US 20180142273A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2018/0142273 A1**

GONZALEZ et al. (43) **Pub. Date: May 24, 2018**

(54) **ITERATIVE PLATFORM FOR THE SYNTHESIS OF ALPHA FUNCTIONALIZED PRODUCTS**

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(21) Appl. No.: **15/566,704**

(22) PCT Filed: **Apr. 15, 2016**

(86) PCT No.: **PCT/US16/27873**

§ 371 (c)(1),
(2) Date: **Oct. 14, 2017**

Related U.S. Application Data

(60) Provisional application No. 62/148,123, filed on Apr. 15, 2015.

Publication Classification

(51) **Int. Cl.**

C12P 13/00	(2006.01)
C12P 7/42	(2006.01)
C12P 7/40	(2006.01)
C12N 9/04	(2006.01)
C12N 9/88	(2006.01)
C12N 9/02	(2006.01)
C12N 9/16	(2006.01)
C12N 9/10	(2006.01)
C12P 7/18	(2006.01)
C12P 7/26	(2006.01)

(52) **U.S. Cl.**

CPC ***C12P 13/001*** (2013.01); ***C12P 7/26*** (2013.01); ***C12P 7/40*** (2013.01); ***C12N 9/0006*** (2013.01); ***C12Y 101/01035*** (2013.01); ***C12Y 101/011*** (2013.01); ***C12N 9/88*** (2013.01); ***C12Y 402/01017*** (2013.01); ***C12Y 402/01059*** (2013.01); ***C12N 9/001*** (2013.01); ***C12Y 103/01038*** (2013.01); ***C12Y 103/01009*** (2013.01); ***C12N 9/16*** (2013.01); ***C12N 9/13*** (2013.01); ***C12Y 208/03008*** (2013.01); ***C12N 9/1029*** (2013.01); ***C12Y 203/01008*** (2013.01); ***C12Y 101/01001*** (2013.01); ***C12N 9/1096*** (2013.01); ***C12P 7/18*** (2013.01); ***C12P 7/42*** (2013.01)

(57) **ABSTRACT**

The use of microorganisms to make alpha-functionalized chemicals and fuels, (e.g. alpha-functionalized carboxylic acids, alcohols, hydrocarbons, amines, and their beta-, and omega-functionalized derivatives), by utilizing an iterative carbon chain elongation pathway that uses functionalized extender units. The core enzymes in the pathway include thiolase, dehydrogenase, dehydratase and reductase. Native or engineered thiolases catalyze the condensation of either unsubstituted or functionalized acyl-CoA primers with an alpha-functionalized acetyl-CoA as the extender unit to generate alpha-functionalized β-keto acyl-CoA. Dehydrogenase converts alpha-functionalized β-keto acyl-CoA to alpha-functionalized β-hydroxy acyl-CoA. Dehydratase converts alpha-functionalized β-hydroxy acyl-CoA to alpha-functionalized enoyl-CoA. Reductase converts alpha-functionalized enoyl-CoA to alpha-functionalized acyl-CoA. The platform can be operated in an iterative manner (i.e. multiple turns) by using the resulting alpha-functionalized acyl-CoA as primer and the aforementioned alpha-functionalized extender unit in subsequent turns of the cycle. Termination pathways acting on any of the four alpha-functionalized CoA thioester intermediates terminate the platform and generate various alpha-functionalized carboxylic acids, alcohols and amines with different β-reduction degree.

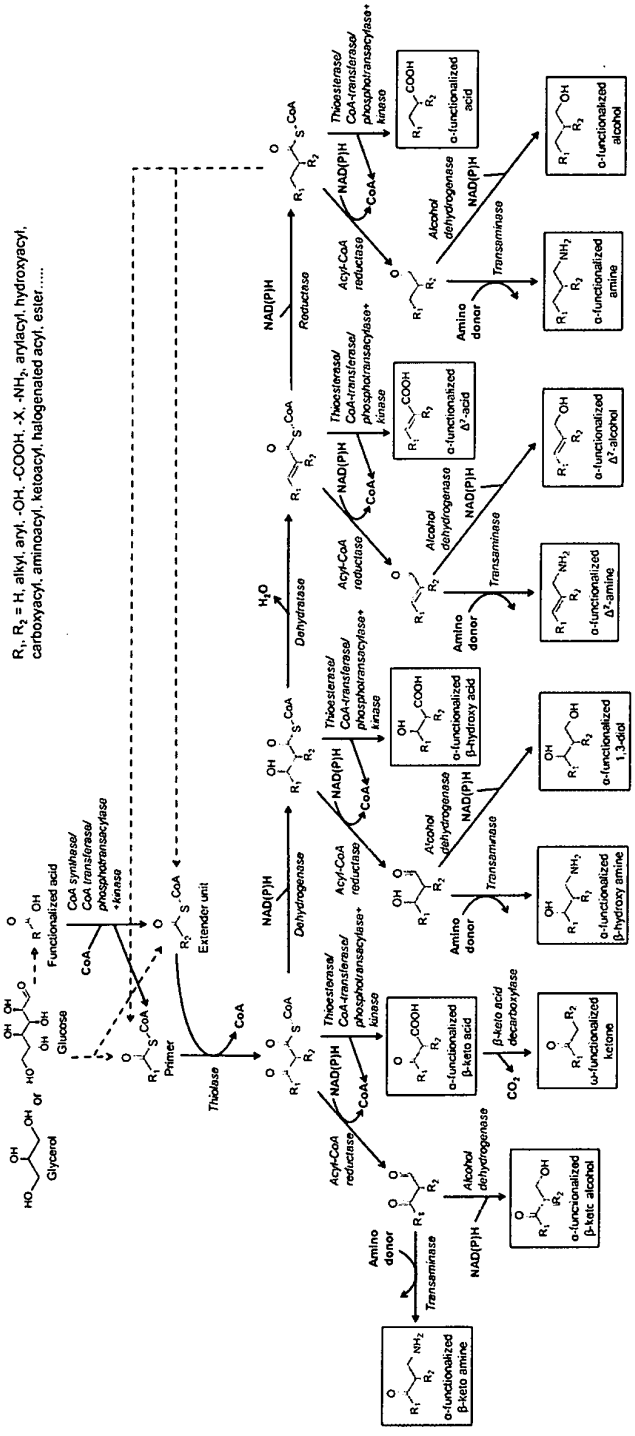

R1, R2 = H, alkyl, aryl, -OH, -COOH, -X, -NH2, arylacyl, hydroxyacyl, carboxyacyl, aminoacyl, ketoacyl, halogenated acyl, ester.....
Glycerol
or
Glucose
Funcionalized acid
CoA synthase/ CoA transferase/ phosphotransacylase +kinase
CoA
Primer
Extender unit
Thiolase
NAD(P)H
Dehydrogenase
Acyl-CoA reductase
Thioesterase/ CoA-transferase/ phosphotransacylase+ kinase
α-functionalized β-keto acid
β-keto acid decarboxylase
ω-functionalized ketone
Alcohol dehydrogenase
α-functionalized β-keto alcohol
Amino donor
Transaminase
α-functionalized β-keto amine
α-functionalized β-hydroxy acid
α-functionalized β-hydroxy amine
α-functionalized 1,3-diol
Dehydratase
H2O
Reductase
α-functionalized Δ2-acid
α-functionalized Δ2-amine
α-functionalized Δ2-alcohol
α-functionalized acid
α-functionalized amine
α-functionalized alcohol

Figure 1

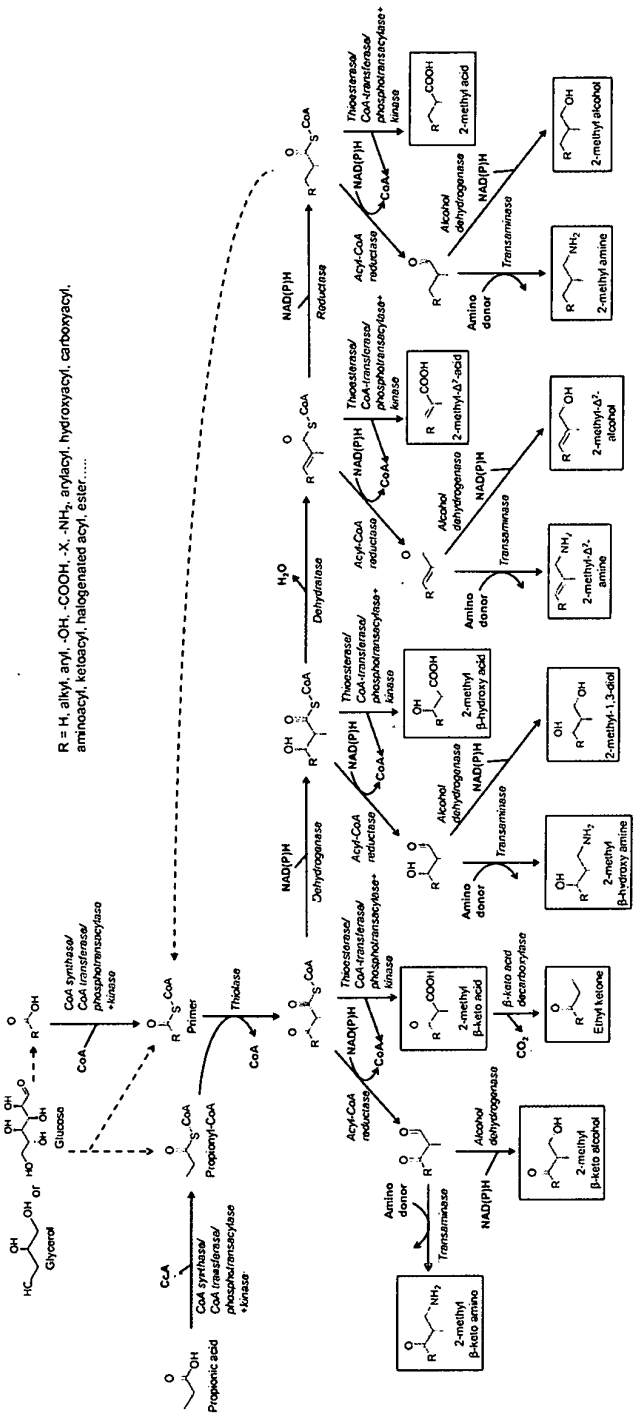

R = H, alkyl, aryl, -OH, -COOH, -X, -NH2, arylacyl, hydroxyacyl, carboxyacyl, aminoacyl, ketoacyl, halogenated acyl, ester.....
Glycerol
Glucose
Propionic acid
Propionyl-CoA
Primer
CoA synthase/ CoA transferase/ phosphotransacylase +kinase
Thiolase
Dehydrogenase
Dehydratase
Reductase
Thioesterase/ CoA-transferase/ phosphotransacylase+ kinase
Acyl-CoA reductase
Alcohol dehydrogenase
Transaminase
Amino donor
β-keto acid decarboxylase
2-methyl β-keto acid
Ethyl ketone
2-methyl β-keto alcohol
2-methyl β-keto amine
2-methyl β-hydroxy acid
2-methyl β-hydroxy amine
2-methyl-1,3-diol
2-methyl-Δ2-acid
2-methyl-Δ2-amine
2-methyl-Δ2-alcohol
2-methyl acid
2-methyl amine
2-methyl alcohol

Figure 2

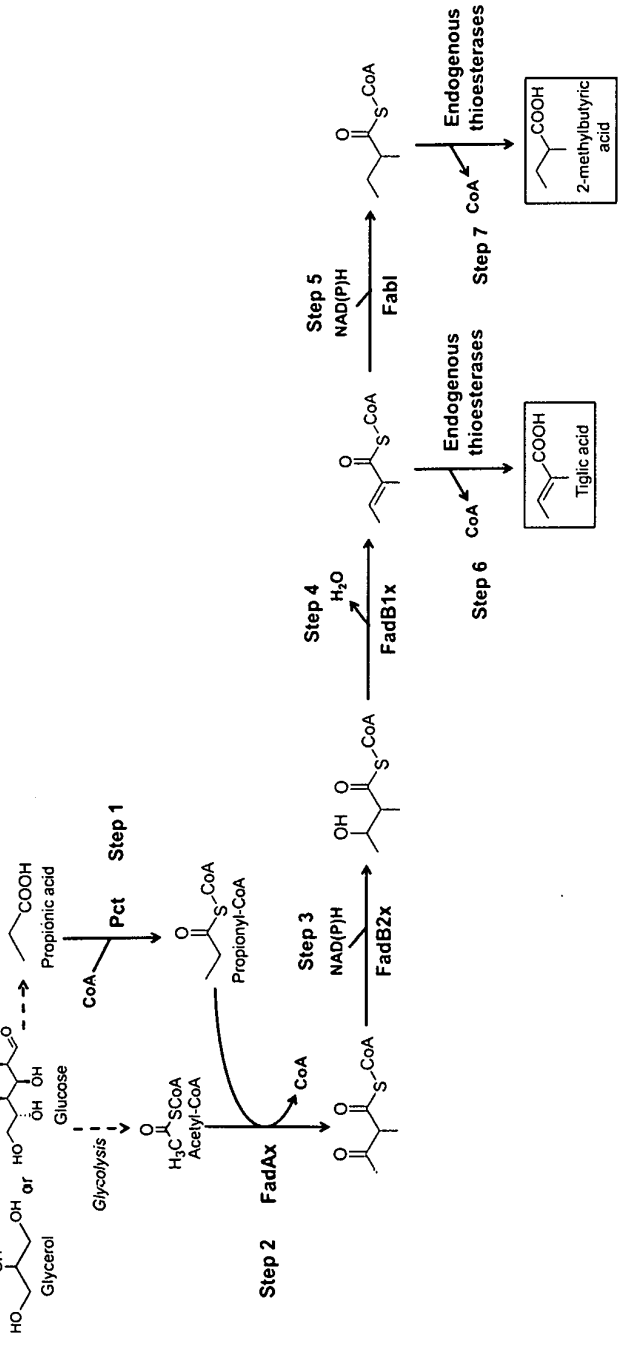

Glycerol
or
Glucose
Glycolysis
Propionic acid
CoA
Pct
Step 1
Propionyl-CoA
Acetyl-CoA
Step 2
FadAx
CoA
Step 3
NAD(P)H
FadB2x
Step 4
H2O
FadB1x
Step 5
NAD(P)H
FabI
Step 6
Endogenous thioesterases
CoA
Tiglic acid
Step 7
Endogenous thioesterases
CoA
2-methylbutyric acid

