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(54) **PRODUCTION OF FATTY ACIDS &
DERIVATIVES THEREOF**

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435/252.33; 435/252.3; 435/252.35; 435/254.21;
435/252.34

(57) **ABSTRACT**

Compositions and methods for production of fatty alcohols
using recombinant microorganisms are provided as well as
fatty alcohol compositions produced by such methods.

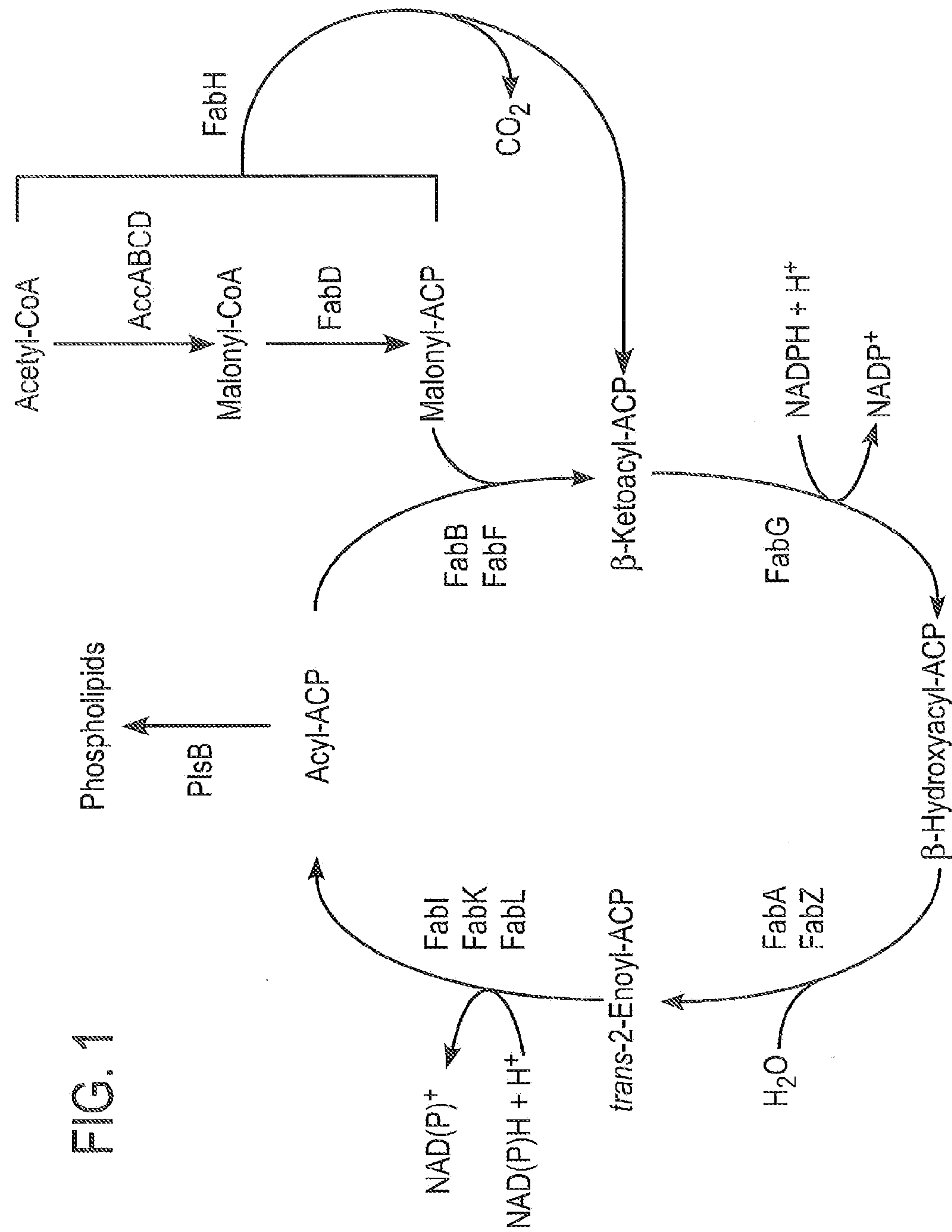
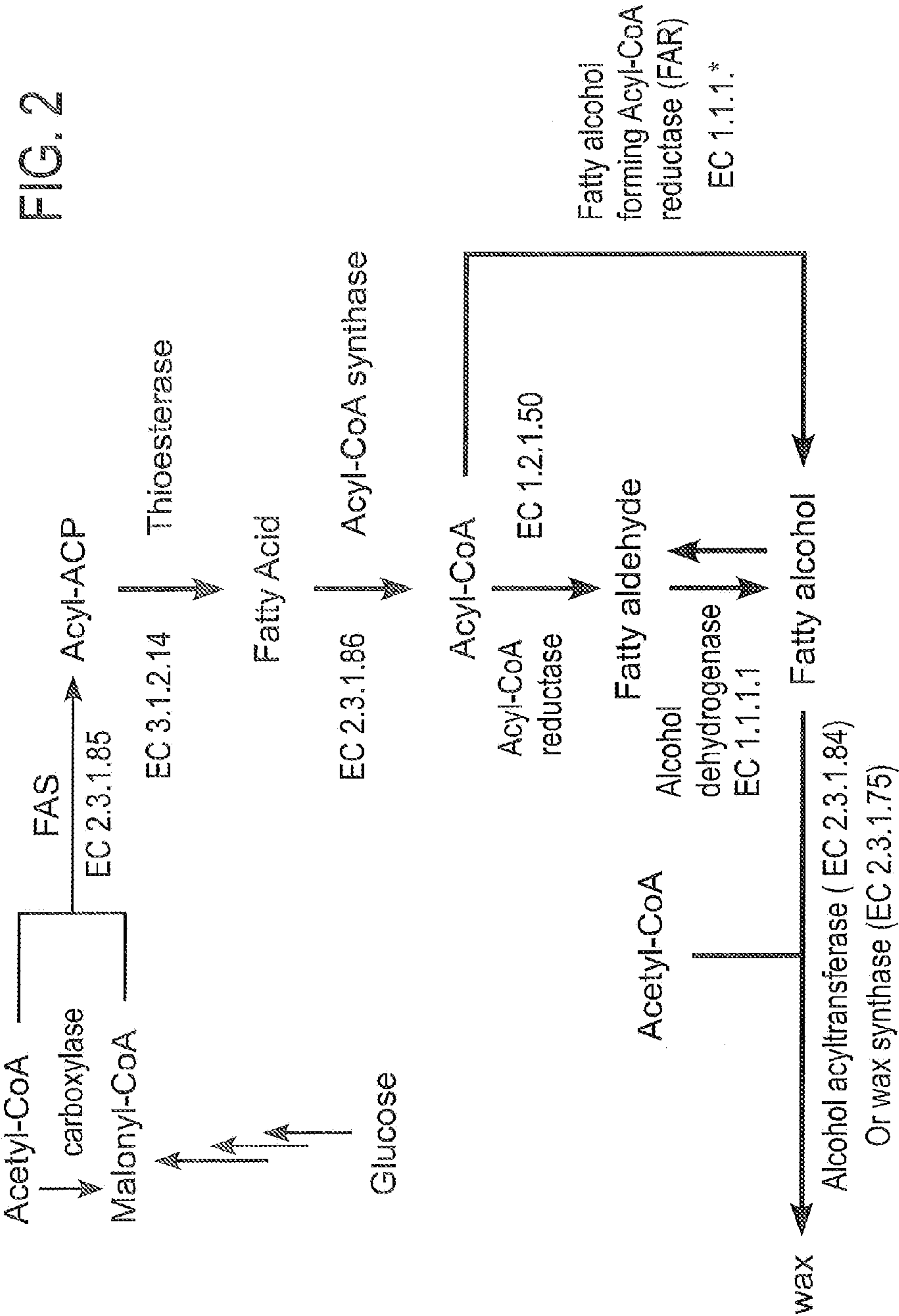
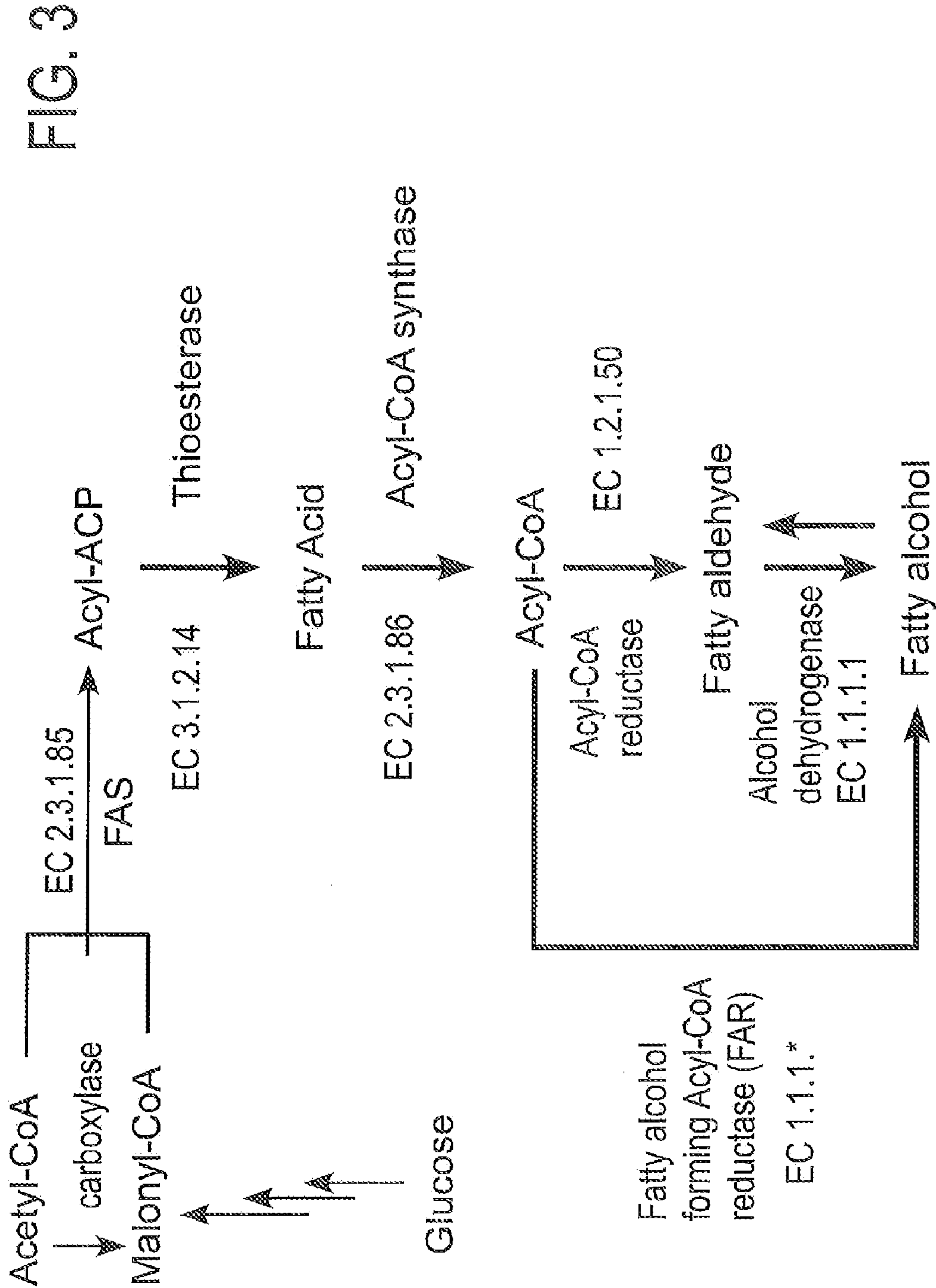
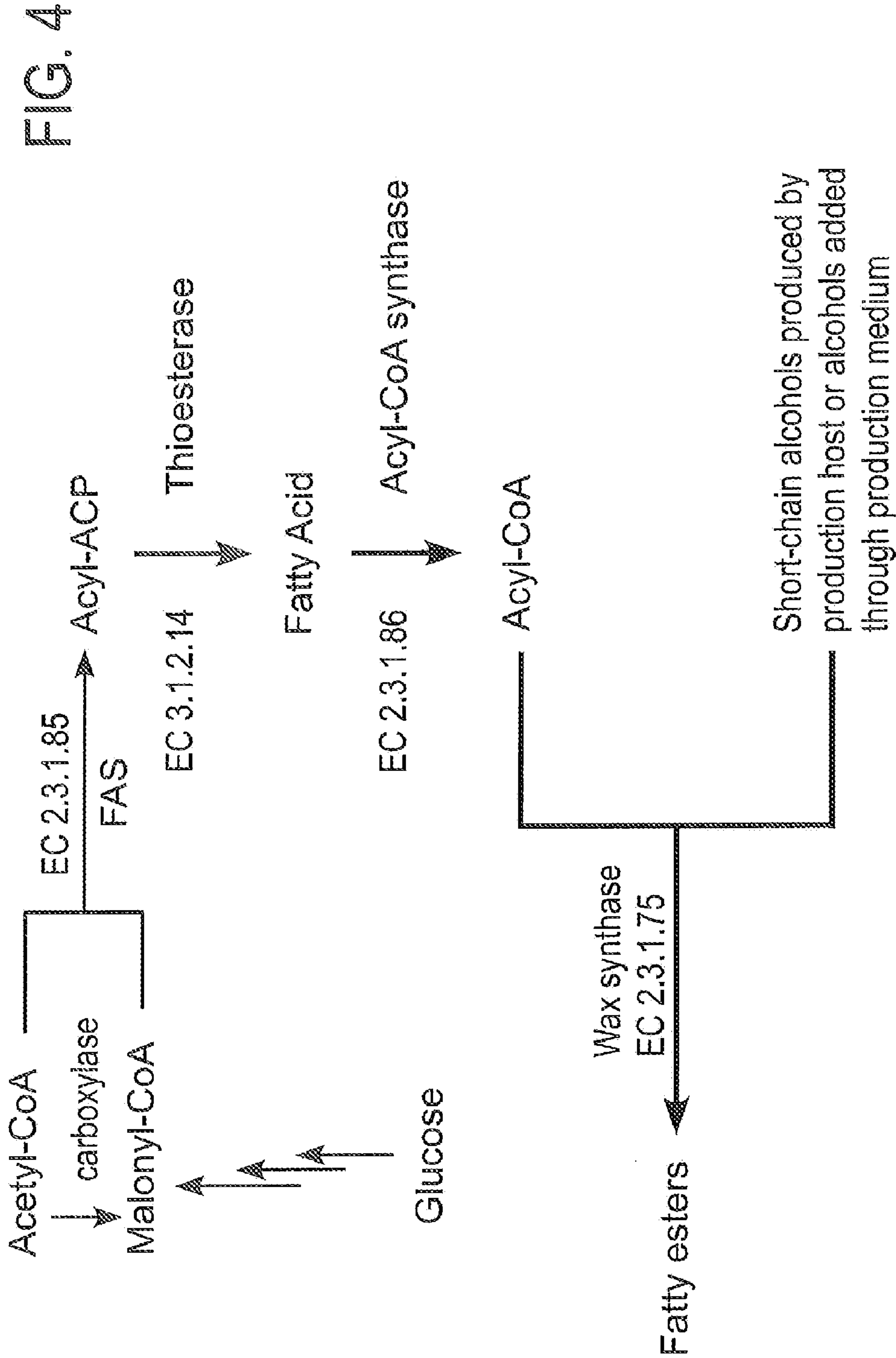


FIG. 1



Fatty alcohol forming acyl-CoA reductase references: Kalscheurer 2006; Metz 2000; Cheng 2004a





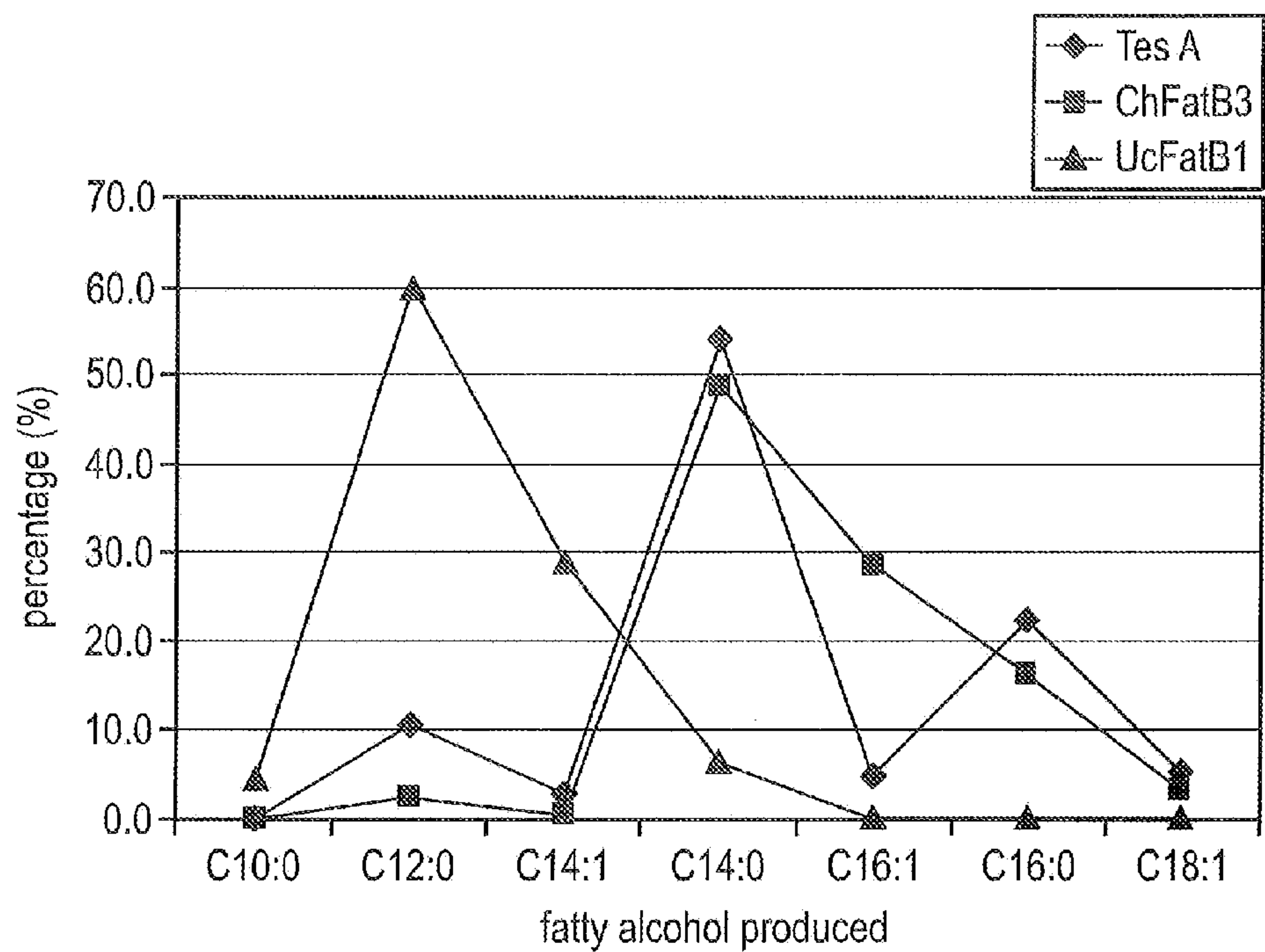


FIG. 5

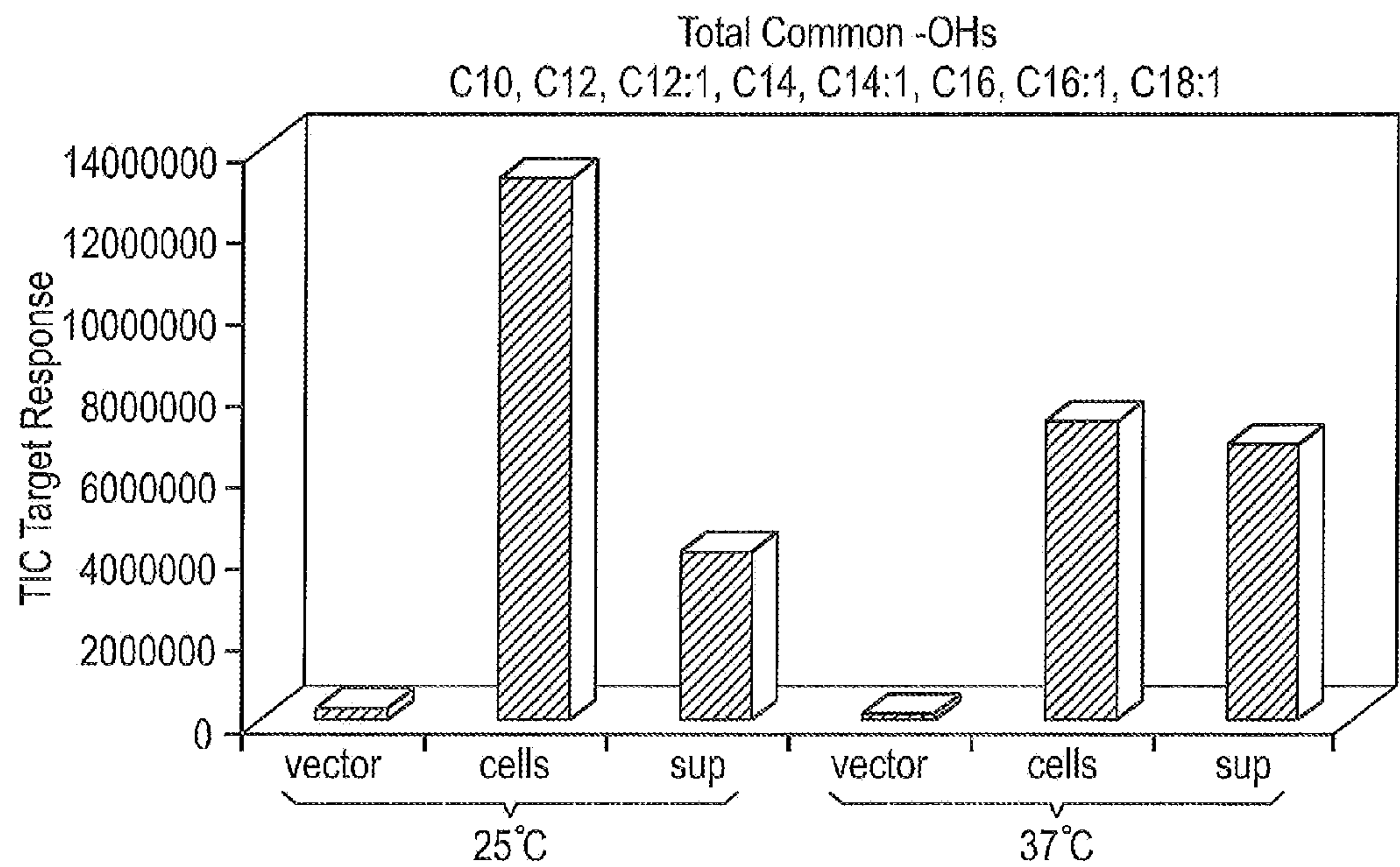


FIG. 6

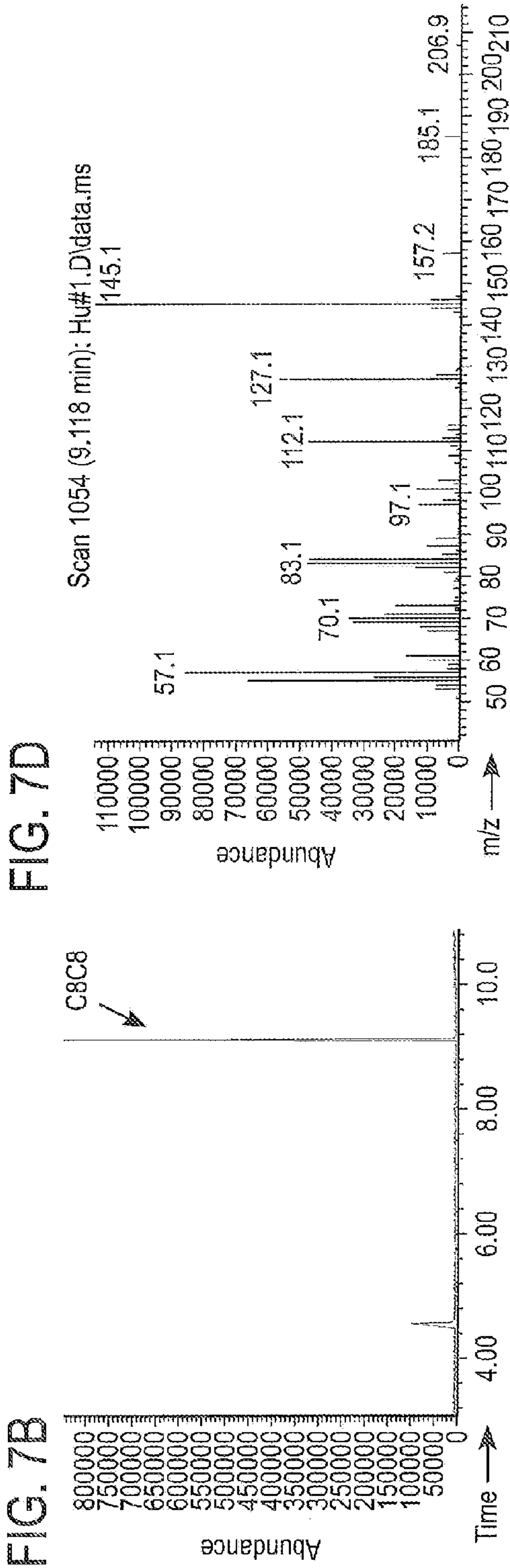
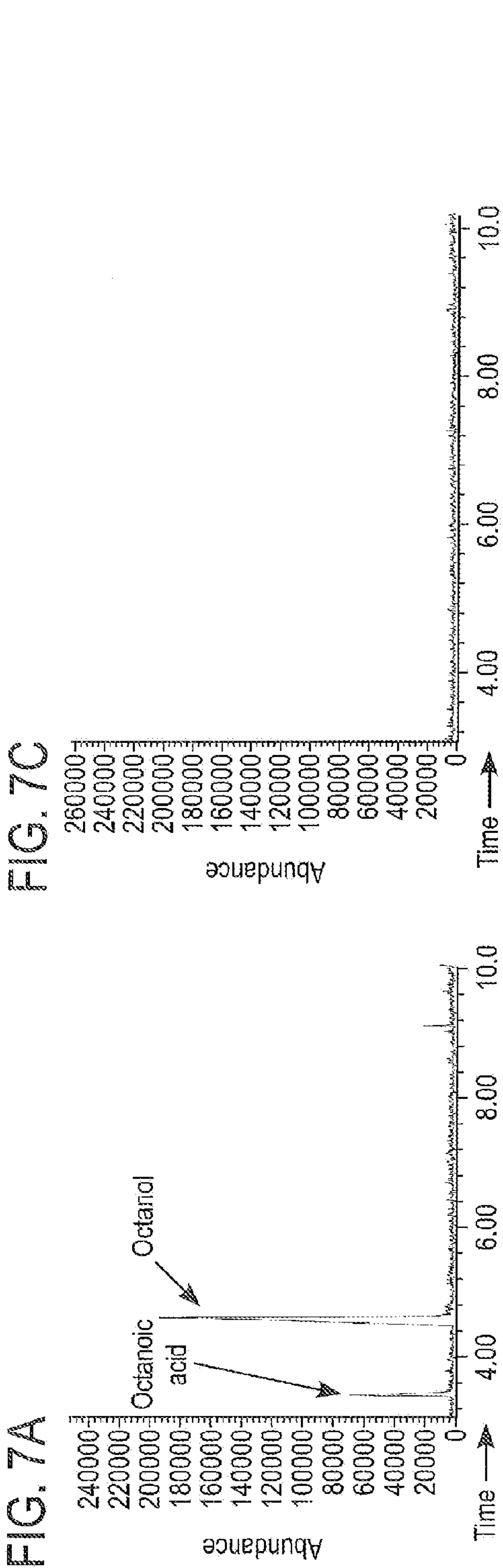
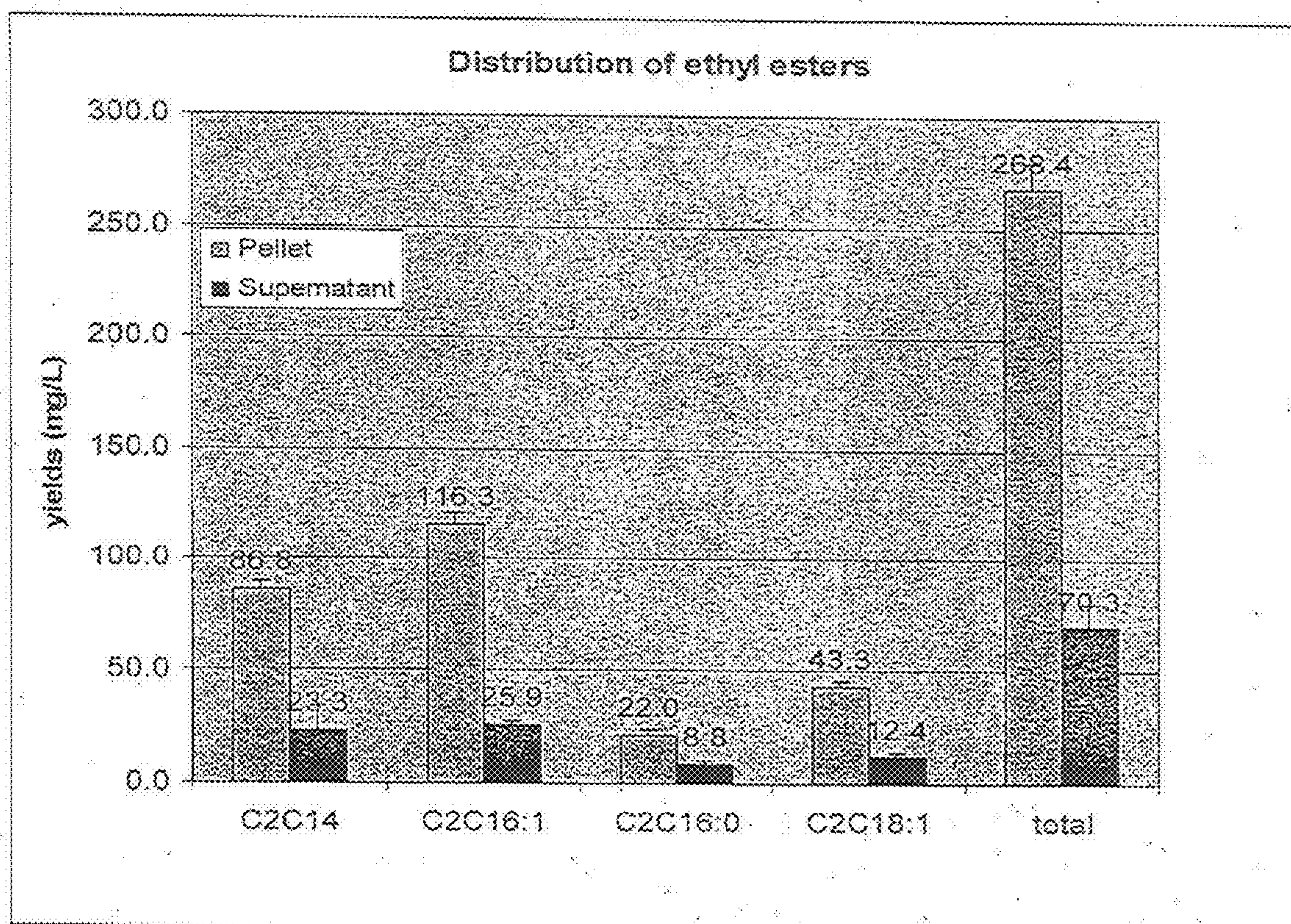


FIG. 8



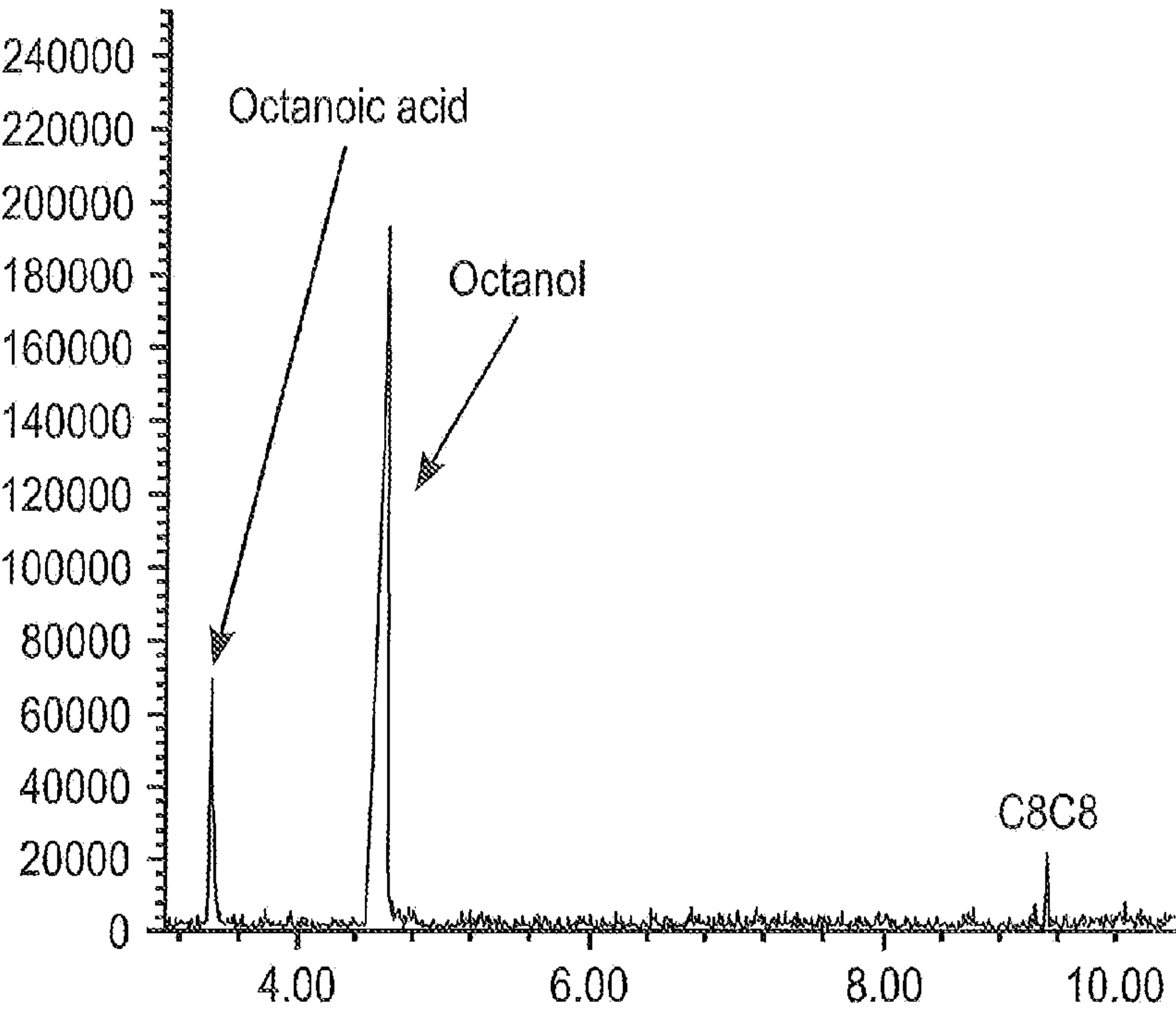


FIG. 9A

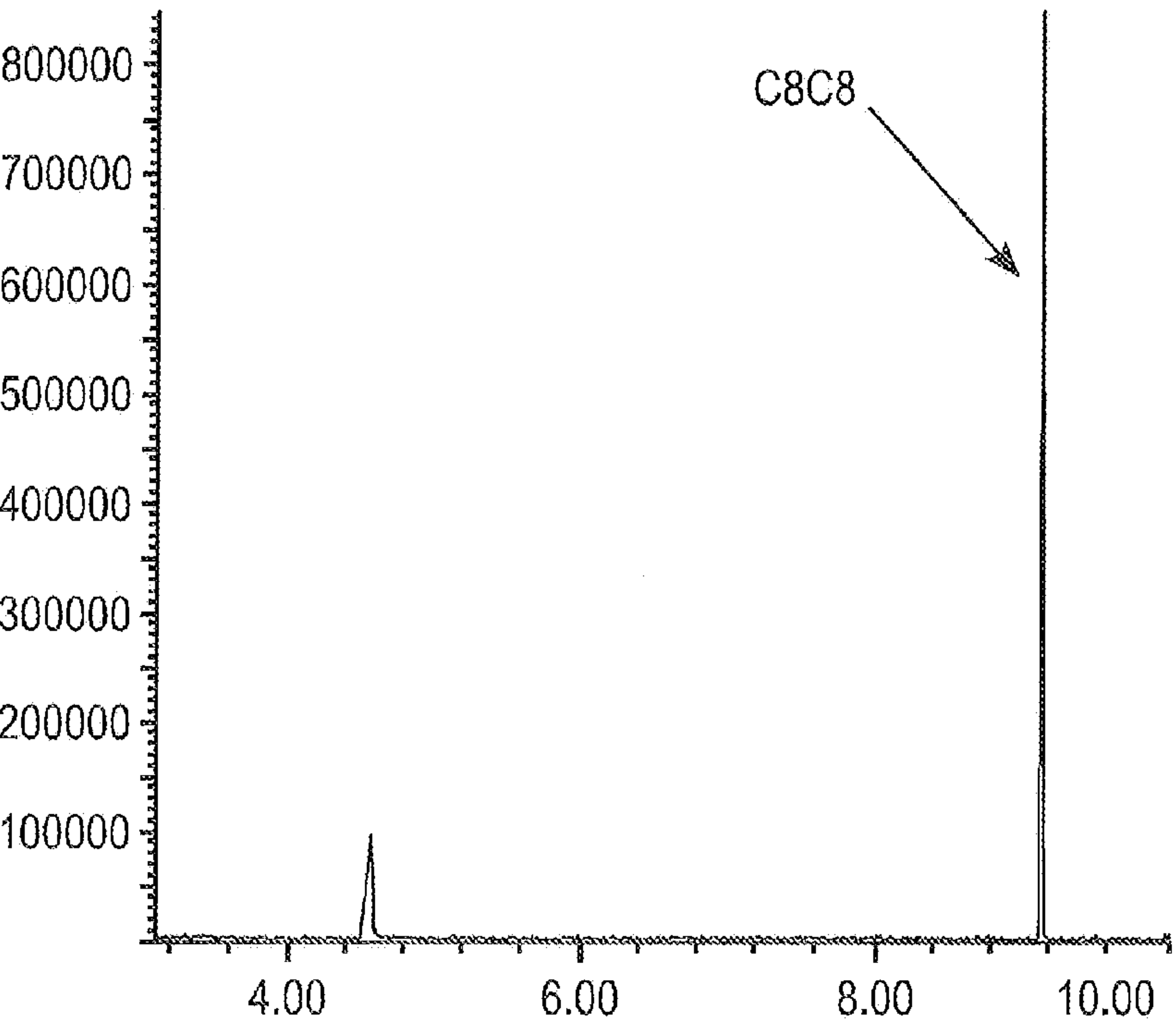


FIG. 9B

FIG. 10

Accession Numbers are from NCBI, GenBank, Release 159.0 as of April 15 2007

EC Numbers are from KEGG, Release 42.0 as of April 2007 (plus daily updates up to and including the date for this patent)

CATEGORY	GENE	NAME	ACCESSION NUMBER	EC	MODIFICATION	USE	ORGANISM
1. Fatty Acid Production Increases / Product Production Increase							
<i>Increase acyl-CoA</i> <i>reduce catabolism of derivatives and intermediates</i> <i>reduce feedback inhibition</i> <i>attenuate other pathways that consume fatty acids</i>							
	accA	Acetyl-CoA carboxylase, subunit	AAC73296, NP_414727	6.4.1.2	Over-express	Increase Malonyl-CoA production	<i>Escherichia coli</i>
	accB	Acetyl-CoA carboxylase, subunit	NP_417721	6.4.1.2	Over-express	Increase Malonyl-CoA production	<i>Escherichia coli</i>
	accC	Acetyl-CoA carboxylase, subunit	NP_417722	6.4.1.2	Over-express	Increase Malonyl-CoA production	<i>Escherichia coli</i>
	accD	Acetyl-CoA carboxylase, subunit	NP_416819	6.4.1.2	Over-express	Increase Malonyl-CoA production	<i>Escherichia coli</i>
	accE	pyruvate dehydrogenase, subunit E1	NP_414656, AAC73226	2.3.1.61, 2.3.1. 1.2.4.1,	Over-express	Increase Acetyl-CoA production	<i>Escherichia coli</i>
	accF	pyruvate dehydrogenase, subunit E2	NP_414657, AAC73227	2.3.1.61, 2.3.1. 1.2.4.1,	Over-express	Increase Acetyl-CoA production	<i>Escherichia coli</i>
	ackA	acetate kinase	AAC75356, NP_416799	2.7.2.1	Delete or reduce	Increase Acetyl-CoA production	<i>Escherichia coli</i>
	ackB	acetate kinase, AckB	BAB81430	2.7.2.1	Delete or reduce	Increase Acetyl-CoA production	<i>Escherichia coli</i>
	acpP	acyl carrier protein	AAC74178	NONE	Over-express	Increase Acetyl-CoA production	<i>Escherichia coli</i>
	fadD	acyl-CoA synthase	AP_002424	2.3.1.86	Over-express	Increase Fatty acid production	<i>Escherichia coli</i> W3110

adhE	alcohol dehydrogenase	AAC74323, CAA47743	1.1.1.1, 1.2.1.10	Delete or reduce	increase Acetyl-CoA production	<i>Escherichia coli</i> W3111
acrl	Aldehyde decarbonylase	BA311024	4.1.99.5	Over-express	increase Acetyl-CoA production	<i>Arabidopsis thaliana</i>
fabA	beta-hydroxydecanoyl thioester dehydrase	NP_415474	4.2.1.60	express	fatty acyl-CoA production	<i>E. coli</i> K12
fabD	[acyl-carrier-protein] S- malonyltransferase	AAC74176	2.3.1.39	Over-express	increase Acetyl-CoA production	<i>E. coli</i> K12
fabF	3-oxoacyl-[acyl-carrier-protein] synthase II	AAC74179	2.3.1.179	Delete or OverExpress	increase Acetyl-CoA production	<i>E. coli</i> K12
fabG	3-oxoacyl-[acyl-carrier-protein] reductase	AAC74177	1.1.1.106	Over-express	increase Acetyl-CoA production	<i>E. coli</i> K12
fabH	3-oxoacyl-[acyl-carrier-protein] synthase III	AAC74175	2.3.1.180	Over-express	increase Acetyl-CoA production	<i>E. coli</i> K12
fabI	enoyl-[acyl-carrier-protein] reductase, NADH-dependent	NP_415804	1.3.1.9	express	fatty acyl-CoA production modulate unsaturated fatty acid production	<i>E. coli</i> K12
fabR	Transcriptional Repressor (3P)-hydroxyacyl acyl carrier protein dehydratase	NP_418398	NONE	Delete or reduce		<i>E. coli</i> K12
fabZ		NP_414732	4.2.1.- 1.3.99.3			<i>E. coli</i> K12
fadE	acyl-CoA dehydrogenase	AAC73325	1.3.99.-	Delete or reduce	increase Acetyl-CoA production	
acrI	Fatty Acyl-CoA reductase	AAC45217	1.2.1.-	Over-express	for fatty alcohol production	<i>E. coli</i> K12
GST	Glutathione synthase	P04425	6.3.2.3	Delete or reduce	increase Acyl-CoA	<i>E. coli</i> K12
gpxA	biosynthetic sn-glycerol 3- phosphate dehydrogenase	AAC76652, NP_418063	EC: 1.1.1.94	Delete or reduce	increase Acetyl-CoA production	<i>E. coli</i> K12
ldhA	lactate dehydrogenase	AAC74462, NP_415298	EC: 1.1.1.28	Delete or reduce	increase Acetyl-CoA production	<i>E. coli</i> K12
Lipase	Triglyceride Lipase	CAA89087, CAA98876	3.1.1.3 4.1.1.9	express	increase Fatty acid production	<i>E. coli</i> K12
	Malonyl-CoA decarboxylase	AAA26500	4.1.1.41	Over-express		<i>Saccharomyces cerevisiae</i> <i>erythraea</i>
panD	aspartate 1-decarboxylase	BA396708	4.1.1.11	Over-express	increase Acyl-CoA	<i>Escherichia coli</i> W3110
panK, a.k.a. coaA	pantothenate kinase	AAC76953	2.7.1.33	Over-express	increase Acetyl-CoA production	

		BAB34380, AAC73227, AAC73226	1.2.4.1	Over-express	increase Acetyl-CoA production	
pdh	Pyruvate dehydrogenase	AAC73989, P09373	EC: 2.3.1.54	Delete or reduce	increase Acetyl-CoA production	
pta	formate acetyltransferase	AAC73611	2.3.1.15	D311E mutation	reduce limits on Acyl-CoA pool	<i>E. coli K12</i>
plsB	acyltransferase	AAC73958, NP_415392	1.2.2.2	Delete or reduce	increase Acetyl-CoA production	
poxB	pyruvate oxidase	AAC73337, NP_416800	2.3.1.8	Delete or reduce	increase Acetyl-CoA production	
pta	phosphotransacetylase				conversion NADH to NADPH or	
udhA	pyridine nucleotide transhydrogenase	CAA46822	1.6.1.1	Over-express	vice versa	
	fixed 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans enoyl-CoA isomerase/enoyl-CoA hydratase and 3-hydroxyacyl-CoA dehydrogenase	AP_005936	1.1.1.35	Delete or reduce	Block fatty acid degradation	<i>E. coli</i>
fadB	3-hydroxyacyl-CoA dehydrogenase; K01692 enoyl-CoA hydratase; K01782 3-hydroxybutyryl-CoA epimerase	AAC73491	5.1.2.3	Delete or reduce	Block fatty acid degradation	<i>E. coli</i>
fadJ	3-ketoacyl-CoA thiolase	BAE77458	2.3.1.16	Delete or reduce	Block fatty acid degradation	<i>E. coli</i>
fadA	beta-ketoacyl-CoA thiolase	AAC73402	1.5.1.29, 1.16	Delete or reduce	Block fatty acid degradation	<i>E. coli</i>
fadI	acyl-coA dehydrogenase	YP_852786	1.3.98.-	Delete or reduce	Block fatty acid degradation	<i>E. coli</i>

2. Structure Control

2A. Chain Length Control

2	tesA	thioester	PGAD41	3.1.2.-	Delete 1 and express	C18 Chain Length	
	tesA without leader sequence	thioesterase	AAC73596, NP_415027	3.1.1.-	express or overexpress	C18:1	<i>E. coli</i>
	fatB	thioesterase	Q41635	3.1.1.-	express or overexpress	C12:0	<i>Umbellularia californica</i>
	(umbellularia)	thioesterase	AAC49269	3.1.1.-	express or overexpress	C8:0 - C10:0	<i>Cuphea hookeri</i>

fatB3	thioesterase	AAC72881	3.1.1.-	express or overexpress	C14:0 - C16:0	<i>Cuphea hookeriana</i>
fatB3 (cinnamomum)	thioesterase	Q39473	3.1.1.-	express or overexpress	C14:0	<i>Cinnamomum camphora</i>
fatB3(M141T)* fatA1	thioesterase	CAA83388	3.1.1.-	express or overexpress	C18:1	<i>Arabidopsis thaliana</i>
(Helianthus)	thioesterase	AAL79361 NP 189147	3.1.1.-	express or overexpress	C18:1	<i>Helianthus annuus</i>
atfata	thioesterase	NP 193041	3.1.1.-	express or overexpress	C18:1	<i>Arabidopsis thaliana</i>
fatA	thioesterase	CAC29306	3.1.1.-	express or overexpress	C18:1	<i>Brassica juncea</i>
fatA (cuphea)	thioesterase	AAC72883	3.1.1.-	express or overexpress	C18:1	<i>Cuphea hookeriana</i>

28. Branching Control

attenuate <i>FabH</i> express <i>FabH</i> from <i>S. glaucescens</i> and knock out endogenous <i>FabH</i> express <i>FabH</i> from <i>B. subtilis</i> and knock out endogenous <i>FabH</i> <i>bkd - E1 -</i> <i>dihydrodipoyl</i> <i>dehydratase</i> <i>subunit</i> <i>bkd - E1 -</i> <i>alpha-beta</i> <i>subunit</i>	EC 1.2.4.4 EC 1.2.4.4	increase branched chain fatty acid derivatives
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*bkd - E2 -
dihydrolipoyl
transacetylase
subunit*

	branched-chain α -ketoacid		EC 1.2.4.4			
bkdA1	decarboxylase α -subunit (E1a)	NP_628006	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdB1	decarboxylase β -subunit (E1b)	NP_628005	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdC1	dihydrolipoyl transacetylase (E2)	NP_638004	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdA2	decarboxylase α -subunit (E1a)	NP_733618	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdB2	decarboxylase β -subunit (E1b)	NP_628019	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdC2	dihydrolipoyl transacetylase (E2)	NP_628018	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces coelicolor</i>
bkdA	decarboxylase α -subunit (E1a)	BAC72074	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdB	decarboxylase β -subunit (E1b)	BAC72075	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdC	dihydrolipoyl transacetylase (E2)	BAC72076	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdF	decarboxylase α -subunit (E1a)	BAC72088	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdG	decarboxylase β -subunit (E1b)	BAC72089	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdH	dihydrolipoyl transacetylase (E2)	BAC72090	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Streptomyces avermitilis</i>
bkdAA	decarboxylase α -subunit (E1a)	NP_390285	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Bacillus subtilis</i>
bkdAB	decarboxylase β -subunit (E1b)	NP_390284	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Bacillus subtilis</i>
bkdB	dihydrolipoyl transacetylase (E2)	NP_390283	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Bacillus subtilis</i>
bkdA1	decarboxylase α -subunit (E1a)	AA465614	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Pseudomonas putida</i>
bkdA2	decarboxylase β -subunit (E1b)	AA465615	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Pseudomonas putida</i>

bkdC	dihydrolipoyl transacetylase (E2)	AA065617	EC 1.2.4.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Pseudomonas putida</i>
lpd	dihydroliposuccinate dehydrogenase (E3)	NP_414658	1.8.1.4	express or Over-Express	make branched-chain acyl-CoA precursors	<i>Escherichia coli</i>
IlvE	branched-chain amino acid aminotransferase	YP_026247	2.6.1.42	express or Over-Express	make branched α -ketoacids	<i>Escherichia coli</i>
IlvB	branched-chain amino acid aminotransferase	AA034406	2.6.1.42	express or Over-Express	make branched α -ketoacids	<i>Lactococcus lactis</i>
IlvE	branched-chain amino acid aminotransferase	NP_745648	2.6.1.42	express or Over-Express	make branched α -ketoacids	<i>Pseudomonas putida</i>
IlvE	branched-chain amino acid aminotransferase	NP_629637	2.6.1.42	express or Over-Express	make branched α -ketoacids	<i>Streptomyces coelicolor</i>
ccr	crotonyl-CoA reductase	NP_630556	1.1.1.9	express or Over-Express	Converting crotonyl-CoA to butyryl-CoA	<i>Streptomyces coelicolor</i>
ccr	crotonyl-CoA reductase	AA053918	1.1.1.9	express or Over-Express	Converting crotonyl-CoA to butyryl-CoA	<i>Streptomyces cinnamonensis</i>
IcmA, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit A	NP_629554	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	<i>Streptomyces coelicolor</i>
IcmA, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit A	AA008713	5.4.99.2	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	<i>Streptomyces cinnamonensis</i>
IcmB, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit B	NP_630904	5.4.99.13	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	<i>Streptomyces coelicolor</i>
IcmB, isobutyryl-CoA mutase	isobutyryl-CoA mutase, subunit B	A0246005	5.4.99.13	express or Over-Express	converting butyryl-CoA to isobutyryl-CoA	<i>Streptomyces cinnamonensis</i>
FabH, ACPs and fabF genes with specificity for branched chain acyl-CoAs						
IlvE		CAC12788	EC2.6.1.42	over express	branched chain amino acid amino transferase	<i>S. carnosus</i>
FabH1	beta-ketoacyl-ACP synthase III	NP_626634	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Streptomyces coelicolor</i>

ACP	acyl-carrier protein	NP_626635	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	<i>Streptomyces coelicolor</i>
FabF	beta-ketoacyl-ACP synthase II	NP_626636	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	<i>Streptomyces coelicolor</i>
FabH3	beta-ketoacyl-ACP synthase III	NP_823466	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Streptomyces avermitilis</i>
FabC3 (ACP)	acyl-carrier protein	NP_823467	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	<i>Streptomyces avermitilis</i>
FabF	beta-ketoacyl-ACP synthase II	NP_823468	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	<i>Streptomyces avermitilis</i>
FabH_A	beta-ketoacyl-ACP synthase III	NP_389015	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Bacillus subtilis</i>
FabH_B	beta-ketoacyl-ACP synthase III	NP_388898	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Bacillus subtilis</i>
ACP	acyl-carrier protein	NP_389474	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	<i>Bacillus subtilis</i>
FabF	beta-ketoacyl-ACP synthase II	NP_389016	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	<i>Bacillus subtilis</i>
SmaIDRAFT_0818	beta-ketoacyl-ACP synthase III	ZP_01643079	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Stenotrophomonas maltophilia</i>
SmaIDRAFT_0821	acyl-carrier protein	ZP_01643063	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	<i>Stenotrophomonas maltophilia</i>
SmaIDRAFT_0822	beta-ketoacyl-ACP synthase II	ZP_01643064	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	<i>Stenotrophomonas maltophilia</i>
FabH	beta-ketoacyl-ACP synthase III	YP_023672	2.3.1.180	express or Over-Express	initiation of branched-chain fatty acid biosynthesis	<i>Legionella pneumophila</i>
ACP	acyl-carrier protein	YP_123673	NONE	express or Over-Express	initiation and elongation of branched-chain fatty acid biosynthesis	<i>Legionella pneumophila</i>
FabF	beta-ketoacyl-ACP synthase II	YP_123676	2.3.1.179	express or Over-Express	elongation of branched-chain fatty acid biosynthesis	<i>Legionella pneumophila</i>
FabH	beta-ketoacyl-ACP synthase III	NP_415809	2.3.1.180	delete or reduce	initiation of branched-chain fatty acid biosynthesis	<i>Escherichia coli</i>

<i>FabF</i> To Produce Cyclic Fatty Acids	beta-ketoacyl-ACP synthase II	NP_415613	2.3.1.179	delete or reduce	elongation of branched-chain fatty acid biosynthesis	<i>Escherichia coli</i>
<i>AnsJ</i>	dehydratase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>AnsK</i>	CoA ligase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>AnsL</i>	dehydrogenase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>CicA</i>	enoyl-CoA reductase	U72144	E1.3.1.34	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>AnsM</i>	oxidoreductase (putative)	not available	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>PinJ</i>	dehydratase (putative)	AAQ84158	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces sp. HK803</i>
<i>PinK</i>	CoA ligase (putative)	AAQ84158	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces sp. HK803</i>
<i>PinL</i>	dehydrogenase (putative)	AAQ84158	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces sp. HK803</i>
<i>CicA</i>	enoyl-CoA reductase	AAQ84160	E1.3.1.34	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces sp. HK803</i>
<i>PinM</i>	oxidoreductase (putative)	AAQ84161	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces sp. HK803</i>
<i>CicB</i>	enoyl-CoA isomerase	AF268489	not available	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces collinus</i>
<i>CicB/CicD</i>	enoyl-CoA isomerase	NP_629292	4.2.1.-	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces coelicolor</i>
<i>CicB/CicD</i>	enoyl-CoA isomerase	NP_824296	4.2.1.-	express or Over-Express	cyclohexylcarbonyl-CoA biosynthesis	<i>Streptomyces overmullis</i>
<u>2C. Saturation Level Control</u>						
<i>Sfa</i> also see <i>FabA</i> in sec. 1	Suppressor of <i>FabA</i>	AAQ79592, AAC44399	Can't find	Over-express	increase monounsaturated fatty acids	<i>E. coli</i>
<i>GnsA</i>	suppressors of the <i>secY</i> null mutation	ABD18647.1	NONE	Over-express	produce unsaturated fatty acids increase unsaturated fatty acid esters	<i>E. coli</i>

OnsB	suppressors of the secE null mutation	AAC74876.1	NONE	Over-express	Increase unsaturated fatty acid esters	<i>E. coli</i>
also see section 3A - items with :0 are unsaturated (no double bonds) and with :1 are saturated (1 double bond)						
fabH	3-oxoacyl-[acyl-carrier-protein] synthase I	BAA16180	EC:2.3.1.41	overexpress	modulate unsaturated fatty acid production	<i>Escherichia coli</i>
fabK	trans-2-enoyl-ACP reductase II	AAP28273	1.3.1.9	express	modulate unsaturated fatty acid production	<i>Streptococcus pneumoniae</i>
fabL	enoyl-(acyl carrier protein)-reductase	AAU39821	1.3.1.9	express	modulate unsaturated fatty acid production	<i>Bacillus licheniformis DSM 13</i>
fabM	trans-2, cis-3-decenoyl-ACP isomerase	BAA05501	5.3.3.14	Over-express	modulate unsaturated fatty acid production	<i>Streptococcus mutans</i>
<u>3. Final Product Output</u>						
<u>3A. Wax Output</u>						
AT3G51970	long-chain-alcohol O-fatty-acyltransferase	NP_190765	2.3.1.75	express	wax production	<i>Arabidopsis thaliana</i>
	thioesterase (see chain length control section)		3.1.2.14	express	increase fatty acid production	
	fatty alcohol forming acyl-CoA reductase		1.1.1.*	express	convert acyl-coa to fatty alcohol	
acrI	acyl-CoA reductase (ACR1)	YP_047869	1.2.1.50	express	convert acyl-coa to fatty alcohol	<i>Acetobacter sp. ADP1</i>
yqhD	alcohol dehydrogenase	AP_003562	1.1.1.1	express	increase produce very long chain length fatty acids	<i>E. coli W3110</i>
ElO1	Fatty acid elongase	BAG98251	2.3.1.74	express		<i>Pichia angusta</i>
plsC	acyltransferase	AAA16614	2.3.1.*	express		<i>Saccharomyces cerevisiae</i>
DAGAT	diacylglycerol acyltransferase	AAF19269	2.3.1.20	express	wax production	<i>Arabidopsis thaliana</i>

aws	acyl-CoA wax alcohol acyltransferase bifunctional wax ester synthase/acyl-CoA:diacylglycerol acyltransferase	AAX34018	Can't find	express	wax production	<i>Roma sapient</i>
ari		AAO17391	2.3.1.20	express	wax production	<i>Acinetobacter sp.</i> <i>ADP1</i>
mws	wax ester synthase (simmondsia)	AAD38041	2.3.1.75	express	wax production	<i>Simmondsia</i> <i>chinensis</i>
3B. Fatty Alcohol Output						
	various thioesterases (refer to Sec. 2A)		3.1.2.14	express	produce	
acr1	acyl-CoA reductase	YP_047869	1.2.1.50	express	produce	<i>Acinetobacter sp.</i> <i>ADP1</i>
yqhD	alcohol dehydrogenase FAR (fatty alcohol forming acyl- CoA reductase)	AP_003562	1.1.1.1	express	produce reduce fatty acyl-CoA to fatty alcohol	<i>Escherichia coli</i> <i>W3110</i>
BroPAR	Mammalian microsomal aldehyde reductase	BAC79425	1.1.1.*	express		<i>Bombyx mori</i>
Akr1a4		NP_067448	1.1.1.21	express	produce	<i>Mus musculus</i> <i>Geobacillus</i> <i>thermodenitrificans</i>
GTNG_1865	Long-chain aldehyde dehydrogenase	YP_00112597	0	1.2.1.48	express	produce
FadD	acyl-CoA synthetase	NP_416319	EC 6.2.1.3	express	produce more	<i>NG80-2</i> <i>E. coli K12</i>
<i>To make Butanol</i>						
atoB	acetyl-CoA acetyltransferase	YP_049382	2.3.1.9	express	produce	<i>Erwinia carotovora</i>
hbd	Beta-hydroxybutyryl-CoA dehydrogenase	BAD51424	1.3.1.157	express	produce	<i>Buergibrio</i> <i>fibrisolens</i>
CPH0095	crotonase	BA879801	4.2.1.17	express	produce	<i>Clostridium</i> <i>perfringens</i>
bcd	butyryl-CoA dehydrogenase	AAM14583	Can't find	express	produce	<i>Clostridium</i> <i>beijerinckii</i>
ALDH	CoA-acylating dehydrogenase	AAT66436	Can't find	express	produce	<i>Clostridium</i> <i>beijerinckii</i>
AdhE	aldehyde-alcohol dehydrogenase	AAN20172	1.2.1.10	express	produce	<i>Escherichia coli</i> <i>CFT073</i>

3C. Fatty Acid Ester Output

thioesterase	see chain length control section		3.1.2.14	express	produce	
acrI	acyl-CoA reductase	YP_047860	1.2.1.50	express	produce	<i>Acinetobacter</i> sp.
adhD	alcohol dehydrogenase	AP_003562	1.1.1.1	express	produce	ADF1 <i>E. Coli</i> K12
AAT	alcohol O-acetyltransferase	AACH3130	2.3.1.84	express	produce	<i>Fragaria x ananassa</i>

4. Export

Wax ester exporter (FATP family, Fatty Acid (long chain) Transport Protein)		NP_524723	NONE	express	export wax	<i>Drosophila melanogaster</i> <i>Rhodococcus erythropolis</i>
ABC transporter:	putative alkane transporter	AAN73268 Atlg51560, AY734542, Atg21090, Atlg51460	NONE	express	export products	
CER5	wax transporter		NONE	express	export products	<i>Arabidopsis thaliana</i>
AtMRP5	Arabidopsis thaliana multidrug resistance-associated	NP_171906	NONE	express	export products	<i>Arabidopsis thaliana</i>
Ami52	ABC transporter Ami52	JCS491	Can't Find	express	export products	<i>Rhodococcus</i> sp.
AtPGP1	GLYCOPROTEIN1	NP_181328	NONE	express	export products	<i>Arabidopsis thaliana</i> <i>Candidatus Proteochlamydia amoebophila</i> GWE25 <i>Candidatus Proteochlamydia amoebophila</i> GWE25
AcrA	putative multidrug-efflux transport protein acrA	CAF23274	NONE	express	export products	<i>Francisella tularensis</i> subsp. <i>novicida</i>
AcrB	probable multidrug-efflux transport protein, acrB	CAF23275	NONE	express	export products	
TolC	Outer membrane protein [Cell envelope biogenesis,	ABD39801	NONE	express	export products	

AcrE AcrF	transmembrane protein affects septum formation and cell membrane permeability	YP_313213	NONE	express	export products	<i>Shigella sonnei</i>
	Acriflavine resistance protein F	P24181	NONE	express	export products	<i>Ss646</i> <i>Escherichia coli</i>
dh1618	multidrug efflux transporter	NP_682408.1		express	export products	<i>Thermosynechococcus elongatus BP-1</i>
dh1619	multidrug efflux transporter	NP_682409.1		express	export products	<i>Thermosynechococcus elongatus BP-1</i>
dh1619	multidrug efflux transporter	NP_680930.1		express	export products	<i>Thermosynechococcus elongatus BP-1</i>
<u>5. Fermentation</u>						
replication checkpoint genes						
umuD	DNA polymerase V, subunit	YP_318152	3.4.21.3	Over-express	increase output efficiency	<i>Shigella sonnei</i>
umuC	DNA polymerase V, subunit	ABC42261	3.4.21.3	Over-express	increase output efficiency	<i>Ss646</i> <i>Escherichia coli</i>
NADH:NADPH transhydrogenase (alpha and beta subunits)		<u>P07081</u>	1.6.1.1			
		<u>P0AB70</u>	1.6.1.2	express	increase output efficiency	<i>Shigella flexneri</i>

** END OF SHEET **

PRODUCTION OF FATTY ACIDS & DERIVATIVES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of copending U.S. patent application Ser. No. 12/278,957, filed Apr. 20, 2010, as the U.S. national phase of Patent Cooperation Treaty Application No. PCT/US2007/11923, filed May 18, 2007, which claims benefit to U.S. Provisional Application Nos. 60/908,547 filed Mar. 28, 2007; U.S. Provisional Application No. 60/801,995 filed May 19, 2006, and U.S. Provisional Application No. 60/802,016 filed May 19, 2006, and, all of which are herein incorporated by reference.

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

[0002] Incorporated by reference in its entirety herein is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 80,354 Byte ASCII (Text) file named "PCT_SeqLstgAs-Filed_05.18.07" created on May 18, 2007. It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for the instant application.

FIELD

[0003] Compositions and methods for production of fatty alcohols using recombinant microorganisms are provided as well as fatty alcohol compositions produced by such methods.

BACKGROUND

[0004] Developments in technology have been accompanied by an increased reliance on fuel sources and such fuel sources are becoming increasingly limited and difficult to acquire. With the burning of fossil fuels taking place at an unprecedented rate, it has likely that the world's fuel demand will soon outweigh the current fuel supplies.

[0005] As a result, efforts have been directed toward harnessing sources of renewable energy, such as sunlight, water, wind, and biomass. The use of biomasses to produce new sources of fuel which are not derived from petroleum sources, (i.e. biofuel) has emerged as one alternative option. Biofuel (biodiesel) is a biodegradable, clean-burning combustible fuel made of long chain alkanes and esters. Biodiesel can be used in most internal combustion diesel engines in either a pure form, which is referred to as "neat" biodiesel, or as a mix in any concentration with regular petroleum diesel. Current methods of making biodiesel involve transesterification of triacylglycerides (mainly vegetable oil) which leads to a mixture of fatty acid esters and the unwanted side product glycerin, thus, providing a product that is heterogeneous and a waste product that causes economic inefficiencies.

SUMMARY

[0006] Disclosed herein are recombinant microorganisms that are capable of synthesizing products derived from the fatty acid biosynthetic pathway (fatty alcohols), and optionally releasing such products into the fermentation broth. Such fatty alcohols are useful, inter alia, specialty chemicals. These specialty chemicals can be used to make additional products,

such as nutritional supplements, polymers, paraffin replacements, and personal care products.

[0007] The recombinant microorganisms disclosed herein can be engineered to yield various fatty alcohol compositions.

[0008] In one example, the disclosure provides a method for modifying a microorganism so that it produces, and optionally releases, fatty alcohols generated from a renewable carbon source. Such microorganisms are genetically engineered, for example, by introducing an exogenous DNA sequence encoding one or more proteins capable of metabolizing a renewable carbon source to produce, and in some examples secrete, a fatty alcohol composition. The modified microorganisms can then be used in a fermentation process to produce useful fatty alcohols using the renewable carbon source (biomass) as a starting material. In some examples, an existing genetically tractable microorganism is used because of the ease of engineering its pathways for controlling growth, production and reducing or eliminating side reactions that reduce biosynthetic pathway efficiencies.

[0009] Provided herein are microorganisms that produce fatty alcohols having defined carbon chain length, branching, and saturation levels. In particular examples, the production of homogeneous products decreases the overall cost associated with fermentation and separation. Microorganisms expressing one or more exogenous nucleic acid sequences encoding at least one thioesterase (EC 3.1.2.14) and at least one fatty alcohol forming acyl-CoA reductase (1.1.1.*) are provided. The thioesterase peptides encoded by the exogenous nucleic acid sequences can be chosen to provide homogeneous products.

[0010] In some examples the microorganism that is engineered to produce the fatty acid derivative is *E. coli*, *Z. mobilis*, *Rhodococcus opacus*, *Ralstonia eutropha*, *Vibrio furnissii*, *Saccharomyces cerevisiae*, *Lactococcus lactis*, *Streptomyces*, *Stenotrophomonas maltophilia*, *Pseudomonas* or *Micrococcus leuteus* and their relatives.

[0011] In addition to being engineered to express exogenous nucleic acid sequences that allow for the production of fatty alcohols, the microorganism can additionally have one or more endogenous genes functionally deleted or attenuated.

[0012] In addition to being engineered to express exogenous nucleic acid sequences that allow for the production of fatty alcohols, the microorganism can additionally have one or more additional genes over-expressed.

[0013] In some examples, the microorganisms described herein produce at least 1 mg of fatty alcohol per liter fermentation broth. In other examples the microorganisms produce at least 100 mg/L, 500 mg/L, 1 g/L, 5 g/L, 10 g/L, 20 g/L, 25 g/L, 30 g/L, 35 g/L, 40 g/L, 50 g/L, 100 g/L, or 120 g/L of fatty alcohol per liter fermentation broth. In some examples, the fatty alcohol is produced and released from the microorganism and in yet other examples the microorganism is lysed prior to separation of the product.

[0014] In some examples, the fatty alcohol includes a carbon chain that is at least 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 carbons long. In some examples at least 50%, 60%, 70%, 80%, 85%, 90%, or 95% of the fatty alcohol product made contains a carbon chain that is 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or 34 carbons long. In yet other examples, at least 60%, 70%, 80%, 85%, 90%, or 95% of the fatty alcohol product contain 1, 2, 3, 4, or 5, points of unsaturation

[0015] Also provided are methods of producing alcohol. These methods include culturing the microorganisms described herein and separating the product from the fermentation broth.

[0016] These and other examples are described further in the following detailed description.

BRIEF DESCRIPTION OF THE FIGURES

[0017] FIG. 1 shows the FAS biosynthetic pathway.

[0018] FIG. 2 shows biosynthetic pathways that produce waxes. Waxes can be produced in a host cell using alcohols produced within the host cell or they can be produced by adding exogenous alcohols in the medium. A microorganism designed to produce waxes will produce wax synthase enzymes (EC 2.3.1.75) using exogenous nucleic acid sequences as well as thioesterase (EC 3.1.2.14) sequences. Other enzymes that can be also modulated to increase the production of waxes include enzymes involved in fatty acid synthesis (FAS enzymes EC 2.3.1.85), acyl-CoA synthase (EC 2.3.1.86), fatty alcohol forming acyl-CoA reductase (EC 1.1.1.*), acyl-CoA reductase (1.2.1.50) and alcohol dehydrogenase (EC 1.1.1.1).

[0019] FIG. 3 shows biosynthetic pathways that produce fatty alcohols. Fatty alcohols having defined carbon chain lengths can be produced by expressing exogenous nucleic acid sequences encoding thioesterases (EC 3.1.2.14), and combinations of acyl-CoA reductases (EC 1.2.1.50), alcohol dehydrogenases (EC 1.1.1.1) and fatty alcohol forming acyl-CoA reductases (FAR, EC 1.1.1.*). Other enzymes that can be also modulated to increase the production of fatty alcohols include enzymes involved in fatty acid synthesis (FAS enzymes EC 2.3.1.85), and acyl-CoA synthase (EC 2.3.1.86).