Figure 3

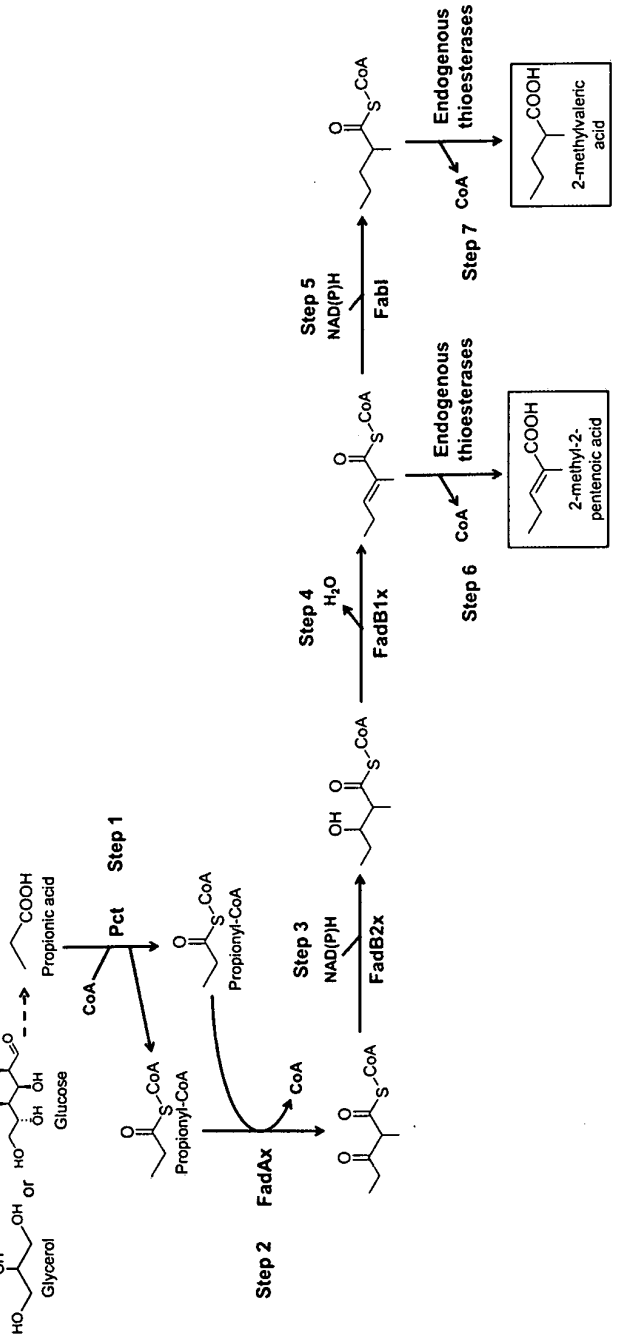

Glycerol
or
Glucose
Propionic acid
Step 1
Pct
CoA
Propionyl-CoA
Step 2
FadAx
CoA
Step 3
NAD(P)H
FadB2x
Step 4
H_2O
FadB1x
Step 5
NAD(P)H
FabI
Step 6
Endogenous thioesterases
CoA
2-methyl-2-pentenoic acid
Step 7
Endogenous thioesterases
CoA
2-methylvaleric acid

Figure 4

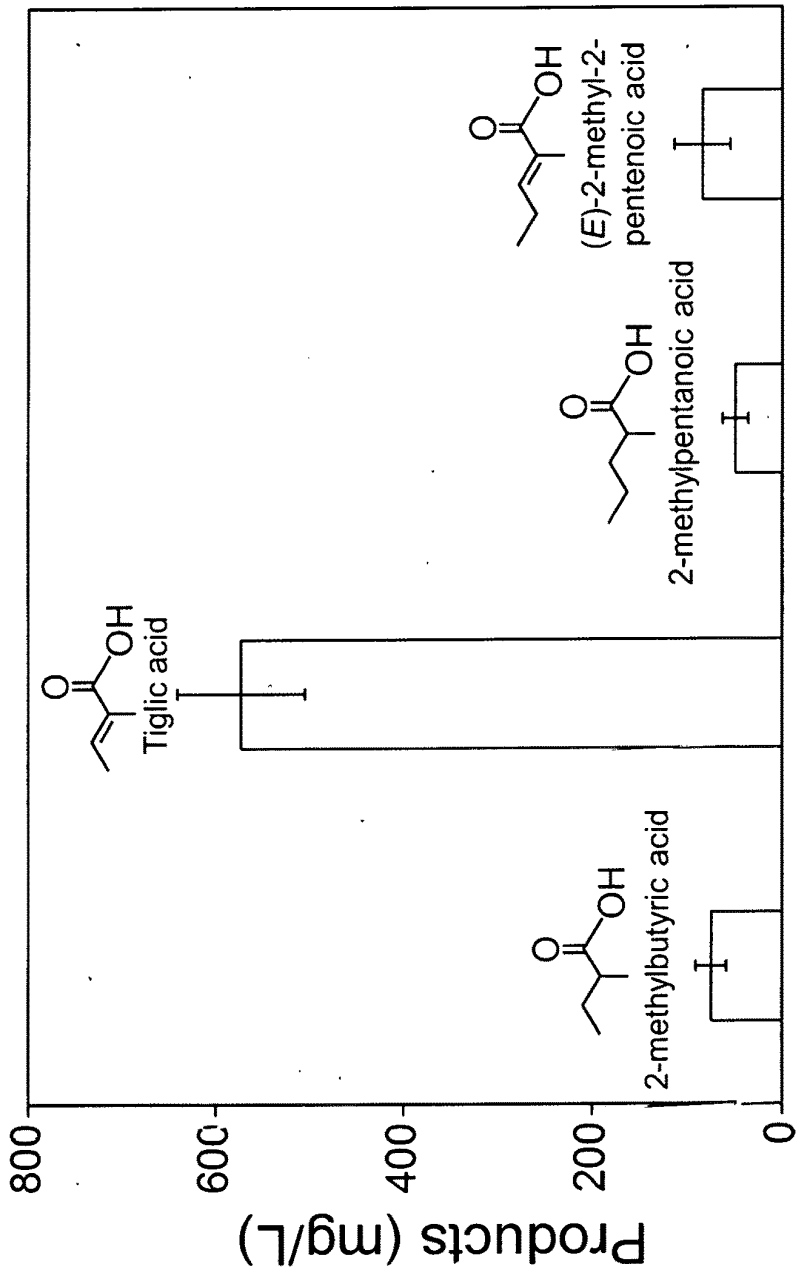

Products (mg/L)
800
600
400
200
0
2-methylbutyric acid
Tiglic acid
2-methylpentanoic acid
(E)-2-methyl-2-pentenoic acid

Figure 5

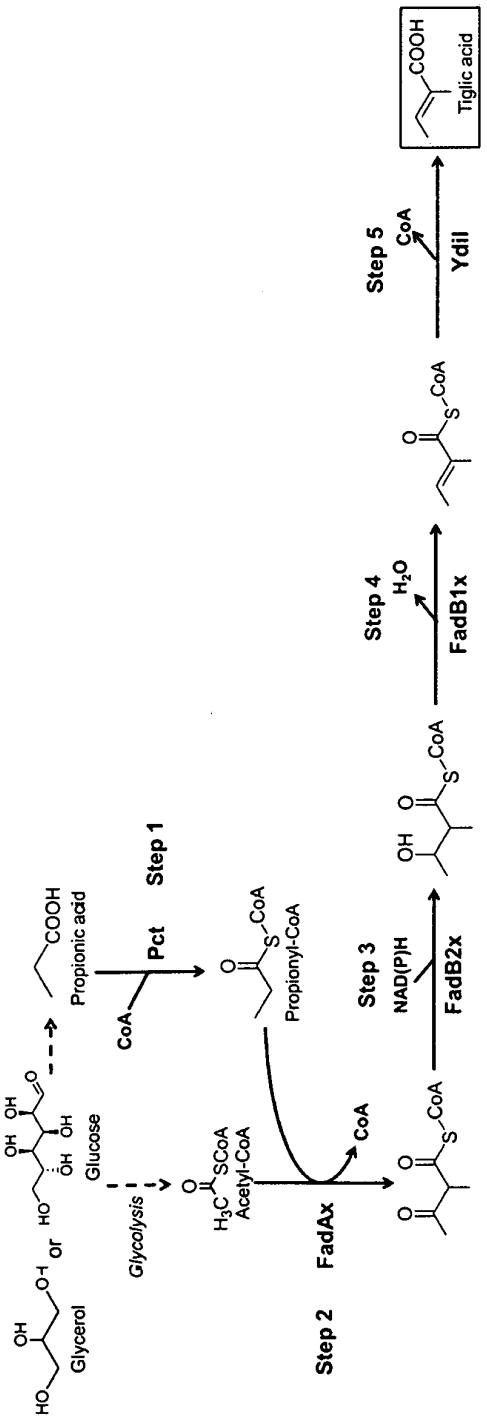

Glycerol
or
Glucose
Glycolysis
Propionic acid
Pct
CoA
Step 1
Acetyl-CoA
Propionyl-CoA
Step 2
FadAx
CoA
Step 3
NAD(P)H
FadB2x
Step 4
H2O
FadB1x
Step 5
CoA
YdiI
Tiglic acid

Figure 6

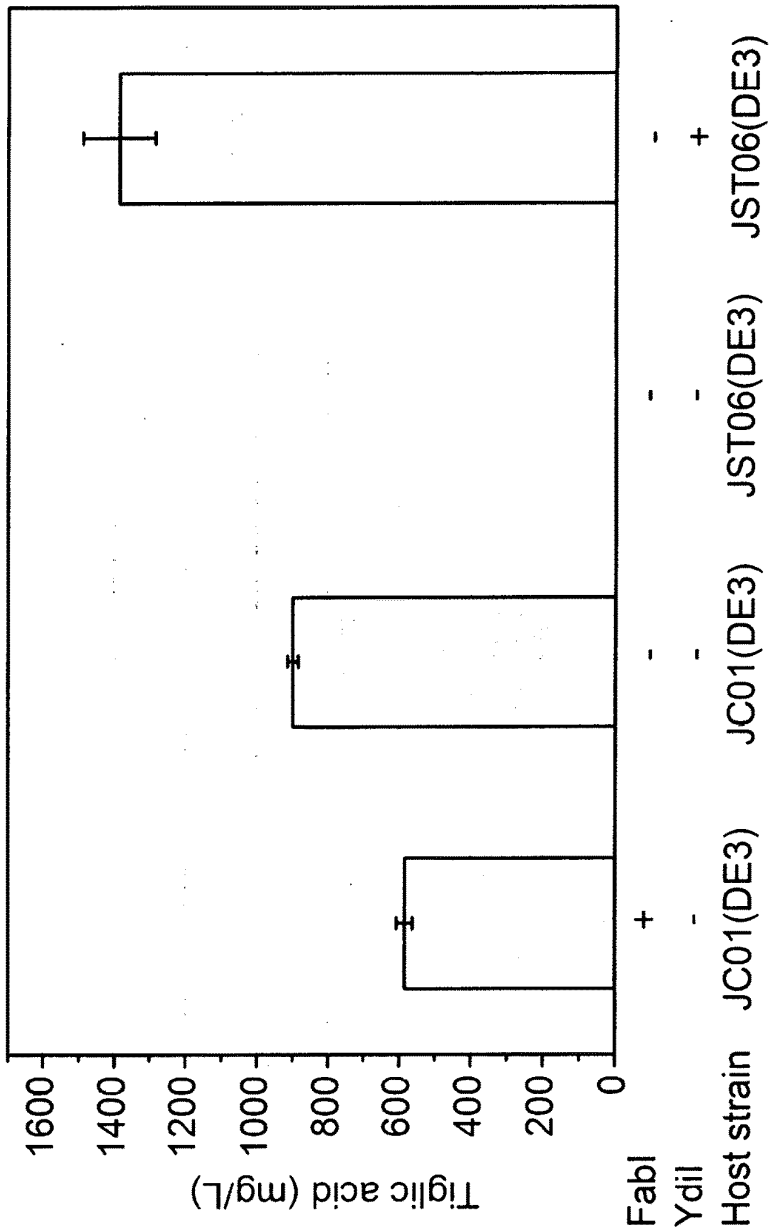

Tiglic acid (mg/L)
1600
1400
1200
1000
800
600
400
200
0
FabI
YdiI
Host strain
+
-
JC01(DE3)
-
-
JC01(DE3)
-
-
JST06(DE3)
-
+
JST06(DE3)

Figure 7

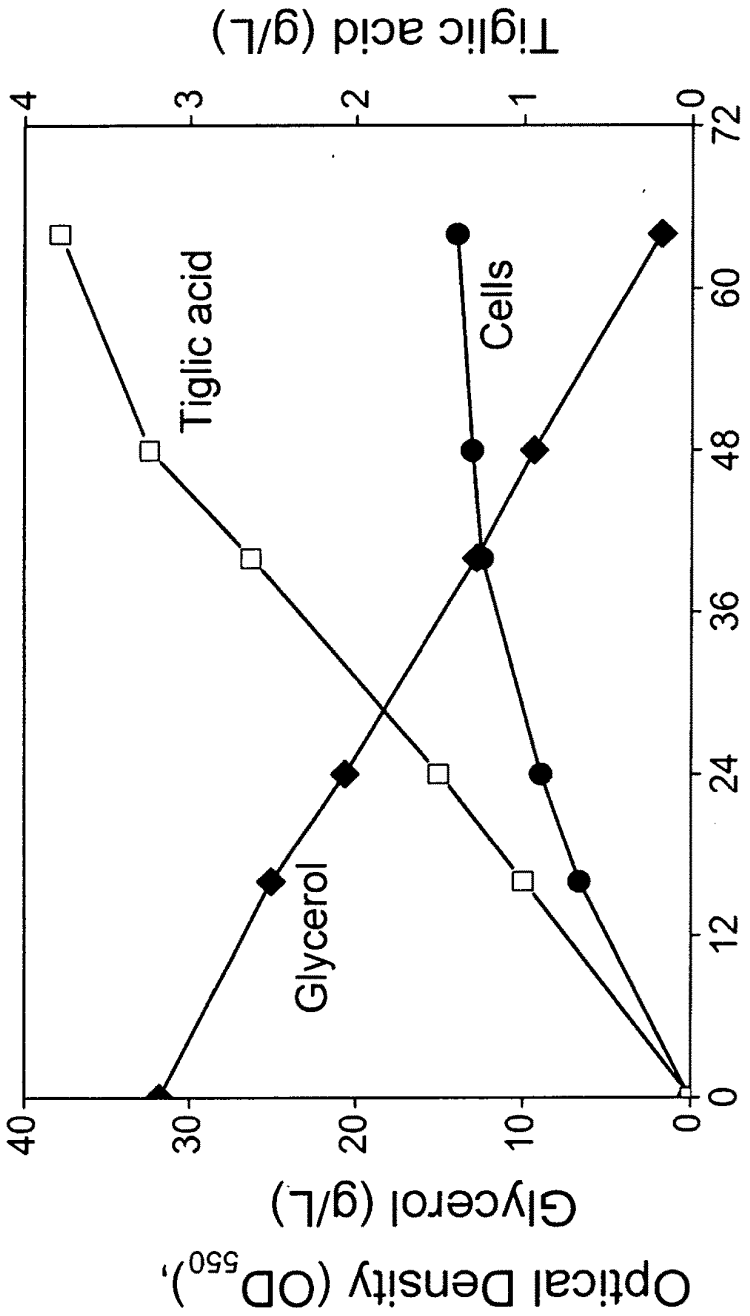

Optical Density (OD550), Glycerol (g/L)
Tiglic acid (g/L)
Time (hr)
Tiglic acid
Cells
Glycerol
0
10
20
30
40
0
1
2
3
4
0
12
24
36
48
60
72

Figure 8

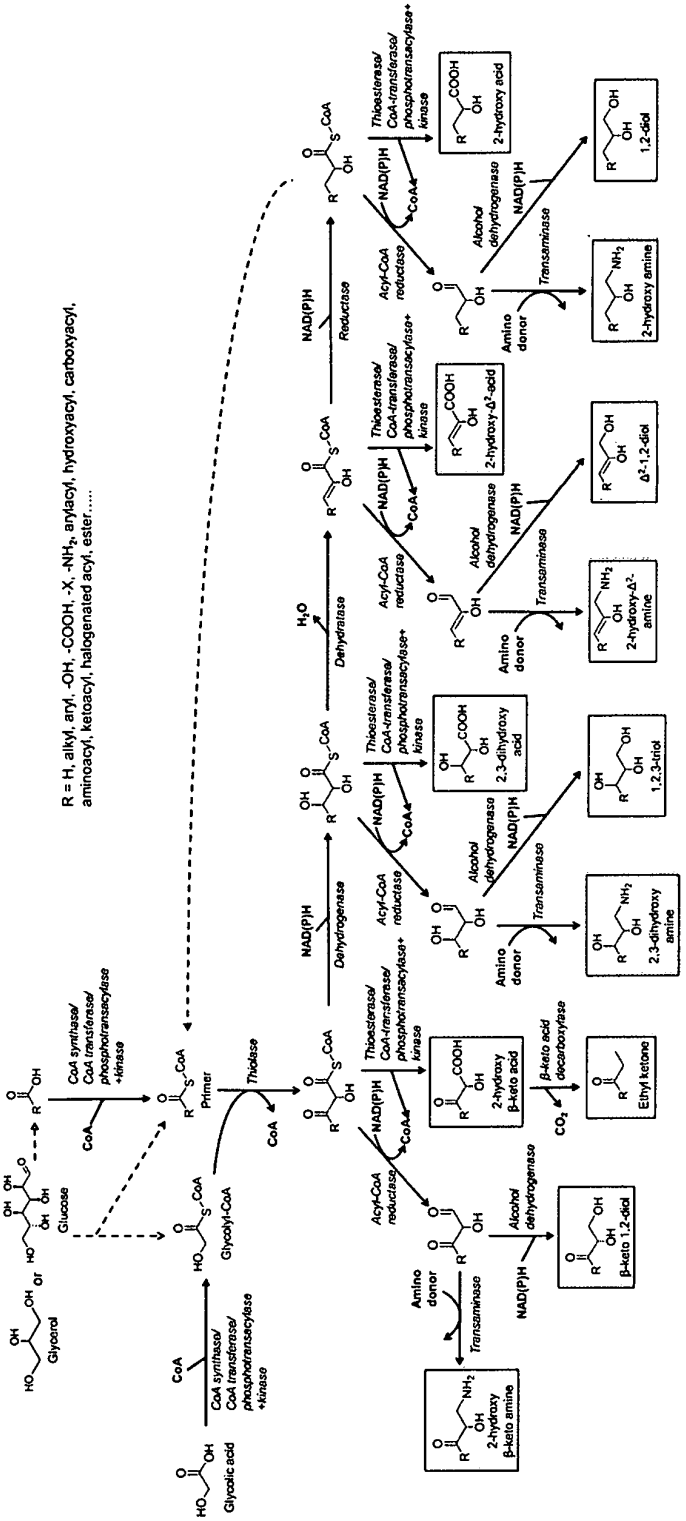

R = H, alkyl, aryl, -OH, -COOH, -X, -NH2, arylacyl, hydroxyacyl, carboxyacyl, aminoacyl, ketoacyl, halogenated acyl, ester.....
Glycerol
Glucose
Glycolic acid
Glycolyl-CoA
CoA synthase/ CoA transferase/ phosphotransacylase +kinase
Primer
Thiolase
Dehydrogenase
Dehydratase
Reductase
Thioesterase/ CoA-transferase/ phosphotransacylase+ kinase
Acyl-CoA reductase
Alcohol dehydrogenase
Transaminase
Amino donor
β-keto acid decarboxylase
2-hydroxy β-keto acid
2-hydroxy β-keto amine
β-keto 1,2-diol
Ethyl ketone
2,3-dihydroxy acid
2,3-dihydroxy amine
1,2,3-triol
2-hydroxy-Δ2-acid
2-hydroxy-Δ2-amine
Δ2-1,2-diol
2-hydroxy acid
2-hydroxy amine
1,2-diol

Figure 9

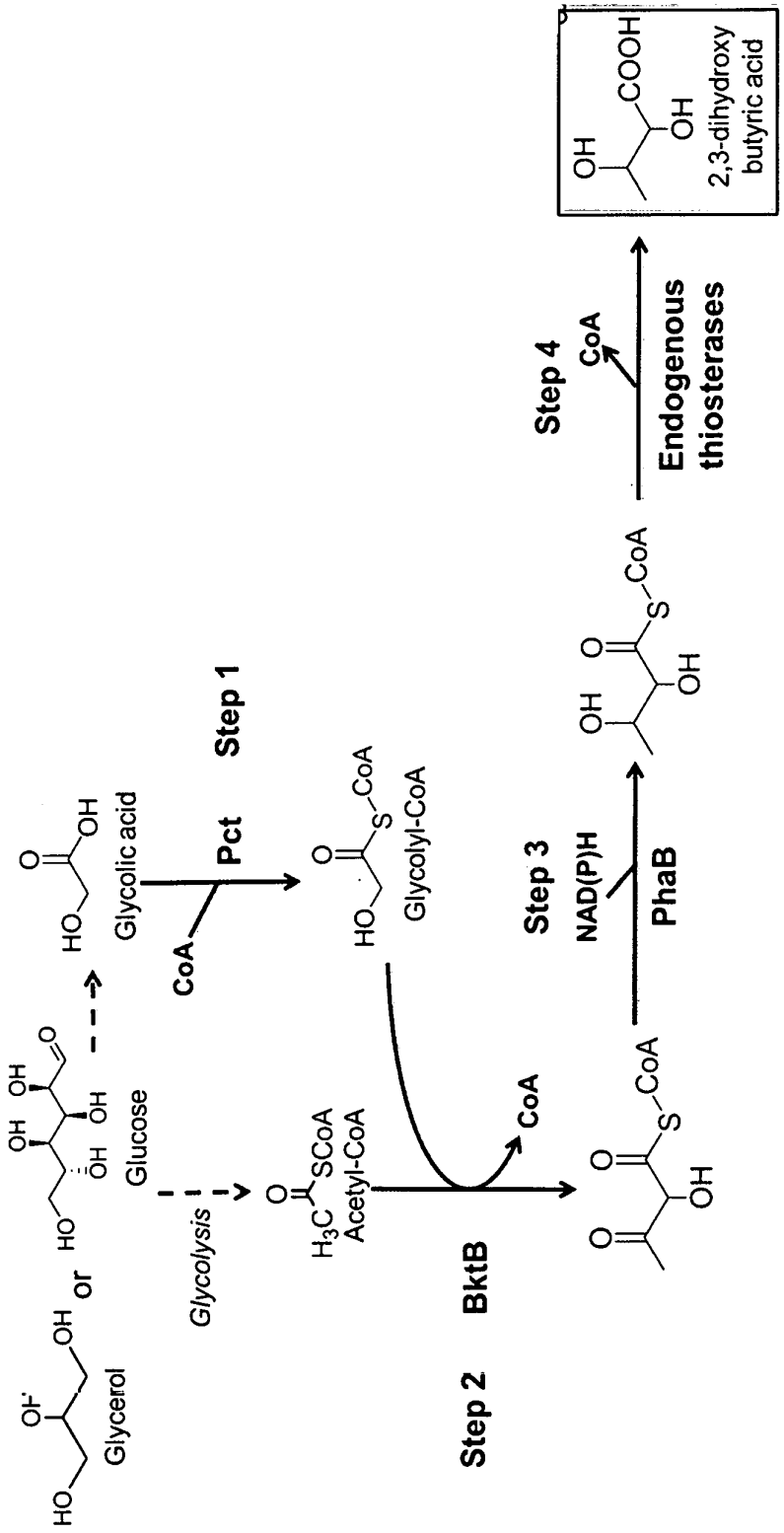

Glycerol
or
Glucose
Glycolysis
Glycolic acid
Pct
CoA
Step 1
Glycolyl-CoA
Acetyl-CoA
Step 2
BktB
CoA
Step 3
NAD(P)H
PhaB
Step 4
CoA
Endogenous thiosterases
2,3-dihydroxy butyric acid

Figure 10

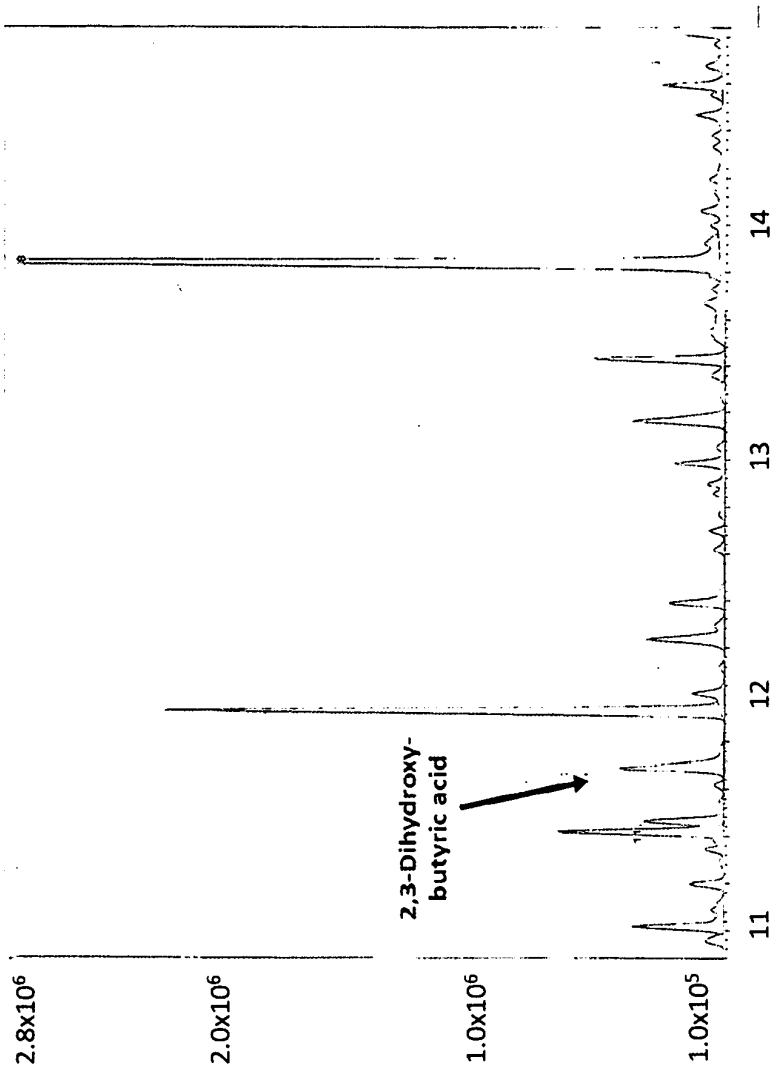

2.8x10^6
2.0x10^6
1.0x10^6
1.0x10^5
2,3-Dihydroxy-butyric acid
11
12
13
14

Figure 11

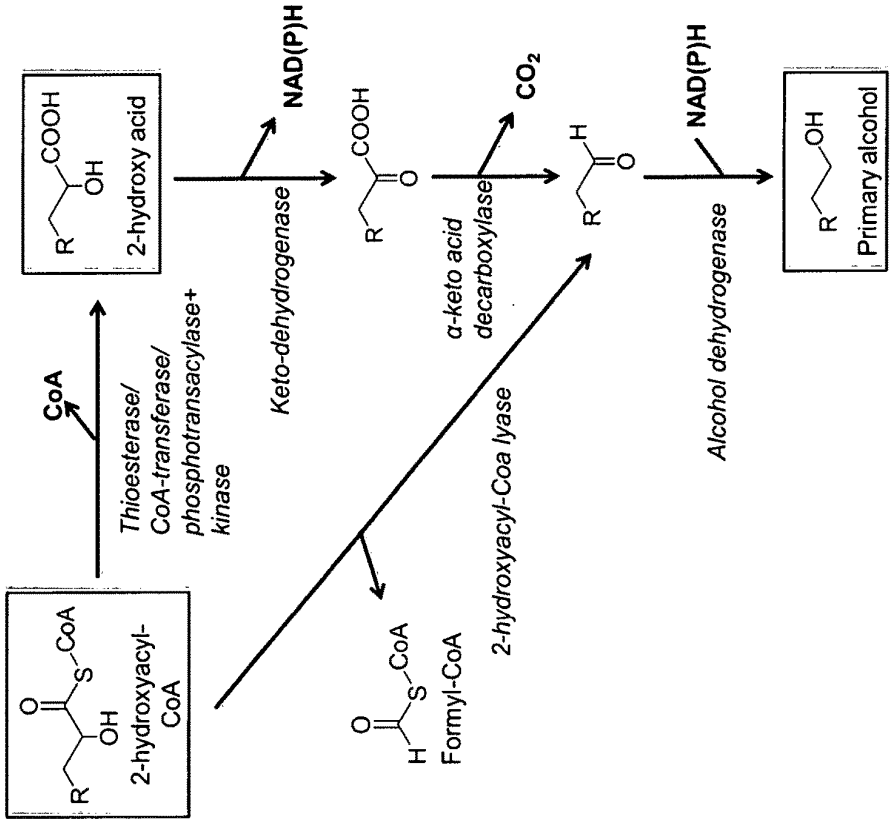

2-hydroxyacyl-CoA
CoA
Thioesterase/
CoA-transferase/
phosphotransacylase+
kinase
2-hydroxy acid
NAD(P)H
Keto-dehydrogenase
α-keto acid
decarboxylase
CO2
NAD(P)H
Alcohol dehydrogenase
Primary alcohol
Formyl-CoA
2-hydroxyacyl-Coa lyase

Figure 12

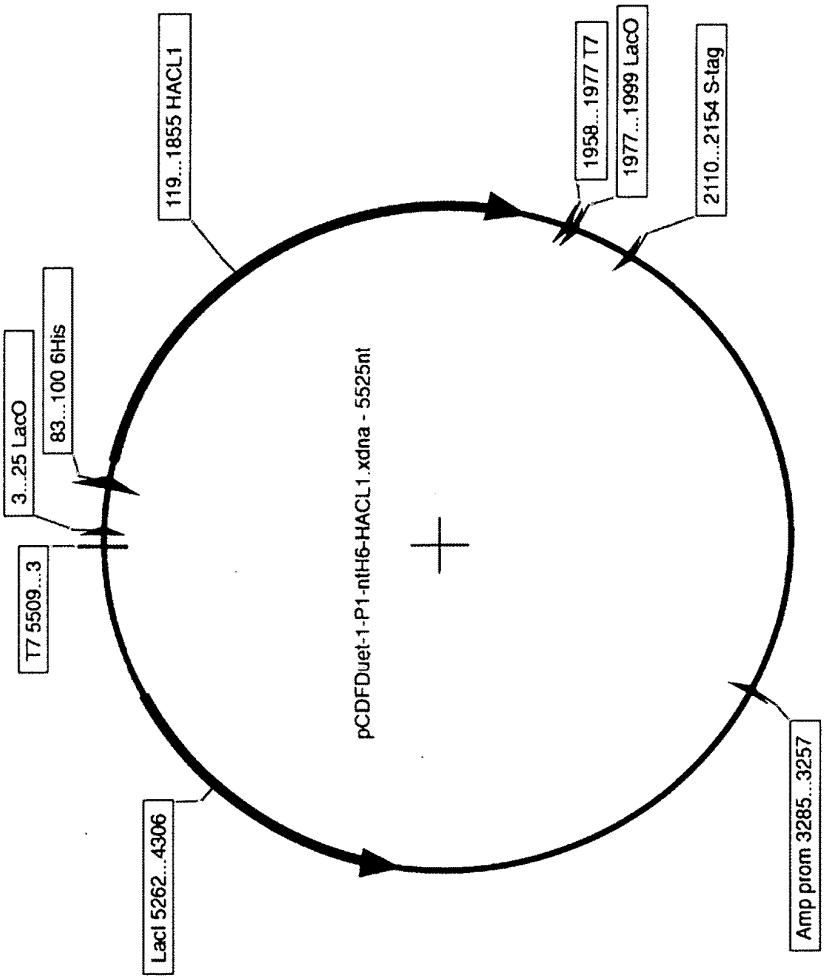

pCDFDuet-1-P1-nlH6-HACL1.xdna - 5525nt
119...1855 HACL1
1958...1977 T7
1977...1999 LacO
2110...2154 S-tag
3...25 LacO
83...100 6His
T7 5509...3
LacI 5262...4306
Amp prom 3285...3257