[0020] FIG. 4 shows biosynthetic pathways that produce fatty acids esters. Fatty acids esters having defined carbon chain lengths can be produced by exogenously expressing various thioesterases (EC 3.1.2.14), combinations of acyl-CoA reductase (1.2.1.50), alcohol dehydrogenases (EC 1.1.1.1), and fatty alcohol forming Acyl-CoA reductase (FAR, EC 1.1.1.*), as well as, acetyl transferase (EC 2.3.1.84). Other enzymes that can be modulated to increase the production of fatty acid esters include enzymes involved in fatty acid synthesis (FAS enzymes EC 2.3.1.85), and acyl-CoA synthase (EC 2.3.1.86).

[0021] FIG. 5 shows fatty alcohol production by the strain described in Example 4, co-transformed with pCDFDuet-1-fadD-acrl and plasmids containing various thioesterase genes. The strains were grown aerobically at 25° C. in M9 mineral medium with 0.4% glucose in shake flasks. Saturated C10, C12, C14, C16 and C18 fatty alcohol were identified. Small amounts of C16:1 and C18:1 fatty alcohols were also detected in some samples. Fatty alcohols were extracted from cell pellets using ethyl acetate and derivatized with N-trimethylsilyl (TMS) imidazole to increase detection.

[0022] FIG. 6 shows the release of fatty alcohols from the production strain. Approximately 50% of the fatty alcohol produced was released from the cells when they were grown at 37° C.

[0023] FIGS. 7A-7D show GS-MS spectrum of octyl octanoate (C8C8) produced by a production hosts expressing alcohol acetyl transferase (AATs, EC 2.3.1.84) and production hosts expressing wax synthase (EC 2.3.1.75). FIG. 7A shows acetyl acetate extract of strain C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid expressed ADP1 (wax synthase). FIG. 7B shows acetyl

acetate extract of strain C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid expressed SAAT. FIG. 7C shows acetyl acetate extract of strain C41 (DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid did not contain ADP1 (wax synthase) or SAAT. FIG. 7D shows the mass spectrum and fragmentation pattern of C8C8 produced by C41(DE3, ΔfadE/pHZ1.43)/pRSET B+pAS004.114B) wherein the pHZ1.43 plasmid expressed SAAT).

[0024] FIG. 8 shows the distribution of ethyl esters made when the wax synthase from *A. baylyi* ADP1 (WSadp1) was co-expressed with thioesterase gene from *Cuphea hookeri-ana* in a production host.

[0025] FIGS. 9A and 9B show chromatograms of GC/MS analysis. FIG. 9A shows a chromatogram of the ethyl extract of the culture of *E. coli* LS9001 strain transformed with plasmids pCDFDuet-1-fadD-WSadp1, pETDuet-1-tesA. Ethanol was fed to fermentations. FIG. 9B shows a chromatogram of ethyl hexadecanoate and ethyl oleate used as reference.

[0026] FIG. 10 shows a table that identifies various genes that can be over-expressed or attenuated to increase fatty acid derivative production. The table also identifies various genes that can be modulated to alter the structure of the fatty acid derivative product. One of ordinary skill in the art will appreciate that some of the genes that are used to alter the structure of the fatty acid derivative will also increase the production of fatty acid derivatives.

ABBREVIATIONS AND TERMS

[0027] The following explanations of terms and methods are provided to better describe the present disclosure and to guide those of ordinary skill in the art in the practice of the present disclosure. As used herein, “comprising” means “including” and the singular forms “a” or “an” or “the” include plural references unless the context clearly dictates otherwise. For example, reference to “comprising a cell” includes one or a plurality of such cells, and reference to “comprising the thioesterase” includes reference to one or more thioesterase peptides and equivalents thereof known to those of ordinary skill in the art, and so forth. The term “or” refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. For example, the phrase “thioesterase activity or fatty alcohol-forming acyl-CoA reductase activity” refers to thioesterase activity, fatty alcohol forming acyl-CoA reductase activity, or a combination of both fatty alcohol forming acyl-CoA reductase activity, and thioesterase activity.

[0028] Unless explained otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. The materials, methods, and examples are illustrative only and not intended to be limiting. Other features of the disclosure are apparent from the following detailed description and the claims.

[0029] Accession Numbers: The accession numbers throughout this description are derived from the NCBI database (National Center for Biotechnology Information) main-

tained by the National Institute of Health, U.S.A. The accession numbers are as provided in the database on Mar. 27, 2007.

[0030] Enzyme Classification Numbers (EC): The EC numbers provided throughout this description are derived from the KEGG Ligand database, maintained by the Kyoto Encyclopedia of Genes and Genomics, sponsored in part by the University of Tokyo. The EC numbers are as provided in the database on Mar. 27, 2007.

[0031] Attenuate: To lessen the impact, activity or strength of something. In one example, the sensitivity of a particular enzyme to feedback inhibition or inhibition caused by a composition that is not a product or a reactant (non-pathway specific feedback) is lessened such that the enzyme activity is not impacted by the presence of a compound. For example, the *fabH* gene and its corresponding amino acid sequence are temperature sensitive and can be altered to decrease the sensitivity to temperature fluctuations. The attenuation of the *fabH* gene can be used when branched amino acids are desired. In another example, an enzyme that has been altered to be less active can be referred to as attenuated.

[0032] A functional deletion of an enzyme can be used to attenuate an enzyme. A functional deletion is a mutation, partial or complete deletion, insertion, or other variation made to a gene sequence or a sequence controlling the transcription of a gene sequence, which reduces or inhibits production of the gene product, or renders the gene product non-functional (i.e. the mutation described herein for the *plsB* gene). For example, functional deletion of *fabR* in *E. coli* reduces the repression of the fatty acid biosynthetic pathway and allows *E. coli* to produce more unsaturated fatty acids (UFAs). In some instances a functional deletion is described as a knock-out mutation.

[0033] One of ordinary skill in the art will appreciate that there are many methods of attenuating enzyme activity. For example, attenuation can be accomplished by introducing amino acid sequence changes via altering the nucleic acid sequence, placing the gene under the control of a less active promoter, expressing interfering RNA, ribozymes or anti-sense sequences that targeting the gene of interest, or through any other technique known in the art.

[0034] Carbon source: Generally refers to a substrate or compound suitable to be used as a source of carbon for prokaryotic or simple eukaryotic cell growth. Carbon sources can be in various forms, including, but not limited to polymers, carbohydrates, acids, alcohols, aldehydes, ketones, amino acids, peptides, etc. These include, for example, various monosaccharides such as glucose, oligosaccharides, polysaccharides, cellulosic material, xylose, and arabinose, disaccharides, such sucrose, saturated or unsaturated fatty acids, succinate, lactate, acetate, ethanol, etc., or mixtures thereof. The carbon source can additionally be a product of photosynthesis, including, but not limited to glucose.

[0035] cDNA (complementary DNA): A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences which determine transcription. cDNA can be synthesized by reverse transcription from messenger RNA extracted from cells.

[0036] Deletion: The removal of one or more nucleotides from a nucleic acid molecule or one or more amino acids from a protein, the regions on either side being joined together.

[0037] Detectable: Capable of having an existence or presence ascertained. For example, production of a product from

a reactant, for example, the production of C18 fatty acids, is detectable using the method provided in Example 11 below.

[0038] DNA: Deoxyribonucleic acid. DNA is a long chain polymer which includes the genetic material of most living organisms (some viruses have genes including ribonucleic acid, RNA). The repeating units in DNA polymers are four different nucleotides, each of which includes one of the four bases, adenine, guanine, cytosine and thymine bound to a deoxyribose sugar to which a phosphate group is attached. Triplets of nucleotides, referred to as codons, in DNA molecules code for amino acid in a peptide. The term codon is also used for the corresponding (and complementary) sequences of three nucleotides in the mRNA into which the DNA sequence is transcribed.

[0039] Endogenous: As used herein with reference to a nucleic acid molecule and a particular cell or microorganism refers to a nucleic acid sequence or peptide that is in the cell and was not introduced into the cell using recombinant engineering techniques. For example, a gene that was present in the cell when the cell was originally isolated from nature. A gene is still considered endogenous if the control sequences, such as a promoter or enhancer sequences that activate transcription or translation have been altered through recombinant techniques.

[0040] Exogenous: As used herein with reference to a nucleic acid molecule and a particular cell refers to any nucleic acid molecule that does not originate from that particular cell as found in nature. Thus, a non-naturally-occurring nucleic acid molecule is considered to be exogenous to a cell once introduced into the cell. A nucleic acid molecule that is naturally-occurring also can be exogenous to a particular cell. For example, an entire coding sequence isolated from cell X is an exogenous nucleic acid with respect to cell Y once that coding sequence is introduced into cell Y, even if X and Y are the same cell type.

[0041] Expression: The process by which a gene's coded information is converted into the structures and functions of a cell, such as a protein, transfer RNA, or ribosomal RNA. Expressed genes include those that are transcribed into mRNA and then translated into protein and those that are transcribed into RNA but not translated into protein (for example, transfer and ribosomal RNAs).

[0042] Fatty ester: Includes any ester made from a fatty acid. The carbon chains in fatty acids can contain any combination of the modifications described herein. For example, the carbon chain can contain one or more points of unsaturation, one or more points of branching, including cyclic branching, and can be engineered to be short or long. Any alcohol can be used to form fatty acid esters, for example alcohols derived from the fatty acid biosynthetic pathway, alcohols produced by the production host through non-fatty acid biosynthetic pathways, and alcohols that are supplied in the fermentation broth.

[0043] Fatty acid derivative: Includes products made in part from the fatty acid biosynthetic pathway of the host organism. The fatty acid biosynthetic pathway includes fatty acid synthase enzymes which can be engineered as described herein to produce fatty acid derivatives, and in some examples can be expressed with additional enzymes to produce fatty acid derivatives having desired carbon chain characteristics. Exemplary fatty acid derivatives include for example, short and long chain alcohols, hydrocarbons, and fatty acid esters including waxes.

[0044] Fermentation Broth: Includes any medium which supports microorganism life (i.e. a microorganism that is actively metabolizing carbon). A fermentation medium usually contains a carbon source. The carbon source can be anything that can be utilized, with or without additional enzymes, by the microorganism for energy.

[0045] Hydrocarbon: includes chemical compounds that containing the elements carbon (C) and hydrogen (H). All hydrocarbons consist of a carbon backbone and atoms of hydrogen attached to that backbone. Sometimes, the term is used as a shortened form of the term “aliphatic hydrocarbon.” There are essentially three types of hydrocarbons: (1) aromatic hydrocarbons, which have at least one aromatic ring; (2) saturated hydrocarbons, also known as alkanes, which lack double, triple or aromatic bonds; and (3) unsaturated hydrocarbons, which have one or more double or triple bonds between carbon atoms, are divided into: alkenes, alkynes, and dienes. Liquid geologically-extracted hydrocarbons are referred to as petroleum (literally “rock oil”) or mineral oil, while gaseous geologic hydrocarbons are referred to as natural gas. All are significant sources of fuel and raw materials as a feedstock for the production of organic chemicals and are commonly found in the Earth’s subsurface using the tools of petroleum geology. Oil reserves in sedimentary rocks are the principal source of hydrocarbons for the energy and chemicals industries. Hydrocarbons are of prime economic importance because they encompass the constituents of the major fossil fuels (coal, petroleum, natural gas, etc.) and biofuels, as well as plastics, waxes, solvents and oils.

[0046] Isolated: An “isolated” biological component (such as a nucleic acid molecule, protein, or cell) has been substantially separated or purified away from other biological components in which the component naturally occurs, such as other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acid molecules and proteins that have been “isolated” include nucleic acid molecules and proteins purified by standard purification methods. The term also embraces nucleic acid molecules and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acid molecules and proteins.

[0047] In one example, isolated refers to a naturally-occurring nucleic acid molecule that is not immediately contiguous with both of the sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally-occurring genome of the organism from which it is derived.

[0048] Microorganism: Includes prokaryotic and eukaryotic microbial species from the Domains Archaea, Bacteria and Eucarya, the latter including yeast and filamentous fungi, protozoa, algae, or higher Protista. The terms “microbial cells” and “microbes” are used interchangeably with the term microorganism.

[0049] Nucleic Acid Molecule: Encompasses both RNA and DNA molecules including, without limitation, cDNA, genomic DNA, and mRNA. Includes synthetic nucleic acid molecules, such as those that are chemically synthesized or recombinantly produced. The nucleic acid molecule can be double-stranded or single-stranded. Where single-stranded, the nucleic acid molecule can be the sense strand or the antisense strand. In addition, nucleic acid molecule can be circular or linear.

[0050] Operably linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relation-

ship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame. Configurations of separate genes that are transcribed in tandem as a single messenger RNA are denoted as operons. Thus placing genes in close proximity, for example in a plasmid vector, under the transcriptional regulation of a single promoter, constitutes a synthetic operon.

[0051] ORF (open reading frame): A series of nucleotide triplets (codons) coding for amino acids without any termination codons. These sequences are usually translatable into a peptide.

[0052] Over-expressed: When a gene is caused to be transcribed at an elevated rate compared to the endogenous transcription rate for that gene. In some examples, over-expression additionally includes an elevated rate of translation of the gene compared to the endogenous translation rate for that gene. Methods of testing for over-expression are well known in the art, for example transcribed RNA levels can be assessed using rtPCR and protein levels can be assessed using SDS page gel analysis.

[0053] Purified: The term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified fatty acid derivative preparation, such as a wax, or a fatty acid ester preparation, is one in which the product is more concentrated than the product is in its environment within a cell. For example, a purified wax is one that is substantially separated from cellular components (nucleic acids, lipids, carbohydrates, and other peptides) that can accompany it. In another example, a purified wax preparation is one in which the wax is substantially-free from contaminants, such as those that might be present following fermentation.

[0054] In one example, a fatty acid ester is purified when at least about 50% by weight of a sample is composed of the fatty acid ester, for example when at least about 60%, 70%, 80%, 85%, 90%, 92%, 95%, 98%, or 99% or more of a sample is composed of the fatty acid ester. Examples of methods that can be used to purify a waxes, fatty alcohols, and fatty acid esters, include the methods described in Example 11 below.

[0055] Recombinant: A recombinant nucleic acid molecule or protein is one that has a sequence that is not naturally occurring, has a sequence that is made by an artificial combination of two otherwise separated segments of sequence, or both. This artificial combination can be achieved, for example, by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acid molecules or proteins, such as genetic engineering techniques. Recombinant is also used to describe nucleic acid molecules that have been artificially manipulated, but contain the same regulatory sequences and coding regions that are found in the organism from which the nucleic acid was isolated. A recombinant cell or microorganism is one that contains an exogenous nucleic acid molecule, such as a recombinant nucleic acid molecule.

[0056] Release: The movement of a compound from inside a cell (intracellular) to outside a cell (extracellular). The movement can be active or passive. When release is active it can be facilitated by one or more transporter peptides and in some examples it can consume energy. When release is passive, it can be through diffusion through the membrane and can be facilitated by continually collecting the desired com-

pound from the extracellular environment, thus promoting further diffusion. Release of a compound can also be accomplished by lysing a cell.

[0057] Surfactants: Substances capable of reducing the surface tension of a liquid in which they are dissolved. They are typically composed of a water-soluble head and a hydrocarbon chain or tail. The water soluble group is hydrophilic and can be either ionic or nonionic, and the hydrocarbon chain is hydrophobic. Surfactants are used in a variety of products, including detergents and cleaners, and are also used as auxiliaries for textiles, leather and paper, in chemical processes, in cosmetics and pharmaceuticals, in the food industry and in agriculture. In addition, they can be used to aid in the extraction and isolation of crude oils which are found hard to access environments or as water emulsions.

[0058] There are four types of surfactants characterized by varying uses. Anionic surfactants have detergent-like activity and are generally used for cleaning applications. Cationic surfactants contain long chain hydrocarbons and are often used to treat proteins and synthetic polymers or are components of fabric softeners and hair conditioners. Amphoteric surfactants also contain long chain hydrocarbons and are typically used in shampoos. Non-ionic surfactants are generally used in cleaning products.

[0059] Transformed or recombinant cell: A cell into which a nucleic acid molecule has been introduced, such as an acyl-CoA synthase encoding nucleic acid molecule, for example by molecular biology techniques. Transformation encompasses all techniques by which a nucleic acid molecule can be introduced into such a cell, including, but not limited to, transfection with viral vectors, conjugation, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

[0060] Under conditions that permit product production: Any fermentation conditions that allow a microorganism to produce a desired product, such as fatty acids, hydrocarbons, fatty alcohols, waxes, or fatty acid esters. Fermentation conditions usually include temperature ranges, levels of aeration, and media selection, which when combined allow the microorganism to grow. Exemplary mediums include broths or gels. Generally, the medium includes a carbon source such as glucose, fructose, cellulose, or the like that can be metabolized by the microorganism directly, or enzymes can be used in the medium to facilitate metabolizing the carbon source. To determine if culture conditions permit product production, the microorganism can be cultured for 24, 36, or 48 hours and a sample can be obtained and analyzed. For example, the cells in the sample or the medium in which the cells were grown can be tested for the presence of the desired product. When testing for the presence of a product assays, such as those provided in the Examples below, can be used.

[0061] Vector: A nucleic acid molecule as introduced into a cell, thereby producing a transformed cell. A vector can include nucleic acid sequences that permit it to replicate in the cell, such as an origin of replication. A vector can also include one or more selectable marker genes and other genetic elements known in the art.

[0062] Wax: A variety of fatty acid esters which form solids or pliable substances under an identified set of physical conditions. Fatty acid esters that are termed waxes generally have longer carbon chains than fatty acid esters that are not waxes. For example, a wax generally forms a pliable substance at room temperature.

DETAILED DESCRIPTION

I. Production of Fatty Acid Derivatives

[0063] The host organism that exogenous DNA sequences are transformed into can be a modified host organism, such as

an organism that has been modified to increase the production of acyl-ACP or acyl-CoA, reduce the catabolism of fatty acid derivatives and intermediates, or to reduce feedback inhibition at specific points in the biosynthetic pathway. In addition to modifying the genes described herein additional cellular resources can be diverted to over produce fatty acids, for example the lactate, succinate and/or acetate pathways can be attenuated, and acetyl-CoA carboxylase (ACC) can be over expressed. The modifications to the production host described herein can be through genomic alterations, extra-chromosomal expression systems, or combinations thereof. An overview of the pathway is provided in FIGS. 1 and 2.

[0064] A. Acetyl-CoA--Malonyl-CoA to Acyl-ACP

[0065] Fatty acid synthase (FAS) is a group of peptides that catalyze the initiation and elongation of acyl chains (Marrakchi et al., *Biochemical Society*, 30:1050-1055, 2002). The acyl carrier protein (ACP) along with the enzymes in the FAS pathway control the length, degree of saturation and branching of the fatty acids produced. Enzymes that can be included in FAS include AccABCD, FabD, FabH, FabG, FabA, FabZ, FabI, FabK, FabL, FabM, FabB, and FabF. Depending upon the desired product one or more of these genes can be attenuated or over-expressed.

[0066] For example, the fatty acid biosynthetic pathway in the production host uses the precursors acetyl-CoA and malonyl-CoA (FIG. 2). *E. coli* or other host organisms engineered to overproduce these components can serve as the starting point for subsequent genetic engineering steps to provide the specific output product (such as, fatty acid esters, hydrocarbons, fatty alcohols). Several different modifications can be made, either in combination or individually, to the host strain to obtain increased acetyl CoA/malonyl CoA/fatty acid and fatty acid derivative production. For example, to increase acetyl CoA production, a plasmid with *pdh*, *panK*, *aceEF*, (encoding the E1p dehydrogenase component and the E2p dihydrolipoamide acyltransferase component of the pyruvate and 2-oxoglutarate dehydrogenase complexes), *fabH/fabD/fabG/acpP/fabF*, and in some examples additional DNA encoding fatty-acyl-CoA reductases and aldehyde decarboxylases, all under the control of a constitutive, or otherwise controllable promoter, can be constructed. Exemplary Genbank accession numbers for these genes are: *pdh* (BAB34380, AAC73227, AAC73226), *panK* (also known as *coaA*, AAC76952), *aceEF* (AAC73227, AAC73226), *fabH* (AAC74175), *fabD* (AAC74176), *fabG* (AAC74177), *acpP* (AAC74178), *fabF* (AAC74179).

[0067] Additionally, *fadE*, *gpsA*, *ldhA*, *pflb*, *adhE*, *pta*, *poxB*, *ackA*, and/or *ackB* can be knocked-out, or their expression levels can be reduced, in the engineered microorganism by transformation with conditionally replicative or non-replicative plasmids containing null or deletion mutations of the corresponding genes, or by substituting promoter or enhancer sequences. Exemplary Genbank accession numbers for these genes are; *fadE* (AAC73325), *gpsA* (AAC76632), *ldhA* (AAC74462), *pflb* (AAC73989), *adhE* (AAC74323), *pta* (AAC75357), *poxB* (AAC73958), *ackA* (AAC75356), and *ackB* (BAB81430).

[0068] The resulting engineered microorganisms can be grown in a desired environment, for example one with limited glycerol (less than 1% w/v in the culture medium). As such, these microorganisms will have increased acetyl-CoA production levels. Malonyl-CoA overproduction can be effected by engineering the microorganism as described above, with DNA encoding *accABCD* (acetyl CoA carboxylase, for

example accession number AAC73296, EC 6.4.1.2) included in the plasmid synthesized de novo. Fatty acid overproduction can be achieved by further including DNA encoding lipase (for example Accessions numbers CAA89087, CAA98876) in the plasmid synthesized de novo.

[0069] In some examples, acetyl-CoA carboxylase (ACC) is over-expressed to increase the intracellular concentration thereof by at least 2-fold, such as at least 5-fold, or at least 10-fold, for example relative to native expression levels.

[0070] In addition, the *plsB* (for example Accession number AAC7701 1) D311E mutation can be used to remove limitations on the pool of acyl-CoA.

[0071] In addition, over-expression of an *sfa* gene (suppressor of *FabA*, for example Accession number AAN79592) can be included in the production host to increase production of monounsaturated fatty acids (Rock et al., *J. Bacteriology* 178:5382-5387, 1996).

[0072] B. Acyl-ACP to Fatty Acid

[0073] To engineer a production host for the production of a homogeneous population of fatty acid derivatives, one or more endogenous genes can be attenuated or functionally deleted and one or more thioesterases can be expressed. For example, C10 fatty acid derivatives can be produced by attenuating thioesterase C18 (for example accession numbers AAC73596 and POADAI), which uses C18:1-ACP and expressing thioesterase C10 (for example accession number Q39513), which uses C10-ACP. Thus, resulting in a relatively homogeneous population of fatty acid derivatives that have a carbon chain length of 10. In another example, C14 fatty acid derivatives can be produced by attenuating endogenous thioesterases that produce non-C14 fatty acids and expressing the thioesterase accession number Q39473 (which uses C14-ACP). In yet another example, C12 fatty acid derivatives can be produced by expressing thioesterases that use C12-ACP (for example accession number Q41635) and attenuating thioesterases that produce non-C12 fatty acids. Acetyl CoA, malonyl CoA, and fatty acid overproduction can be verified using methods known in the art, for example by using radioactive precursors, HPLC, and GC-MS subsequent to cell lysis.

TABLE 1

Thioesterases			
Accession Number	Source Organism	Gene	Preferential product produced
AAC73596	<i>E. coli</i>	<i>tesA</i> without leader sequence	C18:1
Q41635	<i>Umbellularia californica</i>	<i>fatB</i>	C12:0
Q39513;	<i>Cuphea hookeriana</i>	<i>fatB2</i>	C8:0-C10:0
AAC49269	<i>Cuphea hookeriana</i>	<i>fatB3</i>	C14:0-C16:0
Q39473	<i>Cinnamomum camphorum</i>	<i>fatB</i>	C14:0
CAA85388	<i>Arabidopsis thaliana</i>	<i>fatB</i> [M141T]*	C16:1
NP 189147; NP 193041	<i>Arabidopsis thaliana</i>	<i>fatA</i>	C18:1
CAC39106	<i>Bradyrhizobium japonicum</i>	<i>fatA</i>	C18:1
AAC72883	<i>Cuphea hookeriana</i>	<i>fatA</i>	C18:1

*Mayer et al., *BMC Plant Biology* 7:1-11, 2007.

[0074] C. Fatty Acid to Acyl-CoA

[0075] Production hosts can be engineered using known peptides to produce fatty acids of various lengths. One method of making fatty acids involves increasing the expression of, or expressing more active forms of, one or more acyl-CoA synthase peptides (EC 2.3.1.86).

[0076] As used herein, acyl-CoA synthase includes peptides in enzyme classification number EC 2.3.1.86, as well as any other peptide capable of catalyzing the conversion of a fatty acid to acyl-CoA. Additionally, one of ordinary skill in the art will appreciate that some acyl-CoA synthase peptides will catalyze other reactions as well, for example some acyl-CoA synthase peptides will accept other substrates in addition to fatty acids. Such non-specific acyl-CoA synthase peptides are, therefore, also included. Acyl-CoA synthase peptide sequences are publicly available. Exemplary GenBank Accession Numbers are provided in FIG. 10.

[0077] D. Acyl-CoA to Fatty Alcohol

[0078] Production hosts can be engineered using known polypeptides to produce fatty alcohols from acyl-CoA. One method of making fatty alcohols involves increasing the expression of or expressing more active forms of fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), or acyl-CoA reductases (EC 1.2.1.50) and alcohol dehydrogenase (EC 1.1.1.1). Hereinafter fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), acyl-CoA reductases (EC 1.2.1.50) and alcohol dehydrogenase (EC 1.1.1.1) are collectively referred to as fatty alcohol forming peptides. In some examples all three of the fatty alcohol forming genes can be over expressed in a production host, and in yet other examples one or more of the fatty alcohol forming genes can be over-expressed.

[0079] As used herein, fatty alcohol forming peptides include peptides in enzyme classification numbers EC 1.1.1.*, 1.2.1.50, and 1.1.1.1, as well as any other peptide capable of catalyzing the conversion of acyl-CoA to fatty alcohol. Additionally, one of ordinary skill in the art will appreciate that some fatty alcohol forming peptides will catalyze other reactions as well, for example some acyl-CoA reductase peptides will accept other substrates in addition to fatty acids. Such non-specific peptides are, therefore, also included. Fatty alcohol forming peptides sequences are publicly available. Exemplary GenBank Accession Numbers are provided in FIG. 10.

[0080] Fatty alcohols can also be described as hydrocarbon-based surfactants. For surfactant production the microorganism is modified so that it produces a surfactant from a renewable carbon source. Such a microorganism includes a first exogenous DNA sequence encoding a protein capable of converting a fatty acid to a fatty aldehyde and a second exogenous DNA sequence encoding a protein capable of converting a fatty aldehyde to an alcohol. In some examples, the first exogenous DNA sequence encodes a fatty acid reductase. In one embodiment, the second exogenous DNA sequence encodes mammalian microsomal aldehyde reductase or long-chain aldehyde dehydrogenase. In a further example, the first and second exogenous DNA sequences are from a multienzyme complex from *Arthrobacter AK 19*, *Rhodotorula glutinins*, *Acinobacter* sp strain. M-1, or *Candida lipolytica*. In one embodiment, the first and second heterologous DNA sequences are from a multienzyme complex from *Acinobacter* sp strain M-1 or *Candida lipolytica*.

[0081] Additional sources of heterologous DNA sequences encoding fatty acid to long chain alcohol converting proteins

that can be used in surfactant production include, but are not limited to, *Mortierella alpina* (ATCC 32222), *Cryptococcus curvatus*, (also referred to as *Apiotricum curvatum*), *Alcanivorax jadensis* (T9T=DSM 12718=ATCC 700854), *Acinetobacter* sp. HO1-N, (ATCC 14987) and *Rhodococcus opacus* (PD630 DSMZ 44193).

[0082] In one example, the fatty acid derivative is a saturated or unsaturated surfactant product having a carbon atom content limited to between 6 and 36 carbon atoms. In another example, the surfactant product has a carbon atom content limited to between 24 and 32 carbon atoms.

[0083] Appropriate hosts for producing surfactants can be either eukaryotic or prokaryotic microorganisms. Exemplary hosts include *Arthrobacter* AK 19, *Rhodotorula glutinins*, *Acinobacter* sp strain M-1, *Arabidopsis thaliana*, or *Candida lipolytica*, *Saccharomyces cerevisiae*, and *E. coli* engineered to express acetyl CoA carboxylase. Hosts which demonstrate an innate ability to synthesize high levels of surfactant precursors in the form of lipids and oils, such as *Rhodococcus opacus*, *Arthrobacter* AK 19, *Rhodotorula glutinins* *E. coli* engineered to express acetyl CoA carboxylase, and other oleaginous bacteria, yeast, and fungi can also be used.

[0084] E. Fatty Alcohols to Fatty Esters

[0085] Production hosts can be engineered using known polypeptides to produce fatty esters of various lengths. One method of making fatty esters includes increasing the expression of, or expressing more active forms of, one or more alcohol O-acetyltransferase peptides (EC 2.3.1.84). These peptides catalyze the reaction of acetyl-CoA and an alcohol to form CoA and an acetic ester. In some examples the alcohol O-acetyltransferase peptides can be expressed in conjunction with selected thioesterase peptides, FAS peptides and fatty alcohol forming peptides, thus, allowing the carbon chain length, saturation and degree of branching to be controlled. In some cases the bkd operon can be coexpressed to enable branched fatty acid precursors to be produced.

[0086] As used herein, alcohol O-acetyltransferase peptides include peptides in enzyme classification number EC 2.3.1.84, as well as any other peptide capable of catalyzing the conversion of acetyl-CoA and an alcohol to form CoA and an acetic ester. Additionally, one of ordinary skill in the art will appreciate that alcohol O-acetyltransferase peptides will catalyze other reactions as well, for example some alcohol O-acetyltransferase peptides will accept other substrates in addition to fatty alcohols or acetyl-CoA thioester i.e., such as other alcohols and other acyl-CoA thioesters. Such non-specific or divergent specificity alcohol O-acetyltransferase peptides are, therefore, also included. Alcohol O-acetyltransferase peptide sequences are publicly available. Exemplary GenBank Accession Numbers are provided in FIG. 10. Assays for characterizing the activity of a particular alcohol O-acetyltransferase peptides are well known in the art. Engineered O-acetyltransferases and O-acyltransferases can be also created that have new activities and specificities for the donor acyl group or acceptor alcohol moiety. Engineered enzymes could be generated through rational and evolutionary approaches well documented in the art.

[0087] F. Acyl-CoA to Fatty Esters (Biodiesels and Waxes)

[0088] Production hosts can be engineered using known peptides to produce fatty acid esters from acyl-CoA and alcohols. In some examples the alcohols are provided in the fermentation media and in other examples the production host can provide the alcohol as described herein. One of ordinary skill in the art will appreciate that structurally, fatty acid esters

have an A and a B side. As described herein, the A side of the ester is used to describe the carbon chain contributed by the alcohol, and the B side of the ester is used to describe the carbon chain contributed by the acyl-CoA. Either chain can be saturated or unsaturated, branched or unbranched. The production host can be engineered to produce fatty alcohols or short chain alcohols. The production host can also be engineered to produce specific acyl-CoA molecules. As used herein fatty acid esters are esters derived from a fatty acyl-thioester and an alcohol, wherein the A side and the B side of the ester can vary in length independently. Generally, the A side of the ester is at least 1, 2, 3, 4, 5, 6, 7, or 8 carbons in length, while the B side of the ester is 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 carbons in length. The A side and the B side can be straight chain or branched, saturated or unsaturated.

[0089] The production of fatty esters, including waxes from acyl-CoA and alcohols can be engineered using known polypeptides. As used herein waxes are long chain fatty acid esters, wherein the A side and the B side of the ester can vary in length independently. Generally, the A side of the ester is at least 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 carbons in length. Similarly the B side of the ester is at least 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 carbons in length. The A side and the B side can be mono-, di-, tri- unsaturated. The production of fatty esters, including waxes from acyl-CoA and alcohols can be engineered using known polypeptides. One method of making fatty esters includes increasing the expression of or expressing more active forms of one or more wax synthases (EC 2.3.1.75).

[0090] As used herein, wax synthases includes peptides in enzyme classification number EC 2.3.1.75, as well as any other peptide capable of catalyzing the conversion of an acyl-thioester to fatty esters. Additionally, one of ordinary skill in the art will appreciate that some wax synthase peptides will catalyze other reactions as well, for example some wax synthase peptides will accept short chain acyl-CoAs and short chain alcohols to produce fatty esters. Such non-specific wax synthases are, therefore, also included. Wax synthase peptide sequences are publicly available. Exemplary GenBank Accession Numbers are provided in FIG. 10. Methods to identify wax synthase activity are provided in U.S. Pat. No. 7,118,896, which is herein incorporated by reference.

[0091] In particular examples, if the desired product is a fatty ester based biofuel, the microorganism is modified so that it produces a fatty ester generated from a renewable energy source. Such a microorganism includes an exogenous DNA sequence encoding a wax ester synthase that is expressed so as to confer upon said microorganism the ability to synthesize a saturated, unsaturated, or branched fatty ester from a renewable energy source. In some embodiments, the wax ester synthesis proteins include, but are not limited to,: fatty acid elongases, acyl-CoA reductases, acyltransferases or wax synthases, fatty acyl transferases, diacylglycerol acyltransferases, acyl-coA wax alcohol acyltransferases, bifunctional wax ester synthase/acyl-CoA:diacylglycerol acyltransferase selected from a multienzyme complex from *Simmondsia chinensis*, *Acinetobacter* sp. strain ADP1 (formerly *Acinetobacter calcoaceticus* ADP1), *Pseudomonas aeruginosa*, *Fundibacter jadensis*, *Arabidopsis thaliana*, or *Alkaligenes eutrophus*. In one embodiment, the fatty acid elongases, acyl-CoA reductases or wax synthases are from a multienzyme complex from *Alkaligenes eutrophus* and other organisms known in the literature to produce wax and fatty acid esters.

[0092] Additional sources of heterologous DNA encoding wax synthesis proteins useful in fatty ester production include, but are not limited to, *Mortierella alpina* (for example ATCC 32222), *Cryptococcus curvatus*, (also referred to as *Apiotricwn curvatum*), *Alcanivorax jadensis* (for example T9T=DSM 12718=ATCC 700854), *Acinetobacter* sp. HO1-N, (for example ATCC 14987) and *Rhodococcus opacus* (for example PD630, DSMZ 44193).

[0093] The methods of described herein permit production of fatty esters of varied length. In one example, the fatty ester product is a saturated or unsaturated fatty ester product having a carbon atom content between 24 and 46 carbon atoms. In one embodiment, the fatty ester product has a carbon atom content between 24 and 32 carbon atoms. In another embodiment the fatty ester product has a carbon content of 14 and 20 carbons. In another embodiment the fatty ester is the methyl ester of C18:1. In another embodiment the fatty acid ester is the ethyl ester of C16:1. In another embodiment the fatty ester is the methyl ester of C16:1. In another embodiment the fatty acid ester is octadecyl ester of octanol.

[0094] Useful hosts for producing fatty esters can be either eukaryotic or prokaryotic microorganisms. In some embodiments such hosts include, but are not limited to, *Saccharomyces cerevisiae*, *Candida lipolytica*, *E. coli*, *Arthrobacter AK 19*, *Rhodotorula glutinins*, *Acinobacter* sp strain M-1, *Candida lipolytica* and other oleaginous microorganisms.

[0095] In one example the wax ester synthase from *Acinetobacter* sp. ADP1 at locus AAO17391 (described in Kalscheuer and Steinbuchel, *J. Biol. Chem.* 278:8075-8082, 2003, herein incorporated by reference) is used. In another example the wax ester synthase from *Simmondsia chinensis*, at locus AAD38041 is used.