FIGURE 13

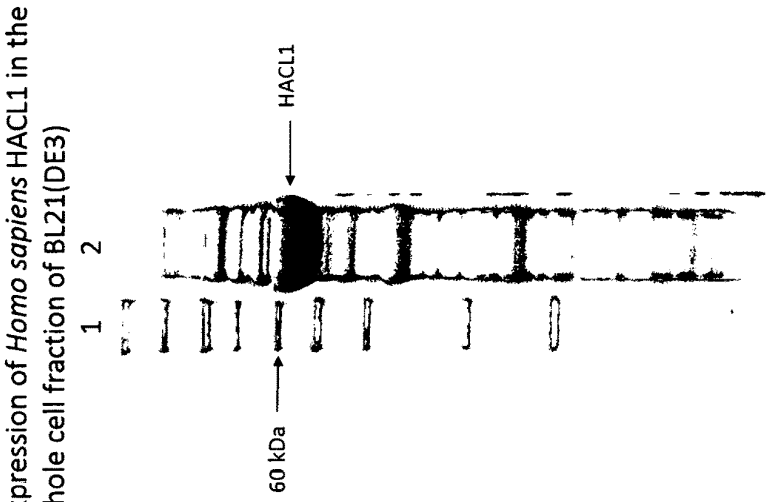

Expression of *Homo sapiens* HACL1 in the whole cell fraction of BL21(DE3)
1
2
HACL1
60 kDa
Lane 1: Ladder;
Lane 2: Whole cell sample of BL21(DE3) pCDFDuet-1-P1-ntH6-HACL1

Figure 14

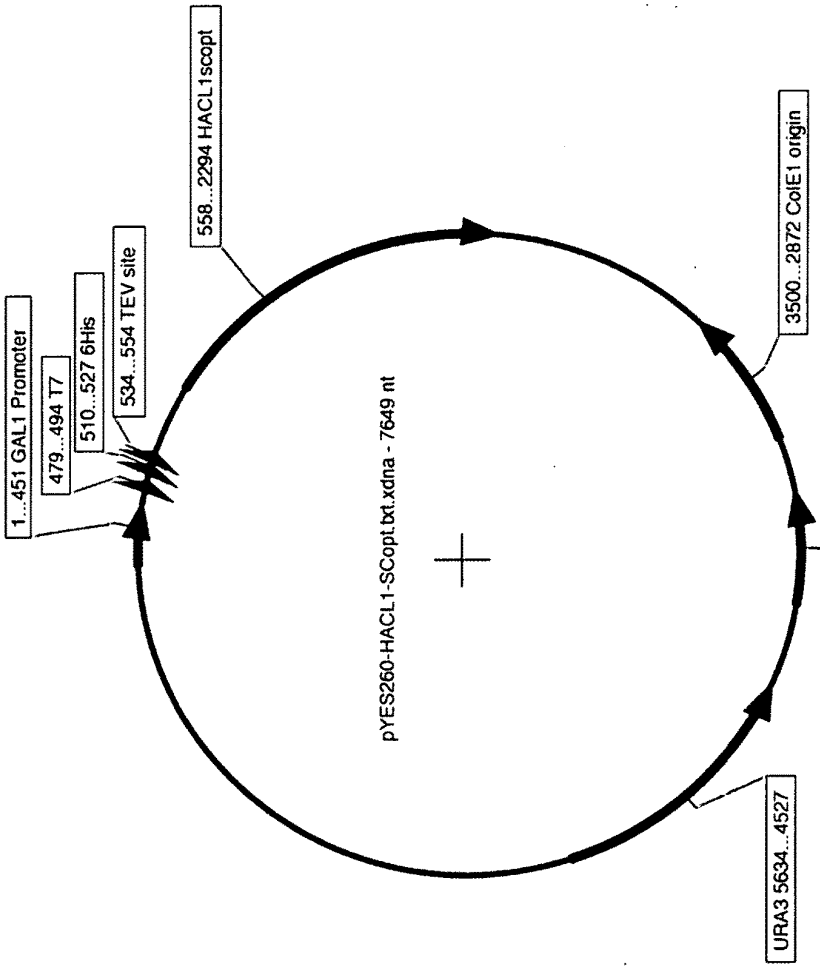
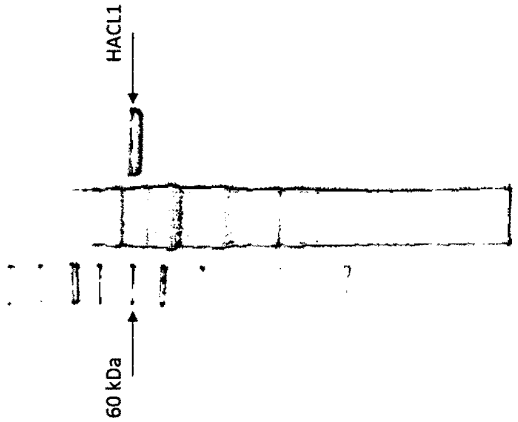

1...451 GAL1 Promoter
479...494 T7
510...527 6His
534...554 TEV site
558...2294 HACL1scopt
3500...2872 ColE1 origin
pYES260-HACL1-SCopt.txt.xdna - 7649 nt
AMPR 4311...3652
URA3 5634...4527

FIGURE 15

Expression and purification of *Homo sapiens* HACL1 in *S. cerevisiae* INVSc1



Lane 1: Ladder;
Lane 2: Cell extract fraction of *S. cerevisiae* pYES260-HACL1-ScOpt;
Lane 3: HACL1 purified from *S. cerevisiae* pYES260-HACL1-ScOpt

Figure 16

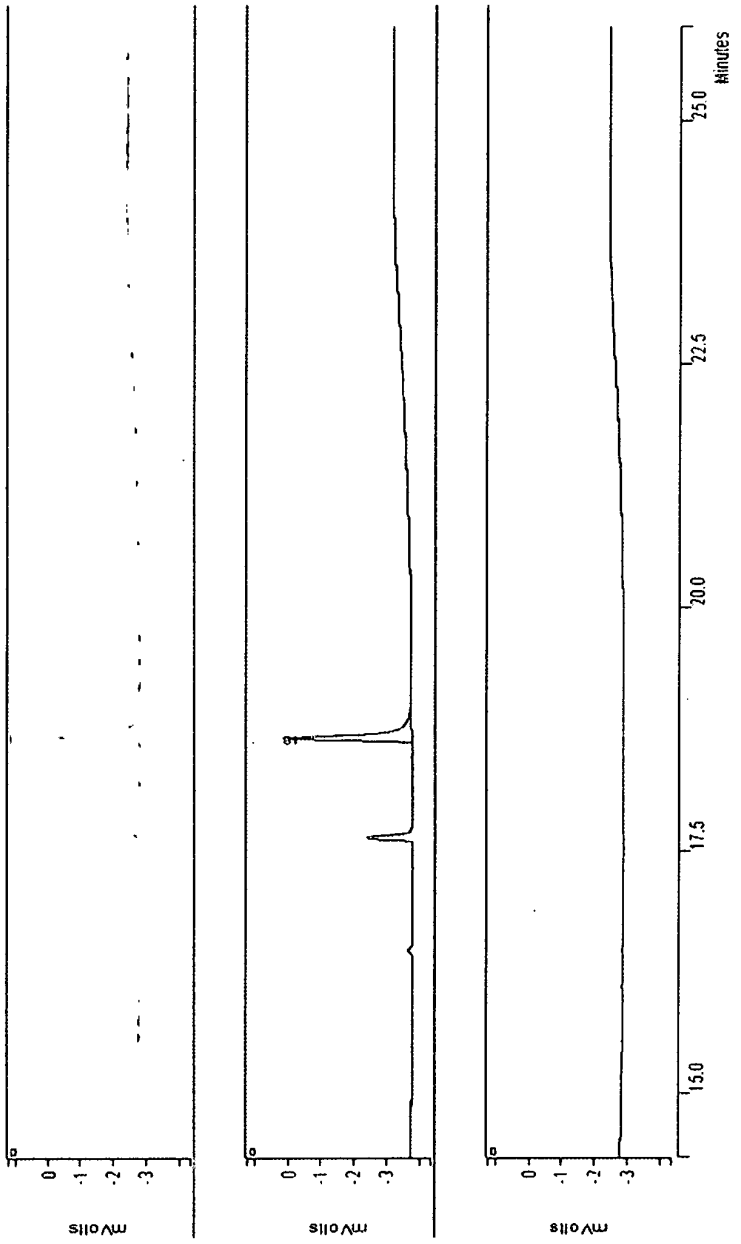


Figure 17

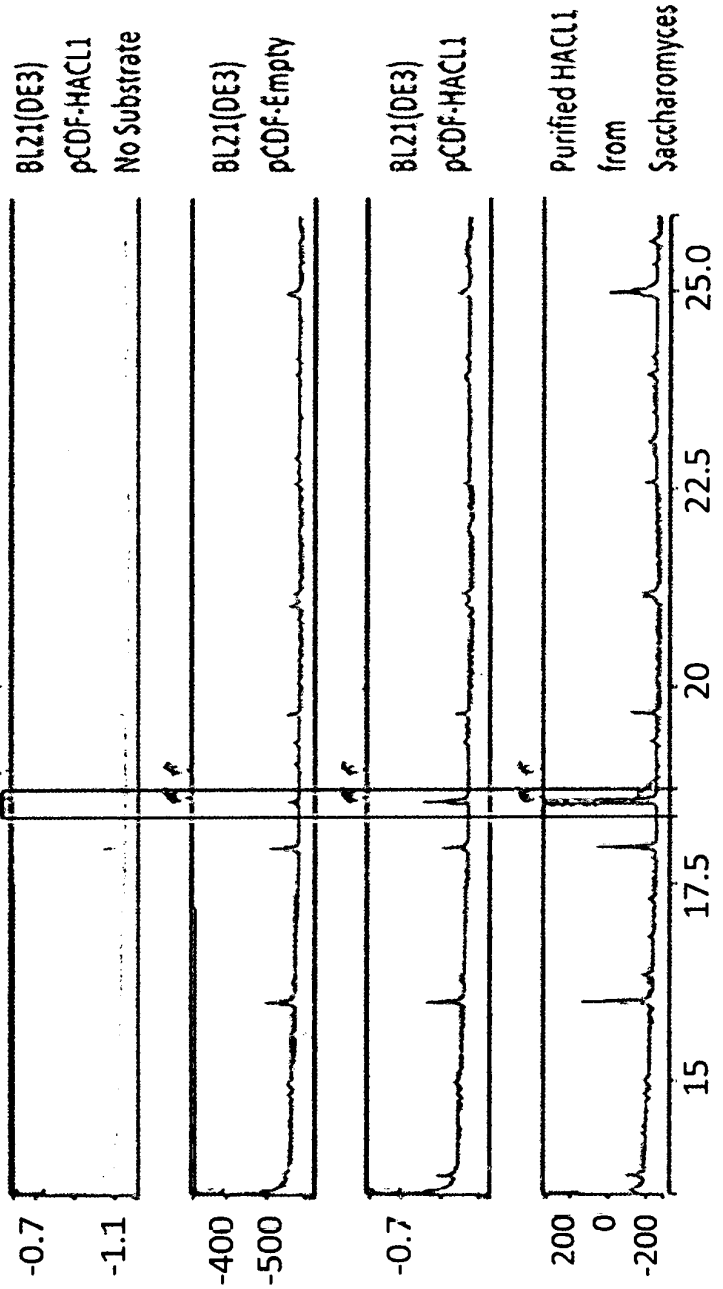

BL21(DE3)
pCDF-HACL1
No Substrate
BL21(DE3)
pCDF-Empty
BL21(DE3)
pCDF-HACL1
Purified HACL1
from
Saccharomyces
-0.7
-1.1
-400
-500
-0.7
200
0
-200
15
17.5
20
22.5
25.0
HACL1 expressed with low induction - 60 minute assay.

Figure 18

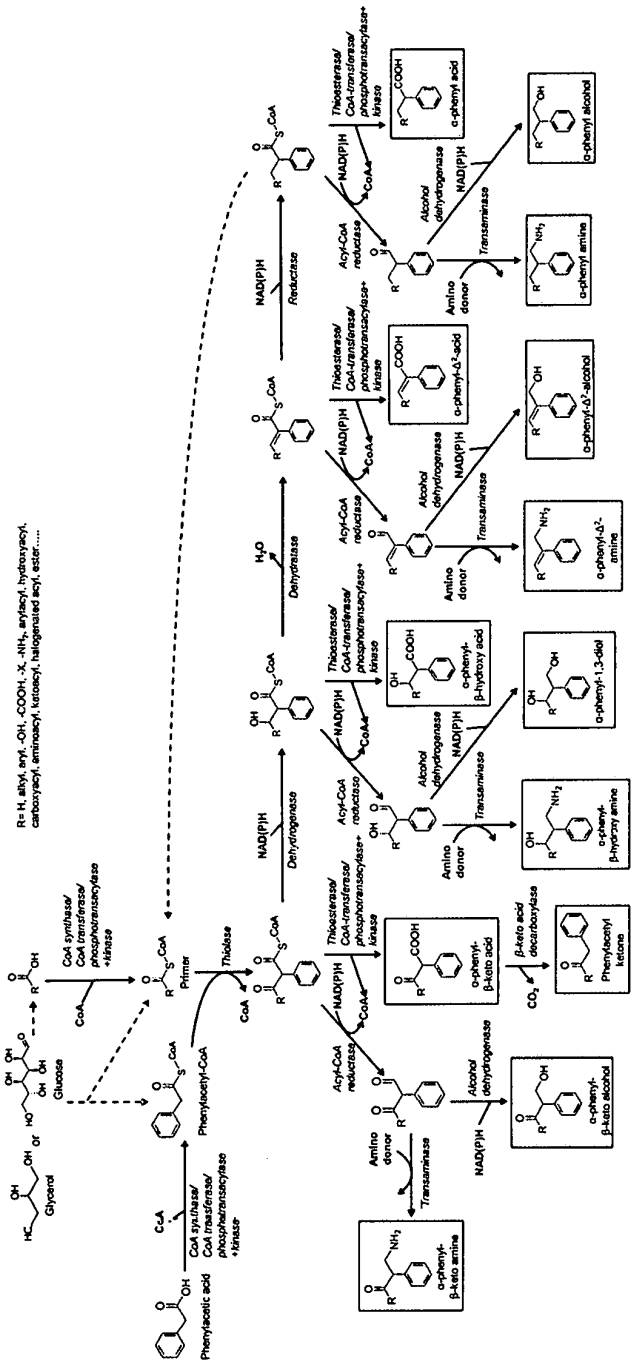

R= H, alkyl, aryl, -OH, -COOH, -X, -NH2, arylacyl, hydroxyacyl, carboxyacyl, aminoacyl, ketoacyl, halogenated acyl, ester....
Glycerol
Glucose
or
Phenylacetic acid
Phenylacetyl-CoA
CoA synthase/ CoA transferase/ phosphotransacylase +kinase
Primer
Thiolase
Dehydrogenase
Dehydratase
Reductase
Thioesterase/ CoA-transferase/ phosphotransacylase+ kinase
Acyl-CoA reductase
Alcohol dehydrogenase
Transaminase
Amino donor
β-keto acid decarboxylase
o-phenyl-β-keto amine
o-phenyl-β-keto alcohol
o-phenyl-β-keto acid
Phenylacetyl ketone
o-phenyl-β-hydroxy amine
o-phenyl-β-hydroxy acid
o-phenyl-1,3-diol
o-phenyl-Δ2-amine
o-phenyl-Δ2-alcohol
o-phenyl-Δ2-acid
o-phenyl amine
o-phenyl alcohol
o-phenyl acid

Figure 19

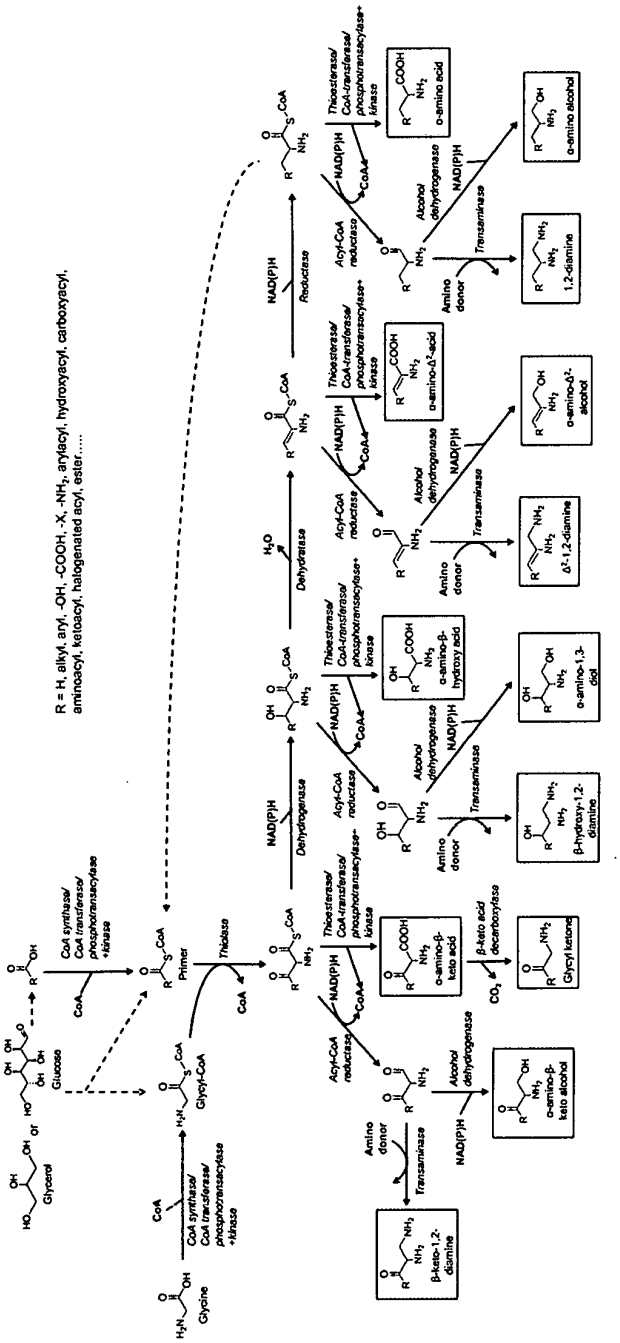

R = H, alkyl, aryl, -OH, -COOH, -X, -NH2, arylacyl, hydroxyacyl, carboxyacyl, aminoacyl, ketoacyl, halogenated acyl, ester....
Glucose
Glycerol
Glycine
Glycyl-CoA
CoA synthase/ CoA transferase/ phosphotransacylase +kinase
Primer
Thiolase
Dehydrogenase
Dehydratase
Reductase
Thioesterase/ CoA-transferase/ phosphotransacylase+ kinase
Acyl-CoA reductase
Alcohol dehydrogenase
Transaminase
Amino donor
NAD(P)H
CoA
H2O
CO2
β-keto acid decarboxylase
α-amino-β-keto acid
Glycyl ketone
β-keto-1,2-diamine
α-amino-β-keto alcohol
β-hydroxy-1,2-diamine
α-amino-1,3-diol
α-amino-β-hydroxy acid
Δ1-1,2-diamine
α-amino-Δ2-alcohol
α-amino-Δ2-acid
1,2-diamine
α-amino alcohol
α-amino acid

Figure 20

FIGURE 21

A recombinant microorganism comprising overexpressed enzymes including 1) a thiolase catalyzing the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA; a 2 hydroxyacyl-CoA dehydrogenase, 3) an enoyl-CoA hydratase, 4) an enoyl-CoA reductase and 5) a termination enzyme such as thioesterase.

A recombinant microorganism comprising an inducible expression vector or inducible integrated sequences for overexpressing enzymes including 1) a thiolase catalyzing the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA; a 2 hydroxyacyl-CoA dehydrogenase, 3) an enoyl-CoA hydratase, 4) an enoyl-CoA reductase and 5) a termination enzyme such as thioesterase.

A recombinant microorganism being a bacteria comprising an inducible expression vector or inducible integrated sequences for overexpressing enzymes including 1) a thiolase catalyzing the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA; a 2 hydroxyacyl-CoA dehydrogenase, 3) an enoyl-CoA hydratase, 4) an enoyl-CoA reductase and 5) a termination enzyme such as thioesterase.

A recombinant microorganism being a *E. coli* comprising an inducible expression vector or inducible integrated sequences for overexpressing enzymes including 1) a thiolase catalyzing the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA; a 2 hydroxyacyl-CoA dehydrogenase, 3) an enoyl-CoA hydratase, 4) an enoyl-CoA reductase and 5) a termination enzyme such as thioesterase.

A genetically engineered microorganism comprising means for:

a) an overexpressed activation enzyme(s) able to produce an alpha-functionalized CoA thioester extender unit, wherein said activation enzyme is selected from:
   i) an acyl-CoA synthase which converts the alpha-functionalized CoA thioester extender unit from an alpha-functionalized acid;
   ii) an acyl-CoA transferase which converts the alpha-functionalized CoA thioester extender unit from an alpha-functionalized acid;
   iii) a phosphotransacylase and a carboxylate kinase which converts the alpha-functionalized CoA thioester extender unit from an alpha-functionalized acid;
   iv) other one or more enzymes that allow the production of the alpha-functionalized CoA thioester extender unit from the carbon source without via the alpha-functionalized acid;

b) an overexpressed activation enzyme(s) able to produce an acyl-CoA primer wherein said activation enzyme is selected from:
   i) an acyl-CoA synthase which converts the acyl-CoA primer from its acid form;
   ii) an acyl-CoA transferase which converts the acyl-CoA primer from its acid form;
   iii) a phosphotransacylase and a carboxylate kinase which converts the acyl-CoA primer from its acid form;
   iv) other one or more enzymes that allow the production of the acyl-CoA primer from the carbon source without via the alpha-functionalized acid;

c) an overexpressed thiolase enzyme that catalyzes the condensation of an acyl-CoA primer with an alpha-functionalized CoA thioester extender unit to form an alpha-functionalized ß-ketoacyl-CoA;

d) an overexpressed 3-hydroxyacyl-CoA dehydrogenase or 3-oxoacyl-[acyl-carrier-protein] reductase enzyme that catalyzes the reduction of said alpha-functionalized ß-ketoacyl-CoA to produce an alpha-functionalized ß-hydroxyacyl-CoA;

e) an overexpressed enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydratase, or 3-hydroxyacyl-[acyl-carrier-protein] dehydratase enzyme that catalyzes the dehydration of said alpha-functionalized ß-hydroxyacyl-CoA to an alpha-functionalized trans-enoyl-CoA;

f) an overexpressed acyl-CoA dehydrogenase, trans-enoyl-CoA reductase, or enoyl-[acyl-carrier-protein] reductase enzyme that catalyzes the reduction of said alpha-functionalized trans-enoyl-CoA to an alpha-functionalized acyl-CoA;

g) iterations of steps b to e, wherein said iteration is achieved by utilizing an alpha-functionalized acyl-CoA-thioester product generated in step e of the last turn as an primer or an extender unit of step b in the next turn of iteration;

h) an overexpressed termination enzyme(s) able to use a substrate selected from the group consisting alpha-functionalized ß-ketoacyl-CoA-thioester products generated in step b, alpha-functionalized ß-hydroxyacyl-CoA-thioester products generated in step c, alpha-functionalized trans-enoyl-CoA-thioester products generated in step d and alpha-functionalized acyl-CoA-thioester products generated in step e, wherein said termination enzyme(s) is selected from:
   i) the group consisting of a thioesterase, or an acyl-CoA transferase, or a phosphotransacylase and a carboxylate kinase catalyzing the conversion of the CoA moiety of substrate CoA thioester to a carboxylic acid group;
   ii) an aldehyde-forming acyl-CoA reductase catalyzing the conversion of the CoA moiety of a substrate to an aldehyde group and an alcohol dehydrogenase catalyzing the conversion of an aldehyde to an alcohol;
   iii) an aldehyde-forming acyl-CoA reductase catalyzing the conversion of the CoA moiety of a substrate to an aldehyde group and a transaminase catalyzing the conversion of an aldehyde to an amine;

i) optionally reduced expressions of fermentation genes leading to reduced production of lactate, acetate, ethanol and succinate; and

wherein said microorganism has an iterative carbon elongation pathway beginning with said acyl-CoA thioester primer and alpha-functionalized CoA thioester extender unit and running in a biosynthetic direction.

Any microorganism as herein described, wherein said acyl-CoA primer is an acyl CoA thioester whose omega group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, halogenated acyl group, and any other

FIGURE 21
functionalized acyl groups.
Any microorganism as herein described, wherein said an alpha-functionalized CoA thioester extender unit is an acyl CoA thioester whose alpha group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, halogenated acyl group, and any other functionalized acyl groups.
Any microorganism as herein described,, wherein said alpha-functionalized acid is the acid form of alpha-functionalized CoA thioester extender unit whose omega group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, halogenated acyl group, and any other functionalized acyl groups.
Any microorganism as herein described, wherein said acid form of acyl-CoA primer has omega group selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, ketoacyl group, aminoacyl group, halogenated acyl group, and any other functionalized acyl groups.
Any microorganism as herein described, wherein said alpha-functionalized acid is supplemented in the media or supplied through the intracellular pathway from the carbon source.
Any microorganism as herein described, wherein said acid form of acyl-CoA primer is supplemented in the media or supplied through the intracellular pathway from the carbon source.
Any microorganism as herein described, wherein said genetically engineered microorganism produces a product selected from the group consisting of β-keto acids, β-keto alcohols, β-keto amines, β-hydroxy acids, 1,3-diols, β-hydroxy amines, Δ^2-fatty alcohols, Δ^2-fatty acids, Δ^2-amines, fatty acids, alcohols and amines whose alpha group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, halogenated acyl group, and any other functionalized acyl groups.
Any microorganism as herein described, wherein said step g uses alpha-functionalized ß-ketoacyl-CoA-thioester products generated in step b as the substrate, further comprising an overexpressed β-keto acid decarboxylase catalyzing the conversion of the ß-keto-acid to a ketone.
Any microorganism as herein described, wherein said genetically engineered microorganism produces a ketone whose omega group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, halogenated acyl group, and any other functionalized acyl groups.
Any microorganism as herein described, wherein said termination pathway i) of step g uses alpha-functionalized acyl-CoA-thioester products generated in step b as the substrate, utilizing glycolyl-CoA as the extender unit and further comprising: an overexpressed keto-dehydrogenase catalyzing the conversion of a 2-hydroxy acid to an alpha-keto acid; an overexpressed alpha-keto acid decarboxylase catalyzing the conversion of an alpha-keto acid to a primary aldehyde; an overexpressed alcohol dehydrogenase catalyzing the conversion of a primary aldehyde to a primary alcohol.
Any microorganism as herein described, utilizing glycolyl-CoA as the extender unit and further comprising: an overexpressed 2-hydroxyacyl-CoA lyase catalyzing the conversion of a 2-hydroxyacyl-CoA, generated from step e, to a primary aldehyde and a formyl-CoA; an overexpressed alcohol dehydrogenase catalyzing the conversion of a primary aldehyde to a primary alcohol.
Any microorganism as herein described, wherein said genetically engineered microorganism produces a primary alcohol.
Any microorganism as herein described, wherein said overexpressed acyl-CoA synthase is encoded by a gene(s) selected from the group consisting of *E. coli sucC, E. coli sucD, E. coli paaK, E. coli prpE, E. coli menE, E. coli fadK, E. coli fadD, Penicillium chrysogenum phl, Salmonella typhimurium LT2 prpE, Bacillus subtilis bioW, Cupriavidus basilensis hmfD, Rhodopseudomonas palustris badA, R. palustris hbaA, Pseudomonas aeruginosa* PAC1 *pqsA, Arabidopsis thaliana 4cl* and other homologs.
Any microorganism as herein described, wherein said overexpressed acyl-CoA transferase is encoded by a gene(s) selected from the group consisting of *E. coli atoD, E. coli scpC, E. coli ydiF, E. coli atoA, E. coli atoD, Clostridium acetobutylicum ctfA, C. acetobutylicum ctfB, Clostridium kluyveri cat2, C. kluyveri cat1, P. putida pcaI, P. putida pcaJ, Megasphaera elsdenii pct, Acidaminococcus fermentans gctA, Acidaminococcus fermentans gctB, Acetobacter aceti aarC* and other homologs.
Any microorganism as herein described, wherein said overexpressed phosphotransacylase is encoded by a gene(s) selected from the group consisting of *Clostridium acetobutylicum ptb, Enterococcus faecalis ptb, Salmonella enterica pduL* and other homologs.
Any microorganism as herein described, wherein said overexpressed carboxylate kinase is encoded by a gene(s) selected from the group consisting of *Clostridium acetobutylicum buk , Enterococcus faecalis buk, Salmonella enterica pduW* and other homologs.
Any microorganism as herein described, wherein said overexpressed thiolase is encoded by a gene(s) selected from the group consisting of *E. coli atoB, E. coli yqeF, E. coli fadA, E. coli fadI, Ralstonia eutropha bktB, Pseudomonas* sp. B13 *caiF, E coli paaJ, Rhodococcus opacus pcaF, Streptomyces* sp. *pcaF, P. putida fadAx, P. putida fadA, Ralstonia eutropha phaA, Acinetobacter* sp. ADP1 *dcaF, Clostridium acetobutylicum thlA, Clostridium acetobutylicum thlB* and other homologs.
Any microorganism as herein described, wherein said overexpressed 3-hydroxyacyl-CoA dehydrogenase or 3-oxoacyl-[acyl-carrier-protein] reductase is encoded by a gene(s) selected from the group consisting of *E. coli fabG, E. coli fadB, E. coli fadJ, E. coli paaH, P. putida fadB, P. putida fadB2x, Acinetobacter* sp. ADP1 *dcaH, Ralstonia eutrophus phaB, Clostridium*