[0096] Optionally a wax ester exporter such as a member of the FATP family can be used to facilitate the release of waxes or esters into the extracellular environment. One example of a wax ester exporter that can be used is fatty acid (long chain) transport protein CG7400-PA, isoform A from *Drosophila melanogaster*, at locus NP_524723.

[0097] G. Acyl-ACP, Acyl-CoA to Hydrocarbon

[0098] A diversity of microorganisms are known to produce hydrocarbons, such as alkanes, olefins, and isoprenoids. Many of these hydrocarbons are derived from fatty acid biosynthesis. The production of these hydrocarbons can be controlled by controlling the genes associated with fatty acid biosynthesis in the native hosts. For example, hydrocarbon biosynthesis in the algae *Botryococcus braunii* occurs through the decarbonylation of fatty aldehydes. The fatty aldehydes are produced by the reduction of fatty acyl—thioesters by fatty acyl-CoA reductase. Thus, the structure of the final alkanes can be controlled by engineering *B. braunii* to express specific genes, such as thioesterases, which control the chain length of the fatty acids being channeled into alkane biosynthesis. Expressing the enzymes that result in branched chain fatty acid biosynthesis in *B. braunii* will result in the production of branched chain alkanes. Introduction of genes effecting the production of desaturation of fatty acids will result in the production of olefins. Further combinations of these genes can provide further control over the final structure of the hydrocarbons produced. To produce higher levels of the native or engineered hydrocarbons, the genes involved in the biosynthesis of fatty acids and their precursors or the degradation to other products can be expressed, overexpressed, or attenuated. Each of these approaches can be applied to the production of alkanes in *Vibrio furnissi* M1 and its functional

homologues, which produces alkanes through the reduction of fatty alcohols (see above for the biosynthesis and engineering of fatty alcohol production). Each of these approaches can also be applied to the production of the olefins produced by many strains of *Micrococcus leuteus*, *Stenotrophomonas maltophilia*, *Jeogalicoccus* sp. (ATCC8456), and related microorganisms. These microorganisms produce long chain internal olefins that are derived from the head to head condensation of fatty acid precursors. Controlling the structure and level of the fatty acid precursors using the methods described herein will result in formation of olefins of different chain length, branching, and level of saturation.

[0099] Hydrocarbons can also be produced using evolved oxido/reductases for the reduction of primary alcohols. Primary fatty alcohols are known to be used to produce alkanes in microorganisms such as *Vibrio furnissi* M1 (Myong-Ok, *J. Bacteriol.*, 187:1426-1429, 2005). An NAD(P)H dependent oxido/reductase is the responsible catalyst. Synthetic NAD(P)H dependent oxidoreductases can be produced through the use of evolutionary engineering and be expressed in production hosts to produce fatty acid derivatives. One of ordinary skill in the art will appreciate that the process of “evolving” a fatty alcohol reductase to have the desired activity is well known (Kolkman and Stemmer *Nat Biotechnol.* 19:423-8, 2001, Ness et al., *Adv Protein Chem.* 55:261-92, 2000, Minshull and Stemmer *Curr Opin Chem Biol.* 3:284-90, 1999, Huisman and Gray *Curr Opin Biotechnol.* August;13:352-8, 2002, and see U.S. patent application 2006/0195947). A library of NAD(P)H dependent oxidoreductases is generated by standard methods, such as error prone PCR, site-specific random mutagenesis, site specific saturation mutagenesis, or site directed specific mutagenesis. Additionally, a library can be created through the “shuffling” of naturally occurring NAD(P)H dependent oxidoreductase encoding sequences. The library is expressed in a suitable host, such as *E. coli*. Individual colonies expressing a different member of the oxido/reductase library is then analyzed for its expression of an oxido/reductase that can catalyze the reduction of a fatty alcohol. For example, each cell can be assayed as a whole cell bioconversion, a cell extract, a permeabilized cell, or a purified enzyme. Fatty alcohol reductases are identified by the monitoring the fatty alcohol dependent oxidation of NAD(P)H spectrophotometrically or fluorometrically. Production of alkanes is monitored by GC/MS, TLC, or other methods. An oxido/reductase identified in this manner is used to produce alkanes, alkenes, and related branched hydrocarbons. This is achieved either in vitro or in vivo. The latter is achieved by expressing the evolved fatty alcohol reductase gene in an organism that produces fatty alcohols, such as those described herein. The fatty alcohols act as substrates for the alcohol reductase which would produce alkanes. Other oxidoreductases can be also engineered to catalyze this reaction, such as those that use molecular hydrogen, glutathione, FADH, or other reductive coenzymes.

II. Genetic Engineering of Production Strain to increase Fatty Acid Derivative Production

[0100] Heterologous DNA sequences involved in a biosynthetic pathway for the production of fatty acid derivatives can be introduced stably or transiently into a host cell using techniques well known in the art for example electroporation, calcium phosphate precipitation, DEAE-dextran mediated transfection, liposome-mediated transfection, conjugation, transduction, and the like. For stable transformation, a DNA sequence can further include a selectable marker, such as,

antibiotic resistance, for example resistance to neomycin, tetracycline, chloramphenicol, kanamycin, genes that complement auxotrophic deficiencies, and the like.

[0101] Various embodiments of this disclosure utilize an expression vector that includes a heterologous DNA sequence encoding a protein involved in a metabolic or biosynthetic pathway. Suitable expression vectors include, but are not limited to, viral vectors, such as baculovirus vectors, phage vectors, such as bacteriophage vectors, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral vectors (e.g. viral vectors based on vaccinia virus, poliovirus, adenovirus, adeno-associated virus, SV40, herpes simplex virus, and the like), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as *E. coli*, *Pseudomonas pisum* and *Saccharomyces cerevisiae*).

[0102] Useful expression vectors can include one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells. The selectable marker gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selectable marker gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*. In alternative embodiments, the selectable marker gene is one that encodes dihydrofolate reductase or confers neomycin resistance (for use in eukaryotic cell culture), or one that confers tetracycline or ampicillin resistance (for use in a prokaryotic host cell, such as *E. coli*).

[0103] The biosynthetic pathway gene product-encoding DNA sequence in the expression vector is operably linked to an appropriate expression control sequence, (promoters, enhancers, and the like) to direct synthesis of the encoded gene product. Such promoters can be derived from microbial or viral sources, including CMV and SV40. Depending on the host/vector system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. can be used in the expression vector (see e.g., Bitter et al., *Methods in Enzymology*, 153:516-544, 1987).

[0104] Suitable promoters for use in prokaryotic host cells include, but are not limited to, promoters capable of recognizing the T4, T3, Sp6 and T7 polymerases, the P_R and P_L promoters of bacteriophage lambda, the trp, recA, heat shock, and lacZ promoters of *E. coli*, the alpha-amylase and the sigma-specific promoters of *B. subtilis*, the promoters of the bacteriophages of *Bacillus*, *Streptomyces* promoters, the int promoter of bacteriophage lambda, the bla promoter of the beta-lactamase gene of pBR322, and the CAT promoter of the chloramphenicol acetyl transferase gene. Prokaryotic promoters are reviewed by Glick, *J. Ind. Microbiol.* 1:277, 1987; Watson et al., *MOLECULAR BIOLOGY OF THE GENE*, 4th Ed., Benjamin Cummins (1987); and Sambrook et al., supra.

[0105] Non-limiting examples of suitable eukaryotic promoters for use within a eukaryotic host are viral in origin and include the promoter of the mouse metallothionein I gene (Hamer et al., *J. Mol. Appl. Gen.* 1:273, 1982); the TK promoter of Herpes virus (McKnight, *Cell* 31:355, 1982); the

SV40 early promoter (Benoist et al., *Nature* (London) 290:304, 1981); the Rous sarcoma virus promoter; the cytomegalovirus promoter (Foecking et al., *Gene* 45:101, 1980); the yeast gal4 gene promoter (Johnston, et al., *PNAS* (USA) 79:6971, 1982; Silver, et al., *PNAS* (USA) 81:5951, 1984); and the IgG promoter (Orlandi et al., *PNAS* (USA) 86:3833, 1989).

[0106] The microbial host cell can be genetically modified with a heterologous DNA sequence encoding a biosynthetic pathway gene product that is operably linked to an inducible promoter. Inducible promoters are well known in the art. Suitable inducible promoters include, but are not limited to promoters that are affected by proteins, metabolites, or chemicals. These include: a bovine leukemia virus promoter, a metallothionein promoter, a dexamethasone-inducible MMTV promoter, a SV40 promoter, a MRP polIII promoter, a tetracycline-inducible CMV promoter (such as the human immediate-early CMV promoter) as well as those from the trp and lac operons.

[0107] In some examples a genetically modified host cell is genetically modified with a heterologous DNA sequence encoding a biosynthetic pathway gene product that is operably linked to a constitutive promoter. Suitable constitutive promoters are known in the art and include, constitutive adenovirus major late promoter, a constitutive MPSV promoter, and a constitutive CMV promoter.

[0108] In some examples a modified host cell is one that is genetically modified with an exogenous DNA sequence encoding a single protein involved in a biosynthesis pathway.

[0109] In other embodiments, a modified host cell is one that is genetically modified with exogenous DNA sequences encoding two or more proteins involved in a biosynthesis pathway--for example, the first and second enzymes in a biosynthetic pathway.

[0110] Where the host cell is genetically modified to express two or more proteins involved in a biosynthetic pathway, those DNA sequences can each be contained in a single or in separate expression vectors. When those DNA sequences are contained in a single expression vector, in some embodiments, the nucleotide sequences will be operably linked to a common control element (e.g., a promoter), e.g., the common control element controls expression of all of the biosynthetic pathway protein-encoding DNA sequences in the single expression vector.

[0111] When a modified host cell is genetically modified with heterologous DNA sequences encoding two or more proteins involved in a biosynthesis pathway, one of the DNA sequences can be operably linked to an inducible promoter, and one or more of the DNA sequences can be operably linked to a constitutive promoter.

[0112] In some embodiments, the intracellular concentration (e.g., the concentration of the intermediate in the genetically modified host cell) of the biosynthetic pathway intermediate can be increased to further boost the yield of the final product. The intracellular concentration of the intermediate can be increased in a number of ways, including, but not limited to, increasing the concentration in the culture medium of a substrate for a biosynthetic pathway; increasing the catalytic activity of an enzyme that is active in the biosynthetic pathway; increasing the intracellular amount of a substrate (e.g., a primary substrate) for an enzyme that is active in the biosynthetic pathway; and the like.

[0113] In some examples the fatty acid derivative or intermediate is produced in the cytoplasm of the cell. The cyto-

plasmic concentration can be increased in a number of ways, including, but not limited to, binding of the fatty acid to coenzyme A to form an acyl-CoA thioester. Additionally, the concentration of acyl-CoAs can be increased by increasing the biosynthesis of CoA in the cell, such as by over-expressing genes associated with pantothenate biosynthesis (panD) or knocking out the genes associated with glutathione biosynthesis (glutathione synthase).

III. Carbon Chain Characteristics

[0114] Using the teachings provided herein a range of products can be produced. These products include hydrocarbons, fatty alcohols, fatty acid esters, and waxes. Some of these products are useful as biofuels and specialty chemicals. These products can be designed and produced in microorganisms. The products can be produced such that they contain branch points, levels of saturation, and carbon chain length, thus, making these products desirable starting materials for use in many applications (FIG. 10 provides a description of the various enzymes that can be used alone or in combination to make various fatty acid derivatives).

[0115] In other examples, the expression of exogenous FAS genes originating from different species or engineered variants can be introduced into the host cell to result in the biosynthesis of fatty acid metabolites structurally different (in length, branching, degree of unsaturation, etc.) as that of the native host. These heterologous gene products can be also chosen or engineered so that they are unaffected by the natural complex regulatory mechanisms in the host cell and, therefore, function in a manner that is more controllable for the production of the desired commercial product. For example the FAS enzymes from *Bacillus subtilis*, *Saccharomyces cerevisiae*, *Streptomyces* spp, *Ralstonia*, *Rhodococcus*, *Corynebacteria*, *Brevibacteria*, *Mycobacteria*, oleaginous yeast, and the like can be expressed in the production host.

[0116] One of ordinary skill in the art will appreciate that when a production host is engineered to produce a fatty acid from the fatty acid biosynthetic pathway that contains a specific level of unsaturation, branching, or carbon chain length the resulting engineered fatty acid can be used in the production of the fatty acid derivatives. Hence, fatty acid derivatives generated from the production host can display the characteristics of the engineered fatty acid. For example, a production host can be engineered to make branched, short chain fatty acids, and then using the teachings provided herein relating to fatty alcohol production (i.e. including alcohol forming enzymes such as FAR) the production host produce branched, short chain fatty alcohols. Similarly, a hydrocarbon can be produced by engineering a production host to produce a fatty acid having a defined level of branching, unsaturation, and/or carbon chain length, thus, producing a homogenous hydrocarbon population. Moreover, when an unsaturated alcohol, fatty acid ester, or hydrocarbon is desired the fatty acid biosynthetic pathway can be engineered to produce low levels of saturated fatty acids and an additional desaturase can be expressed to lessen the saturated product production.

[0117] A. Saturation

[0118] Production hosts can be engineered to produce unsaturated fatty acids by engineering the production host to over-express fabB, or by growing the production host at low temperatures (for example less than 37° C.). FabB has preference to cis- δ^3 decenoyl-ACP and results in unsaturated fatty acid production in *E. coli*. Over-expression of FabB resulted

in the production of a significant percentage of unsaturated fatty acids (de Mendoza et al., *J. Biol. Chem.*, 258:2098-101, 1983). These unsaturated fatty acids can then be used as intermediates in production hosts that are engineered to produce fatty acid derivatives, such as fatty alcohols, esters, waxes, olefins, alkanes, and the like. One of ordinary skill in the art will appreciate that by attenuating fabA, or over-expressing FabB and expressing specific thioesterases (described below), unsaturated fatty acid derivatives having a desired carbon chain length can be produced. Alternatively, the repressor of fatty acid biosynthesis, FabR (Genbank accession NP_418398), can be deleted, which will also result in increased unsaturated fatty acid production in *E. coli* (Zhang et al., *J. Biol. Chem.* 277:pp. 15558, 2002.). Further increase in unsaturated fatty acids may be achieved by over-expression of FabM (trans-2, cis-3-decenoyl-ACP isomerase, Genbank accession DAA05501) and controlled expression of FabK (trans-2-enoyl-ACP reductase II, Genbank accession NP_357969) from *Streptococcus pneumoniae* (Marrakchi et al., *J. Biol. Chem.* 277: 44809, 2002), while deleting *E. coli* Fab I ((trans-2-enoyl-ACP reductase, Genbank accession NP_415804). Additionally, to increase the percentage of unsaturated fatty acid esters, the microorganism can also have fabB (encoding β -ketoacyl-ACP synthase I, Accessions: BAA16180, EC:2.3.1.41), Sfa (encoding a suppressor of fabA, Accession: AAC44390) and gnsA and gnsB (both encoding secG null mutant suppressors, a.k.a. cold shock proteins, Accession: ABD18647.1, AAC74076.1) over-expressed.

[0119] In some examples, the endogenous fabF gene can be attenuated, thus, increasing the percentage of palmitoleate (C16:1) produced.

[0120] B. Branching Including Cyclic Moieties

[0121] Fatty acid derivatives can be produced that contain branch points, cyclic moieties, and combinations thereof, using the teachings provided herein.

[0122] Microorganisms that naturally produce straight fatty acids (sFAs) can be engineered to produce branched chain fatty acids (brFAs) by expressing one or more exogenous nucleic acid sequences. For example, *E. coli* naturally produces straight fatty acids (sFAs). To engineer *E. coli* to produce brFAs, several genes can be introduced and expressed that provide branched precursors (bkd operon) and allow initiation of fatty acid biosynthesis from branched precursors (fabH). Additionally, the organism can express genes for the elongation of brFAs (e.g. ACP, FabF) and/or deleting the corresponding *E. coli* genes that normally lead to sFAs and would compete with the introduced genes (e.g. FabH, FabF).

[0123] The branched acyl-CoAs 2-methyl-buturyl-CoA, isovaleryl-CoA and isobutyryl-CoA are the precursors of brFA. In most brFA-containing microorganisms they are synthesized in two steps (described in detail below) from branched amino acids (isoleucine, leucine and valine) (Kadena, *Microbiol. Rev.* 55: pp. 288, 1991). To engineer a microorganism to produce brFAs, or to overproduce brFAs, expression or over-expression of one or more of the enzymes in these two steps can be engineered. For example, in some instances the production host may have an endogenous enzyme that can accomplish one step and therefore, only enzymes involved in the second step need to be expressed recombinantly.

[0124] The first step in forming branched fatty acids is the production of the corresponding α -keto acids by a branched-

chain amino acid aminotransferase. *E. coli* has such an enzyme, IlvE (EC 2.6.1.42; Genbank accession YP_026247). In some examples, a heterologous branched-chain amino acid aminotransferase may not be expressed. However, *E. coli* IlvE or any other branched-chain amino acid aminotransferase, e.g. ilvE from *Lactococcus lactis* (Genbank accession AAF34406), ilvE from *Pseudomonas putida* (Genbank accession NP_745648) or ilvE from *Streptomyces coelicolor* (Genbank accession NP_629657) can be over-expressed in a host microorganism, should the aminotransferase reaction turn out to be rate limiting in brFA biosynthesis in the host organism chosen for fatty acid derivative production.

[0125] The second step, the oxidative decarboxylation of the α -ketoacids to the corresponding branched-chain acyl-CoA, is catalyzed by a branched-chain α -keto acid dehydrogenase complexes (bkd; EC 1.2.4.4.) (Denoya et al. *J. Bacteriol.* 177:pp. 3504, 1995), which consist of E1 α / β (decarboxylase), E2 (dihydrolipoyl transacylase) and E3 (dihydrolipoyl dehydrogenase) subunits and are similar to pyruvate and α -ketoglutarate dehydrogenase complexes. Table 2 shows potential bkd genes from several microorganisms, that can be expressed in a production host to provide branched-chain acyl-CoA precursors. Basically, every microorganism that possesses brFAs and/or grows on branched-chain amino acids can be used as a source to isolate bkd genes for expression in production hosts such as, for example, *E. coli*. Furthermore, *E. coli* has the E3 component (as part of its pyruvate dehydrogenase complex; 1pd, EC 1.8.1.4, Genbank accession NP_414658), it can therefore, be sufficient to only express the E1 α / β and E2 bkd genes.

TABLE 2

Bkd genes from selected microorganisms		
Organism	Gene	Genbank Accession #
<i>Streptomyces coelicolor</i>	bkdA1 (E1 α)	NP_628006
	bkdB1 (E1 α)	NP_628005
	bkdC1 (E2)	NP_638004
<i>Streptomyces coelicolor</i>	bkdA2 (E1 α)	NP_733618
	bkdB2 (E1 α)	NP_628019
	bkdC2 (E2)	NP_628018
<i>Streptomyces avermitilis</i>	bkdA (E1a)	BAC72074
	bkdB (E1b)	BAC72075
	bkdC (E2)	BAC72076
<i>Streptomyces avermitilis</i>	bkdF (E1 α)	BAC72088
	bkdG (E1 α)	BAC72089
	bkdH (E2)	BAC72090
<i>Bacillus subtilis</i>	bkdAA (E1 α)	NP_390288
	bkdAB (E1 α)	NP_390288
	bkdB (E2)	NP_390288
<i>Pseudomonas putida</i>	bkdA1 (E1 α)	AAA65614
	bkdA2 (E1 α)	AAA65615
	bkdC (E2)	AAA65617

[0126] In another example, isobutyryl-CoA can be made in a production host, for example in *E. coli* through the co-expression of a crotonyl-CoA reductase (Ccr, EC 1.1.1.9) and isobutyryl-CoA mutase (large subunit IcmA, EC 5.4.99.2; small subunit IcmB, EC 5.4.99.13) (Han and Reynolds *J. Bacteriol.* 179:pp. 5157, 1997). Crotonyl-CoA is an intermediate in fatty acid biosynthesis in *E. coli* and other microorganisms. Examples for ccr and icm genes from selected microorganisms are given in Table 3.

TABLE 3

Ccr and icm genes from selected microorganisms		
Organism	Gene	Genbank Accession #
<i>Streptomyces coelicolor</i>	ccr	NP_630556
	icmA	NP_629554
	icmB	NP_630904
<i>Streptomyces cinnamonensis</i>	ccr	AAD53915
	icmA	AAC08713
	icmB	AJ246005

[0127] In addition to expression of the bkd genes (see above), the initiation of brFA biosynthesis utilizes β -ketoacyl-acyl-carrier-protein synthase III (FabH, EC 2.3.1.41) with specificity for branched chain acyl CoAs (Li et al. *J. Bacteriol.* 187:pp. 3795, 2005). Examples of such FabHs are listed in Table 4. FabH genes that are involved in fatty acid biosynthesis of any brFA-containing microorganism can be expressed in a production host. The Bkd and FabH enzymes from production hosts that do not naturally make brFA may not support brFA production and therefore, Bkd and FabH can be expressed recombinantly. Similarly, the endogenous level of Bkd and FabH production may not be sufficient to produce brFA, therefore, they can be over-expressed. Additionally, other components of fatty acid biosynthesis machinery can be expressed such as acyl carrier proteins (ACPs) and β -ketoacyl-acyl-carrier-protein synthase II candidates are acyl carrier proteins (ACPs) and β -ketoacyl-acyl-carrier-protein synthase II (fabF, EC 2.3.1.41) (candidates are listed in Table 4). In addition to expressing these genes, some genes in the endogenous fatty acid biosynthesis pathway may be attenuated in the production host. For example, in *E. coli* the most likely candidates to interfere with brFA biosynthesis are fabH (Genbank accession # NP_415609) and/or fabF genes (Genbank accession #NP_415613).

[0128] As mentioned above, through the combination of expressing genes that support brFA synthesis and alcohol synthesis branched chain alcohols can be produced. For example, when an alcohol reductase such as AcrI from *Acinetobacter baylyi* ADP1 is coexpressed with a bkd operon, *E. coli* can synthesize isopentanol, isobutanol or 2-methyl butanol. Similarly, when AcrI is coexpressed with ccr/icm genes, *E. coli* can synthesize isobutanol.

[0129] In order to convert a production host such as *E. coli* into an organism capable of synthesizing co-cyclic fatty acids (cyFAs), several genes need to be introduced and expressed that provide the cyclic precursor cyclohexylcarbonyl-CoA (Cropp et al. *Nature Biotech.* 18:pp. 980, 2000). The genes listed in Table 4 (fabH, ACP and fabF) can then be expressed to allow initiation and elongation of ω -cyclic fatty acids. Alternatively, the homologous genes can be isolated from microorganisms that make cyFAs and expressed in *E. coli*.

TABLE 4

FabH, ACP and fabF genes from selected microorganisms with brFAs		
Organism	Gene	Genbank Accession #
<i>Streptomyces coelicolor</i>	fabH1	NP_626634
	ACP	NP_626635
	fabF	NP_626636
<i>Streptomyces avermitilis</i>	fabH3	NP_823466
	fabC3 (ACP)	NP_823467
	fabF	NP_823468

TABLE 4-continued

FabH, ACP and fabF genes from selected microorganisms with brFAs		
Organism	Gene	Genbank Accession #
<i>Bacillus subtilis</i>	fabH_A	NP_389015
	fabH_B	NP_388898
	ACP	NP_389474
	fabF	NP_389016
<i>Stenotrophomonas maltophilia</i>	SmalDRAFT_0818 (FabH)	ZP_01643059
	SmalDRAFT_0821 (ACP)	ZP_01643063
	SmalDRAFT_0822 (FabF)	ZP_01643064
<i>Legionella pneumophila</i>	FabH	YP_123672
	ACP	YP_123675
	fabF	YP_123676

[0130] Expression of the following genes are sufficient to provide cyclohexylcarbonyl-CoA in *E. coli*: ansJ, ansK, ansL, chcA and ansM from the ansatrienin gene cluster of *Streptomyces collinus* (Chen et al., *Eur. J. Biochem.* 261:pp. 1999, 1999) or plmJ, plmL, chcA and plmM from the phoslactomycin B gene cluster of *Streptomyces* sp. HK803 (Pala-niappan et al., *J. Biol. Chem.* 278:pp. 35552, 2003) together with the chcB gene (Patton et al. *Biochem.*, 39:pp. 7595, 2000) from *S. collinus*, *S. avermitilis* or *S. coelicolor* (see Table 5 for Genbank accession numbers).

TABLE 5

Genes for the synthesis of cyclohexylcarbonyl-CoA		
Organism	Gene	Genbank Accession #
<i>Streptomyces collinus</i>	ansJK	U72144*
	ansL	
	chcA	
	ansL	
<i>Streptomyces</i> sp. HK803	chcB	AF268489
	pmlJK	AAQ84158
	pmlL	AAQ84159
	chcA	AAQ84160
	pmlM	AAQ84161
<i>Streptomyces coelicolor</i>	chcB/caiD	NP_629292
<i>Streptomyces avermitilis</i>	chcB/caiD	NP_629292

Only chcA is annotated in Genbank entry U72144, ansJKLM are according to Chen et al. (*Eur. J. Biochem.* 261: pp. 1999, 1999)

[0131] The genes listed in Table 4 (fabH, ACP and fabF) are sufficient to allow initiation and elongation of co-cyclic fatty acids, because they can have broad substrate specificity. In the event that coexpression of any of these genes with the ansJKLM/chcAB or pm1JKLM/chcAB genes from Table 5 does not yield cyFAs, fabH, ACP and/or fabF homologs from microorganisms that make cyFAs can be isolated (e.g. by using degenerate PCR primers or heterologous DNA probes) and coexpressed. Table 6 lists selected microorganisms that contain co-cyclic fatty acids.

TABLE 6

Examples of microorganisms that contain ω -cyclic fatty acids	
Organism	Reference
<i>Curtobacterium pusillum</i>	ATCC19096
<i>Alicyclobacillus acidoterrestris</i>	ATCC49025
<i>Alicyclobacillus acidocaldarius</i>	ATCC27009
<i>Alicyclobacillus cycloheptanicum</i> *	Moore, <i>J. Org. Chem.</i> 62: pp. 2173, 1997.

*uses cycloheptylcarbonyl-CoA and not cyclohexylcarbonyl-CoA as precursor for cyFA biosynthesis

[0132] C. Ester characteristics

[0133] One of ordinary skill in the art will appreciate that an ester includes an A side and a B side. As described herein, the B side is contributed by a fatty acid produced from de novo synthesis in the host organism. In some instances where the host is additionally engineered to make alcohols, including fatty alcohols, the A side is also produced by the host organism. In yet other examples the A side can be provided in the medium. As described herein, by selecting the desired thioesterase genes the B side, and when fatty alcohols are being made the A side, can be designed to have certain carbon chain characteristics. These characteristics include points of unsaturation, branching, and desired carbon chain lengths. Exemplary methods of making long chain fatty acid esters, wherein the A and B side are produced by the production host are provided in Example 6, below. Similarly, Example 5 provides methods of making medium chain fatty acid esters. When both the A and B side are contributed by the production host and they are produced using fatty acid biosynthetic pathway intermediates they will have similar carbon chain characteristics. For example, at least 50%, 60%, 70%, or 80% of the fatty acid esters produced will have A sides and B sides that vary by 6, 4, or 2 carbons in length. The A side and the B side will also display similar branching and saturation levels.

[0134] In addition to producing fatty alcohols for contribution to the A side, the host can produce other short chain alcohols such as ethanol, propanol, isopropanol, isobutanol, and butanol for incorporation on the A side using techniques well known in the art. For example, butanol can be made by the host organism. To create butanol producing cells, the LS9001 strain (described in Example 1, below) can be further engineered to express atoB (acetyl-CoA acetyltransferase) from *Escherichia coli* K12, β -hydroxybutyryl-CoA dehydrogenase from *Butyrivibrio fibrisolvens*, crotonase from *Clostridium beijerinckii*, butyryl CoA dehydrogenase from *Clostridium beijerinckii*, CoA-acylating aldehyde dehydrogenase (ALDH) from *Cladosporium fulvum*, and adhE encoding an aldehyde-alcohol dehydrogenase of *Clostridium acetobutylicum* in the pBAD24 expression vector under the prpBCDE promoter system. Similarly, ethanol can be produced in a production host using the methods taught by Kalscheuer et al., *Microbiology* 152:2529-2536, 2006, which is herein incorporated by reference.

IV. Fermentation

[0135] The production and isolation of fatty acid derivatives can be enhanced by employing specific fermentation techniques. One method for maximizing production while reducing costs is increasing the percentage of the carbon source that is converted to hydrocarbon products. During normal cellular lifecycles carbon is used in cellular functions including producing lipids, saccharides, proteins, organic acids, and nucleic acids. Reducing the amount of carbon necessary for growth-related activities can increase the efficiency of carbon source conversion to output. This can be achieved by first growing microorganisms to a desired density, such as a density achieved at the peak of the log phase of growth. At such a point, replication checkpoint genes can be harnessed to stop the growth of cells. Specifically, quorum sensing mechanisms (reviewed in Camilli and Bassler *Science* 311:1113, 2006; Venturi *FEMS Microbio Rev* 30:274-291, 2006; and Reading and Sperandio *FEMS Microbiol Lett* 254:1-11, 2006) can be used to activate genes such as p53,

p21, or other checkpoint genes. Genes that can be activated to stop cell replication and growth in *E. coli* include umuDC genes, the over-expression of which stops the progression from stationary phase to exponential growth (Murli et al., *J. of Bact.* 182:1127, 2000). UmuC is a DNA polymerase that can carry out translesion synthesis over non-coding lesions--the mechanistic basis of most UV and chemical mutagenesis. The umuDC gene products are used for the process of translesion synthesis and also serve as a DNA damage checkpoint. UmuDC gene products include UmuC, UmuD, umuD', UmuD', UmuD'₂C, UmuD'₂ and UmuD₂. Simultaneously, the product producing genes would be activated, thus minimizing the need for replication and maintenance pathways to be used while the fatty acid derivative is being made.

[0136] The percentage of input carbons converted to hydrocarbon products is a cost driver. The more efficient (i.e. the higher the percentage), the less expensive the process. For oxygen-containing carbon sources (i.e. glucose and other carbohydrate based sources), the oxygen must be released in the form of carbon dioxide. For every 2 oxygen atoms released, a carbon atom is also released leading to a maximal theoretical metabolic efficiency of about 34% (w/w) (for fatty acid derived products). This figure, however, changes for other hydrocarbon products and carbon sources. Typical efficiencies in the literature are about <5%. Engineered microorganisms which produce hydrocarbon products can have greater than 1, 3, 5, 10, 15, 20, 25, and 30% efficiency. In one example microorganisms will exhibit an efficiency of about 10% to about 25%. In other examples, such microorganisms will exhibit an efficiency of about 25% to about 30%, and in other examples such microorganisms will exhibit >30% efficiency.

[0137] In some examples where the final product is released from the cell, a continuous process can be employed. In this approach, a reactor with organisms producing fatty acid derivatives can be assembled in multiple ways. In one example, a portion of the media is removed and let to sit. Fatty acid derivatives are separated from the aqueous layer, which will in turn, be returned to the fermentation chamber.

[0138] In one example, the fermentation chamber will enclose a fermentation that is undergoing a continuous reduction. In this instance, a stable reductive environment would be created. The electron balance would be maintained by the release of carbon dioxide (in gaseous form). Efforts to augment the NADH and NADP/H balance can also facilitate in stabilizing the electron balance.

[0139] The availability of intracellular NADPH can be also enhanced by engineering the production host to express an NADH:NADPH transhydrogenase. The expression of one or more NADH:NADPH transhydrogenase converts the NADH produced in glycolysis to NADPH which enhances the production of fatty acid derivatives.

[0140] Disclosed herein is a system for continuously producing and exporting fatty acid derivatives out of recombinant host microorganisms via a transport protein. Many transport and efflux proteins serve to excrete a large variety of compounds and can be evolved to be selective for a particular type of fatty acid derivatives. Thus, in some embodiments an exogenous DNA sequence encoding an ABC transporter will be functionally expressed by the recombinant host microorganism, so that the microorganism exports the fatty acid derivative into the culture medium. In one example, the ABC transporter is an ABC transporter from *Caenorhabditis elegans*, *Arabidopsis thaliana*, *Alkaligenes eutrophus* or

Rhodococcus erythropolis (locus AAN73268). In another example, the ABC transporter is an ABC transporter chosen from CER5 (locuses At1g51500 or AY734542), AtMRP5, AmiS2 and AtPGPI. In some examples, the ABC transporter is CER5. In yet another example, the CER5 gene is from *Arabidopsis* (locuses At1g51500, AY734542, At3g21090 and At1g51460).

[0141] The transport protein, for example, can also be an efflux protein selected from: AcrAB, TolC and AcrEF from *E. coli*, or tll1618, tll1619 and tll0139 from *Thermosynechococcus elongatus* BP-1.

[0142] In addition, the transport protein can be, for example, a fatty acid transport protein (FATP) selected from *Drosophila melanogaster*, *Caenorhabditis elegans*, *Mycobacterium tuberculosis* or *Saccharomyces cerevisiae* or any one of the mammalian FATP's. The FATPs can additionally be resynthesized with the membranous regions reversed in order to invert the direction of substrate flow. Specifically, the sequences of amino acids composing the hydrophilic domains (or membrane domains) of the protein, could be inverted while maintaining the same codons for each particular amino acid. The identification of these regions is well known in the art.

[0143] Production hosts can also be chosen for their endogenous ability to release fatty acid derivatives. The efficiency of product production and release into the fermentation broth can be expressed as a ratio intracellular product to extracellular product. In some examples the ratio can be 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, or 1:5.

[0144] The production host can be additionally engineered to express recombinant cellulosomes, such as those described in PCT application number PCT/US2007/003736, which will allow the production host to use cellulosic material as a carbon source. For example, the production host can be additionally engineered to express invertases (EC 3.2.1.26) so that sucrose can be used as a carbon source.

[0145] Similarly, the production host can be engineered using the teachings described in U.S. Pat. Nos. 5,000,000, 5,028,539, 5,424,202, 5,482,846, and 5,602,030 to Ingram et al. so that the production host can assimilate carbon efficiently and use cellulosic materials as carbon sources.

IV. Post Production Processing

[0146] The fatty acid derivatives produced during fermentation can be separated from the fermentation media. Any technique known for separating fatty acid derivatives from aqueous media can be used. One exemplary separation process provided herein is a two phase (bi-phasic) separation process. This process involves fermenting the genetically engineered production hosts under conditions sufficient to produce a fatty acid derivative, allowing the derivative to collect in an organic phase and separating the organic phase from the aqueous fermentation broth. This method can be practiced in both a batch and continuous fermentation setting.

[0147] Bi-phasic separation uses the relative immiscibility of fatty acid derivatives to facilitate separation. Immiscible refers to the relative inability of a compound to dissolve in water and is defined by the compound's partition coefficient. The partition coefficient, P, is defined as the equilibrium concentration of compound in an organic phase (in a bi-phasic system the organic phase is usually the phase formed by the fatty acid derivative during the production process, however, in some examples an organic phase can be provided (such as a layer of octane to facilitate product separation)

divided by the concentration at equilibrium in an aqueous phase (i.e. fermentation broth). When describing a two phase system the P is usually discussed in terms of logP. A compound with a logP of 10 would partition 10:1 to the organic phase, while a compound of logP of 0.1 would partition 10:1 to the aqueous phase. One of ordinary skill in the art will appreciate that by choosing a fermentation broth and the organic phase such that the fatty acid derivative being produced has a high logP value, the fatty acid derivative will separate into the organic phase, even at very low concentrations in the fermentation vessel.

[0148] The fatty acid derivatives produced by the methods described herein will be relatively immiscible in the fermentation broth, as well as in the cytoplasm. Therefore, the fatty acid derivative will collect in an organic phase either intracellularly or extracellularly. The collection of the products in an organic phase will lessen the impact of the fatty acid derivative on cellular function and will allow the production host to produce more product. Stated another way, the concentration of the fatty acid derivative will not have as significant of an impact on the host cell.

[0149] The fatty alcohols, fatty acid esters, waxes, and hydrocarbons produced as described herein allow for the production of Komogeneous compounds wherein at least 60%, 70%, 80%, 90%, or 95% of the fatty alcohols, fatty acid esters, and waxes produced will have carbon chain lengths that vary by less than 4 carbons, or less than 2 carbons. These compounds can also be produced so that they have a relatively uniform degree of saturation, for example at least 60%, 70%, 80%, 90%, or 95% of the fatty alcohols, fatty acid esters, hydrocarbons and waxes will be mono-, di-, or tri-unsaturated. These compounds can be used directly as fuels, personal care additives, nutritional supplements. These compounds can also be used as feedstock for subsequent reactions for example transesterification, hydrogenation, catalytic cracking via either hydrogenation, pyrolysis, or both or epoxidations reactions to make other products.

V. Fuel Compositions

[0150] The fatty acid derivatives described herein can be used as fuel. One of ordinary skill in the art will appreciate that depending upon the intended purpose of the fuel different fatty acid derivatives can be produced and used. For example, for automobile fuel that is intended to be used in cold climates a branched fatty acid derivative may be desirable and using the teachings provided herein, branched hydrocarbons, fatty acid esters, and alcohols can be made. Using the methods described herein fuels comprising relatively homogeneous fatty acid derivatives that have desired fuel qualities can be produced. Such fuels can be characterized by carbon fingerprinting, their lack of impurities when compared to petroleum derived fuels or bio-diesel derived from triglycerides and, moreover, the fatty acid derivative based fuels can be combined with other fuels or fuel additives to produce fuels having desired properties.

[0151] A. Carbon Fingerprinting

[0152] Biologically produced fatty acid derivatives represent a new feedstock for fuels, such as alcohols, diesel and gasoline. Some biofuels made using fatty acid derivatives have not been produced from renewable sources and as such, are new compositions of matter. These new fuels can be distinguished from fuels derived from petrochemical carbon on the basis of dual carbon-isotopic fingerprinting. Additionally, the specific source of biosourced carbon (e.g. glucose vs.

glycerol) can be determined by dual carbon-isotopic fingerprinting (see, U.S. Pat. No. 7,169,588, which is herein incorporated by reference).

[0153] This method usefully distinguishes chemically-identical materials, and apportions carbon in products by source (and possibly year) of growth of the biospheric (plant) component. The isotopes, ^{14}C and ^{13}C , bring complementary information to this problem. The radiocarbon dating isotope (^{14}C), with its nuclear half life of 5730 years, clearly allows one to apportion specimen carbon between fossil ("dead") and biospheric ("alive") feedstocks [Currie, L. A. "Source Apportionment of Atmospheric Particles," Characterization of Environmental Particles, J. Buffle and H. P. van Leeuwen, Eds., 1 of Vol. I of the IUPAC Environmental Analytical Chemistry Series (Lewis Publishers, Inc) (1992) 3-74]. The basic assumption in radiocarbon dating is that the constancy of ^{14}C concentration in the atmosphere leads to the constancy of ^{14}C in living organisms. When dealing with an isolated sample, the age of a sample can be deduced approximately by the relationship $t = (-5730/0.693) \ln(A/A_{\text{sub.O}})$ (Equation 5) where t =age, 5730 years is the half-life of radiocarbon, and A and $A_{\text{sub.O}}$ are the specific ^{14}C activity of the sample and of the modern standard, respectively [Hsieh, Y., Soil Sci. Soc. Am J., 56, 460, (1992)]. However, because of atmospheric nuclear testing since 1950 and the burning of fossil fuel since 1850, ^{14}C has acquired a second, geochemical time characteristic. Its concentration in atmospheric CO_2 --and hence in the living biosphere--approximately doubled at the peak of nuclear testing, in the mid-1960s. It has since been gradually returning to the steady-state cosmogenic (atmospheric) baseline isotope rate ($^{14}\text{C}/^{12}\text{C}$) of ca. 1.2×10^{12} , with an approximate relaxation "half-life" of 7-10 years. (This latter half-life must not be taken literally; rather, one must use the detailed atmospheric nuclear input/decay function to trace the variation of atmospheric and biospheric ^{14}C since the onset of the nuclear age.) It is this latter biospheric ^{14}C time characteristic that holds out the promise of annual dating of recent biospheric carbon. ^{14}C can be measured by accelerator mass spectrometry (AMS), with results given in units of "fraction of modern carbon" (f_M). f_M is defined by National Institute of Standards and Technology (NIST) Standard Reference Materials (SRMs) 4990B and 4990C, known as oxalic acids standards HOxI and HOxII, respectively. The fundamental definition relates to 0.95 times the $^{14}\text{C}/^{12}\text{C}$ isotope ratio HOxI (referenced to AD 1950). This is roughly equivalent to decay-corrected pre-Industrial Revolution wood. For the current living biosphere (plant material), f_M approx 1.1.

[0154] The stable carbon isotope ratio ($^{13}\text{C}/^{12}\text{C}$) provides a complementary route to source discrimination and apportionment. The $^{13}\text{C}/^{12}\text{C}$ ratio in a given biosourced material is a consequence of the $^{13}\text{C}/^{12}\text{C}$ ratio in atmospheric carbon dioxide at the time the carbon dioxide is fixed and also reflects the precise metabolic pathway. Regional variations also occur. Petroleum, C3 plants (the broadleaf), C.sub.4 plants (the grasses), and marine carbonates all show significant differences in $^{13}\text{C}/^{12}\text{C}$ and the corresponding $\delta^{13}\text{C}$ values. Furthermore, lipid matter of C3 and C4 plants analyze differently than materials derived from the carbohydrate components of the same plants as a consequence of the metabolic pathway. Within the precision of measurement, ^{13}C shows large variations due to isotopic fractionation effects, the most significant of which for the instant invention is the photosynthetic mechanism. The major cause of differences in the carbon isotope ratio in plants is closely associated with differ-

ences in the pathway of photosynthetic carbon metabolism in the plants, particularly the reaction occurring during the primary carboxylation, i.e., the initial fixation of atmospheric CO₂. Two large classes of vegetation are those that incorporate the “C3” (or Calvin-Benson) photosynthetic cycle and those that incorporate the “C4” (or Hatch-Slack) photosynthetic cycle. C3 plants, such as hardwoods and conifers, are dominant in the temperate climate zones. In C3 plants, the primary CO₂ fixation or carboxylation reaction involves the enzyme ribulose-1,5-diphosphate carboxylase and the first stable product is a 3-carbon compound. C4 plants, on the other hand, include such plants as tropical grasses, corn and sugar cane. In C4 plants, an additional carboxylation reaction involving another enzyme, phosphoenol-pyruvate carboxylase, is the primary carboxylation reaction. The first stable carbon compound is a 4-carbon acid which is subsequently decarboxylated. The CO₂ thus released is refixed by the C3 cycle.

[0155] Both C4 and C3 plants exhibit a range of ¹³C/¹²C isotopic ratios, but typical values are ca. -10 to -14 per mil (C4) and -21 to -26 per mil (C3) [Weber et al., J. Agric. Food Chem., 45, 2942 (1997)]. Coal and petroleum fall generally in this latter range. The ¹³C measurement scale was originally defined by a zero set by pee dee belemnite (PDB) limestone, where values are given in parts per thousand deviations from this material. The “Δ¹³C”, values are in parts per thousand (per mil), abbreviated ‰, and are calculated as follows:

$$\delta^{13}C \equiv \frac{(^{13}C/^{12}C)_{\text{sample}} - (^{13}C/^{12}C)_{\text{standard}}}{(^{13}C/^{12}C)_{\text{standard}}} \times 100\% \quad (\text{Equation 6})$$

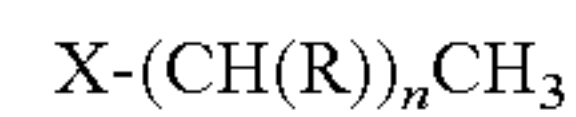
Since the PDB reference material (RM) has been exhausted, a series of alternative RMs have been developed in cooperation with the IAEA, USGS, NIST, and other selected international isotope laboratories. Notations for the per mil deviations from PDB is Δ¹³C. Measurements are made on CO₂ by high precision stable ratio mass spectrometry (IRMS) on molecular ions of masses 44, 45 and 46.

[0156] The fatty acid derivatives and the associated biofuels, chemicals, and mixtures may be completely distinguished from their petrochemical derived counterparts on the basis of ¹⁴C (fM) and dual carbon-isotopic fingerprinting, indicating new compositions of matter.

[0157] The fatty acid derivatives described herein have utility in the production of biofuels and chemicals. The new fatty acid derivative based product compositions provided by the instant invention additionally may be distinguished on the basis of dual carbon-isotopic fingerprinting from those materials derived solely from petrochemical sources. The ability to distinguish these products is beneficial in tracking these materials in commerce. For example, fuels or chemicals comprising both “new” and “old” carbon isotope profiles may be distinguished from fuels and chemicals made only of “old” materials. Hence, the instant materials may be followed in commerce on the basis of their unique profile and for the purposes of defining competition, and for determining shelf life.

[0158] In some examples a biofuel composition is made that includes a fatty acid derivative having δ¹³C of from about -10.9 to about -15.4, wherein the fatty acid derivative accounts for at least about 85% of biosourced material (derived from a renewable resource such as cellulosic materials

and sugars) in the composition. In other examples, the biofuel composition includes a fatty acid derivative having the formula



[0159] wherein X represents CH₃, —CH₂OR¹; —C(O)OR²; or —C(O)NR³R⁴;

[0160] R is, for each n, independently absent, H or lower aliphatic;

[0161] n is an integer from 8 to 34, such as from 10 to 24; and

[0162] R¹, R², R³ and R⁴ independently are selected from H and lower alkyl. Typically, when R is lower aliphatic, R represents a branched, unbranched or cyclic lower alkyl or lower alkenyl moiety. Exemplary R groups include, without limitation, methyl, isopropyl, isobutyl, sec-butyl, cyclopentenyl and the like. The fatty acid derivative is additionally characterized as having a δ¹³C of from about -10.9 to about -15.4; and the fatty acid derivative accounts for at least about 85% of biosourced material in the composition. In some examples the fatty acid derivative in the biofuel composition is characterized by having a fraction of modern carbon (f_M¹⁴C) of at least about 1.003, 1.010, or 1.5.

[0163] B. Fatty Acid Derivatives

[0164] The centane number (CN), viscosity, melting point, and heat of combustion for various fatty acid esters have been characterized in for example, Knothe, *Fuel Processing Technology* 86:1059-1070, 2005, which is herein incorporated by reference. Using the teachings provided herein a production host can be engineered to produce anyone of the fatty acid esters described in the Knothe, *Fuel Processing Technology* 86:1059-1070, 2005.

[0165] Alcohols (short chain, long chain, branched or unsaturated) can be produced by the production hosts described herein. Such alcohols can be used as fuels directly or they can be used to create an ester, i.e. the A side of an ester as described above. Such ester alone or in combination with the other fatty acid derivatives described herein are useful a fuels.

[0166] Similarly, hydrocarbons produced from the microorganisms described herein can be used as biofuels. Such hydrocarbon based fuels can be designed to contain branch points, defined degrees of saturation, and specific carbon lengths. When used as biofuels alone or in combination with other fatty acid derivatives the hydrocarbons can be additionally combined with additives or other traditional fuels (alcohols, diesel derived from triglycerides, and petroleum based fuels).

[0167] C. Impurities

[0168] The fatty acid derivatives described herein are useful for making bio-fuels. These fatty acid derivatives are made directly from fatty acids and not from the chemical processing of triglycerides. Accordingly, fuels comprising the disclosed fatty acid derivatives will contain less of the impurities than are normally associated with bio-fuels derived from triglycerides, such as fuels derived from vegetable oils and fats.

[0169] The crude fatty acid derivative bio-fuels described herein (prior to mixing the fatty acid derivative with other fuels such as traditional fuels) will contain less transesterification catalyst than petrochemical diesel or bio-diesel. For example, the fatty acid derivative can contain less than about 2%, 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% of a transesterification catalyst or an impurity resulting from a transesterification catalyst. Transesterification catalysts

include for example, hydroxide catalysts such as NaOH, KOH, LiOH, and acidic catalysts, such as mineral acid catalysts and Lewis acid catalysts. Catalysts and impurities resulting from transesterification catalysts include, without limitation, tin, lead, mercury, cadmium, zinc, titanium, zirconium, hafnium, boron, aluminum, phosphorus, arsenic, antimony, bismuth, calcium, magnesium, strontium, uranium, potassium, sodium, lithium, and combinations thereof.

[0170] Similarly, the crude fatty acid derivative bio-fuels described herein (prior to mixing the fatty acid derivative with other fuels such as petrochemical diesel or bio-diesel) will contain less glycerol (or glycerin) than bio-fuels made from triglycerides. For example, the fatty acid derivative can contain less than about 2%, 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% glycerol.

[0171] The crude biofuel derived from fatty acid derivatives will also contain less free alcohol (i.e. alcohol that is used to create the ester) than bio-diesel made from triglycerides. This is in-part due to the efficiency of utilization of the alcohol by the production host. For example, the fatty acid derivative will contain less than about 2%, 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% free alcohol.

[0172] Biofuel derived from the disclosed fatty acid derivatives can be additionally characterized by its low concentration of sulfur compared to petroleum derived diesel. For example, biofuel derived from fatty acid derivatives can have less than about 2%, 1.5%, 1.0%, 0.5%, 0.3%, 0.1%, 0.05%, or 0% sulfur.

[0173] D. Additives

[0174] Fuel additives are used to enhance the performance of a fuel or engine. For example, fuel additives can be used to alter the freezing/gelling point, cloud point, lubricity, viscosity, oxidative stability, ignition quality, octane level, and flash point. In the United States, all fuel additives must be registered with Environmental Protection Agency and companies that sell the fuel additive and the name of the fuel additive are publicly available on the agency website and also by contacting the agency. One of ordinary skill in the art will appreciate that the fatty acid derivatives described herein can be mixed with one or more such additives to impart a desired quality.

[0175] One of ordinary skill in the art will also appreciate that the fatty acid derivatives described herein are can be mixed with other fuels such as bio-diesel derived from triglycerides, various alcohols such as ethanol and butanol, and petroleum derived products such as gasoline. In some examples, a fatty acid derivative, such as C16:1 ethyl ester or C18:1 ethyl ester, is produced which has a low gel point. This low gel point fatty acid derivative is mixed with bio-diesel made from triglycerides to lessen the overall gelling point of the fuel. Similarly, a fatty acid derivative such as C16:1 ethyl ester or C18:1 ethyl ester can be mixed with petroleum derived diesel to provide a mixture that is at least and often greater than 5% biodiesel. In some examples, the mixture includes at least 20% or greater of the fatty acid derivative.

[0176] For example, a biofuel composition can be made that includes at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90% or 95% of a fatty acid derivative that includes a carbon chain that is 8:0, 10:0, 12:0, 14:0, 14:1, 16:0, 16:1, 18:0, 18:1, 18:2, 18:3, 20:0, 20:1, 20:2, 20:3, 22:0, 22:1 or 22:3. Such biofuel compositions can additionally include at least one additive selected from a cloud point lowering additive that can lower the cloud point to less than about 5° C., or 0° C., a surfactant, or a microemulsion, at least about 5%, 10%, 15%, 20%, 30%, 40%, 50%, 60%, 70% or 80%, 85%,

90%, or 95% diesel fuel from triglycerides, petroleum derived gasoline or diesel fuel from petroleum.

EXAMPLES

[0177] FIG. 1 is a diagram of the FAS pathway showing the enzymes directly involved in the synthesis of acyl-ACP. To increase the production of waxes/fatty acid esters, and fatty alcohols one or more of the enzymes can be over expressed or mutated to reduce feedback inhibition. Additionally, enzymes that metabolize the intermediates to make non-fatty acid based products (side reactions) can be functionally deleted or attenuated to increase the flux of carbon through the fatty acid biosynthetic pathway. Examples 1, 2, and 8 below provide exemplary production hosts that have been modified to increase fatty acid production.

[0178] FIGS. 2, 3 and 4 show biosynthetic pathways that can be engineered to make fatty alcohols and wax/fatty acid esters, respectively. As illustrated in FIG. 2 the conversion of each substrate (acetyl-CoA, malonyl-CoA, acyl-ACP, fatty acid, and acyl-CoA) to each product (acetyl-CoA, malonyl-CoA, acyl-ACP, fatty acid, and acyl-CoA) can be accomplished using several different polypeptides that are members of the enzyme classes indicated. The Examples below describe microorganisms that have been engineered or can be engineered to produce specific fatty alcohols and waxes/fatty acid esters and hydrocarbons.

Example 1

Production Host Construction

[0179] An exemplary production host is LS9001. LS9001 was produced by modifying C41(DE3) from Overexpress.com (Saint Beausine, France) to functionally deleting the *fadE* gene (acyl-CoA dehydrogenase).

[0180] Briefly, the *fadE* knock-out strain of *E. coli* was made using primers YafV_NotI and Ivry_OI to amplify about 830 by upstream of *fadE* and primers Lpcaf_ol and LpcaR_Bam to amplify about 960 by downstream of *fadE*. Overlap PCR was used to create a construct for in frame deletion of the complete *fadE* gene. The *fadE* deletion construct was cloned into the temperature sensitive plasmid pKOV3, which contained a *SacB* gene for counterselection, and a chromosomal deletion of *fadE* was made according to the method of Link et al., *J. Bact.* 179:6228-6237, 1997. The resulting strain was not capable of degrading fatty acids and fatty acyl-CoAs (this functional deletion is herein designated as Δ *fadE*).

[0181] Additional modifications that can be included in a production host include introducing a plasmid carrying the four genes which are responsible for acetyl-CoA carboxylase activity in *E. coli* (*accA*, *B*, *C*, and *D*, Accessions: NP_414727, NP_417721, NP_417722, NP_416819, EC 6.4.1.2). The *accABCD* genes were cloned in two steps as bicistronic operons into the *NcoI*/*HindIII* and *NdeI*/*AvrII* sites of pACYCDuct-1 (Novagen, Madison, Wis.) the resulting plasmid was termed pAS004.126.

[0182] Additional modifications that can be included in a production host include the following: over-expression of *aceEF* (encoding the E1p dehydrogase component and the E2p dihydrolipoamide acyltransferase component of the pyruvate and 2-oxoglutarate dehydrogenase complexes); and *fabH/fabD/fabG/acpP/fabF* (encoding FAS) from any organism known in the art to encode such proteins, including for example *E. coli*, *Nitrosomonas europaea* (ATCC 19718), *Bacillus subtilis*, *Saccharomyces cerevisiae*, *Streptomyces*

spp, *Ralstonia*, *Rhodococcus*, *Corynebacteria*, *Brevibacteria*, *Mycobacteria*, oleaginous yeast, and the like can be expressed in the production host. Similarly, production hosts can be engineered to express accABCD (encoding acetyl co-A carboxylase) from *Pisum sativum* instead of, or in addition to, the *E. coli* homologues. However, when the production host is also producing butanol it is less desirable to express the *Pisum sativum* homologue.

[0183] In some exemplary production hosts, genes can be knocked out or attenuated using the method of Link, et al., *J. Bacteriol.* 179:6228-6237, 1997. For example, genes that can be knocked out or attenuated include gpsA (encoding biosynthetic sn-glycerol 3-phosphate dehydrogenase, accession NP_418065, EC: 1.1.1.94); ldhA (encoding lactate dehydrogenase, accession NP_415898, EC: 1.1.1.28); pflb (encoding formate acetyltransferase 1, accessions: P09373, EC: 2.3.1.54); adhE (encoding alcohol dehydrogenase, accessions: CAA47743, EC: 1.1.1.1, 1.2.1.10); pta (encoding phosphotransacetylase, accessions: NP_416800, EC: 2.3.1.8); poxB (encoding pyruvate oxidase, accessions: NP_415392, EC: 1.2.2.2); ackA (encoding acetate kinase, accessions: NP_416799, EC: 2.7.2.1) and combinations thereof.

[0184] Similarly, the PlsB[D311E] mutation can be introduced into LS9001 to attenuate PlsB using the method described above for the fadE deletion. Once introduced, this mutation will decrease the amount of carbon being diverted to phospholipid production (see, FIG. 1). Briefly, an allele encoding PlsB[D311E] is made by replacing the GAC codon for aspartate 311 with a GAA codon for glutamate. The altered allele is made by gene synthesis and the chromosomal plsB wildtype allele is exchanged for the mutant plsB [D311E] allele using the method of Link et al. (see above).

Example 2

Production Host Modifications

[0185] The following plasmids were constructed for the expression of various proteins that are used in the synthesis of fatty acid derivatives. The constructs were made using standard molecular biology methods and all the cloned genes were put under the control of IPTG-inducible promoters (T7, tac or lac promoters).

[0186] The 'tesA gene (thioesterase A gene accession NP_415027 without leader sequence (Cho and Cronan, *J. Biol. Chem.*, 270:4216-9, 1995, EC: 3.1.1.5, 3.1.2.-) of *E. coli* was cloned into NdeI/AvrII digested pETDuet-1 (pETDuet-1 described herein is available from Novagen, Madison, Wis.). Genes encoding for FatB-type plant thioesterases (TEs) from *Umbellularia California*, *Cuphea hookeriana* and *Cinnamomum camphorum* (accessions: UcFatB1=AAA34215, ChFatB2=AAC49269, ChFatB3=AAC72881, CcFatB=AAC49151) were individually cloned into three different vectors: (i) NdeI/AvrII digested pETDuet-1, (ii) XhoI/HindIII digested pBluescript KS+ (Stratagene, La Jolla, Calif.) (used to create N-terminal lacZ::TE fusion proteins) and (iii) XbaI/HindIII digested pMAL-c2X (New England Lab, Ipswich, Mass.) (used to create n-terminal MalE::TE fusions). The fadD gene (encoding acyl-CoA synthetase) from *E. coli* was cloned into a NcoI/HindIII digested pCDFDuet-1 derivative, which contained the acrl gene (acyl-CoA reductase) from *Acinetobacter baylyi* ADP1 within its NdeI/AvrII sites. Table 7 provides a summary of the plasmids generated to make several exemplary production strains, one

of ordinary skill in the art will appreciate that different plasmids and genomic modifications can be used to achieve similar strains

TABLE 7

Summary of Plasmids used in Production hosts		
Plasmid	Source Organism Gene Product	Accession No., EC number
pETDuet-1-tesA	<i>E. coli</i> TesA	Accessions: NP_415027, EC: 3.1.1.5, 3.1.2.—
pETDuet-1-TEuc	<i>Umbellularia</i>	Q41635
pBluescript-TEuc	<i>California</i>	AAA34215
pMAL-c2X-TEuc	UcFatB1	
pETDuet-1-TEch	<i>Cuphea hookeriana</i>	ABB71581
pBluescript-TEch	ChFatB2	AAC49269
pMAL-c2X-TEch	ChFatB3	AAC72881
pETDuet-1-TEcc	<i>Cinnamomum</i>	AAC49151
pBluescript-TEcc	<i>camphorum</i>	
TEci	CcFatB	
pCDFDuet-1-fadD-acrl	<i>E. coli</i>	fadD: Accessions NP_416319, EC 6.2.1.3 acrl: Accessions YP_047869

[0187] The chosen expression plasmids contain compatible replicons and antibiotic resistance markers, so that a four-plasmid expression system can be established. Therefore, LS9001 can be co-transformed with (i) any of the TE-expressing plasmids, (ii) the FadD-expressing plasmid, which also expresses acrl and (iii) wax synthase expression plasmid. When induced with IPTG, the resulting strain will produce increased concentrations of fatty-alcohols from carbon sources such as glucose. The carbon chain length and degree of saturation of the fatty alcohol produced is dependent on the thioesterase gene that is expressed.

Example 3

Production of Fatty Alcohol in the Recombinant *E. coli* Strain

[0188] Fatty alcohols were produced by expressing a thioesterase gene and an acyl-CoA reductase gene (FAR) exogenously in a production host. More specifically, plasmids pCDFDuet-1-fadD-acrl (acyl-CoA reductase) and pETDuet-1-'tesA (thioesterase) were transformed into *E. coli* strain LS9001 (described in Example 1) and corresponding transformants were selected in LB plate supplemented with 100 mg/L of spectinomycin and 50 mg/L of carbenicillin. Four transformants of LS9001/pCDFDuet-1-fadD-acrl were independently inoculated into 3 mL of M9 medium supplemented with 50 mg/L of carbenicillin and 100 mg/L of spectinomycin. The samples containing the transformants were grown in at 25° C. in a shaker (250 rpm) until they reached 0.5 OD₆₀₀. 1.5 mL of each sample was transferred into a 250 mL flask containing 30 mL of the medium described above. The resulting culture was grown at 25° C. in a shaker until the culture reached between 0.5-1.0 OD₆₀₀. IPTG was then added to a final concentration of 1 mM, and growth continued for 40 hours.

[0189] The cells were then spun down at 4000 rpm and the cell pellets were suspended in 1.0 mL of methanol. 3 mL of ethyl acetate was then mixed with the suspended cells. 3 mL of H₂O were then added to the mixture and the mixture was sonicated for 20 minutes. The resulting sample was centrifuged at 4000 rpm for 5 minutes and the organic phase (the upper phase) which contained fatty alcohol and was subjected

to GC/MS analysis. Total alcohol (including tetradecanol, hexadecanol, hexadecenol and octadecenol) yield was about 1-10 mg/L. When an *E. coli* strain carrying only empty vectors was cultured in the same way, only 0.2-0.5 mg/L of fatty alcohols were found in the ethyl acetate extract.

Example 4

Production and Release of Fatty Alcohol from Production Host

[0190] *Acrl* (acyl-CoA reductase) was expressed in *E. coli* grown on glucose as the sole carbon and energy source. The *E. coli* produced small amounts of fatty alcohols such as dodecanol (C12:0-OH), tetradecanol (C14:0-OH) and hexadecanol (C16:0-OH). In other samples, *FadD* (acyl-CoA synthetase) was expressed together with *acrl* in *E. coli* and a five-fold increase in fatty alcohol production was observed.

[0191] In other samples, *acrl*, *fadD*, *accABCD* (acetyl-CoA Carboxylase) (plasmid carrying *accABCD* constructed as described in Example 1) were expressed along with various individual thioesterases (TEs) in wildtype *E. coli* C41(DE3) and an *E. coli* C41(DE3 Δ *fadE*), a strain lacking acyl-CoA dehydrogenase. This resulted in additional increases in fatty alcohol production and modulating the profiles of fatty alcohols (see FIG. 5). For example, over-expression of *E. coli* 'tesA (pETDuet-1-'tesA) in this system achieved approximately a 60-fold increase in C12:0-OH, C14:0-OH and C16:0-OH with C14:0-OH being the major fatty alcohol. A very similar result was obtained when the *ChFatB3* enzyme (FatB3 from *Cuphea hookeriana* in pMAL-c2X-TEcu) was expressed. When the *UcFatB1* enzyme (FatB1 from *Umbellularia californica* in pMAL-c2X-TEuc) was expressed, fatty alcohol production increased approximately 20-fold and C12:0-OH was the predominant fatty alcohol.

[0192] Expression of *ChFatB3* and *UcFatB1* also led to the production of significant amounts of the unsaturated fatty alcohols C16:1-OH and C14:1-OH, respectively. The presence of fatty alcohols was also found in the supernatant of samples generated from the expression of *tesA* (FIG. 6). At 37° C. approximately equal amounts of fatty alcohols were found in the supernatant and in the cell pellet, whereas at 25° C. approximately 25% of the fatty alcohols were found in the supernatant.

Example 5

Medium Chain Fatty Acid Esters

[0193] Alcohol acetyl transferases (AATs, EC 2.3.1.84), which is responsible for acyl acetate production in various plants, can be used to produce medium chain length waxes, such as octyl octanoate, decyl octanoate, decyl decanoate, and the like. Fatty esters, synthesized from medium chain alcohol (such as C6, C8) and medium chain acyl-CoA (or fatty acids, such as C6 or C8) have a relative low melting point. For example, hexyl hexanoate has a melting point of -55° C. and octyl octanoate has a melting point of -18 to -17° C. The low melting points of these compounds makes them good candidates for use as biofuels.

[0194] In this example, a SAAT gene was co-expressed in a production host C41(DE3, Δ *fadE*) with *fadD* from *E. coli* and *acrl* (alcohol reductase from *A. baylyi* ADP1) and octanoic acid was provided in the fermentation broth. This resulted in the production of octyl octanoate. Similarly, when the wax

synthase gene from *A. baylyi* ADP1 was expressed in the production host instead of the SAAT gene octyl octanoate was produced.

[0195] A recombinant SAAT gene was synthesized using DNA 2.0 (Menlo Park, Calif. 94025). The synthesized DNA was based on the published gene sequence (accession number AF193789) and modified to eliminate the *NcoI* site. The synthesized SAAT gene (as a *Bam*HI-*Hind*III fragment) was cloned in pRSET B (Invitrogen, Calsbad, Calif.), linearized with *Bam*HI and *Hind*III. The resulted plasmid, pHZ1.63A was cotransformed into an *E. coli* production host with pAS004.114B, which carries a *fadD* gene from *E. coli* and *acrl* gene from *A. baylyi* ADP1. The transformants were grown in 3 mL of M9 medium with 2% of glucose. After IPTG induction and the addition of 0.02% of octanoic acid, the culture was continued at 25° C. from 40 hours. After that, 3 mL of acetyl acetate was added to the whole culture and mixed several times with mixer. The acetyl acetate phase was analyzed by GC/MS.

[0196] Surprising, in the acetyl acetate extract, there is no acyl acetate found. However, a new compound was found and the compound was octyl octanoate. Whereas the control strain without the SAAT gene [C41(DE3, Δ *fadE*)/pRSET B+pAS004.114B] did not produce octyl octanoate. Also the strain [C41(DE3, Δ *fadE*)/pHZ1.43 B+pAS004.114B], in which the wax synthase gene from *A. baylyi* ADP1 was carried by pHZ1.43 produced octyl octanoate (see FIGS. 7B).

[0197] The finding that SAAT activity produces octyl octanoate has not reported before and makes it possible to produce medium chain waxes such as octyl octanoate, octyl decanoate, which have low melting point and are good candidates to be use for biofuel to replace triglyceride based biodiesel.

Example 6

Production of Wax Ester in *E. coli* Strain LS9001

[0198] Wax esters were produced by engineering an *E. coli* production host to express a fatty alcohol forming acyl-CoA reductase, thioesterase, and a wax synthase. Thus, the production host produced both the A and the B side of the ester and the structure of both sides was influenced by the expression of the thioesterase gene.

[0199] More specifically, wax synthase from *A. baylyi* ADP1 (termed WSadp1, accessions AA017391, EC: 2.3.175) was amplified with the following primers using genomic DNA from *A. baylyi* ADP1 as the template. The primers were (1) WSadp1_NdeI, 5'- TCATATGCGCCCATACATCCG -3' and (2) WSadp1_Avr, 5'- TCCTAGGAGGGCTAATT-TAGCCCTTTAGTT-3'. The PCR product was digested with *NdeI* and *AvrII* and cloned into pCOALDeut-1 to give pHZ 1.43. The plasmid carrying WSadp1 was then co-transformed into *E. coli* strain LS9001 with both pETDuet-1-'tesA and pCDFDuet-1-*fadD*-*acrl* and transformants were selected in LB plates supplemented with 50 mg/L of kanamycin, 50 mg/L of carbenicillin and 100 mg/L of spectinomycin. Three transformants were inoculated in 3 mL of LBKCS (LB broth supplement with 50 mg/L of kanamycin, 50 mg/L of carbenicillin, 100 mg/L of spectinomycin and 10 g/L of glucose) and cultured at 37° C. shaker (250 rpm). When the cultures reached 0.5 OD₆₀₀, 1.5 mL of each culture was transferred into 250 mL flasks containing 50 mL of LBKCS and the flasks were grown in a shaker (250 rpm) at 37° C. until the culture reached 0.5-1.0 OD₆₀₀. IPTG was then added to a final con-

centration of 1 mM. The induced cultures were grown at 37° C. shaker for another 40-48 hours.

[0200] The culture was then placed into 50 mL conical tubes and the cells were spun down at 3500 ×g for 10 minutes. The cell pellet was then mixed with 5 mL of ethyl acetate. The ethyl acetate extract was analyzed with GC/MS. The intracellular yield of waxes (including C16C16, C14:1C16, C18:1C18:1, C2C14, C2C16, C2C16:1, C16C16:1 and C2C18:1) was about 10 mg/L. When an *E. coli* strain only carrying empty vectors was cultured in the same way, only 0.2 mg/L of wax was found in the ethyl acetate extract.

Example 7

Production and Release of Fatty-Ethyl Ester from Production Host

[0201] The LS9001 strain was modified by transforming it with the plasmids carrying a wax synthase gene from *A. baylyi* (plasmid pHZ1.43), a thioesterase gene from *Cuphea hookeriana* (plasmid pMAL-c2X-TEcu) and a fadD gene from *E. coli* (plasmid pCDFDuet-1-fadD). This recombinant strain was grown at 25° C. in 3 mL of M9 medium with 50 mg/L of kanamycin, 100 mg/L of carbenicillin and 100 mg/L of spectinomycin. After IPTG induction, the media was adjusted to a final concentration of 1% ethanol and 2% glucose. The culture was allowed to grow for 40 hours after IPTG

Example 8

The Influence of Various Thioesterases on the Composition of Fatty-Ethyl Esters Produced in Recombinant *E. coli* Strains

[0202] The thioesterases FatB3 (*C. hookeriana*), TesA (*E. coli*), and FatB (*U. californica*) were expressed simultaneously with wax synthase (*A. baylyi*). A plasmid termed pHZ1.61 was constructed by replacing the NotI/AvrII fragment (carrying the acrl gene) with the NotI-AvrII fragment from pHZ1.43 so that fadD and the ADP1 wax synthase were in one plasmid and both coding sequences were under the control of separate T7 promoter. The construction of pHZ1.61 made it possible to use a two plasmid system instead of the three plasmid system as described in Example 6. pHZ1.61 was then co-transformed into *E. coli* C41(DE3, ΔfadE) with one of the various plasmids carrying the different thioesterase genes stated above.

[0203] The total fatty acid ethyl esters (supernatant and intracellular fatty acid ethyl esters) produced by these transformants were evaluated using the technique described herein. The yields and the composition of fatty acid ethyl esters are summarized in Table 8.