FIGURE 21
acetobutylicum hbd and other homologs.
Any microorganism as herein described, wherein said overexpressed enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydratase, or 3-hydroxyacyl-[acyl-carrier-protein] dehydratase is encoded by a gene(s) selected from the group consisting of *E. coli fabA, E. coli fabZ, E. coli fadB, E. coli fadJ, E. coli paaF, P. putida fadB, P. putida fadB1x, Acinetobacter* sp. ADP1 *dcaE, Clostridium acetobutylicum crt, Aeromonas caviae phaJ* and other homologs.
Any microorganism as herein described, wherein said acyl-CoA dehydrogenase, trans-enoyl-CoA reductase, or enoyl-[acyl-carrier-protein] reductase is encoded by a gene(s) selected from the group consisting of *E. coli fadE, E. coli ydiO, Euglena gracilis* TER, *Treponema denticola* TER, *Clostridium acetobutylicum* TER, *E. coli fabI, Enterococcus faecalis fabK, Bacillus subtilis fabL, Vibrio cholerea fabV* and other homologs.
Any microorganism as herein described, wherein said overexpressed thioesterase is encoded by a gene(s) selected from the group consisting of *E. coli tesA, E. coli tesB, E. coli yciA, E. coli fadM, E. coli ydiI, E. coli ybgC, E. coli paaI, Mus musculus acot8, Alcanivorax borkumensis tesB2, Fibrobacter succinogenes Fs2108, Prevotella ruminicola Pr655, Prevotella ruminicola Pr1687, Lycopersicon hirsutum f glabratum mks2* and other homologs.
Any microorganism as herein described, wherein said overexpressed aldehyde-forming acyl-CoA reductase is encoded by a gene(s) selected from the group consisting *Acinetobacter calcoaceticus acr1, Acinetobacter sp Strain* M-1 *acrM, Clostridium beijerinckii ald, E. coli eutE, Salmonella enterica eutE, E. coli mhpF, Clostridium kluyveri sucD* and other homologs.
Any microorganism as herein described, wherein said overexpressed alcohol dehydrogenase is encoded by a gene(s) selected from the group consisting *E. coli betA, E. coli dkgA, E. coli eutG, E. coli fucO, E. coli ucpA, E. coli yahK, E. coli ybbO, E. coli ybdH, E. coli yiaY, E. coli yjgB, Saccharomyces cerevisiae ADH6, Clostridium kluyveri 4hbD, Acinetobacter* sp. SE19 *chnD* and other homologs.
Any microorganism as herein described, wherein said overexpressed transaminase is encoded by a gene(s) selected from the group consisting of *Arabidopsis thaliana* At3g22200, *Alcaligenes denitrificans aptA, Bordetella bronchiseptica* BB0869, *Bordetella parapertussis* BPP0784, *Brucella melitensis* BAWG_0478, *Burkholderia pseudomallei* BP1026B_I0669, *Chromobacterium violaceum* CV2025, *Oceanicola granulosus* OG2516_07293, *Paracoccus denitrificans* PD1222 Pden_3984, *Caulobacter crescentus* CC_3143, *Pseudogulbenkiania ferrooxidans* ω-TA, *Pseudomonas putida* ω -TA, *Ralstonia solanacearum* ω -TA, *Rhizobium meliloti* SMc01534, *Vibrio fluvialis* ω -TA, *Bacillus megaterium* SC6394 ω –TA, *Mus musculus abaT, Flavobacterium lutescens lat, Streptomyces clavuligerus lat, E. coli gabT, E. coli puuE, E. coli ygjG* and other homologs.
Any microorganism as herein described,, wherein said overexpressed β-keto acid decarboxylase is encoded by a gene(s) selected from the group consisting of *Clostridium acetobutylicum adc, Lycopersicon hirsutum f glabratum mks1* and other homologs.
Any microorganism as herein described, wherein said overexpressed keto-dehydrogenase is encoded by a gene(s) selected from the group consisting of *E. coli ldhA, E. coli lldD, E. coli leuB, Clostridium beijerinckii adh, Acidaminococcus fermentans hgdH, E. coli serA, Gordonia* sp. TY-5 *adh1, Gordonia* sp. TY-5 *adh2, Gordonia* sp. TY-5 *adh3, Rhodococcus ruber adh-A* and other homologs.
Any microorganism as herein described, wherein said overexpressed alpha-keto acid decarboxylase is encoded by a gene(s) selected from the group consisting *Lactococcus lactis kivd, Saccharomyces cerevisiae PDC1, S. cerevisiae PDC5, S. cerevisiae PDC6, S. cerevisiae ARO10, S. cerevisiae THI3, Zymomonas mobilis pdc* and other homologs.
Any microorganism as herein described, wherein said overexpressed 2-hydroxyacyl-CoA lyase is encoded by a gene(s) selected from the group consisting *Homo sapiens hacl1, Rattus norvegicus hacl1, Dictyostelium discoideum hacl1, Mus musculus hacl1* and other homologs.
Any microorganism as herein described, wherein said reduced expressions of fermentation enzymes are Δ*adhE*, (Δ*pta* or Δ*ackA* or Δ*ackApta*), Δ*poxB*, Δ*ldhA*, and Δ*frdA* and less acetate, lactate, ethanol and succinate are thereby produced.
Any microorganism as herein described, comprising one or more of the following mutations: fadR, atoC(c), ΔarcA, Δcrp, crp*.
Any microorganism herein described, said overexpressed enzymes being under the control of an inducible promoter, preferably multiple enzymes under the control of a single promoter, preferably allowing for coordinate expression of the enzymes. In one embodiment, the enzymes are expressed off an expression vector, but in another one or more are integrated into the genome.
A method of making alpha functionalized products, comprising growing any microorganism described herein in a nutrient broth under conditions such that said enzymes are overexpressed, said microorganism producing alpha functionalized product using said overexpressed enzymes, and isolating said alpha functionalized product.

ITERATIVE PLATFORM FOR THE SYNTHESIS OF ALPHA FUNCTIONALIZED PRODUCTS

PRIOR RELATED APPLICATIONS

[0001] This application claims priority to U.S. Ser. No. 62/148,123, ITERATIVE PLATFORM FOR THE SYNTHESIS OF ALPHA FUNCTIONALIZED PRODUCTS, filed Apr. 15, 2015 and expressly incorporated by reference herein in its entirety for all purposes.

FEDERALLY SPONSORED RESEARCH STATEMENT

[0002] Not applicable.

FIELD OF THE DISCLOSURE

[0003] This disclosure generally relates to the use of recombinant microorganisms to make various products.

BACKGROUND OF THE DISCLOSURE

[0004] Reactions that catalyze the iterative formation of carbon-carbon bonds are instrumental for many metabolic pathways, such as the biosynthesis of fatty acids, polyketides, and many other molecules with applications ranging from biofuels and green chemicals to therapeutic agents. These pathways typically start with small precursor metabolites that serve as building blocks that are subsequently condensed and modified in an iterative fashion until the desired chain length and functionality are achieved.

[0005] Most iterative carbon—carbon bond forming reactions in natural biological systems take place through a Claisen condensation mechanism in which the nucleophilic α-anion of an acyl-thioester, serving as the extender unit, attacks the electrophilic carbonyl carbon of another acyl-thioester, serving as the primer. Depending on how the nucleophilic α-anion is generated, the Claisen condensation reaction can be classified as decarboxylative or non-decarboxylative.

[0006] Many natural iterative carbon chain elongation pathways, like fatty acid and polyketide biosynthesis pathways, utilize decarboxylative Claisen condensation reactions with malonyl thioesters as extender units. Their potential products include fatty acids, alcohols, polyketides, esters, alkanes and alkenes with diverse chain lengths, structures and functionalities due to usage of functionalized primers, usage of α-functionalized malonyl thioesters as extender units and diverse pathways for termination of carbon chain elongation and subsequent product modification. However, despite the structural and functional diversity of these products, the use of malonyl thioester as a C2 extender unit requires the ATP-dependent activation of acetyl-CoA to malonyl-CoA, which in turn limits the energy efficiency of these pathways. Furthermore, owing to the decarboxylation mechanism, the β-site of extender units of the decarboxylative Claisen condensation must be a carboxylic group, restricting the range of extender units and potentially limiting the diversity of products that can be generated through these carbon chain elongation pathways.

[0007] In order to overcome this limitation, we have recently implemented a novel approach by driving beta-oxidation in reverse to make fatty acids instead of degrading them (see US20130316413, WO2013036812, each incorporated by reference in its entirety for all purposes). Unlike the fatty acid biosynthesis pathway, the reversal of the β-oxidation cycle operates with coenzyme-A (CoA) thioester intermediates and uses acetyl-CoA directly for acyl-chain elongation (rather than first requiring ATP-dependent activation to malonyl-CoA). In these pathways, thiolases catalyze the non-decarboxylative Claisen condensation in which acetyl-CoA, instead of malonyl thioesters, serves as the extender unit, and subsequent β-reduction reactions by hydroxyacyl-CoA dehydrogenases (HACDs), enoyl-CoA hydratases (ECHs) and enoyl-CoA reductases (ECRs) enable iteration. Compared to pathways utilizing decarboxylative Claisen condensation, these pathways are more energy efficient due to less ATP consumption for the supply of extender unit acetyl-CoA than malonyl thioesters. However, these thiolases only utilize acetyl-CoA as the extender unit, thus limiting the functionality of synthesized products. A novel non-decarboxylative Claisen condensation reaction able to accept wider range of extender units and proceed in an iterative manner is required to diversify the product range of carbon-chain elongation.

[0008] This disclosure demonstrates a general CoA-dependent carbon elongation platform based on the use of de novo thiolase-catalyzed non-decarboxylative Claisen condensation which accepts functionalized primers and extender units, along with suitable HACDs, ECHs and ECRs (FIG. **1**) to complete one turn of the 2-carbon additive cycle. Wide-ranging product diversity (FIG. **1**) from this iterative platform is achieved through the use of primers with or without functionalization (R1 in FIG. **1**) and extender units with alpha-functionalization (R2 in FIG. **1**) in combination with pathway termination to various product classes by multiple pathways from any intermediate with various β-reduction degrees. The proposed platform possesses the potential for the high product diversity of a biosynthetic pathway combined with the high efficiency of a fermentative pathway.

SUMMARY OF THE DISCLOSURE

[0009] This disclosure generally relates to the use of microorganisms to make alpha-functionalized chemicals and fuels, (e.g. alpha-functionalized carboxylic acids, alcohols, hydrocarbons, amines, and their beta-, and omega-functionalized derivatives), by utilizing an iterative carbon chain elongation pathway that uses functionalized extender units. The core enzymes in the pathway include thiolases, dehydrogenases, dehydratases and reductases. Native or engineered thiolases catalyze the condensation of either unsubstituted or functionalized acyl-CoA primers with an alpha-functionalized acetyl-CoA as the extender unit to generate alpha-functionalized β-keto acyl-CoA. Dehydrogenases convert alpha-functionalized β-keto acyl-CoA to alpha-functionalized β-hydroxy acyl-CoA. Dehydratases convert alpha-functionalized β-hydroxy acyl-CoA to alpha-functionalized enoyl-CoA. Reductases convert alpha-functionalized enoyl-CoA to alpha-functionalized acyl-CoA. The platform can be operated in an iterative manner (i.e. multiple turns) by using the resulting alpha-functionalized acyl-CoA as primer and either acetyl-CoA or the aforementioned alpha-functionalized extender unit in subsequent turns of the cycle. Termination pathways acting on any of the four alpha-functionalized CoA thioester intermediates terminate the platform and generate various alpha-functionalized carboxylic acids, alcohols and amines with different β-reduction degrees.

[0010] This disclosure demonstrates a general CoA-dependent carbon elongation platform based on the use of thiolase-catalyzed non-decarboxylative Claisen condensations that accept alpha-functionalized extender units, along with suitable hydroxyacyl-CoA dehydrogenases (HACDs), enoyl-CoA hydratases (ECHs) and enoyl-CoA reductases (ECRs). A wide-range of alpha-functionalized product families (e.g. alpha-functionalized carboxylic acids, alcohols, hydrocarbons, amines, and their beta-, and omega-functionalized derivatives) can be obtained through this iterative platform.

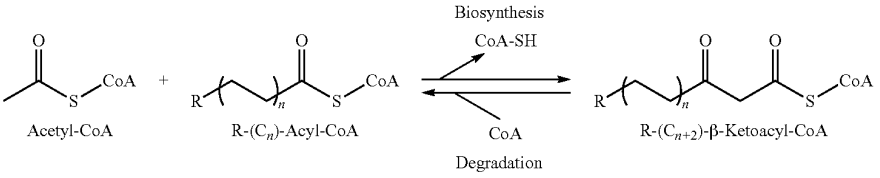
[0011] The technology entails developing a new pathway that is based on native or engineered thiolases capable of catalyzing the condensation of either unsubstituted or functionalized acyl-CoA primers with an alpha-functionalized acetyl-CoA as the extender unit. This has been reported in neither the scientific, peer-reviewed literature nor the patent literature.

[0012] The process involves performing traditional fermentations using industrial organisms (such as *E. coli, S. cerevisiae*) that convert different feedstocks into longer-chain products (e.g. alpha-functionalized carboxylic acids, alcohols, amines, and their beta-, and omega-functionalized derivatives or hydrocarbons). These organisms are considered workhorses of modern biotechnology. Media preparation, sterilization, inoculum preparation, and fermentation are the main steps of the process.

[0013] As used herein, a "primer" is a starting molecule for iterative carbon elongation platform. The "initial primer" or "initiating primer" can be simply acetyl-CoA or other unsubstituted or functionalized acyl-CoAs. As the chain grows by adding extender units in each cycle, the primer will accordingly increase in size.

[0014] As used herein, an "extender unit" is the donor of carbons in each cycle of the iterative carbon elongation platform. In this disclosure, the extender unit is alpha-functionalized acetyl-CoAs.

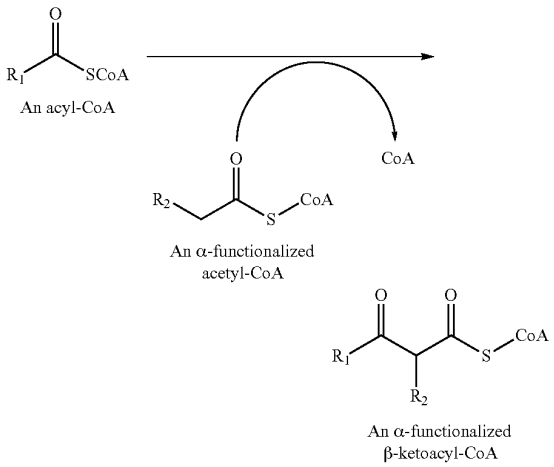
[0015] Thiolases are ubiquitous enzymes that have key roles in many vital biochemical pathways, including the beta-oxidation pathway of fatty acid degradation and various biosynthetic pathways. Members of the thiolase family can be divided into two broad categories: degradative thiolases (EC 2.3.1.16), and biosynthetic thiolases (EC 2.3.1.9). The forward and reverse reactions are shown below:



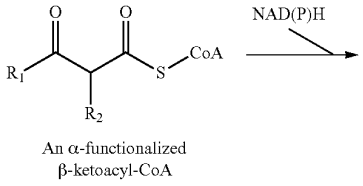
[0016] These two different types of thiolase are found both in eukaryotes and in prokaryotes: acetoacetyl-CoA thiolase (EC:2.3.1.9) and 3-ketoacyl-CoA thiolase (EC:2.3.1.16). 3-ketoacyl-CoA thiolase (also called thiolase I) has a broad chain-length specificity for its substrates and is involved in degradative pathways such as fatty acid beta-oxidation. Acetoacetyl-CoA thiolase (also called thiolase II) is specific for the thiolysis of acetoacetyl-CoA and involved in biosynthetic pathways such as poly beta-hydroxybutyric acid synthesis or steroid biogenesis.

[0017] Furthermore, the degradative thiolases can be made to run in the forward direction by building up the level of left hand side reactants (primer and extender unit), thus driving the equilibrium in the forward direction and/or by overexpressing same or by expressing a mutant of same.

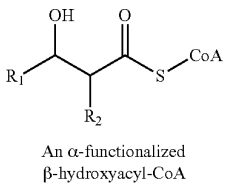
[0018] As used herein, a "thiolase" is an enzyme that catalyzes the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA as the carbon donor for chain elongation to produce an unsubstituted or omega-functionalized alpha-functionalized β-keto acyl-CoA in a non-decarboxylative condensation reaction:



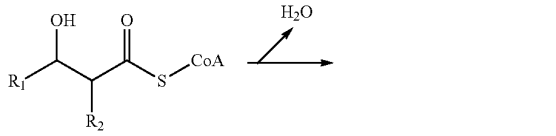
[0019] As used herein, a "hydroxyacyl-CoA dehydrogenase" or "HACD", is an enzyme that catalyzes the reduction of an unsubstituted or omega-functionalized alpha-functionalized β-keto acyl-CoA to an unsubstituted or omega-functionalized alpha-functionalized β-hydroxy acyl-CoA:



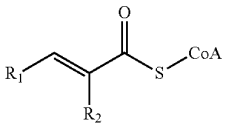
-continued



[0020] As used herein, an "enoyl-CoA hydratase" or "ECH" is an enzyme that catalyzes the dehydration of an unsubstituted or omega-functionalized or alpha-functionalized β-hydroxy acyl-CoA to an unsubstituted or omega-functionalized or alpha-functionalized enoyl-CoA:

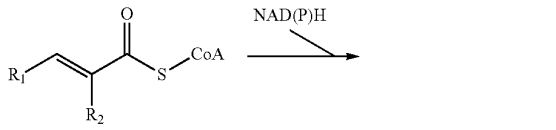


An α-functionalized β-hydroxyacyl-CoA

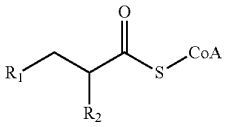


An α-functionalized enoyl-CoA

[0021] As used herein, an "enoyl-CoA reductase" or "ECR" is an enzyme that catalyzes the reduction of an unsubstituted or omega-functionalized or alpha-functionalized transenoyl-CoA to an unsubstituted or omega-functionalized of alpha-functionalized acyl-CoA:



An α-functionalized enoyl-CoA



An α-functionalized acyl-CoA

[0022] As used herein, "termination pathway" refers to one or more enzymes (or genes encoding same) that will pull reaction CoA thioester intermediates out the iterative cycle and produce the desired end product.

[0023] As used herein, an "alpha functionalized product" is a carboxylic acid, alcohols, hydrocarbons, or amine, wherein the alpha position is the second carbon and has an R group that is not hydrogen (R preferably being e.g., alkyl, aryl, —OH, —COOH, or —X, but including others). Note that the second carbon is defined with respect to the—coA end, and the numbering is retained even when the—coA is removed. Such alpha functionalized products can be further modified herein, and thus include beta-, and omega-functionalized derivatives.

[0024] As used herein, the expressions "microorganism," "microbe," "strain" and the like may be used interchangeably and all such designations include their progeny. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same function or biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

[0025] As used herein, reference to a "cell" is generally understood to include a culture of such cells, as the work described herein is done in cultures having 10^{9-15} cells.

[0026] As used herein, "growing" cells used it its art accepted manner, referring to exponential growth of a culture of cells, not the few cells that may not have completed their cell cycle at stationary phase or have not yet died in the death phase or after harvesting.

[0027] As used in the claims, "homolog" means an enzyme with at least 50% identity to one of the listed sequences and also having the same general catalytic activity, although of course Km, Kcat and the like can vary. While higher identity (60%, 70%, 80%) and the like may be preferred, it is typical for bacterial sequences to diverge significantly (40-60%), yet still be identifiable as homologs, while mammalian species tend to diverge less (80-90%).

[0028] Reference to proteins herein can be understood to include reference to the gene encoding such protein. Thus, a claimed "permease" protein can include the related gene encoding that permease. However, it is preferred herein to refer to the protein by standard name per ecoliwiki or HUGO since both enzymatic and gene names have varied widely, especially in the prokaryotic arts.

[0029] Once an exemplary protein is obtained, many additional examples of proteins with similar activity can be identified by BLAST search. Further, every protein record is linked to a gene record, making it easy to design overexpression vectors. Many of the needed enzymes are already available in vectors, and can often be obtained from cell depositories or from the researchers who cloned them. But, if necessary, new clones can be prepared based on available sequence information using RT-PCR techniques. Thus, it should be easily possible to obtain all of the needed enzymes for overexpression.

[0030] Another way of finding suitable enzymes/proteins for use in the invention is to consider other enzymes with the same EC number, since these numbers are assigned based on the reactions performed by a given enzyme. An enzyme that thus be obtained, e.g., from AddGene or from the author of the work describing that enzyme, and tested for functionality as described herein. In addition, many sites provide lists of proteins that all catalyze the same reaction.

[0031] Understanding the inherent degeneracy of the genetic code allows one of ordinary skill in the art to design multiple nucleotides that encode the same amino acid sequence. NCBI™ provides codon usage databases for optimizing DNA sequences for protein expression in various species. Using such databases, a gene or cDNA may be "optimized" for expression in *E. coli,* yeast, algal or other species using the codon bias for the species in which the gene will be expressed.

[0032] Initial cloning experiments have proceeded in *E. coli* for convenience since most of the required genes are already available in plasmids suitable for bacterial expression, but the addition of genes to bacteria is of nearly universal applicability. Indeed, since recombinant methods were invented in the 70's and are now so commonplace, even school children perform genetic engineering experiments using bacteria. Such species include e.g., *Bacillus,*

Streptomyces, Azotobacter, Trichoderma, Rhizobium, Pseudomonas, Micrococcus, Nitrobacter, Proteus, Lactobacillus, Pediococcus, Lactococcus, Salmonella, Streptococcus, Paracoccus, Methanosarcina, and *Methylococcus,* or any of the completely sequenced bacterial species. Indeed, hundreds of bacterial genomes have been completely sequenced, and this information greatly simplifies both the generation of vectors encoding the needed genes, as well as the planning of a recombinant engineering protocol. Such species are listed along with links at http://en.wikipedia.org/wiki/List_of_sequenced_bacterial_genomes.

[0033] Additionally, yeasts, such as *Saccharomyces,* are a common species used for microbial manufacturing, and many species can be successfully transformed. Indeed, yeast are already available that express recombinant thioesterases—one of the termination enzymes described herein—and the reverse beta oxidation pathway has also been achieved in yeast. Other species include but are not limited to *Candida, Aspergillus, Arxula adeninivorans, Candida boidinii, Hansenula polymorpha* (*Pichia angusta*), *Kluyveromyces lactis, Pichia pastoris,* and *Yarrowia lipolytica,* to name a few.

[0034] It is also possible to genetically modify many species of algae, including e.g., *Spirulina, Apergillus, Chlamydomonas, Laminaria japonica, Undaria pinnatifida, Porphyra, Eucheuma, Kappaphycus, Gracilaria, Monostroma, Enteromorpha, Arthrospira, Chlorella, Dunaliella, Aphanizomenon, Isochrysis, Pavlova, Phaeodactylum, Ulkenia, Haematococcus, Chaetoceros, Nannochloropsis, Skeletonema, Thalassiosira,* and *Laminaria japonica,* and the like. Indeed, the microalga *Pavlova lutheri* is already being used as a source of economically valuable docosahexaenoic (DHA) and eicosapentaenoic acids (EPA), and *Crypthecodinium cohnii* is the heterotrophic algal species that is currently used to produce the DHA used in many infant formulas.

[0035] Furthermore, a number of databases include vector information and/or a repository of vectors and can be used to choose vectors suitable for the chosen host species. See e.g., AddGene.org which provides both a repository and a searchable database allowing vectors to be easily located and obtained from colleagues. See also Plasmid Information Database (PlasmID) and DNASU having over 191,000 plasmids. A collection of cloning vectors of *E. coli* is also kept at the National Institute of Genetics as a resource for the biological research community. Furthermore, vectors (including particular ORFS therein) are usually available from colleagues.

[0036] The enzymes can be added to the genome or via expression vectors, as desired. Preferably, multiple enzymes are expressed in one vector or multiple enzymes can be combined into one operon by adding the needed signals between coding regions. Further improvements can be had by overexpressing one or more, or even all of the enzymes, e.g., by adding extra copies to the cell via plasmid or other vector. Initial experiments may employ expression plasmids hosting 3 or more ORFs for convenience, but it may be preferred to insert operons or individual genes into the genome for long term stability.

[0037] Still further improvements in yield can be had by reducing competing pathways, such as those pathways for making e.g., acetate, formate, ethanol, and lactate, and it is already well known in the art how to reduce or knockout these pathways. See e.g., the Rice patent portfolio by Ka-Yiu San and George Bennett (U.S. Pat. No. 7,569,380, U.S. Pat. No. 7,262,046, U.S. Pat. No. 8,962,272, U.S. Pat. No. 8,795,991) and patents by these inventors (U.S. Pat. No. 8,129,157 and U.S. Pat. No. 8,691,552) (each incorporated by reference herein in its entirety for all purposes). Many others have worked in this area as well.

[0038] In calculating "% identity" the unaligned terminal portions of the query sequence are not included in the calculation. The identity is calculated over the entire length of the reference sequence, thus short local alignments with a query sequence are not relevant (e.g., % identity=number of aligned residues in the query sequence/length of reference sequence). Alignments are performed using BLAST homology alignment as described by Tatusova T A & Madden T L (1999) *FEMS Microbiol. Lett.* 174:247-250, and available through the NCBI web site. The default parameters were used, except the filters were turned OFF.

[0039] "Operably associated" or "operably linked", as used herein, refer to functionally coupled nucleic acid or amino acid sequences.

[0040] "Recombinant" is relating to, derived from, or containing genetically engineered material. In other words, the genetics of an organism was intentionally manipulated by the hand of man in some way.

[0041] "Reduced activity" is defined herein to be at least a 75% reduction in protein activity, as compared with an appropriate control species (e.g., the wild type gene in the same host species). Preferably, at least 80, 85, 90, 95% reduction in activity is attained, and in the most preferred embodiment, the activity is eliminated (100%). Proteins can be inactivated with inhibitors, by mutation, or by suppression of expression or translation, by knock-out, by adding stop codons, by frame shift mutation, and the like. All reduced activity genes or proteins are signified herein by "−".

[0042] By "null" or "knockout" what is meant is that the mutation produces undetectable active protein. A gene can be completely (100%) reduced by knockout or removal of part of all of the gene sequence. Use of a frame shift mutation, early stop codon, point mutations of critical residues, or deletions or insertions, and the like, can also completely inactivate (100%) gene product by completely preventing transcription and/or translation of active protein. All null mutants herein are signified by Δ.

[0043] "Overexpression" or "overexpressed" is defined herein to be at least 150% of protein activity as compared with an appropriate control species, or any detectable expression in a species that lacks the activity altogether. Preferably, the activity is increased 100-500% or even ten fold. Overexpression can be achieved by mutating the protein to produce a more active form or a form that is resistant to inhibition, by removing inhibitors, or adding activators, and the like. Overexpression can also be achieved by removing repressors, adding multiple copies of the gene to the cell, or up-regulating the endogenous gene, and the like. All overexpressed genes or proteins are signified herein by "+".

[0044] In certain species it is possible to genetically engineer the endogenous protein to be overexpressed by changing the regulatory sequences or removing repressors. However, overexpressing the gene by inclusion on selectable plasmids or other vectors that exist in hundreds of copies in the cell may be preferred due to its simplicity and ease of

exerting externals controls, although permanent modifications to the genome may be preferred in the long term for stability reasons.

[0045] The term "endogenous" or "native" means that a gene originated from the species in question, without regard to subspecies or strain, although that gene may be naturally or intentionally mutated, or placed under the control of a promoter that results in overexpression or controlled expression of said gene. Thus, genes from *Clostridia* would not be endogenous to *Escherichia,* but a plasmid expressing a gene from *E. coli* or would be considered to be endogenous to any genus of *Escherichia,* even though it may now be overexpressed.

[0046] "Expression vectors" are used in accordance with the art accepted definition of a plasmid, virus or other propagatable sequence designed for protein expression in cells. There are thousands of such vectors commercially available, and typically each has an origin of replication (ori); a multiple cloning site; a selectable marker; ribosome binding sites; a promoter and often enhancers; and the needed termination sequences. Most expression vectors are inducible, although constitutive expressions vectors also exist.

[0047] As used herein, "inducible" means that gene expression can be controlled by the hand of man, by adding e.g., a ligand to induce expression from an inducible promoter. Exemplary inducible promoters include the lac operon, inducible by IPTG, the yeast AOX1 promoter inducible with methanol, the strong LAC4 promoter inducible with lactate, and the like. Low level of constitutive protein synthesis may occur even in expression vectors with tightly controlled promoters.

[0048] As used herein, an "integrated sequence" means the sequence has been integrated into the host genome, as opposed to being maintained on an expression vector. It will still be expressible, and preferably is inducible as well.

[0049] The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims or the specification means one or more than one, unless the context dictates otherwise.

[0050] The term "about" means the stated value plus or minus the margin of error of measurement or plus or minus 10% if no method of measurement is indicated.

[0051] The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or if the alternatives are mutually exclusive.

[0052] The terms "comprise", "have", "include" and "contain" (and their variants) are open-ended linking verbs and allow the addition of other elements when used in a claim.

[0053] The phrase "consisting of" is closed, and excludes all additional elements.

[0054] The phrase "consisting essentially of" excludes additional material elements, but allows the inclusions of non-material elements that do not substantially change the nature of the invention, such as instructions for use, buffers, background mutations that do not effect the invention, and the like.

[0055] The following abbreviations are used herein:

ABBREVIATION	TERM
Box-R	Beta oxidation pathway in reverse.
FAS	Fatty acid biosynthesis
ACP	Acyl carrier protein
CoA	Coenzyme A
HACD	Hydroxyacyl-CoA dehydrogenases
ECH	Enoyl-CoA hydratase
ECR	Enoyl-CoA reductase
HACL	2-hydroxyacyl-CoA lyase

BRIEF DESCRIPTION OF THE DRAWINGS

[0056] FIG. **1**: Platform for the synthesis of alpha-functionalized carboxylic acids, alcohols and amines. Acyl-CoA primer, which is either unsubstituted or functionalized, and alpha-functionalized extender unit are mainly activated from their acid form, which can be either supplemented in the media or derived from carbon sources. Primer and extender unit can also be derived from carbon sources without the need to generate their acid forms. The platform is composed of thiolases, dehydrogenases, dehydratases and reductases. Thiolases catalyze a condensation between acyl-CoA primer and alpha-functionalized acyl-CoA extender and generates alpha-functionalized β-keto acyl-CoA. Dehydrogenases convert alpha-functionalized β-keto acyl-CoA to alpha-functionalized β-hydroxy acyl-CoA. Dehydratases convert alpha-functionalized β-hydroxy acyl-CoA to alpha-functionalized enoyl-CoA. Reductases convert alpha-functionalized enoyl-CoA to alpha-functionalized acyl-CoA. Iterative operation can be realized by using alpha-functionalized acyl-CoA as primer and either acetyl-CoA or alpha-functionalized acetyl-CoA as extender unit in subsequent turns of the platform. Termination pathways starting from four alpha-functionalized CoA thioester intermediates terminate the platform and generate various alpha-functionalized carboxylic acids, alcohols and amines with different β-reduction degrees. There are three types of termination pathways: thioesterase/CoA-transferase/phosphotransacylase+kinase, which generates carboxylic acids; acyl-CoA reductase and alcohol dehydrogenase which generate alcohols; acyl-CoA reductase and transaminase which generate amine. R_1 and R_2 mean functionalized group from primer and extender unit respectively. Dashed line means multiple reaction steps or iteration.

[0057] FIG. **2**: Proposed platform depicted in FIG. **1** and its products utilizing propionyl-CoA as the extender unit (R_2 in FIG. **1** =–CH_3).

[0058] FIG. **3**: Example pathway of synthesis of tiglic acid (trans-2-methyl-2-butenoic acid) and 2-methylbutyric acid through the proposed platform with acetyl-CoA as the primer and propionyl-CoA as the extender unit. Propionyl-CoA is activated by Pct from propionic acid (Step 1). The platform is composed of thiolase FadAx, which catalyzes the condensation between primer acetyl-CoA and extender unit propionyl-CoA to 2-methyl acetoacetyl-CoA (Step 2); dehydrogenase FadB2x, which converts 2-methyl acetoacetyl-CoA to 2-methyl-3-hydroxybutyryl-CoA (Step 3); dehydratase FadB1x, which converts 2-methyl-3-hydroxybutyryl-CoA to tiglyl-CoA (Step 4); reductase FabI, which reduces tiglyl-CoA to 2-methylbutyryl-CoA (Step 5). Termination reactions by endogenous thioesterases from tiglyl-CoA (Step 6) and 2-methylbutyryl-CoA (Step 7) finally generate products tiglic acid and 2-methylbutyric acid.

[0059] FIG. **4**: Example pathway of synthesis of trans-2-methyl-2-pentenoic acid and 2-methylvaleric acid through the proposed platform with propionyl-CoA as the primer and the extender unit. Propionyl-CoA is activated by Pct from propionic acid (Step 1). The platform is composed of thiolase FadAx, which catalyzes the condensation between two molecules of propionyl-CoA to 2-methyl-3-oxopentanoyl-CoA (Step 2); dehydrogenase FadB2x, which converts 2-methyl-3-oxopentanoyl-CoA to 2-methyl-3-hydroxypentanoyl-CoA (Step 3); dehydratase FadB1x, which converts 2-methyl-3-hydroxypentanoyl-CoA to 2-methyl-2-pentenoyl-CoA (Step 4); reductase FabI, which reduces 2-methyl-2-pentenoyl-CoA to 2-methylvaleryl-CoA (Step 5). Termination reactions by endogenous thioesterases from 2-methyl-2-pentenoyl-CoA (Step 6) and 2-methylvaleryl-CoA (Step 7) finally generate products 2-methyl-2-pentenoic acid and 2-methylvaleric acid.