TABLE 8

The yields (mg/L) and the composition of fatty acid ethyl esters by recombinant <i>E. coli</i> C41(DE3, ΔfadE)/pHZ1.61 and plasmids carrying various thioesterase genes.								
Thioesterases	C2C10	C2C12:1	C2C12	C2C14:1	C2C14	C2C16:1	C2C16	C2C18:1
TesA	0.0	0.0	6.5	0.0	17.5	6.9	21.6	18.1
ChFatB3	0.0	0.0	0.0	0.0	10.8	12.5	11.7	13.8
ucFatB	6.4	8.5	25.3	14.7	0.0	4.5	3.7	6.7
pMAL	0.0	0.0	0.0	0.0	5.6	0.0	12.8	7.6

Note:

TesA, pETDuet-1-tesA; chFatB3, pMAL-c2X-TEcu; ucFatB, pMAL-c2X-TEuc; pMAL, pMAL-c2X, the empty vector for thioesterase genes used in the study.

induction. The cells were separated from the spent medium by centrifugation at 3500 ×g for 10 minutes). The cell pellet was re-suspended with 3 mL of M9 medium. The cell suspension and the spent medium were then extracted with 1 volume of ethyl acetate. The resulting ethyl acetate phases from the cells suspension and the supernatant were subjected to GC-MS analysis. The results showed that the C16 ethyl ester was the most prominent ester species (as expected for this thioesterase, see Table 1), and that 20% of the fatty acid ester produced was released from the cell (see FIG. 8). A control *E. coli* strain C41(DE3, ΔfadE) containing pCOLA-Duet-1 (empty vector for the wax synthase gene), pMAL-c2X-TEuc (containing fatB from *U. californica*) and pCDFDuet-1-fadD (fadD gene from *E. coli*) failed to produce detectable amounts of fatty ethyl esters. The fatty acid esters were quantified using commercial palmitic acid ethyl ester as the reference. Fatty acid esters were also made using the methods described herein except that methanol, or isopropanol was added to the fermentation broth and the expected fatty acid esters were produced.

Example 9

Production Host Construction

[0204] The genes that control fatty acid production are conserved between microorganisms. For example, Table 9 identifies the homologues of many of the genes described herein which are known to be expressed in microorganisms that produce hydrocarbons. To increase fatty acid production and, therefore, hydrocarbon production in microorganisms such as those identified in Table 9, heterologous genes, such as those from *E. coli* can be expressed. One of ordinary skill in the art will also appreciate that genes that are endogenous to the microorganisms provided in Table 9 can also be over-expressed, or attenuated using the methods described herein. Moreover, genes that are described in FIG. 10 can be expressed or attenuated in microorganisms that endogenously produce hydrocarbons to allow for the production of specific hydrocarbons with defined carbon chain length, saturation points, and branch points.

[0205] For example, exogenous nucleic acid sequences encoding acetyl-CoA carboxylase are introduced into *K. radiotolerans*. The following genes comprise the acetyl-CoA

carboxylase protein product in *K. radiotolerans*; acetyl CoA carboxylase, alpha subunit (accA/ZP_00618306), acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB/ZP_00618387), acetyl-CoA carboxylase, biotin carboxylase subunit (accC/ZP_00618040), and acetyl-CoA carboxylase, beta (carboxyltransferase) subunit (accD/ZP_00618306). These genes are cloned into a plasmid such that they make a synthetic acetyl-CoA carboxylase operon (accABCD) under

the control of a *K. radiotolerans* expression system such as the expression system disclosed in Ruyter et al., *Appl Environ Microbiol.* 62:3662-3667, 1996. Transformation of the plasmid into *K. radiotolerans* will enhance fatty acid production. The hydrocarbon producing strain of *K. radiotolerans* can also be engineered to make branched, unsaturated hydrocarbons having specific carbon chain lengths using the methods disclosed herein.

TABLE 9

Hydrocarbon Production Hosts			
Organism	Gene Name	Accession No./Seq ID/Loci	EC No.
<i>Desulfovibrio desulfuricans</i> G20	accA	YP_388034	6.4.1.2
<i>Desulfovibrio desulfuricans</i> G22	accC	YP_388573/YP_388033	6.3.4.14, 6.4.1.2
<i>Desulfovibrio desulfuricans</i> G23	accD	YP_388034	6.4.1.2
<i>Desulfovibrio desulfuricans</i> G28	fabH	YP_388920	2.3.1.180
<i>Desulfovibrio desulfuricans</i> G29	fabD	YP_388786	2.3.1.39
<i>Desulfovibrio desulfuricans</i> G30	fabG	YP_388921	1.1.1.100
<i>Desulfovibrio desulfuricans</i> G31	acpP	YP_388922/YP_389150	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Desulfovibrio desulfuricans</i> G32	fabF	YP_388923	2.3.1.179
<i>Desulfovibrio desulfuricans</i> G33	gpsA	YP_389667	1.1.1.94
<i>Desulfovibrio desulfuricans</i> G34	ldhA	YP_388173/YP_390177	1.1.1.27, 1.1.1.28
<i>Erwinia (micrococcus) amylovora</i>	accA	942060-943016	6.4.1.2
<i>Erwinia (micrococcus) amylovora</i>	accB	3440869-3441336	6.4.1.2
<i>Erwinia (micrococcus) amylovora</i>	accC	3441351-3442697	6.3.4.14, 6.4.1.2
<i>Erwinia (micrococcus) amylovora</i>	accD	2517571-2516696	6.4.1.2
<i>Erwinia (micrococcus) amylovora</i>	fadE	1003232-1000791	1.3.99.—
<i>Erwinia (micrococcus) amylovora</i>	plsB(D311E)	333843-331423	2.3.1.15
<i>Erwinia (micrococcus) amylovora</i>	aceE	840558-843218	1.2.4.1
<i>Erwinia (micrococcus) amylovora</i>	aceF	843248-844828	2.3.1.12
<i>Erwinia (micrococcus) amylovora</i>	fabH	1579839-1580789	2.3.1.180
<i>Erwinia (micrococcus) amylovora</i>	fabD	1580826-1581749	2.3.1.39
<i>Erwinia (micrococcus) amylovora</i>	fabG	CAA74944	1.1.1.100
<i>Erwinia (micrococcus) amylovora</i>	acpP	1582658-1582891	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Erwinia (micrococcus) amylovora</i>	fabF	1582983-1584221	2.3.1.179
<i>Erwinia (micrococcus) amylovora</i>	gpsA	124800-125810	1.1.1.94
<i>Erwinia (micrococcus) amylovora</i>	ldhA	1956806-1957789	1.1.1.27, 1.1.1.28
<i>Kineococcus radiotolerans</i> SRS30216	accA	ZP_00618306	6.4.1.2
<i>Kineococcus radiotolerans</i> SRS30216	accB	ZP_00618387	6.4.1.2
<i>Kineococcus radiotolerans</i> SRS30216	accC	ZP_00618040/ ZP_00618387	6.3.4.14, 6.4.1.2
<i>Kineococcus radiotolerans</i> SRS30216	accD	ZP_00618306	6.4.1.2

TABLE 9-continued

Hydrocarbon Production Hosts			
Organism	Gene Name	Accession No./Seq ID/Loci	EC No.
<i>Kineococcus radiotolerans</i> SRS30216	fadE	ZP_00617773	1.3.99.—
<i>Kineococcus radiotolerans</i> SRS30216	plsB(D311E)	ZP_00617279	2.3.1.15
<i>Kineococcus radiotolerans</i> SRS30216	aceE	ZP_00617600	1.2.4.1
<i>Kineococcus radiotolerans</i> SRS30216	aceF	ZP_00619307	2.3.1.12
<i>Kineococcus radiotolerans</i> SRS30216	fabH	ZP_00618003	2.3.1.180
<i>Kineococcus radiotolerans</i> SRS30216	fabD	ZP_00617602	2.3.1.39
<i>Kineococcus radiotolerans</i> SRS30216	fabG	ZP_00615651	1.1.1.100
<i>Kineococcus radiotolerans</i> SRS30216	acpP	ZP_00617604	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Kineococcus radiotolerans</i> SRS30216	fabF	ZP_00617605	2.3.1.179
<i>Kineococcus radiotolerans</i> SRS30216	gpsA	ZP_00618825	1.1.1.94
<i>Kineococcus radiotolerans</i> SRS30216	ldhA	ZP_00618879	1.1.1.27, 1.1.1.28
<i>Rhodospirillum rubrum</i>	accA	YP_425310	6.4.1.2
<i>Rhodospirillum rubrum</i>	accB	YP_427521	6.4.1.2
<i>Rhodospirillum rubrum</i>	accC	YP_427522/YP_425144/ YP_427028/ YP_426209/YP_427404	6.3.4.14, 6.4.1.2
<i>Rhodospirillum rubrum</i>	accD	YP_428511	6.4.1.2
<i>Rhodospirillum rubrum</i>	fadE	YP_427035	1.3.99.—
<i>Rhodospirillum rubrum</i>	aceE	YP_427492	1.2.4.1
<i>Rhodospirillum rubrum</i>	aceF	YP_426966	2.3.1.12
<i>Rhodospirillum rubrum</i>	fabH	YP_426754	2.3.1.180
<i>Rhodospirillum rubrum</i>	fabD	YP_425507	2.3.1.39
<i>Rhodospirillum rubrum</i>	fabG	YP_425508/YP_425365	1.1.1.100
<i>Rhodospirillum rubrum</i>	acpP	YP_425509	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Rhodospirillum rubrum</i>	fabF	YP_425510/YP_425510/ YP_425285	2.3.1.179
<i>Rhodospirillum rubrum</i>	gpsA	YP_428652	1.1.1.94
<i>Rhodospirillum rubrum</i>	ldhA	YP_426902/YP_428871	1.1.1.27, 1.1.1.28
<i>Vibrio furnissii</i>	accA	1, 16	6.4.1.2
<i>Vibrio furnissii</i>	accB	2, 17	6.4.1.2
<i>Vibrio furnissii</i>	accC	3, 18	6.3.4.14, 6.4.1.2
<i>Vibrio furnissii</i>	accD	4, 19	6.4.1.2
<i>Vibrio furnissii</i>	fadE	5, 20	1.3.99.—
<i>Vibrio furnissii</i>	plsB(D311E)	6, 21	2.3.1.15
<i>Vibrio furnissii</i>	aceE	7, 22	1.2.4.1
<i>Vibrio furnissii</i>	aceF	8, 23	2.3.1.12
<i>Vibrio furnissii</i>	fabH	9, 24	2.3.1.180
<i>Vibrio furnissii</i>	fabD	10, 25	2.3.1.39
<i>Vibrio furnissii</i>	fabG	11, 26	1.1.1.100
<i>Vibrio furnissii</i>	acpP	12, 27	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Vibrio furnissii</i>	fabF	13, 28	2.3.1.179
<i>Vibrio furnissii</i>	gpsA	14, 29	1.1.1.94
<i>Vibrio furnissii</i>	ldhA	15, 30	1.1.1.27, 1.1.1.28
<i>Stenotrophomonas maltophilia</i> R551-3	accA	ZP_01643799	6.4.1.2
<i>Stenotrophomonas maltophilia</i> R551-3	accB	ZP_01644036	6.4.1.2
<i>Stenotrophomonas maltophilia</i> R551-3	accC	ZP_01644037	6.3.4.14, 6.4.1.2
<i>Stenotrophomonas maltophilia</i> R551-3	accD	ZP_01644801	6.4.1.2

TABLE 9-continued

Hydrocarbon Production Hosts			
Organism	Gene Name	Accession No./Seq ID/Loci	EC No.
<i>Stenotrophomonas maltophilia</i> R551-3	fadE	ZP_01645823	1.3.99.—
<i>Stenotrophomonas maltophilia</i> R551-3	plsB(D311E)	ZP_01644152	2.3.1.15
<i>Stenotrophomonas maltophilia</i> R551-3	aceE	ZP_01644724	1.2.4.1
<i>Stenotrophomonas maltophilia</i> R551-3	aceF	ZP_01645795	2.3.1.12
<i>Stenotrophomonas maltophilia</i> R551-3	fabH	ZP_01643247	2.3.1.180
<i>Stenotrophomonas maltophilia</i> R551-3	fabD	ZP_01643535	2.3.1.39
<i>Stenotrophomonas maltophilia</i> R551-3	fabG	ZP_01643062	1.1.1.100
<i>Stenotrophomonas maltophilia</i> R551-3	acpP	ZP_01643063	3.1.26.3, 1.6.5.3, 1.6.99.3
<i>Stenotrophomonas maltophilia</i> R551-3	fabF	ZP_01643064	2.3.1.179
<i>Stenotrophomonas maltophilia</i> R551-3	gpsA	ZP_01643216	1.1.1.94
<i>Stenotrophomonas maltophilia</i> R551-3	ldhA	ZP_01645395	1.1.1.27, 1.1.1.28

For Table 9, Accession Numbers are from GenBank, Release 159.0 as of Apr. 15, 2007, EC Numbers are from KEGG, Release 42.0 as of April 2007 (plus daily updates up to and including May 09, 2007), results for *Erwinia amylovora* strain Ea273 are taken from the Sanger sequencing center, completed shotgun sequence as of May 9, 2007, positions for *Erwinia* represent locations on the Sanger psuedo-chromosome, sequences from *Vibrio furnisii* M1 are from the LS9 VFM1 pseudochromosome, v2 build, as of Sep. 28, 2006, and include the entire gene, and may also include flanking sequence.

Example 10

Additional Exemplary Production strains

[0206] Table 10, below provides additional exemplary production strains. Two example biosynthetic pathways are described for producing fatty acids, fatty alcohols, and wax esters. A genetically engineered host can be produced by cloning the expression of the accABCD genes from *E. coli*, the 'tesA gene from *E. coli*, and fadD gene from *E. coli* into a host cell. Host cells can be selected from *E. coli*, yeast, add to the list. These genes can also be transformed into a host cell that is modified to contain one or more of the genetic manipulations described in Examples 1 and 2, above.

Example 11

Fermentation

[0207] Host microorganisms can be also engineered to express umuC and umuD from *E. coli* in pBAD24 under the prpBCDE promoter system through de novo synthesis of this gene with the appropriate end-product production genes. For small scale hydrocarbon product production, *E. coli* BL21 (DE3) cells harbouring pBAD24 (with ampicillin resistance and the end-product synthesis pathway) as well as pUMVC1 (with kanamycin resistance and the acetyl CoA/malonyl CoA over-expression system) are incubated overnight at at 37° C. shaken at >200 rpm 2 L flasks in 500 ml LB medium supplemented with 75 µg/mL ampicillin and 50 µg/ml kanamycin until cultures reached an OD₆₀₀ of >0.8. Upon achieving an OD₆₀₀ of >0.8, cells are supplemented with 25 mM sodium propionate (pH 8.0) to activate the engineered gene systems for production as well as to stop cellular proliferation (through activation of umuC and umuD proteins). Induction

is performed for 6 hours at 30° C. After incubation, media is examined for product using GC- MS (as described below).

[0208] For large scale product production, the engineered microorganisms are grown in 10 L, 100 L or larger batches, fermented and induced to express desired products based on the specific genes encoded in plasmids as appropriate. *E. coli* BL21(DE3) cells harbouring pBAD24 (with ampicillin resistance and the end-product synthesis pathway) as well as pUMVC1 (with kanamycin resistance and the acetyl-CoA/malonyl-CoA over-expression system) are incubated from a 500 mL seed culture for 10 L fermentations (5 L for 100 L fermentations) in LB media (glycerol free) at 37° C. shaken at >200 rpm until cultures reached an OD₆₀₀ of >0.8 (typically 16 hours) incubated with 50 µg/mL kanamycin and 75 µg/mL ampicillin. Media is treated with continuously supplemented to maintain a 25 mM sodium propionate (pH 8.0) to activate the engineered in gene systems for production as well as to stop cellular proliferation (through activation of umuC and umuD proteins). Media is continuously supplemented with glucose to maintain a concentration 90 g/100 mL. After the first hour of induction, aliquots of no more than 10% of the total cell volume are removed each hour and allowed to sit unaggitated so as to allow the hydrocarbon product to rise to the surface and undergo a spontaneous phase separation. The hydrocarbon component is then collected and the aqueous phase returned to the reaction chamber. The reaction chamber is operated continuously. When the OD.sub.600 drops below 0.6, the cells are replaced with a new batch grown from a seed culture.

[0209] For wax ester production, subsequent to isolation, the wax esters are washed briefly in 1 M HCl to split the ester bond, and returned to pH 7 with extensive washing with distilled water.

Example 12

Product Characterization

[0210] To characterize and quantify the fatty alcohols and fatty acid esters, gas chromatography (GC) coupled with electron impact mass spectra (MS) detection was used. Fatty alcohol samples were first derivatized with an excess of N-trimethylsilyl (TMS) imidazole to increase detection sensitivity. Fatty acid esters did not required derivatization. Both fatty alcohol-TMS derivatives and fatty acid esters were dissolved in an appropriate volatile solvent, like ethyl acetate. The samples were analyzed on a 30 m DP-5 capillary column using the following method. After a 14 splitless injection onto the GC/MS column, the oven is held at 100° C. for 3 minutes. The temperature was ramped up to 320° C. at a rate of 20° C./minute. The oven was held at 320° C. for an additional 5 minutes. The flow rate of the carrier gas helium was 1.3 mL/minute. The MS quadrupole scans from 50 to 550 m/z. Retention times and fragmentation patterns of product peaks were compared with authentic references to confirm peak identity.

[0211] For example, hexadeconic acid ethyl ester eluted at 10.18 minutes (FIGS. 9A and 9B). The parent ion of 284 mass units was readily observed. More abundant were the daughter

ions produced during mass fragmentation. This included the most prevalent daughter ion of 80 mass units. The derivatized fatty alcohol hexadecanol-TMS eluted at 10.29 minutes and the parent ion of 313 could be observed. The most prevalent ion was the M-14 ion of 299 mass units.

[0212] Quantification was carried out by injecting various concentrations of the appropriate authentic references using the GC/MS method described above. This information was used to generate a standard curve with response (total integrated ion count) versus concentration.

Equivalents

[0213] While specific examples of the subject inventions are explicitly disclosed herein, the above specification and examples herein are illustrative and not restrictive. Many variations of the inventions will become apparent to those skilled in the art upon review of this specification including the examples. The full scope of the inventions should be determined by reference to the examples, along with their full scope of equivalents, and the specification, along with such variations.

SEQUENCE LISTING

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<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 1

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gggcatggca agtggcacag atggctcgcc atccacaacg tccttacacc ttagattaca    240
tcaacaacat gtttacggag ttogatgaac tagccgggtga ccgtgcattt gctgacgaca    300
aagcgatcgt gggcgggcatg gcccgccttag atggtcgccc tgtgatgggtg attggtcatc    360
agaaaggccg tgaaaccctg gaaaaagtaa aacgtaactt tgggatgcca aagccagaag    420
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<210> SEQ ID NO 2

<211> LENGTH: 564

<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 2

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gcagctcaat tgagctgtct tattcacaag ataaaagaga aagaaacaat ggatattcgt    120
aaaatcaaga agcttatcga attgggtgaa gagtcaggca ttgctgagct agaaatttct    180
gaaggtgaag aatcggtacg catcagtcgt cacggtgtcg cccagttgc acctatccag    240
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tatgcagcac ctgcaccaat ggcagcgcca gtagcagcac ctgcagcagc gccagtcgct	300
gaagcaccag cagcagccaa aacgcctgcg ggccacatgg ttctttctcc aatggtgggt	360
acgttctacc gttcaccaag tccagatgca aaatcattca tcgaagtggg tcaaactgtg	420
aaagcgggtg acacattgtg catcgttgaa gcgatgaaaa tgatgaacca aatcgaagca	480
gacaagtctg gtgtagtgac cgagatcctt gttgaagacg gtcaggccgt agaattcgac	540
cagccacttg ttgtcatcga ataa	564

<210> SEQ ID NO 3
 <211> LENGTH: 1344
 <212> TYPE: DNA
 <213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 3

atgctagata agttagtcat cgcgaaaccga ggcgaaattg cgcttcgtat tcttcgtgca	60
tgtaaagagt tgggcatcaa aactggtgcc gttcactcca cagcagaccg cgatctaaaa	120
cacgtcctgc tggcggatga aaccgtatgt atcggccctg caaaaggcat cgatagctac	180
ttgaacattc cacgcatcat ttcagccgct gaagtgaccg gcgcagtggc catccaccgc	240
ggttacggct tcctgtctga aaatgcggaac tttgctgaac aagttgagcg cagcggcttt	300
atcttcgtgg gtccaaaagc cgacaccatc cgctgatgg gcgataaagt gtcagccatc	360
accgcgatga agaaagcagg cgttccttgt gtaccgggtt ctgacgggtc tctggacaac	420
gatgaagtga aaaaccgtgc acacgcgaaa cgcatgtggt acccagtgat catcaaagcc	480
tctggtggcg gcggcggtcg cggatatgct gtggttcgca gcgaagcggg actgggtcaat	540
gccatcagca tgaccctgac agaagcgaaa gcggcggttc acaacgacat ggtttacatg	600
gagaaatacc tcgaaaaccc acgtcacgtt gaagtccaag ttctggccga tggtcagggc	660
agcgcgatcc acttgggtga acgcgactgt tccatgcagc gtcgtcacca gaaagtagtg	720
gaagaagcgc cagcaccagg cattactgaa gagatgcgta agtacatcgg tgaacgctgt	780
accctgctgt gtatcgaaat cggttaccgc ggccgaggta cgtttgagtt cctgtacgaa	840
aacggcgaat tctacttcat cgaaatgaac acacgtattc aggttgaaca cccagtgact	900
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ctgtcgttca cacaagacga catcaaaatt cgtggccatg cgatggaatg ccgtatcaac	1020
gcggaagacc cagaacgctt cctaccttgc ccaggcaaga tcaccgcttt ccaactacca	1080
ggtggcatgg gcgtgcgttg ggaatcacac atctactcag gctacaccgt accggcgtag	1140
tacgactcga tgatcggaac actgatcacc tttggtgaga accgtgacgt cgcgattgca	1200
cggatgcgta acgcgctcga tgagatgatt gtggaaggta tcaaaaccaa cattccactg	1260
cagcaagtaa tcatgaaaga tgagaacttc caacacgggtg gcaccaacat ccactatctg	1320
gagaaaaagc tggggctgca ataa	1344

<210> SEQ ID NO 4
 <211> LENGTH: 927
 <212> TYPE: DNA
 <213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 4

atgagctggc ttgagaagat tttagaaaaa agcaacatcg gaagttcacg taaagcgtct	60
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atccctgaag	gggtttggac	caaatgtaca	tcgtgtgaac	aggtgcttta	ttacgctgaa	120
ctagagcgca	atcttgaagt	ttgtccgaag	tgtaatcatc	acatgcgtat	gaaggcgcg	180
cgtcgtcttg	aaacgttctt	ggacgaagca	aaccgttacg	aaatcgcgga	cgaactcgaa	240
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cagaagagca	gtggcgaaaa	agatgcgctg	atttgtgatga	aaggcgagtt	gatgacgatt	360
ccagtcgtgg	cgtgtgcgtt	tgaattctcg	ttcatggg	gttcaatggg	gtcggttgtc	420
ggtgcgcgtt	tcgtgcgtgc	agttgaagcg	gcgattgaag	cgaactgtgg	tctggtctgt	480
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atgatcggtg	accgtcgtga	aatgcgtcag	cgtgtggctg	gcctgctggc	gaaaatgaca	840
cgtcaggagt	cgccgctggt	ggtttctgtg	aacgatgcgc	caaatgaagc	cgcatattct	900
gtaccagaag	cgaacaaaaa	agggtaa				927

<210> SEQ ID NO 5

<211> LENGTH: 2445

<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 5

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tttgggccag	tgggtatcat	cagctggg	ctgtacttag	ccgctatcgc	ggtattggca	180
gtcccgtcaa	tccgtcaaag	tctcatcagc	ggtaagacac	taaaggattt	caaaaaagta	240
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gccgaactgt	tcaaaggcaa	accggactgg	caacagctga	gccatatcaa	agcgcccaca	360
ctttctgccc	aagaacaggc	gttcctcgat	ggcccagtga	acgaagtgtg	cgccatgggtg	420
aacgactatc	aggtgactca	cgaattggcg	gatttgcctc	cggaagtgtg	gcaataacctg	480
aaagaccaca	aatttttcgc	catgatcatt	aagaagcagt	acggcggcct	ggaattttcc	540
gcgtacgcgc	aatcgctggt	gctacaaaag	ctgacggg	tatcggg	gctctcttcc	600
accgtcggcg	tgccgaactc	tctcgggccc	ggcgaactgc	tgcaacatta	cggcaccgac	660
gatcagaaag	attactacct	ccctcgtttg	gcggaaggca	aagagattcc	atgtttcgcg	720
ctgaccagcc	cagaagcggg	ctctgatg	ggctcgatc	cggattacgg	catcgtgtgc	780
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gggctatttg	gcgacaaaaa	agagattggc	atcacgtgtg	ctttgatccc	gacacacctc	960
aaaggggtgg	aaatcggcaa	tcgtcacttc	ccattgaacg	tgccgttcca	aaatggcccc	1020
acgcgcgcga	acgatctatt	tgtgccgctg	gacttcatca	tcgggtggccc	atcgatggcc	1080
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tcgaactcaa	ctggcggcat	caaagcggcg	gcaatggcaa	cgggcgctta	tgcgcgcatt	1200
cgtcgtcagt	tcaagcaacc	cattggtcac	atggaaggga	ttgaagaacc	tttggcgcgc	1260
cttgcaggga	acgcttacgt	gatggatgca	gcgagcaacc	tactgtcgc	ggggattgat	1320
gccggcgaaa	aaccatcggg	tatttctgcg	attgtgaagt	atcactgtac	ccaccgcggc	1380
caacgctcaa	tcacgatgc	aatggacatc	gtcggcggca	aaggcatctg	tttgggcccc	1440
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aacattctga	cccgtccat	gatcatcttt	ggtcaggggtg	ctattcgctg	ccatccgtac	1560
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gccgcgctgg	ctggccatgt	cagctttacc	atgagtaact	tggtgcgctg	catctggttt	1680
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actgcacata	acgcggtcgg	caagattgaa	ctggcggtga	atgtgattct	tcaagcagaa	2220
ccggtgttcg	acaaggtatg	caaagcgtg	aacgaacgtc	gccattcac	gcaattggat	2280
caagtggcac	aatgtggcct	tgagcaaaaag	ctgatcaccg	agcaagaagc	cgaactgctg	2340
atcgaagccg	agcaacaccg	cttatacacc	atcaatgtgg	atgactttgc	gccgcaggag	2400
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<210> SEQ ID NO 6

<211> LENGTH: 2424

<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 6

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aaaggtagcg	tcattccatc	caatccgatc	gatgatctcg	agattgatat	taacaagccg	120
atcgtctatg	cactaccctt	tcgctccaat	gtcgacctgt	tgacgctgca	aacgcctgcg	180
ttacaagccg	gcctgccgga	tccgttagaa	ccgtgacca	ttcatagtca	cacgctgaaa	240
cgttacgtgt	tcctctcgtc	gcgccccacg	ctgctgcaag	atgacaatca	ggtgccgacc	300
gattctatcg	ccacattcag	cgaaatgctc	agcctgcac	aagaagattc	ggagttggat	360
gtgcagggtca	ttcctgccac	cgtcctgtgg	ggacgcaaac	cgggcaaaga	aggtcgggaa	420
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ggcaccgatg	cctcgattgc	ccacaagctg	gcacgtgtgg	cgcgcattca	cttctcacgt	600
cagaagctgg	cggcgtctgg	gccgaacctg	ccacaacgcc	accagttggt	ccaacgcttg	660
atgaattccc	cagcgatcga	aaaagcgatt	gctgatgaag	cggccgcgaa	gaacatctcg	720

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ggcttgaaca tcaataacgc cgcgacgggt cgcgcttggt cacaagatgg tcacgagatt	900
gtgtatgtgc cctgtcacgc cagccacatg gattacctgt tgctgtcata cgtgttgat	960
cacgaaggca tgggtgcccc gcacattgca gcaggattta acctcaactt cttcccggcc	1020
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gagcaagtgc ccgagtggac acaagacatc gatgccatgg gcgccagcaa accccagtgg	1500
atgacaccgg tgggtgaacaa gctcgcgacg aagatgatga cgcacattaa cgatgcagcg	1560
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aatcagtcga ttctgatgac ctactaccgc aacaacatca ttcacctgct ggcggtgcca	1860
tcactgattg cgcagatgct gatccgtcag caacaaatgc cgggtggaaca gattcagacc	1920
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caactcgatg aggtggtgat gcattatctc gctgagctgc aacgccaaac actggtgacg	2040
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cgcaccatct ctgagacgct gcaacgctac gcgatcacgc tcaacctgtt ggtggctaac	2160
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gtcacgctca aacagcaagg ttacctgac agcgatggca actgccacct cgaccagacc	2340
aagcacttct cgcgcatgct ctacaccatg ctttaccctg aagtgcgcct gactattcag	2400
gaaagtatct gtcaggtgga ataa	2424

<210> SEQ ID NO 7

<211> LENGTH: 2661

<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 7

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gaaaaagcac gtctagacgg cgttgatatg ccaactggta ttacaactaa ctacatcaac	180
acgattcctg cggcgcaaga accggcatac ccaggcgaca cgaccattga acgtcgtatt	240
cgttcgatca ttcggttgaa cgcgatcatg atcgttctgc gtgcatcgaa gaaagacctg	300

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gatctgggcg gccacatggc atcattccag tcttcagctg cgttctatga aacatgtttc	360
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catatttctc cagggattta cgcgcgtgca ttcgttgaag gccgcctgac agaagaacaa	480
ctggataact tccgtcaaga agtggatggc aaaggatttc cttcctaccc acacccgaaa	540
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cagcgcgttt acgcgttctt gggcgacggg gagatggatg agccagaatc acgtgggtgcc	720
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ccagagacag cagcgtctgt tgcgtgacatg actgacgacg aagtgttcgc cctgaaacgt	1080
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cgtccaaccg ttatcctcgc gaagactgta aaaggttacg gcatgggtga tgcggctcaa	1200
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cgtgcactga acattctgtt gaaagacaaa aatattggta agaacatcgt tcctatcatt	1560
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gccgaagcgc aagtacctta catcgcttca gtgatgggaa ctgaaccagc aatcgctgca	2400
accgactaca tgaagaacta cgctgaccaa gtgcgcgctg tcattcctgc agagtcttac	2460
aaagtgcctg gtactgacgg ctteggctcg tcagacagcc gtgagaacct acgtcgtcac	2520
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actaaccgcg tatacgctta a 2661

<210> SEQ ID NO 8
<211> LENGTH: 1893
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 8

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aaagcttcta tggaagttcc tgcgtctcag gccggtattg tcaaagaaat caaagttgtg 180
actggtgata aagtcacaac tggctcactg atcatggtgt ttgaagcgga aggtgcagca 240
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gcgccagcag cggcagcgcc agctcaggca gcggctccag cagcagcgcc agcggtagca 600
gcagataaag aagttaacgt gccagatata ggcggcgatg aagttgaagt gactgaaatc 660
atggttgacg ttggcgacat ggtgagcgaa gagcaatctc tgatcactgt ggaaggcgac 720
aaagcgtcga tggaagttcc tgcaccattc gcgggtaaag tgaaagcgat caaagtcgcg 780
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ccggcagctg tttcagcacc agctcaagcc gcagcacctg cagcagcggc accgaaagct 900
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tctgacatgc aaggcggctg tttcaccatc tctagtctgg gtggtatcgg cggtagacga 1680
ttcacaccaa tcgtgaatgc accagaagta ggtattctgg gtgtgtctaa gtctgaaatg 1740
aagccagtgt ggaacggcaa agaatttgcg ccacgtctgc aactgcctct gtctctgtca 1800
tacgaccacc gtgtgatcga tggcgcgga ggtgcacgct tcatcactta cttgaacggg 1860
tgctgagcg acattcgtcg tctggttctg taa 1893

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<210> SEQ ID NO 9
<211> LENGTH: 951
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 9

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atgtatagca aaatttttagg tacaggcagc tacctgccat ctcagggtgcg tactaacgcg      60
gatttagaga aaatggtaga tacaagtgat gagggtgattg tcacgcgtac tgggtattcgc     120
gagcgtcgta ttgccgcaga taatgaaacc gttgccgata tgggctttta cgccggcgcaa     180
aacgctattg agatggcggg cattgataaa aacgacatcg atttaatcat ccttgccacg     240
accagtagca gtcacacggt cccttcgtct gcctgtcagg tgcaagcgaa actgggcatt     300
aaagggttgc cagcgtttga ccttgccgca gcgtgttctg gttttatcta cggattgtca     360
gtcgcggatc aacacatcaa atcgggcatg tgtaaaaacg tgctgggtgat tggtgccgat     420
gcgttgtcaa aaacgtgtga cccaaccgat cgctcaacca ttatcctgtt tggatgatgg      480
gcgggtgcgg ttgtggttgg tgccagtga gaacctggca ttttgctgac tcatgtttac     540
gctgatggtc aattcggcga cctgctcagc ctggaagtac cagagcgtgg cggatgatgtg     600
gacaaatggc tatatatggc cggcaacgaa gtgttcaaag tggcgggtgac gcagctttca     660
aaactggtca aagacacgct ggcagccaac aatatgcaca agtctgaact agactggttg     720
gtaccgcata aagcgaacta tcgcattatt tctgcgacgg cgaaaaaatt gtcgatgtcg     780
ctggatcaag tggatgatcac gttggaccgt catgggaaca cgtctgctgc aacgggtgccg     840
acggcactgg acgaagcggg acgtgatggc cggatcaaac ggggtcagac gctactttta     900
gaagcctttg gtggtggttt cacctggggg tctgcgttag tgaagtctta a              951
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<210> SEQ ID NO 10
<211> LENGTH: 924
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 10

```
atgagcaagt ttgctatcgt atttccaggt caaggttctc aagcgggttg tatgcttgcc      60
gagcttggcg aacagtatga cgtagttaaa caaactttcg cagaagcgtc tgacgcactg     120
ggttacgacc tatgggcatt ggttcagaac ggtcctgttg aagatctcaa ccagactttc     180
cgtacgcaac ctgcactgct ggcgtcttct gtggcgatgtt ggcgtgtatg gcaagcgtg     240
ggtcttgagc agccagaagt gctggcaggc cacagccttg gtgaatactc tgcactgggt     300
tgtgccggtg tgattgattt taaagccgcg atcaaattgg tcgaactgcg tggatcaactg     360
atgcaagaag cagtacctgc aggaaccggc gcaatgtacg cgatcatcgg tttggatgat     420
gcggcgattg ccaaagcgtg tgaagacgct gcgcaaggcg acgtgggtgc tccgggtgaac     480
ttcaactcac caggccaagt ggtcattgcc ggtcagaaag atgcggtaga acgcgcgggc     540
gcactgtgta aagaagcggg cgcgaaacgt gcactgccac tgccgggtgc agtgccctca     600
cactgcgcgc tgatgaaacc tgcagcagaa aaactggctg tggcgctaga agcgttgag     660
ttcaacgcgc cgcaaatccc agtgattaac aacgtggacg ttgcgacaga aacggatcca     720
gcgaaaatca aagatgcgtt ggttcgtcaa ctacacagcc cagtccgctg gacagaaggc     780
gtggagaaga tggcagcaca aggcattgaa aaactaattg aagttggccc aggcaaagta     840
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ctgactgggtt tgactaaacg tattgtgaaa acgcttgatg cagcagcagt gaacgacatc 900
gcttcactgg aagccgttaa gtaa 924

<210> SEQ ID NO 11
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 11

atgagtaatt tcatgaacct ggaaggcaaa attgtcctgg ttactggcgc aagccgtggt 60
atcggtaaag caatcgcgga actattgggt gaacgtgggtg ccacagtgat tggtaacagcg 120
accagcgaaa gcggcgcgaga tgcgatcagt gcgtacctag gcgacaacgg caaaggtctg 180
gcgttgaatg tgacagatgt agcgtctatc gaatccgtgc tgaaaagcat taacgatgaa 240
ttcggcggtg ttgatattct ggtgaacaac gcgggtatca cgcgtgacaa cctgctgatg 300
cgtatgaaag atgacgagtg gaccgatatt ctggatacca acttgacgtc gatcttcctg 360
ctgtctaaag ctgtacttcg tggcatgatg aaaaaacgcc aaggccgtat cattaatgtc 420
ggttctgttg tcggtacaat gggtaacgcg ggtcaaaca actacgcagc cgcaaaagcg 480
ggcgtaatcg gctttacgaa gtcaatggca cgtgaagttg catcccggtg cgtgaccgtg 540
aacacagttg caccaggttt catcgaaacg gatatgacaa aagcgctgaa tgacgaccaa 600
cgtgctgcta cacttgaca agtgccagca ggtcgtctgg gtgatccag tgaaatcgca 660
tccgcggttg cattcttggc atctccagaa gcagcgtaca ttaccggtga aactctgcac 720
gttaacggcg gaatgtacat ggtttaa 747

<210> SEQ ID NO 12
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 12

gaagtgaacg gaacttggtc ggtaaaatgt tgacttcgtc caaaacttgt caatgaaatg 60
cgcaagattt gtgcatgata tatgtcaaaa atggtgtgaa ttccggttaa aatcgccaaa 120
tttgtggttt gaccagcaag gtcccccttg caactttcac tagtttgaat aaactacgga 180
atcatcgcat taggcgaaat ctgtaaagga aaagaaaaaa tgagcaacat cgaagaacgc 240
gtaaagaaaa tcatcggtga acagctaggc gtagacgaag cagaagtga aaacgaagct 300
tctttcgttg aagacctagg tgcggattct ctagacactg ttgagcttgt tatggctctg 360
gaagaagaat tcgacactga gattcctgat gaagaagcag agaaaatcac tactgttcaa 420
gctgcgatcg attacgtaaa cagcgctcag taatgtctct ccccgaggcg ccctctggcc 480
gcctgagttt ttctcactca tctataatct ctcatagaat tttca 525

<210> SEQ ID NO 13
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 13

atgatcgtgt ccaagcgtcg tgctggtgtc actggcatgg gtatgttgct accggtaggc 60
aacactgtag aatcttcttg gaaagccctg ctagctggct aaagtggat cgtgaatctc 120

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gaacactttg atacaacaaa tttctcaact cgtttcgcag gtctggtaaa agatttcaac 180
tgcgaagagt acatgtctaa aaaagatgcc cgtaaaatgg atttatttat ccagtacggg 240
attgctgcgg gcatccaagc gctagacgat tctgggtctgg tgatcactga agaaaacgcg 300
ccacgcgtcg gtgttgcaat cggctcgggc atcgggtggc ttgatttgat cgaaaaaggt 360
catcaagcgc ttatggagaa aggtccacgt aaagtgagcc cattcttcgt cccctcaacc 420
atcgtgaaca tggttgccgg taacttatct atcatgcgtg gtcttcgtgg tccaaacatc 480
gcgatttcaa ctgcatgtac cacaggttta cataacatcg gccacgcggc gcgtatgatt 540
gcatacggcg atgcggaagc gatggttgct ggtggtagtg aaaaagcgtc taccctctg 600
ggtatggctg gcttcgggtg cgctaaagcg ctgtctacac gcaacgatga acctgcaaaa 660
gcttctcgcc cttgggacaa agaccgtgac ggttttggtc tgggtgacgg cgcaggcgtg 720
atggttctgg aaggatacga acacgcaaaa gcgcgtggcg cgaaaatcta cgcagaaatc 780
gtaggcttcg gtatgtccgg tgacgcgtac cacatgactt cgccaagcga agatggttca 840
ggtggcgcgc tggctatgga agcggcgatg cgtgatgcag cactagcggg tacacaaatc 900
ggctacgtga acgcgcacgg tacgtcaaca ccagcagggtg acgtagcggg agtgaaaggt 960
atcaaacgtg cacttggcga agacgggtgc aaacaagtag tgatctcttc aaccaaatac 1020
atgaccggtc acctactggg tgctgcaggc tcggtagaag ccatcattac cgtgatgtct 1080
ctggttgacc aaatcggtcc gccaaaccatc aacctggata atccagaaga aggtttgggc 1140
gtggatttgg ttccgcacac agcacgtaaa gtggaaggca tggaatacgc gatgtgtaac 1200
tcgtttggct ttggtggcac aaacgggtca ctgatcttca agcgcgtata a 1251

<210> SEQ ID NO 14

<211> LENGTH: 1035

<212> TYPE: DNA

<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 14

atgactgatt cacacacaaa caatgcttac ggtaaagcga tcgccatgac cgtcattggc 60
gcgggttcgt acggcacatc tctggccatt tctttggctc gcaacggcgc caatgttgct 120
ctgtggggac acgatccggt ccacatggcg cgtttggaag cggaacgtgc taaccacgaa 180
ttcctccctg acatcgattt tccaccgtcg ctgatcattg aatccgattt gcaaaaagcg 240
gtgcaagcga gccgcgatct gctgggtggg gtgccaagcc atgtgtttgc gattgtgctc 300
aacagcctgc aaccttactt gcgagaagat acccgatatc gctgggcaac caaaggggtg 360
gaaccggaca caggacgttt gctgcaagat gtggcgcacg acgtgctggg tgaatcccat 420
ccattggcgg tgctgtctgg cccgacgttt gcgaaagagc tggcgatggg tatgccact 480
gcgatttcag tggcatcgcc tgacgcgcag tttgtcgccg atctgcagga aaagattcac 540
tgcagcaaaa ccttccgtgt ttatgccaac agcgatttca tcggcatgca actggggggc 600
gctgtgaaga acgtgattgc cattggtgcg gggatgtcgg atggcatcgg ctttgggtgcc 660
aacgctcgta cggcgtgat taccgtggg ttggcgaaa tgaccgtct gggcgcgcg 720
ctgggcgcgc agccggaaac cttcatgggc atggcggggc tgggtgattt ggtgctgacg 780
tgtaccgata accaatcgcg caaccgtcgt tttggtttgg ccttgggcca aggcaaagat 840
gtcgatacgg cgcaacaaga tatcgggtcaa gtggtggaag ggtatcgga caccaaagag 900

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gtgtggctac tggcgcaacg catgggcgtg gagatgccaa tagttgaaca aatttatcaa	960
gtattgtatc aaggaaagga cgcgcgatg gcagcacaag atttgctggc gcgcgataaa	1020
aaagcagaac gataa	1035
<210> SEQ ID NO 15	
<211> LENGTH: 855	
<212> TYPE: DNA	
<213> ORGANISM: Vibrio furnisii	
<400> SEQUENCE: 15	
gtggtgtgtg cgtttgtgaa cgacgatttg agtgcgaccg tgttggaaga actgtatcaa	60
gggggcactc gcctgatcgc catgcgctgc gcgggctttg ataaagtgga tttagacgcc	120
gcaaaacgca ttggcatgca ggtggttcgc gtacctcgt attcaccaga agcggtgga	180
gagcacgcgg tcgggttgat gatgtgtctg aaccgccgtt accacaaagc gtatcagcgc	240
acacgtgagg ccaacttctc gttggaaggc ttggtgggct ttaacttcta tggcaaaacc	300
gtgggtgtga ttggttcagg caagattggc attgcagcga tgcgtatcct caaaggcctt	360
ggcatgaaca ttctctgctt tgaccctgat gaaaacccat tggccattga aatcggcgcg	420
aaatacgttc aattgccgga gctgtatgca aacagcgaca tcattacgt gcactgccc	480
atgaccaaag aaaactacca cctgctggat gagcaagcgt tcgctcaaat gaaggatggg	540
gtgatgatca tcaataccag ccgtggcgaa ttgcttgatt cagtcgcagc cattgaagcg	600
ctcaaacgtg gccgtattgg cgcgctgggc ttagacgtat acgacaacga aaaagatctg	660
ttcttccaag acaagtcgaa cgatgtgatt gtagatgacg tgttccgccg cctgtccgcc	720
tgccataacg tgctgtttac cggccatcag gcgtttttga cagaagatgc cctgcacaat	780
atcgcgcaaa ccacgcttaa caacgtgctg gcgtttgagc aaggcaccaa atctggaaac	840
gaattagtta actaa	855
<210> SEQ ID NO 16	
<211> LENGTH: 177	
<212> TYPE: PRT	
<213> ORGANISM: Vibrio furnisii	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (2)..(2)	
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid	
<400> SEQUENCE: 16	
Phe Xaa Asn Leu Glu Lys Pro Ile Val Glu Leu Glu Ala Lys Ile Gln	
1 5 10 15	
Ala Leu Arg Asp Val Ser Arg His Gly Gly Gly Thr Ser Val Asp Leu	
20 25 30	
Glu Lys Glu Ile Glu Gln Leu Glu Lys Lys Ser Leu Glu Leu Lys Lys	
35 40 45	
Lys Ile Phe Gly Asp Leu Gly Ala Trp Gln Val Ala Gln Met Ala Arg	
50 55 60	
His Pro Gln Arg Pro Tyr Thr Leu Asp Tyr Ile Asn Asn Met Phe Thr	
65 70 75 80	
Glu Phe Asp Glu Leu Ala Gly Asp Arg Ala Phe Ala Asp Asp Lys Ala	
85 90 95	
Ile Val Gly Gly Met Ala Arg Leu Asp Gly Arg Pro Val Met Val Ile	

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100						105						110					
Gly	His	Gln	Lys	Gly	Arg	Glu	Thr	Arg	Glu	Lys	Val	Lys	Arg	Asn	Phe		
	115						120					125					
Gly	Met	Pro	Lys	Pro	Glu	Gly	Tyr	Arg	Lys	Ala	Leu	Arg	Leu	Met	Glu		
	130					135					140						
Met	Ala	Glu	Arg	Phe	Asn	Met	Pro	Ile	Ile	Thr	Phe	Ile	Asp	Thr	Ala		
145					150					155					160		
Gly	Ala	Tyr	Pro	Gly	Val	Gly	Ala	Glu	Glu	Arg	Gly	Gln	Ser	Glu	Ala		
				165					170					175			
Ile																	
<210> SEQ ID NO 17																	
<211> LENGTH: 187																	
<212> TYPE: PRT																	
<213> ORGANISM: Vibrio furnisii																	
<400> SEQUENCE: 17																	
Met	Asn	Ser	Leu	Cys	Arg	Gln	Pro	Phe	Ala	Arg	Cys	Lys	Gln	Ser	Lys		
1				5					10					15			
Pro	Lys	His	Ser	Ala	Ala	Gln	Leu	Ser	Cys	Leu	Ile	His	Lys	Ile	Lys		
			20					25					30				
Glu	Lys	Glu	Thr	Met	Asp	Ile	Arg	Lys	Ile	Lys	Lys	Leu	Ile	Glu	Leu		
		35					40					45					
Val	Glu	Glu	Ser	Gly	Ile	Ala	Glu	Leu	Glu	Ile	Ser	Glu	Gly	Glu	Glu		
	50					55					60						
Ser	Val	Arg	Ile	Ser	Arg	His	Gly	Val	Ala	Pro	Val	Ala	Pro	Ile	Gln		
65					70				75						80		
Tyr	Ala	Ala	Pro	Ala	Pro	Met	Ala	Ala	Pro	Val	Ala	Ala	Pro	Ala	Ala		
			85					90					95				
Ala	Pro	Val	Ala	Glu	Ala	Pro	Ala	Ala	Ala	Lys	Thr	Pro	Ala	Gly	His		
			100					105					110				
Met	Val	Leu	Ser	Pro	Met	Val	Gly	Thr	Phe	Tyr	Arg	Ser	Pro	Ser	Pro		
		115					120					125					
Asp	Ala	Lys	Ser	Phe	Ile	Glu	Val	Gly	Gln	Thr	Val	Lys	Ala	Gly	Asp		
	130					135					140						
Thr	Leu	Cys	Ile	Val	Glu	Ala	Met	Lys	Met	Met	Asn	Gln	Ile	Glu	Ala		
145					150					155					160		
Asp	Lys	Ser	Gly	Val	Val	Thr	Glu	Ile	Leu	Val	Glu	Asp	Gly	Gln	Ala		
				165					170					175			
Val	Glu	Phe	Asp	Gln	Pro	Leu	Val	Val	Ile	Glu							
			180					185									
<210> SEQ ID NO 18																	
<211> LENGTH: 447																	
<212> TYPE: PRT																	
<213> ORGANISM: Vibrio furnisii																	
<400> SEQUENCE: 18																	
Met	Leu	Asp	Lys	Leu	Val	Ile	Ala	Asn	Arg	Gly	Glu	Ile	Ala	Leu	Arg		
1				5					10					15			
Ile	Leu	Arg	Ala	Cys	Lys	Glu	Leu	Gly	Ile	Lys	Thr	Val	Ala	Val	His		
			20					25					30				
Ser	Thr	Ala	Asp	Arg	Asp	Leu	Lys	His	Val	Leu	Leu	Ala	Asp	Glu	Thr		
		35					40					45					

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Val	Cys	Ile	Gly	Pro	Ala	Lys	Gly	Ile	Asp	Ser	Tyr	Leu	Asn	Ile	Pro	50	55	60
Arg	Ile	Ile	Ser	Ala	Ala	Glu	Val	Thr	Gly	Ala	Val	Ala	Ile	His	Pro	65	70	75
Gly	Tyr	Gly	Phe	Leu	Ser	Glu	Asn	Ala	Asp	Phe	Ala	Glu	Gln	Val	Glu	85	90	95
Arg	Ser	Gly	Phe	Ile	Phe	Val	Gly	Pro	Lys	Ala	Asp	Thr	Ile	Arg	Leu	100	105	110
Met	Gly	Asp	Lys	Val	Ser	Ala	Ile	Thr	Ala	Met	Lys	Lys	Ala	Gly	Val	115	120	125
Pro	Cys	Val	Pro	Gly	Ser	Asp	Gly	Pro	Leu	Asp	Asn	Asp	Glu	Val	Lys	130	135	140
Asn	Arg	Ala	His	Ala	Lys	Arg	Ile	Gly	Tyr	Pro	Val	Ile	Ile	Lys	Ala	145	150	155
Ser	Gly	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Val	Val	Arg	Ser	Glu	Ala	165	170	175
Glu	Leu	Val	Asn	Ala	Ile	Ser	Met	Thr	Arg	Ala	Glu	Ala	Lys	Ala	Ala	180	185	190
Phe	Asn	Asn	Asp	Met	Val	Tyr	Met	Glu	Lys	Tyr	Leu	Glu	Asn	Pro	Arg	195	200	205
His	Val	Glu	Val	Gln	Val	Leu	Ala	Asp	Gly	Gln	Gly	Ser	Ala	Ile	His	210	215	220
Leu	Gly	Glu	Arg	Asp	Cys	Ser	Met	Gln	Arg	Arg	His	Gln	Lys	Val	Val	225	230	235
Glu	Glu	Ala	Pro	Ala	Pro	Gly	Ile	Thr	Glu	Glu	Met	Arg	Lys	Tyr	Ile	245	250	255
Gly	Glu	Arg	Cys	Thr	Arg	Ala	Cys	Ile	Glu	Ile	Gly	Tyr	Arg	Gly	Ala	260	265	270
Gly	Thr	Phe	Glu	Phe	Leu	Tyr	Glu	Asn	Gly	Glu	Phe	Tyr	Phe	Ile	Glu	275	280	285
Met	Asn	Thr	Arg	Ile	Gln	Val	Glu	His	Pro	Val	Thr	Glu	Met	Val	Thr	290	295	300
Gly	Val	Asp	Leu	Ile	Lys	Glu	Gln	Leu	Arg	Ile	Ala	Ala	Gly	Gln	Pro	305	310	315
Leu	Ser	Phe	Thr	Gln	Asp	Asp	Ile	Lys	Ile	Arg	Gly	His	Ala	Met	Glu	325	330	335
Cys	Arg	Ile	Asn	Ala	Glu	Asp	Pro	Glu	Arg	Phe	Leu	Pro	Cys	Pro	Gly	340	345	350
Lys	Ile	Thr	Arg	Phe	His	Ser	Pro	Gly	Gly	Met	Gly	Val	Arg	Trp	Glu	355	360	365
Ser	His	Ile	Tyr	Ser	Gly	Tyr	Thr	Val	Pro	Ala	Tyr	Tyr	Asp	Ser	Met	370	375	380
Ile	Gly	Lys	Leu	Ile	Thr	Phe	Gly	Glu	Asn	Arg	Asp	Val	Ala	Ile	Ala	385	390	395
Arg	Met	Arg	Asn	Ala	Leu	Asp	Glu	Met	Ile	Val	Glu	Gly	Ile	Lys	Thr	405	410	415
Asn	Ile	Pro	Leu	Gln	Gln	Val	Ile	Met	Lys	Asp	Glu	Asn	Phe	Gln	His	420	425	430
Gly	Gly	Thr	Asn	Ile	His	Tyr	Leu	Glu	Lys	Lys	Leu	Gly	Leu	Gln		435	440	445

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<210> SEQ ID NO 19
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Vibrio furnisii

<400> SEQUENCE: 19

Met Ser Trp Leu Glu Lys Ile Leu Glu Lys Ser Asn Ile Gly Ser Ser
1          5          10          15

Arg Lys Ala Ser Ile Pro Glu Gly Val Trp Thr Lys Cys Thr Ser Cys
          20          25          30

Glu Gln Val Leu Tyr Tyr Ala Glu Leu Glu Arg Asn Leu Glu Val Cys
          35          40          45

Pro Lys Cys Asn His His Met Arg Met Lys Ala Arg Arg Arg Leu Glu
          50          55          60

Thr Phe Leu Asp Glu Ala Asn Arg Tyr Glu Ile Ala Asp Glu Leu Glu
65          70          75          80

Pro Gln Asp Lys Leu Lys Phe Lys Asp Ser Lys Arg Tyr Lys Glu Arg
          85          90          95

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

Met Lys Gly Glu Leu Met Thr Ile Pro Val Val Ala Cys Ala Phe Glu
          115          120          125

Phe Ser Phe Met Gly Gly Ser Met Gly Ser Val Val Gly Ala Arg Phe
          130          135          140

Val Arg Ala Val Glu Ala Ala Ile Glu Ala Asn Cys Gly Leu Val Cys
145          150          155          160

Phe Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ala Leu Met Ser Leu
          165          170          175

Met Gln Met Ala Lys Thr Ser Ala Ala Leu Glu Arg Leu Thr Ala Lys
          180          185          190

Gly Leu Pro Phe Ile Ser Val Met Thr Asp Pro Thr Met Gly Gly Val
          195          200          205

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

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

Glu Glu Leu Pro Glu Gly Phe Gln Arg Ser Glu Phe Leu Leu Glu His
          245          250          255

Gly Ala Ile Asp Met Ile Val Asp Arg Arg Glu Met Arg Gln Arg Val
          260          265          270

Ala Gly Leu Leu Ala Lys Met Thr Arg Gln Glu Ser Pro Leu Val Val
          275          280          285

Ser Val Asn Asp Ala Pro Asn Glu Ala Ala Tyr Ser Val Pro Glu Ala
          290          295          300

Asn Lys Lys Gly
305

<210> SEQ ID NO 20
<211> LENGTH: 814
<212> TYPE: PRT
<213> ORGANISM: Vibrio furnisii

<400> SEQUENCE: 20
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Met	Asp	Ile	Leu	Leu	Ser	Ile	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Gly	1	5	10	15
Cys	Leu	Tyr	His	Arg	Thr	Ser	Leu	Met	Thr	Ala	Leu	Ala	Ala	Leu	Thr	20	25	30	
Val	Thr	Met	Leu	Val	Leu	Ser	Leu	Phe	Gly	Pro	Val	Gly	Ile	Ile	Ser	35	40	45	
Trp	Ala	Leu	Tyr	Leu	Ala	Ala	Ile	Ala	Val	Leu	Ala	Val	Pro	Ser	Ile	50	55	60	
Arg	Gln	Ser	Leu	Ile	Ser	Gly	Lys	Thr	Leu	Lys	Val	Phe	Lys	Lys	Val	65	70	75	80
Leu	Pro	Ala	Met	Ser	Gln	Thr	Glu	Lys	Glu	Ala	Leu	Asp	Ala	Gly	Thr	85	90	95	
Val	Trp	Trp	Glu	Ala	Glu	Leu	Phe	Lys	Gly	Lys	Pro	Asp	Trp	Gln	Gln	100	105	110	
Leu	Ser	His	Ile	Lys	Ala	Pro	Thr	Leu	Ser	Ala	Glu	Glu	Gln	Ala	Phe	115	120	125	
Leu	Asp	Gly	Pro	Val	Asn	Glu	Val	Cys	Ala	Met	Val	Asn	Asp	Tyr	Gln	130	135	140	
Val	Thr	His	Glu	Leu	Ala	Asp	Leu	Pro	Pro	Glu	Val	Trp	Gln	Tyr	Leu	145	150	155	160
Lys	Asp	His	Lys	Phe	Phe	Ala	Met	Ile	Ile	Lys	Lys	Gln	Tyr	Gly	Gly	165	170	175	
Leu	Glu	Phe	Ser	Ala	Tyr	Ala	Gln	Ser	Leu	Val	Leu	Gln	Lys	Leu	Thr	180	185	190	
Gly	Val	Ser	Gly	Val	Leu	Ser	Ser	Thr	Val	Gly	Val	Pro	Asn	Ser	Leu	195	200	205	
Gly	Pro	Gly	Glu	Leu	Leu	Gln	His	Tyr	Gly	Thr	Asp	Asp	Gln	Lys	Asp	210	215	220	
Tyr	Tyr	Leu	Pro	Arg	Leu	Ala	Glu	Gly	Lys	Glu	Ile	Pro	Cys	Phe	Ala	225	230	235	240
Leu	Thr	Ser	Pro	Glu	Ala	Gly	Ser	Asp	Ala	Gly	Ser	Ile	Pro	Asp	Tyr	245	250	255	
Gly	Ile	Val	Cys	Lys	Asp	Glu	Trp	Glu	Gly	Lys	Glu	Val	Leu	Gly	Met	260	265	270	
Arg	Leu	Thr	Trp	Asn	Lys	Arg	Tyr	Ile	Thr	Leu	Ala	Pro	Val	Ala	Thr	275	280	285	
Val	Leu	Gly	Leu	Ala	Phe	Lys	Leu	Arg	Asp	Pro	Asp	Gly	Leu	Leu	Gly	290	295	300	
Asp	Gln	Lys	Glu	Ile	Gly	Ile	Thr	Cys	Ala	Leu	Ile	Pro	Thr	His	Leu	305	310	315	320
Lys	Gly	Val	Glu	Ile	Gly	Asn	Arg	His	Phe	Pro	Leu	Asn	Val	Pro	Phe	325	330	335	
Gln	Asn	Gly	Pro	Thr	Arg	Ala	Asn	Asp	Leu	Phe	Val	Pro	Leu	Asp	Phe	340	345	350	
Ile	Ile	Gly	Gly	Pro	Ser	Met	Ala	Gly	Gln	Gly	Trp	Arg	Met	Leu	Val	355	360	365	
Glu	Cys	Leu	Ser	Val	Gly	Arg	Gly	Ile	Thr	Leu	Pro	Ser	Asn	Ser	Thr	370	375	380	
Gly	Gly	Ile	Lys	Ala	Ala	Ala	Met	Ala	Thr	Gly	Ala	Tyr	Ala	Arg	Ile	385	390	395	400
Arg	Arg	Gln	Phe	Lys	Gln	Pro	Ile	Gly	His	Met	Glu	Gly	Ile	Glu	Glu				

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405								410					415			
Pro	Leu	Ala	Arg	Leu	Ala	Gly	Asn	Ala	Tyr	Val	Met	Asp	Ala	Ala	Ser	
			420					425					430			
Asn	Leu	Thr	Val	Ala	Gly	Ile	Asp	Ala	Gly	Glu	Lys	Pro	Ser	Val	Ile	
		435					440					445				
Ser	Ala	Ile	Val	Lys	Tyr	His	Cys	Thr	His	Arg	Gly	Gln	Arg	Ser	Ile	
	450					455					460					
Ile	Asp	Ala	Met	Asp	Ile	Val	Gly	Gly	Lys	Gly	Ile	Cys	Leu	Gly	Pro	
465					470					475					480	
Ser	Asn	Phe	Leu	Ala	Arg	Gly	Tyr	Gln	Gly	Ser	Pro	Ile	Ala	Ile	Thr	
			485						490					495		
Val	Glu	Gly	Ala	Asn	Ile	Leu	Thr	Arg	Ser	Met	Ile	Ile	Phe	Gly	Gln	
			500					505					510			
Gly	Ala	Ile	Arg	Cys	His	Pro	Tyr	Val	Leu	Lys	Glu	Met	Glu	Ala	Ala	
		515					520					525				
Tyr	Ser	Asp	Ser	Ala	Asn	Ala	Val	Glu	Gln	Phe	Asp	Ala	Ala	Leu	Ala	
	530					535					540					
Gly	His	Val	Ser	Phe	Thr	Met	Ser	Asn	Leu	Val	Arg	Cys	Ile	Trp	Phe	
545					550					555					560	
Gly	Leu	Thr	Asp	Gly	Leu	Gly	Ser	Ala	Ala	Pro	Thr	Lys	Asp	Ala	Thr	
			565						570					575		
Lys	Arg	Tyr	Tyr	Gln	Gln	Leu	Asn	Arg	Tyr	Ser	Ala	Asn	Leu	Ala	Leu	
			580					585					590			
Leu	Ala	Asp	Ile	Ser	Met	Ala	Val	Leu	Gly	Gly	Ser	Leu	Lys	Arg	Lys	
		595					600					605				
Glu	Arg	Leu	Ser	Ala	Arg	Leu	Gly	Asp	Ile	Leu	Ser	Gln	Leu	Tyr	Leu	
	610					615					620					
Ser	Ser	Ala	Thr	Leu	Lys	Arg	Phe	Glu	Asn	Asp	Gly	Arg	Pro	Ala	Glu	
625					630					635					640	
Asp	Leu	Ala	Leu	Val	His	Trp	Gly	Leu	Gln	Asp	Ser	Leu	Lys	Gln	Thr	
			645						650					655		
Glu	Val	Ala	Ile	Asp	Glu	Phe	Leu	Ala	Asn	Phe	Pro	Asn	Lys	Val	Ile	
		660						665					670			
Gly	Lys	Ala	Leu	Arg	Val	Leu	Ile	Met	Pro	Phe	Gly	Arg	Val	Arg	Lys	
		675				680						685				
Ala	Pro	Asn	Asp	Lys	Leu	Asp	Ser	Lys	Val	Ala	Gln	Ile	Ile	Gln	Thr	
	690					695					700					
Pro	Ser	Ala	Thr	Arg	Ser	Arg	Ile	Gly	Arg	His	Gln	Tyr	Leu	Glu	Pro	
705					710					715					720	
Thr	Ala	His	Asn	Ala	Val	Gly	Lys	Ile	Glu	Leu	Ala	Leu	Asn	Val	Ile	
			725						730					735		
Leu	Gln	Ala	Glu	Pro	Val	Phe	Asp	Lys	Val	Cys	Lys	Ala	Leu	Asn	Glu	
			740					745					750			
Arg	Arg	Pro	Phe	Thr	Gln	Leu	Asp	Gln	Val	Ala	Gln	Cys	Gly	Leu	Glu	
		755					760					765				
Gln	Lys	Leu	Ile	Thr	Glu	Gln	Glu	Ala	Glu	Leu	Leu	Ile	Glu	Ala	Glu	
	770					775					780					
Gln	His	Arg	Leu	Tyr	Thr	Ile	Asn	Val	Asp	Asp	Phe	Ala	Pro	Gln	Glu	
785					790					795					800	
Leu	Ala	Ala	Lys	Lys	Ser	Gln	Pro	Lys	Leu	Val	Glu	Val	Ala			
			805						810							

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<210> SEQ ID NO 21
<211> LENGTH: 807
<212> TYPE: PRT
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 21

Met Ser Ser Gly His Ser Phe Ser Arg Ser Leu Leu Lys Leu Pro Leu
1 5 10 15

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

Leu Glu Ile Asp Ile Asn Lys Pro Ile Val Tyr Ala Leu Pro Phe Arg
35 40 45

Ser Asn Val Asp Leu Leu Thr Leu Gln Thr His Ala Leu Gln Ala Gly
50 55 60

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

Arg Tyr Val Phe Ile Ser Ser Arg Pro Thr Leu Leu Gln Asp Asp Asn
85 90 95

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

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

Leu Trp Gly Arg Lys Pro Gly Lys Glu Gly Arg Glu Arg Pro Tyr Leu
130 135 140

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

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

Ala Asp Ser His Gly Thr Asp Ala Ser Ile Ala His Lys Leu Ala Arg
180 185 190

Val Ala Arg Ile His Phe Ser Arg Gln Lys Leu Ala Ala Ser Gly Pro
195 200 205

Asn Leu Pro Gln Arg His Gln Leu Phe Gln Arg Leu Met Asn Ser Pro
210 215 220

Ala Ile Glu Lys Ala Ile Ala Asp Glu Ala Ala Ala Lys Asn Ile Ser
225 230 235 240

Leu Glu Lys Ala Arg Lys Glu Ala His Asp Met Leu Asp Glu Ile Ala
245 250 255

Ala Asp Phe Ser Tyr Ser Leu Val Arg Lys Gly Asp Arg Ile Leu Gly
260 265 270

Trp Leu Trp Asn Arg Ile Tyr Gln Gly Leu Asn Ile Asn Asn Ala Ala
275 280 285

Thr Val Arg Arg Leu Ala Gln Asp Gly His Glu Ile Val Tyr Val Pro
290 295 300

Cys His Arg Ser His Met Asp Tyr Leu Leu Leu Ser Tyr Val Leu Tyr
305 310 315 320

His Glu Gly Met Val Pro Pro His Ile Ala Ala Gly Ile Asn Leu Asn
325 330 335

Phe Phe Pro Ala Gly Pro Ile Phe Arg Arg Gly Gly Ala Phe Phe Ile
340 345 350

Arg Arg Ser Phe Lys Gly Asn Lys Leu Tyr Ser Thr Ile Phe Arg Glu

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	355					360					365				
Tyr	Leu	Ala	Glu	Leu	Phe	Ala	Lys	Gly	Tyr	Ser	Val	Glu	Tyr	Phe	Ser
	370					375					380				
Glu	Gly	Gly	Arg	Ser	Arg	Thr	Gly	Arg	Leu	Leu	Gln	Ala	Lys	Thr	Gly
385					390					395					400
Met	Leu	Ala	Met	Thr	Ile	Gln	Ala	Met	Leu	Arg	Gly	Leu	Asn	Arg	Pro
				405					410					415	
Val	Thr	Leu	Val	Pro	Val	Tyr	Ile	Gly	Tyr	Glu	His	Val	Met	Glu	Val
			420					425					430		
Gly	Thr	Tyr	Ala	Lys	Glu	Leu	Arg	Gly	Lys	Arg	Lys	Glu	Lys	Glu	Asn
		435					440					445			
Ala	Ser	Leu	Val	Leu	Arg	Thr	Ile	Arg	Lys	Leu	Arg	Asn	Phe	Gly	Gln
	450					455					460				
Gly	Tyr	Val	Asn	Phe	Gly	Glu	Pro	Ile	Pro	Leu	Asn	Gln	Phe	Leu	Asn
465					470					475					480
Glu	Gln	Val	Pro	Glu	Trp	Thr	Gln	Asp	Ile	Asp	Ala	Met	Gly	Ala	Ser
				485					490					495	
Lys	Pro	Gln	Trp	Met	Thr	Pro	Val	Val	Asn	Lys	Leu	Ala	Thr	Lys	Met
			500					505					510		
Met	Thr	His	Ile	Asn	Asp	Ala	Ala	Ala	Ala	Asn	Ala	Met	Thr	Leu	Cys
		515					520					525			
Ala	Thr	Ala	Leu	Leu	Ala	Ser	Arg	Gln	Arg	Ala	Leu	Ala	Arg	Asp	Asn
	530					535					540				
Leu	Val	Lys	Gln	Ile	Asp	Cys	Tyr	Leu	Gln	Leu	Leu	Arg	Asn	Val	Pro
545					550					555					560
Tyr	Ser	Asn	Thr	Tyr	Thr	Val	Pro	Ser	Asp	Ser	Ala	Glu	Ser	Leu	Val
				565					570					575	
Gln	His	Ala	Glu	Ser	Leu	Asp	Lys	Phe	Val	Val	Glu	Thr	Asp	Thr	Met
			580					585					590		
Gly	Asp	Ile	Ile	Ser	Leu	Asp	Arg	Asn	Gln	Ser	Ile	Leu	Met	Thr	Tyr
		595					600					605			
Tyr	Arg	Asn	Asn	Ile	Ile	His	Leu	Leu	Ala	Leu	Pro	Ser	Leu	Ile	Ala
	610					615					620				
Gln	Met	Leu	Ile	Arg	Gln	Gln	Gln	Met	Pro	Val	Glu	Gln	Ile	Gln	Thr
625					630					635					640
Cys	Val	Ala	Lys	Val	Tyr	Pro	Phe	Leu	Lys	Gln	Glu	Leu	Phe	Leu	Ser
				645					650					655	
His	Asp	Glu	Thr	Gln	Leu	Asp	Glu	Val	Val	Met	His	Tyr	Leu	Ala	Glu
			660					665					670		
Leu	Gln	Arg	Gln	Gln	Leu	Val	Thr	Leu	Asp	Asp	Gly	Ile	Ala	Thr	Ile
		675					680					685			
Asn	Gln	Ala	Gln	Thr	Gln	Val	Leu	Met	Leu	Leu	Gly	Arg	Thr	Ile	Ser
	690					695					700				
Glu	Thr	Leu	Gln	Arg	Tyr	Ala	Ile	Thr	Leu	Asn	Leu	Leu	Val	Ala	Asn
705					710					715					720
Pro	Glu	Leu	Gly	Lys	Ser	Asp	Leu	Glu	Ser	Lys	Ser	Gln	Glu	Ile	Ala
				725					730					735	
Gln	Arg	Leu	Gly	Arg	Leu	His	Gly	Ile	Asn	Ala	Pro	Glu	Phe	Phe	Asp
			740					745					750		
Lys	Gly	Val	Phe	Ser	Ser	Met	Phe	Val	Thr	Leu	Lys	Gln	Gln	Gly	Tyr
		755					760					765			

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Leu	Asp	Ser	Asp	Gly	Asn	Cys	His	Leu	Asp	Gln	Thr	Lys	His	Phe	Ser	
770						775					780					
Arg	Met	Leu	Tyr	Thr	Met	Leu	Tyr	Pro	Glu	Val	Arg	Leu	Thr	Ile	Gln	
785					790					795					800	
Glu	Ser	Ile	Cys	Gln	Val	Glu										
				805												
<210> SEQ ID NO 22																
<211> LENGTH: 886																
<212> TYPE: PRT																
<213> ORGANISM: Vibrio furnisii																
<400> SEQUENCE: 22																
Met	Ser	Asp	Met	Lys	His	Asp	Val	Asp	Ala	Leu	Glu	Thr	Gln	Glu	Trp	
1				5					10					15		
Leu	Ala	Ala	Leu	Glu	Ser	Val	Val	Arg	Glu	Glu	Gly	Val	Glu	Arg	Ala	
			20					25					30			
Gln	Tyr	Leu	Leu	Glu	Glu	Val	Leu	Glu	Lys	Ala	Arg	Leu	Asp	Gly	Val	
		35					40					45				
Asp	Met	Pro	Thr	Gly	Ile	Thr	Thr	Asn	Tyr	Ile	Asn	Thr	Ile	Pro	Ala	
	50					55					60					
Ala	Gln	Glu	Pro	Ala	Tyr	Pro	Gly	Asp	Thr	Thr	Ile	Glu	Arg	Arg	Ile	
65					70					75					80	
Arg	Ser	Ile	Ile	Arg	Trp	Asn	Ala	Ile	Met	Ile	Val	Leu	Arg	Ala	Ser	
				85					90					95		
Lys	Lys	Asp	Leu	Asp	Leu	Gly	Gly	His	Met	Ala	Ser	Phe	Gln	Ser	Ser	
			100					105					110			
Ala	Ala	Phe	Tyr	Glu	Thr	Cys	Phe	Asn	His	Phe	Phe	Arg	Ala	Pro	Asn	
		115					120					125				
Glu	Lys	Asp	Gly	Gly	Asp	Leu	Val	Tyr	Tyr	Gln	Gly	His	Ile	Ser	Pro	
	130					135					140					
Gly	Ile	Tyr	Ala	Arg	Ala	Phe	Val	Glu	Gly	Arg	Leu	Thr	Glu	Glu	Gln	
145					150					155					160	
Leu	Asp	Asn	Phe	Arg	Gln	Glu	Val	Asp	Gly	Lys	Gly	Ile	Pro	Ser	Tyr	
				165					170					175		
Pro	His	Pro	Lys	Leu	Met	Pro	Glu	Phe	Trp	Gln	Phe	Pro	Thr	Val	Ser	
			180					185					190			
Met	Gly	Leu	Gly	Pro	Ile	Ala	Ser	Ile	Tyr	Gln	Ala	Arg	Phe	Leu	Lys	
		195					200					205				
Tyr	Leu	Glu	Gly	Arg	Gly	Met	Lys	Asp	Thr	Ala	Glu	Gln	Arg	Val	Tyr	
	210					215					220					
Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser	Arg	Gly	Ala	
225					230					235					240	
Ile	Ser	Phe	Ala	Ala	Arg	Glu	Lys	Leu	Asp	Asn	Leu	Cys	Phe	Leu	Ile	
				245					250					255		
Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Met	Gly	Asn	Gly	Lys	
			260					265					270			
Ile	Ile	Gln	Glu	Leu	Glu	Gly	Leu	Phe	Lys	Gly	Ala	Gly	Trp	Asn	Val	
		275					280					285				
Val	Lys	Val	Ile	Trp	Gly	Asn	Asn	Trp	Asp	Ser	Leu	Leu	Ala	Lys	Asp	
	290					295					300					
Thr	Ser	Gly	Lys	Leu	Leu	Gln	Leu	Met	Asn	Glu	Thr	Ile	Asp	Gly	Asp	

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305				310					315					320		
Tyr	Gln	Thr	Phe	Lys	Ala	Lys	Asp	Gly	Ala	Tyr	Val	Arg	Glu	His	Phe	
				325						330						335
Phe	Gly	Lys	Tyr	Pro	Glu	Thr	Ala	Ala	Leu	Val	Ala	Asp	Met	Thr	Asp	
				340						345						350
Asp	Glu	Val	Phe	Ala	Leu	Lys	Arg	Gly	Gly	His	Glu	Ser	Ser	Lys	Leu	
				355						360						365
Tyr	Ala	Ala	Phe	Lys	Asn	Ala	Gln	Asp	Thr	Lys	Gly	Arg	Pro	Thr	Val	
				370						375						380
Ile	Leu	Ala	Lys	Thr	Val	Lys	Gly	Tyr	Gly	Met	Gly	Asp	Ala	Ala	Gln	
385														400		
Gly	Lys	Asn	Ile	Ala	His	Gln	Val	Lys	Lys	Met	Asp	Met	Thr	His	Val	
				405						410						415
Ile	Ala	Met	Arg	Asn	Arg	Leu	Gly	Leu	Gln	Asp	Ile	Ile	Ser	Asp	Glu	
				420						425						430
Glu	Val	Asn	Asn	Leu	Pro	Tyr	Leu	Lys	Leu	Glu	Glu	Gly	Ser	Lys	Glu	
				435						440						445
Phe	Glu	Tyr	Leu	His	Ala	Arg	Arg	Lys	Ala	Leu	His	Gly	Tyr	Thr	Pro	
				450						455						460
Gln	Arg	Leu	Pro	Lys	Phe	Thr	Gln	Glu	Leu	Val	Ile	Pro	Glu	Leu	Glu	
465														480		
Glu	Phe	Lys	Pro	Leu	Leu	Glu	Glu	Gln	Lys	Arg	Glu	Ile	Ser	Ser	Thr	
				485						490						495
Met	Ala	Tyr	Val	Arg	Ala	Leu	Asn	Ile	Leu	Leu	Lys	Asp	Lys	Asn	Ile	
				500						505						510
Gly	Lys	Asn	Ile	Val	Pro	Ile	Ile	Ala	Asp	Glu	Ala	Arg	Thr	Phe	Gly	
				515						520						525
Met	Glu	Gly	Leu	Phe	Arg	Gln	Ile	Gly	Ile	Tyr	Asn	Pro	His	Gly	Gln	
				530						535						540
Thr	Tyr	Thr	Pro	Glu	Asp	Arg	Gly	Val	Val	Ser	Tyr	Tyr	Lys	Glu	Asp	
545														560		
Thr	Ala	Gly	Gln	Val	Leu	Gln	Glu	Gly	Ile	Asn	Glu	Leu	Gly	Ala	Met	
				565						570						575
Ser	Ser	Trp	Val	Ala	Ala	Ala	Thr	Ser	Tyr	Ser	Thr	Asn	Asn	Leu	Pro	
				580						585						590
Met	Ile	Pro	Phe	Tyr	Ile	Tyr	Tyr	Ser	Met	Phe	Gly	Phe	Gln	Arg	Val	
				595						600						605
Gly	Asp	Met	Ala	Trp	Met	Ala	Gly	Asp	Gln	Gln	Ala	Arg	Gly	Phe	Leu	
				610						615						620
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Asn	Gly	Glu	Gly	Leu	Gln	
625														640		
His	Glu	Asp	Gly	His	Ser	His	Ile	Gln	Ala	Ala	Thr	Ile	Pro	Asn	Cys	
				645						650						655
Ile	Ser	Tyr	Asp	Pro	Thr	Phe	Ala	Tyr	Glu	Val	Ala	Val	Ile	Met	Gln	
				660						665						670
Asp	Gly	Ile	Arg	Arg	Met	Tyr	Gly	Asp	Gln	Glu	Asn	Val	Phe	Tyr	Tyr	
				675						680						685
Met	Thr	Leu	Met	Asn	Glu	Asn	Tyr	Ala	His	Pro	Ala	Met	Pro	Glu	Gly	
				690						695						700
Ala	Glu	Glu	Gly	Ile	Arg	Lys	Gly	Ile	Tyr	Lys	Leu	Glu	Thr	Leu	Ser	
705														720		

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Gly Ser Lys Gly Lys Val Gln Leu Met Ser Ser Gly Thr Ile Met Asn
 725 730 735
 Glu Val Arg Lys Ala Ala Val Ile Leu Ser Glu Glu Tyr Gly Ile Ala
 740 745 750
 Ser Asp Val Tyr Ser Val Thr Ser Phe Asn Glu Leu Ala Arg Asp Gly
 755 760 765
 Gln Asn Val Glu Arg Tyr Asn Met Leu His Pro Glu Ala Glu Ala Gln
 770 775 780
 Val Pro Tyr Ile Ala Ser Val Met Gly Thr Glu Pro Ala Ile Ala Ala
 785 790 795 800
 Thr Asp Tyr Met Lys Asn Tyr Ala Asp Gln Val Arg Ala Phe Ile Pro
 805 810 815
 Ala Glu Ser Tyr Lys Val Leu Gly Thr Asp Gly Phe Gly Arg Ser Asp
 820 825 830
 Ser Arg Glu Asn Leu Arg Arg His Phe Glu Val Asn Ala Gly Tyr Val
 835 840 845
 Val Val Ala Ala Leu Asn Glu Leu Ala Lys Arg Gly Glu Val Glu Lys
 850 855 860
 Ser Val Val Ala Glu Ala Ile Lys Lys Phe Asp Ile Asp Thr Glu Lys
 865 870 875 880
 Thr Asn Pro Leu Tyr Ala
 885

<210> SEQ ID NO 23
 <211> LENGTH: 630
 <212> TYPE: PRT
 <213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 23

Met Ala Ile Glu Ile Tyr Val Pro Asp Ile Gly Ala Asp Glu Val Glu
 1 5 10 15
 Val Thr Glu Ile Leu Val Ser Val Gly Asp Lys Val Glu Glu Glu Gln
 20 25 30
 Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val Pro Ala
 35 40 45
 Ser Gln Ala Gly Ile Val Lys Glu Ile Lys Val Val Thr Gly Asp Lys
 50 55 60
 Val Thr Thr Gly Ser Leu Ile Met Val Phe Glu Ala Glu Gly Ala Ala
 65 70 75 80
 Ala Ala Ala Pro Ala Pro Ala Ala Glu Ala Ala Pro Val Ala Ala Ala
 85 90 95
 Pro Ala Ala Val Glu Leu Lys Glu Val Asn Val Pro Asp Ile Gly Gly
 100 105 110
 Asp Glu Val Glu Val Thr Glu Ile Met Val Ala Val Gly Asp Thr Val
 115 120 125
 Ser Glu Glu Gln Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met
 130 135 140
 Glu Val Pro Ala Pro Phe Ala Gly Thr Val Lys Glu Ile Lys Ile Ala
 145 150 155 160
 Ser Gly Asp Lys Val Thr Thr Gly Ser Leu Ile Met Val Phe Glu Val
 165 170 175
 Ala Gly Ser Gly Ala Pro Ala Ala Ala Ala Pro Ala Gln Ala Ala Ala

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180							185					190			
Pro	Ala	Ala	Ala	Pro	Ala	Val	Ala	Ala	Asp	Lys	Glu	Val	Asn	Val	Pro
		195					200					205			
Asp	Ile	Gly	Gly	Asp	Glu	Val	Glu	Val	Thr	Glu	Ile	Met	Val	Ala	Val
	210					215					220				
Gly	Asp	Met	Val	Ser	Glu	Glu	Gln	Ser	Leu	Ile	Thr	Val	Glu	Gly	Asp
225					230					235					240
Lys	Ala	Ser	Met	Glu	Val	Pro	Ala	Pro	Phe	Ala	Gly	Lys	Val	Lys	Ala
				245					250					255	
Ile	Lys	Val	Ala	Ala	Gly	Asp	Lys	Val	Ser	Thr	Gly	Ser	Leu	Ile	Met
			260					265					270		
Val	Phe	Glu	Val	Ala	Gly	Ala	Ala	Pro	Ala	Ala	Val	Ser	Ala	Pro	Ala
		275					280					285			
Gln	Ala	Ala	Ala	Pro	Ala	Ala	Ala	Ala	Pro	Lys	Ala	Glu	Ala	Pro	Ala
	290					295					300				
Ala	Ala	Ala	Pro	Ala	Ala	Ala	Thr	Gly	Asp	Phe	Gln	Glu	Asn	Asn	Glu
305					310					315					320
Tyr	Ala	His	Ala	Ser	Pro	Val	Val	Arg	Arg	Leu	Ala	Arg	Glu	Phe	Gly
				325					330					335	
Val	Asn	Leu	Ser	Lys	Val	Lys	Gly	Ser	Gly	Arg	Lys	Ser	Arg	Ile	Leu
			340					345					350		
Lys	Glu	Asp	Val	Gln	Asn	Tyr	Val	Lys	Glu	Ala	Leu	Lys	Arg	Leu	Glu
		355					360					365			
Ser	Gly	Ala	Ala	Ser	Ala	Ala	Ser	Gly	Lys	Gly	Asp	Gly	Ala	Ala	Leu
	370					375					380				
Gly	Leu	Leu	Pro	Trp	Pro	Lys	Val	Asp	Phe	Ser	Lys	Phe	Gly	Asp	Thr
385					390					395					400
Glu	Ile	Gln	Pro	Leu	Ser	Arg	Ile	Lys	Lys	Ile	Ser	Gly	Ala	Asn	Leu
				405					410					415	
His	Arg	Asn	Trp	Val	Met	Ile	Pro	His	Val	Thr	Gln	Trp	Asp	Asn	Ala
			420					425					430		
Asp	Ile	Thr	Glu	Leu	Glu	Ala	Phe	Arg	Lys	Glu	Gln	Asn	Ala	Ile	Glu
		435					440					445			
Ala	Lys	Lys	Asp	Thr	Gly	Met	Lys	Ile	Thr	Pro	Leu	Val	Phe	Ile	Met
	450					455					460				
Lys	Ala	Ala	Ala	Lys	Ala	Leu	Glu	Ala	Phe	Pro	Ala	Phe	Asn	Ser	Ser
465					470					475					480
Leu	Ser	Glu	Asp	Gly	Glu	Ser	Leu	Ile	Leu	Lys	Lys	Tyr	Val	Asn	Ile
				485					490					495	
Gly	Ile	Ala	Val	Asp	Thr	Pro	Asn	Gly	Leu	Val	Val	Pro	Val	Phe	Lys
			500					505					510		
Asp	Val	Asn	Lys	Lys	Gly	Ile	Tyr	Glu	Leu	Ser	Glu	Glu	Leu	Ala	Val
		515					520					525			
Val	Ser	Lys	Lys	Ala	Arg	Ala	Gly	Lys	Leu	Thr	Ala	Ser	Asp	Met	Gln
						535					540				
Gly	Gly	Cys	Phe	Thr	Ile	Ser	Ser	Leu	Gly	Gly	Ile	Gly	Gly	Thr	Ala
545					550					555					560
Phe	Thr	Pro	Ile	Val	Asn	Ala	Pro	Glu	Val	Gly	Ile	Leu	Gly	Val	Ser
				565					570					575	
Lys	Ser	Glu	Met	Lys	Pro	Val	Trp	Asn	Gly	Lys	Glu	Phe	Ala	Pro	Arg
			580					585					590		

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Leu Gln Leu Pro Leu Ser Leu Ser Tyr Asp His Arg Val Ile Asp Gly
595 600 605
Ala Glu Gly Ala Arg Phe Ile Thr Tyr Leu Asn Gly Cys Leu Ser Asp
610 615 620
Ile Arg Arg Leu Val Leu
625 630

<210> SEQ ID NO 24
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 24

Met Tyr Ser Lys Ile Leu Gly Thr Gly Ser Tyr Leu Pro Ser Gln Val
1 5 10 15
Arg Thr Asn Ala Asp Leu Glu Lys Met Val Asp Thr Ser Asp Glu Trp
20 25 30
Ile Val Thr Arg Thr Gly Ile Arg Glu Arg Arg Ile Ala Ala Asp Asn
35 40 45
Glu Thr Val Ala Asp Met Gly Phe Tyr Ala Ala Gln Asn Ala Ile Glu
50 55 60
Met Ala Gly Ile Asp Lys Asn Asp Ile Asp Leu Ile Ile Leu Ala Thr
65 70 75 80
Thr Ser Ser Ser His Thr Phe Pro Ser Ser Ala Cys Gln Val Gln Ala
85 90 95
Lys Leu Gly Ile Lys Gly Cys Pro Ala Phe Asp Leu Ala Ala Ala Cys
100 105 110
Ser Gly Phe Ile Tyr Gly Leu Ser Val Ala Asp Gln His Ile Lys Ser
115 120 125
Gly Met Cys Lys Asn Val Leu Val Ile Gly Ala Asp Ala Leu Ser Lys
130 135 140
Thr Cys Asp Pro Thr Asp Arg Ser Thr Ile Ile Leu Phe Gly Asp Gly
145 150 155 160
Ala Gly Ala Val Val Val Gly Ala Ser Glu Glu Pro Gly Ile Leu Ser
165 170 175
Thr His Val Tyr Ala Asp Gly Gln Phe Gly Asp Leu Leu Ser Leu Glu
180 185 190
Val Pro Glu Arg Gly Gly Asp Val Asp Lys Trp Leu Tyr Met Ala Gly
195 200 205
Asn Glu Val Phe Lys Val Ala Val Thr Gln Leu Ser Lys Leu Val Lys
210 215 220
Asp Thr Leu Ala Ala Asn Asn Met His Lys Ser Glu Leu Asp Trp Leu
225 230 235 240
Val Pro His Gln Ala Asn Tyr Arg Ile Ile Ser Ala Thr Ala Lys Lys
245 250 255
Leu Ser Met Ser Leu Asp Gln Val Val Ile Thr Leu Asp Arg His Gly
260 265 270
Asn Thr Ser Ala Ala Thr Val Pro Thr Ala Leu Asp Glu Ala Val Arg
275 280 285
Asp Gly Arg Ile Lys Arg Gly Gln Thr Leu Leu Leu Glu Ala Phe Gly
290 295 300
Gly Gly Phe Thr Trp Gly Ser Ala Leu Val Lys Phe

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305	310	315
<210> SEQ ID NO 25		
<211> LENGTH: 307		
<212> TYPE: PRT		
<213> ORGANISM: Vibrio furnisii		
<400> SEQUENCE: 25		
Met Ser Lys Phe Ala Ile Val Phe Pro Gly Gln Gly Ser Gln Ala Val		
1 5 10 15		
Gly Met Leu Ala Glu Leu Gly Glu Gln Tyr Asp Val Val Lys Gln Thr		
20 25 30		
Phe Ala Glu Ala Ser Asp Ala Leu Gly Tyr Asp Leu Trp Ala Leu Val		
35 40 45		
Gln Asn Gly Pro Val Glu Asp Leu Asn Gln Thr Phe Arg Thr Gln Pro		
50 55 60		
Ala Leu Leu Ala Ser Ser Val Ala Ile Trp Arg Val Trp Gln Ala Leu		
65 70 75 80		
Gly Leu Glu Gln Pro Glu Val Leu Ala Gly His Ser Leu Gly Glu Tyr		
85 90 95		
Ser Ala Leu Val Cys Ala Gly Val Ile Asp Phe Lys Ala Ala Ile Lys		
100 105 110		
Leu Val Glu Leu Arg Gly Gln Leu Met Gln Glu Ala Val Pro Ala Gly		
115 120 125		
Thr Gly Ala Met Tyr Ala Ile Ile Gly Leu Asp Asp Ala Ala Ile Ala		
130 135 140		
Lys Ala Cys Glu Asp Ala Ala Gln Gly Asp Val Val Ser Pro Val Asn		
145 150 155 160		
Phe Asn Ser Pro Gly Gln Val Val Ile Ala Gly Gln Lys Asp Ala Val		
165 170 175		
Glu Arg Ala Gly Ala Leu Cys Lys Glu Ala Gly Ala Lys Arg Ala Leu		
180 185 190		
Pro Leu Pro Val Ser Val Pro Ser His Cys Ala Leu Met Lys Pro Ala		
195 200 205		
Ala Glu Lys Leu Ala Val Ala Leu Glu Ala Leu Glu Phe Asn Ala Pro		
210 215 220		
Gln Ile Pro Val Ile Asn Asn Val Asp Val Ala Thr Glu Thr Asp Pro		
225 230 235 240		
Ala Lys Ile Lys Asp Ala Leu Val Arg Gln Leu His Ser Pro Val Arg		
245 250 255		
Trp Thr Glu Gly Val Glu Lys Met Ala Ala Gln Gly Ile Glu Lys Leu		
260 265 270		
Ile Glu Val Gly Pro Gly Lys Val Leu Thr Gly Leu Thr Lys Arg Ile		
275 280 285		
Val Lys Thr Leu Asp Ala Ala Ala Val Asn Asp Ile Ala Ser Leu Glu		
290 295 300		
Ala Val Lys		
305		
<210> SEQ ID NO 26		
<211> LENGTH: 248		
<212> TYPE: PRT		
<213> ORGANISM: Vibrio furnisii		

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<400> SEQUENCE: 26

Met	Ser	Asn	Phe	Met	Asn	Leu	Glu	Gly	Lys	Ile	Val	Leu	Val	Thr	Gly
1				5					10					15	
Ala	Ser	Arg	Gly	Ile	Gly	Lys	Ala	Ile	Ala	Glu	Leu	Leu	Val	Glu	Arg
			20					25					30		
Gly	Ala	Thr	Val	Ile	Gly	Thr	Ala	Thr	Ser	Glu	Ser	Gly	Ala	Asp	Ala
			35				40					45			
Ile	Ser	Ala	Tyr	Leu	Gly	Asp	Asn	Gly	Lys	Gly	Leu	Ala	Leu	Asn	Val
	50					55					60				
Thr	Asp	Val	Ala	Ser	Ile	Glu	Ser	Val	Leu	Lys	Ser	Ile	Asn	Asp	Glu
65					70					75				80	
Phe	Gly	Gly	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp
				85				90						95	
Asn	Leu	Leu	Met	Arg	Met	Lys	Asp	Asp	Glu	Trp	Thr	Asp	Ile	Leu	Asp
			100					105					110		
Thr	Asn	Leu	Thr	Ser	Ile	Phe	Arg	Leu	Ser	Lys	Ala	Val	Leu	Arg	Gly
		115					120					125			
Met	Met	Lys	Lys	Arg	Gln	Gly	Arg	Ile	Ile	Asn	Val	Gly	Ser	Val	Val
	130					135					140				
Gly	Thr	Met	Gly	Asn	Ala	Gly	Gln	Thr	Asn	Tyr	Ala	Ala	Ala	Lys	Ala
145					150					155				160	
Gly	Val	Ile	Gly	Phe	Thr	Lys	Ser	Met	Ala	Arg	Glu	Val	Ala	Ser	Arg
				165					170					175	
Gly	Val	Thr	Val	Asn	Thr	Val	Ala	Pro	Gly	Phe	Ile	Glu	Thr	Asp	Met
			180					185					190		
Thr	Lys	Ala	Leu	Asn	Asp	Asp	Gln	Arg	Ala	Ala	Thr	Leu	Ala	Gln	Val
		195					200					205			
Pro	Ala	Gly	Arg	Leu	Gly	Asp	Pro	Arg	Glu	Ile	Ala	Ser	Ala	Val	Ala
	210					215					220				
Phe	Leu	Ala	Ser	Pro	Glu	Ala	Ala	Tyr	Ile	Thr	Gly	Glu	Thr	Leu	His
225					230					235				240	
Val	Asn	Gly	Gly	Met	Tyr	Met	Val								
				245											

<210> SEQ ID NO 27
<211> LENGTH: 77
<212> TYPE: PRT
<213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 27

Met	Ser	Asn	Ile	Glu	Glu	Arg	Val	Lys	Lys	Ile	Ile	Val	Glu	Gln	Leu
1				5					10					15	
Gly	Val	Asp	Glu	Ala	Glu	Val	Lys	Asn	Glu	Ala	Ser	Phe	Val	Glu	Asp
			20					25					30		
Leu	Gly	Ala	Asp	Ser	Leu	Asp	Thr	Val	Glu	Leu	Val	Met	Ala	Leu	Glu
		35					40					45			
Glu	Glu	Phe	Asp	Thr	Glu	Ile	Pro	Asp	Glu	Glu	Ala	Glu	Lys	Ile	Thr
	50					55					60				
Thr	Val	Gln	Ala	Ala	Ile	Asp	Tyr	Val	Asn	Ser	Ala	Gln			
65					70					75					

<210> SEQ ID NO 28
<211> LENGTH: 416

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<212> TYPE: PRT
<213> ORGANISM: Vibrio furnisii

<400> SEQUENCE: 28

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

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

Gly Gln Ser Gly Ile Val Asn Ile Glu His Phe Asp Thr Thr Asn Phe
          35           40           45

Ser Thr Arg Phe Ala Gly Leu Val Lys Asp Phe Asn Cys Glu Glu Tyr
          50           55           60

Met Ser Lys Lys Asp Ala Arg Lys Met Asp Leu Phe Ile Gln Tyr Gly
65           70           75           80

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

Glu Glu Asn Ala Pro Arg Val Gly Val Ala Ile Gly Ser Gly Ile Gly
          100          105          110

Gly Leu Asp Leu Ile Glu Lys Gly His Gln Ala Leu Met Glu Lys Gly
          115          120          125

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

Val Ala Gly Asn Leu Ser Ile Met Arg Gly Leu Arg Gly Pro Asn Ile
145          150          155          160

Ala Ile Ser Thr Ala Cys Thr Thr Gly Leu His Asn Ile Gly His Ala
          165          170          175

Ala Arg Met Ile Ala Tyr Gly Asp Ala Glu Ala Met Val Ala Gly Gly
          180          185          190

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

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

Trp Asp Lys Asp Arg Asp Gly Phe Val Leu Gly Asp Gly Ala Gly Val
225          230          235          240

Met Val Leu Glu Gly Tyr Glu His Ala Lys Ala Arg Gly Ala Lys Ile
          245          250          255

Tyr Ala Glu Ile Val Gly Phe Gly Met Ser Gly Asp Ala Tyr His Met
          260          265          270

Thr Ser Pro Ser Glu Asp Gly Ser Gly Gly Ala Leu Ala Met Glu Ala
          275          280          285

Ala Met Arg Asp Ala Ala Leu Ala Gly Thr Gln Ile Gly Tyr Val Asn
          290          295          300

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

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

Ser Thr Lys Ser Met Thr Gly His Leu Leu Gly Ala Ala Gly Ser Val
          340          345          350

Glu Ala Ile Ile Thr Val Met Ser Leu Val Asp Gln Ile Val Pro Pro
          355          360          365

Thr Ile Asn Leu Asp Asn Pro Glu Glu Gly Leu Gly Val Asp Leu Val
          370          375          380

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Pro His Thr Ala Arg Lys Val Glu Gly Met Glu Tyr Ala Met Cys Asn
 385 390 395 400

Ser Phe Gly Phe Gly Gly Thr Asn Gly Ser Leu Ile Phe Lys Arg Val
 405 410 415

<210> SEQ ID NO 29
 <211> LENGTH: 344
 <212> TYPE: PRT
 <213> ORGANISM: *Vibrio furnisii*

<400> SEQUENCE: 29

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

Thr Val Ile Gly Ala Gly Ser Tyr Gly Thr Ser Leu Ala Ile Ser Leu
 20 25 30

Ala Arg Asn Gly Ala Asn Val Val Leu Trp Gly His Asp Pro Val His
 35 40 45

Met Ala Arg Leu Glu Ala Glu Arg Ala Asn His Glu Phe Leu Pro Asp
 50 55 60

Ile Asp Phe Pro Pro Ser Leu Ile Ile Glu Ser Asp Leu Gln Lys Ala
 65 70 75 80

Val Gln Ala Ser Arg Asp Leu Leu Val Val Val Pro Ser His Val Phe
 85 90 95

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

Ile Cys Trp Ala Thr Lys Gly Leu Glu Pro Asp Thr Gly Arg Leu Leu
 115 120 125

Gln Asp Val Ala His Asp Val Leu Gly Glu Ser His Pro Leu Ala Val
 130 135 140

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

Ala Ile Ser Val Ala Ser Pro Asp Ala Gln Phe Val Ala Asp Leu Gln
 165 170 175

Glu Lys Ile His Cys Ser Lys Thr Phe Arg Val Tyr Ala Asn Ser Asp
 180 185 190

Phe Ile Gly Met Gln Leu Gly Gly Ala Val Lys Asn Val Ile Ala Ile
 195 200 205

Gly Ala Gly Met Ser Asp Gly Ile Gly Phe Gly Ala Asn Ala Arg Thr
 210 215 220

Ala Leu Ile Thr Arg Gly Leu Ala Glu Met Thr Arg Leu Gly Ala Ala
 225 230 235 240

Leu Gly Ala Gln Pro Glu Thr Phe Met Gly Met Ala Gly Leu Gly Asp
 245 250 255

Leu Val Leu Thr Cys Thr Asp Asn Gln Ser Arg Asn Arg Arg Phe Gly
 260 265 270

Leu Ala Leu Gly Gln Gly Lys Asp Val Asp Thr Ala Gln Gln Asp Ile
 275 280 285

Gly Gln Val Val Glu Gly Tyr Arg Asn Thr Lys Glu Val Trp Leu Leu
 290 295 300

Ala Gln Arg Met Gly Val Glu Met Pro Ile Val Glu Gln Ile Tyr Gln
 305 310 315 320

Val Leu Tyr Gln Gly Lys Asp Ala Arg Met Ala Ala Gln Asp Leu Leu

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325330335

Ala Arg Asp Lys Lys Ala Glu Arg

340

<210> SEQ ID NO 30

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Vibrio furnisii

<400> SEQUENCE: 30

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

15

Glu Leu Tyr Gln Gly Gly Thr Arg Leu Ile Ala Met Arg Cys Ala Gly

202530

Phe Asp Lys Val Asp Leu Asp Ala Ala Lys Arg Ile Gly Met Gln Val

354045

Val Arg Val Pro Ala Tyr Ser Pro Glu Ala Val Ala Glu His Ala Val

505560

Gly Leu Met Met Cys Leu Asn Arg Arg Tyr His Lys Ala Tyr Gln Arg

65707580

Thr Arg Glu Ala Asn Phe Ser Leu Glu Gly Leu Val Gly Phe Asn Phe

859095

Tyr Gly Lys Thr Val Gly Val Ile Gly Ser Gly Lys Ile Gly Ile Ala

100105110

Ala Met Arg Ile Leu Lys Gly Leu Gly Met Asn Ile Leu Cys Phe Asp

115120125

Pro Tyr Glu Asn Pro Leu Ala Ile Glu Ile Gly Ala Lys Tyr Val Gln

130135140

Leu Pro Glu Leu Tyr Ala Asn Ser Asp Ile Ile Thr Leu His Cys Pro

145150155160

Met Thr Lys Glu Asn Tyr His Leu Leu Asp Glu Gln Ala Phe Ala Gln

165170175

Met Lys Asp Gly Val Met Ile Ile Asn Thr Ser Arg Gly Glu Leu Leu

180185190

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

195200205

Leu Gly Leu Asp Val Tyr Asp Asn Glu Lys Asp Leu Phe Phe Gln Asp

210215220

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

225230235240

Cys His Asn Val Leu Phe Thr Gly His Gln Ala Phe Leu Thr Glu Asp

245250255

Ala Leu His Asn Ile Ala Gln Thr Thr Leu Asn Asn Val Leu Ala Phe

260265270

Glu Gln Gly Thr Lys Ser Gly Asn Glu Leu Val Asn

275280

What is claimed is:

1. A method of producing a fatty alcohol composition in a recombinant microorganism, comprising the steps of:

(a) genetically engineering a microorganism to comprise a nucleic acid sequence encoding a polypeptide having acetyl-CoA carboxylase activity (EC 6.4.1.2), and a

nucleic acid sequence encoding a polypeptide having fatty alcohol forming activity, resulting in a recombinant microorganism;

(b) culturing the recombinant microorganism in a culture medium containing a carbon source under conditions effective to overexpress the acetyl-CoA carboxylase polypeptide and the polypeptide having fatty alcohol

forming activity, wherein a fatty alcohol composition is produced by said cultured recombinant microorganism; and

(c) optionally recovering the fatty alcohol composition from the cell culture.

2. The method of claim **1**, further comprising genetically engineering said microorganism to comprise at least one nucleic acid sequence encoding a polypeptide having thioesterase activity, wherein said thioesterase polypeptide is expressed.

3. The method of claim **1**, wherein said polypeptide having fatty alcohol forming activity is (i) a fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), or (ii) an acyl-CoA reductase (EC 1.2.1.50) and an alcohol dehydrogenase (EC 1.1.1.1).

4. The method of claim **2**, wherein said polypeptide having fatty alcohol forming activity is (i) a fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), or (ii) an acyl-CoA reductase (EC 1.2.1.50) and an alcohol dehydrogenase (EC 1.1.1.1).

5. The method of claim **4**, wherein said polypeptide having fatty alcohol forming activity is a fatty alcohol forming acyl-CoA reductase.

6. The method of claim **1**, wherein said the fatty alcohol composition comprises one or more of saturated or unsaturated C12, C14 or C16 fatty alcohols.

7. A recombinant microorganism comprising:

(a) a nucleic acid sequence encoding a branched chain alpha-keto acid dehydrogenase 60 (Bkd) operon including branched-chain α -keto acid decarboxylase α and β subunits (E1 α/β), a dihydrolipoyl transacylase component (E2), and a dihydrolipoyl dehydrogenase component (E3); and

(b) a nucleic acid sequence encoding a β -ketoacyl-ACP synthase III protein

(FabH, EC 2.3.1.41) with specificity for a branched chain acyl CoA molecule, wherein at least one nucleic acid sequence according to (a) or (b) is exogenous to the recombinant microorganism and wherein the recombinant microorganism produces a branched fatty acid derivative when cultured in the presence of a carbon source under conditions effective to express the nucleic acid sequences according to (a) and (b).

8. The recombinant microorganism according to claim **7**, wherein the nucleic acid sequence encoding the FabH protein with specificity for a branched chain acyl CoA molecule is exogenous to the recombinant microorganism and the expression of a FabH endogenous to the recombinant microorganism and lacking specificity for a branched chain acyl CoA molecule is attenuated.

9. The recombinant microorganism according to claim **7**, further comprising a nucleic acid sequence encoding at least one polypeptide having thioesterase activity.

10. The recombinant microorganism according to claim **9**, further comprising a nucleic acid sequence encoding a polypeptide having fatty alcohol forming activity.

11. The recombinant microorganism according to claim **10**, wherein said polypeptide having fatty alcohol forming activity is (i) a fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), or (II) acyl-CoA reductases (EC 1.2.1.50) and alcohol dehydrogenase (EC 1.1.1.1).

12. The recombinant microorganism according to claim **11**, wherein said polypeptide having fatty alcohol forming activity is a fatty alcohol forming acyl-CoA reductase.

13. A recombinant microorganism culture, comprising: the recombinant microorganism according to claim **11** and a fermentation medium comprising a carbon source.

14. A branched fatty alcohol composition produced by the recombinant microorganism culture according to claim **13**, wherein said fatty alcohol composition comprises one or more of saturated or unsaturated C12, C14 and C16 fatty alcohols.

15. A branched fatty alcohol composition obtained from the supernatant of the recombinant microorganism culture of claim **13** wherein the fatty alcohol composition comprises C₁₂ and C₁₄ fatty alcohols.

16. A branched fatty alcohol composition obtained from the supernatant of the recombinant microorganism culture of claim **13**, wherein the fatty alcohol composition comprises unsaturated fatty alcohols.

17. A branched fatty alcohol composition obtained from the supernatant of the recombinant microorganism culture of claim **13**, wherein the fatty alcohol composition comprises saturated fatty alcohols.

18. A method of producing a branched fatty alcohol composition in a recombinant microorganism, comprising the steps of:

(a) obtaining a genetically engineered recombinant microorganism according to claim **11**;

(b) culturing the recombinant microorganism in a culture medium containing a carbon source under conditions effective to express said: (i) Bkd operon; (ii) FabH;

(iii) a nucleic acid sequence encoding a polypeptide having fatty alcohol forming activity; and (iv) nucleic acid sequence encoding a polypeptide having thioesterase activity; and

(c) optionally recovering the branched fatty alcohol composition from the cell culture.

19. The method of claim **18**, wherein said polypeptide having fatty alcohol forming activity is (i) a fatty alcohol forming acyl-CoA reductase (FAR, EC 1.1.1.*), or (II) an acyl-CoA reductase (EC 1.2.1.50) and an alcohol dehydrogenase (EC 1.1.1.1).

20. The recombinant microorganism according to claim **19**, wherein said polypeptide having fatty alcohol forming activity is a fatty alcohol forming acyl-CoA reductase.

* * * * *