[0060] FIG. **5**: Titers of alpha-methylated products synthesized through the utilization of propionyl-CoA as the extender unit with either acetyl-CoA or propionyl-CoA priming. These products were produced from the *E. coli* strain overexpressing enzymes catalyzing Steps 1-5 depicted in FIG. **3**-**4**. JC01(DE3), an *E. coli* strain deficient of mixed-acid fermentations, served as the host strain. The engineered strains were grown for 48 hours under 37° C. in 20 mL LB-like MOPS media supplemented with 20 g/L glycerol and 20 mM propionic acid.

[0061] FIG. **6**: Pathway for the improved production of tiglic acid through the proposed platform with acetyl-CoA as the primer and propionyl-CoA as the extender unit. Propionyl-CoA is activated by Pct from propionic acid (Step 1). Thiolase FadAx condenses acetyl-CoA and propionyl-CoA to 2-methyl acetoacetyl-CoA (Step 2). Dehydrogenase FadB2x converts 2-methyl acetoacetyl-CoA to 2-methyl-3-hydroxybutyryl-CoA (Step 3). Dehydratase FadB1x converts 2-methyl-3-hydroxybutyryl-CoA to tiglyl-CoA (Step 4). Finally, thioesterase YdiI can remove the CoA from tiglyl-CoA to generate the product tiglic acid (Step 5).

[0062] FIG. **7**: Results of improvement of tiglic acid production by removal of overexpression of FabI (ECR), addition of overexpression of YdiI (a thioesterase) and usage of JST06(DE3) as the host strain. JST06(DE3) is an *E. coli* strain deficient of mixed-acid fermentations, thioesterases. The engineered strains were grown for 48 h at 37° C. in 20 mL LB-like MOPS media supplemented with 20 g/L glycerol and 20 mM propionic acid.

[0063] FIG. **8**: Time course for tiglic acid production from JST06(DE3) strain overexpressing Pct, FadAx, FadB2x, FadB1x and YdiI in a fermentation conducted in a controlled bioreactor. The fermentation was performed under 37° C. in LB-like MOPS media supplemented with 30 g/L glycerol, and 20 mM propionic acid which was added at 0, 24, and 48 h.

[0064] FIG. **9**: Proposed platform depicted in FIG. **1** and its products utilizing glycolyl-CoA as the extender unit (R2 in FIG. **1** =—OH).

[0065] FIG. **10**: Example pathway of synthesis of 2,3-dihydroxy-butyric acid through the proposed platform with acetyl-CoA as the primer and propionyl-CoA as the extender unit. Glycolyl-CoA is activated by Pct from glycolic acid (Step 1). Then, condensation by thiolase BktB converts glycolyl-CoA and acetyl-CoA to 2-hydroxy acetoacetyl-CoA (Step 2). Dehydrogenase PhaB converts 2-hydroxy acetoacetyl-CoA to 2,3-dihydroxy-butyryl-CoA (Step 3). CoA removal by endogenous thioesterases convert 2,3-dihydroxy-butyryl-CoA to the product 2,3-dihydroxy-butyric acid (Step 4).

[0066] FIG. **11**: Peak of product 2,3-dihydroxy-butyric acid in the GC-MS chromatogram of the fermentation sample from MG1655(DE3) ΔglcD (pET-P1-bktB-phaB-P2-phaJ) (pCDF-P1-pct-P2-tdTER). The strain was grown in 50 mL LB media supplemented with 10 g/L glucose and 40 mM glycolate for 96 hours under 30° C. in 250 mL flask.

[0067] FIG. **12**: Derivatization pathway of product 2-hydroxy acid and intermediate 2-hydroxyacyl-CoA of the proposed platform utilizing glycolyl-CoA as the extender unit depicted in FIG. **3**, to a primary alcohol product. 2-hydroxyacyl-CoA can be degraded to primary aldehyde and formyl-CoA by 2-hydroxyacyl-CoA lyase. 2-hydroxy acid can be converted to α-keto acid by keto-dehydrogenase and α-keto acid can be decarboxylated to primary aldehyde by α-keto acid to primary aldehyde. Primary aldehyde is finally reduced to primary alcohol by alcohol dehydrogenase.

[0068] FIG. **13**: Vector map of pCDFDuet-1-P1-ntH6-HACL1 for overexpression and purification of codon-optimized 2-hydroxyacyl-CoA lyase HACL1 from *Homo sapiens* in *E coli*.

[0069] FIG. **14**: SDS-PAGE analysis result of overexpression of *Homo sapiens* HACL1 in *E. coli*.

[0070] FIG. **15**: Vector map of pYES260-HACL1-SCopt for overexpression and purification of codon-optimized 2-hydroxyacyl-CoA lyase HACL1 from *Homo sapiens* in *Saccharomyces cerevisiae*.

[0071] FIG. **16**: SDS-PAGE analysis result of overexpression and purification of *Homo sapiens* HACL1 in *S. cerevisiae*.

[0072] FIG. **17**: GC-FID chromatograms of pentadecanal content in HACL1 degradative reaction (forward reaction) mixtures after extraction with hexane. HACL1 was expressed and purified from *S. cerevisiae*. Top: pentadecanal standard; Middle: HACL1 assay sampled; Bottom: no enzyme control. In samples containing HACL1, a pentadecanal peak is seen, while there is no peak in the sample in which enzyme was omitted.

[0073] FIG. **18**: GC-FID chromatograms of pentadecanal content demonstrating HACL1 activity in *E. coli* BL21 (DE3) crude extract. The peak of pentadecanal is shown in the square.

[0074] FIG. **19**: Proposed platform depicted in FIG. **1** and its products utilizing phenylacetyl-CoA as the extender unit (R_2 in FIG. **1** =–Ph).

[0075] FIG. **20**: Proposed platform depicted in FIG. **1** and its products utilizing phenylacetyl-CoA as the extender unit (R_2 in FIG. **1** =–NH_2).

[0076] FIG. **21**. A partial listing of embodiments of the invention, any one or more of which can be combined with any other.

DETAILED DESCRIPTION

[0077] This disclosure generally relates to the use of microorganisms to make alpha-functionalized chemicals and fuels, (e.g. alpha-functionalized carboxylic acids, alcohols, hydrocarbons, amines, and their beta-, and omega-functionalized derivatives), by utilizing a novel iterative carbon chain elongation pathway that uses functionalized extender units to grow a carbon chain by two carbon units.

[0078] The core enzymes in the pathway include thiolase, dehydrogenase, dehydratase and reductase. Native or engineered thiolases catalyze the condensation of either unsubstituted or functionalized acyl-CoA primers with an alpha-functionalized acetyl-CoA as the extender unit to generate alpha-functionalized β-keto acyl-CoA. Dehydrogenase converts alpha-functionalized β-keto acyl-CoA to alpha-functionalized β-hydroxy acyl-CoA. Dehydratase converts alpha-functionalized β-hydroxy acyl-CoA to alpha-functionalized enoyl-CoA. Reductase converts alpha-functionalized enoyl-CoA to alpha-functionalized acyl-CoA.

[0079] The platform can be operated in an iterative manner (i.e. multiple turns) by using the resulting alpha-functionalized acyl-CoA as primer and the aforementioned omega-functionalized extender unit in subsequent turns of the cycle. Various termination pathways

[0080] (FIG. **1** and Table 4) acting on any of the four alpha-functionalized CoA thioester intermediates terminate the platform and generate various alpha-functionalized carboxylic acids, alcohols and amines with different β-reduction degrees.

[0081] Thioesterase or CoA transferase or phosphotransacylase+carboxylate kinase can terminate the platform by converting the alpha-functionalized acyl-CoAs to alpha-functionalized carboxylic acids. If alpha-functionalized carboxylic acids has keto group at the beta-site, it can then be converted to ketone through reactions by beta-keto acid decarboxylase. Acyl-CoA reductases can terminate the platform by converting the alpha-functionalized acyl-CoAs to alpha-functionalized aldehydes. Alpha-functionalized aldehydes can then be converted to alpha-functionalized alcohols and alpha-functionalized amines through reactions by alcohol dehydrogenase and transaminase respectively.

[0082] This disclosure also relates to a novel primary alcohol synthesis incorporating the proposed iterative platform using glycolyl-CoA (alpha-hydroxy acetyl-CoA) as the extender unit. When the platform uses glycolyl-CoA as the extender unit, it generates alpha-hydroxyacyl-CoA, which can be converted to primary alcohol by termination pathways selected from: a) 2-hydroxyacyl-CoA lyase (HACL) that converts alpha-hydroxyacyl-CoA to primary aldehyde with one less carbon and formyl-CoA, and alcohol dehydrogenase subsequently converts the primary aldehyde to primary alcohol; b) acid-forming termination enzyme selected from thioesterase, CoA transferase and phosphotransacylase+carboxylate kinase that converts alpha-hydroxyacyl-CoA to alpha-hydroxy acid, keto-dehydrogenase that converts alpha-hydroxy acid to alpha-keto acid, alpha-keto acid decarboxylase that converts alpha-keto acid to primary aldehyde with one less carbon and alcohol dehydrogenase subsequently converts the primary aldehyde to primary alcohol.

[0083] Many examples of thiolase enzymes which can potentially catalyze the non-decarboxylative condensation of an acyl-CoA primer and acetyl-CoA extender unit are provided herein and Table 1 provides several additional examples which can also serve as templates for engineered variants:

TABLE 1

Example Thiolase Enzymes (EC Number 2.3.1.—)

Source organism and gene name	Protein Accession Numbers
E. coli atoB	NP_416728.1
E. coli yqeF	NP_417321.2
E. coli fadA	YP_026272.1
E. coli fadI	NP_416844.1
Streptomyces collinus fadA	Q93C88
Ralstonia eutropha bktB	AAC38322.1
Pseudomonas sp. Strain B13 catF	AAL02407.1
E coli paaJ	NP_415915.1
Pseudomonas putida pcaF	AAA85138.1
Rhodococcus opacus pcaF	YP_002778248.1
Streptomyces sp. pcaF	AAD22035.1
Ralstonia eutropha phaA	AEI80291.1
Clostridium acetobutylicum thlA	AAC26023.1
Clostridium acetobutylicum thlB	AAC26026.1

[0084] This technology takes the above thiolase initiated pathway one step further to make alpha functionalized products. The method entails developing a new pathway that is based on native or engineered thiolases capable of catalyzing the condensation of either unsubstituted or functionalized acyl-CoA primers with an omega-functionalized acetyl-CoA as the extender unit. This has been reported in neither the scientific, peer-reviewed literature nor the patent literature.

[0085] Materials that can be used with the invention include those in Tables 2-5 below.

TABLE 2

Activation enzymes

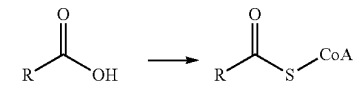
Reaction	Illustration	EC Numbers	Enzyme names	source organism and gene name	Protein Accession Numbers
Carboxylic acid → Acyl-CoA (including acyl-CoA primer, and α-functionalized acetyl-CoA acting as the extender unit)		6.2.1.-	Acyl-CoA synthetase	*E. coli* PaaK *E. coli* sucCD *E. coli* fadK *E. coli* fadD *E. coli* prpE *E. coli* menE *Penicillium chrysogenum* phl *Salmonella typhimurium* LT2 prpE *Bacillius subtilis* bioW *Cupriavidus basilensis* hmfD *Rhodopseudomonas palustris* badA	NP_415916.1 NP_415256.1 NP_415257.1 NP_416216.4 NP_416319.1 NP_414869.1 NP_416763.1 CAJ15517.1 AAL19325.1 AAC00261.1 ADE20402.1 CAJ18317.1

TABLE 2-continued

Activation enzymes					
Reaction	Illustration	EC Numbers	Enzyme names	source organism and gene name	Protein Accession Numbers
				R. palustris hbaA	CAE26113.1
				Pseudomonas aeruginosa PAO1 pqsA	NP_249687.1
				Arabidopsis thaliana 4cl	Q42524.1
		2.8.3-	CoA transferase	*E. coli* atoD	NP_416725.1
				E. coli atoA	NP_416726.1
				E. coli scpC	NP_417395.1
				Clostridium kluyveri cat1	AAA92346.1
				Clostridium kluyveri cat2	AAA92344.1
				Clostridium acetobutylicum ctfAB	NP_149326.1, NP_149327.1
				Pseudomonas putida pcaIJ	NP_746081.1 NP_746082.1
				Megasphaera elsdenii pct	WP_014015705.1
				Acidaminococcus fermentans gctAB	CAA57199.1 CAA57200.1
				Acetobacter aceti aarC	AGG68319.1
				E. coli ydiF	NP_416209.1
		2.3.1.-; 2.7.2.1; 2.7.2.15	Phosphotransacylase + Carboxylate kinase	*Clostridium acetobutylicum* ptb	NP_349676.1
				Enterococcus faecalis ptb	AAD55374.1
				Salmonella enterica pduL	AAD39011.1
				Clostridium acetobutylicum buk	AAK81015.1
				Enterococcus faecalis buk	AAD55375.1
				Salmonella enterica pduW	AAD39021.1

TABLE 3

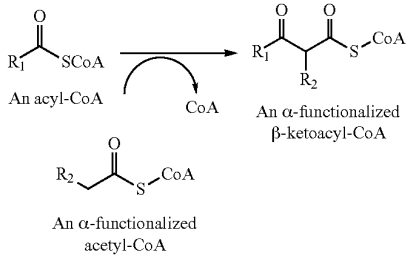
Reactions of the platform						
Reaction	Illustration	EC Numbers	Enzyme Names	Source organism and gene name	Protein Accession Numbers
Acyl-CoA + α-functionalized acetyl-CoA → α-functionalized β-ketoacyl-CoA		2.3.1-	Thiolase	*E. coli* atoB	NP_416728.1
				E. coli yqeF	NP_417321.2
				E. coli fadA	YP_026272.1
				E. coli fadI	NP_416844.1
				Ralstonia eutropha bktB	AAC38322.1
				Pseudomonas sp. Strain B13 catF	AAL02407.1
				E coli paaJ	NP_415915.1
				Pseudomonas putida pcaF	AAA85138.1
				Rhodococcus opacus pcaF	YP_002778248.1
				Streptomyces sp. pcaF	AAD22035.1
				Ralstonia eutropha phaA	AEI80291.1
				Clostridium acetobutylicum thlA	AAC26023.1
				Clostridium acetobutylicum thlB	AAC26026.1
				Pseudomonas putida fadA	AAK18168.1
				P. putida fadAx	AAK18171.1

TABLE 3-continued

Reactions of the platform

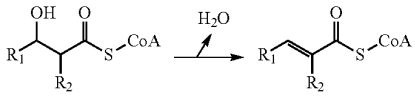
Reaction	Illustration	EC Numbers	Enzyme Names	Source organism and gene name	Protein Accession Numbers
				Acinetobacter sp. ADP1 dcaF	CAG68532.1
				E. coli paaJ	NP_415915.1
α-functionalized β-ketoacyl-CoA → α-functionalized β-hydroxyacyl-CoA	 An α-functionalized β-ketoacyl-CoA → An α-functionalized β-hydroxyacyl-CoA	1.1.1.35; 1.1.1.36	Hydroxyacyl-CoA dehydrogenase	*E. coli* fadB	NP_418288.1
				E. coli fadJ	NP_416843.1
				E. coli paaH	NP_415913.1
				P. putida fadB	AAK18167.2
				P. putida fadB2x	AAK18170.1
				Acinetobacter sp. ADP1 dcaH	CAG68533.1
				Ralstonia eutrophus phaB	P14697.1
				Clostridium acetbutylicum hbd	AAA95971.1
			3-oxoacyl-[acyl-carrier-protein] reductase	*E. coli* fabG	NP_415611.1
α-functionalized β-hydroxyacyl-CoA → α-functionalized enoyl-CoA	 An α-functionalized β-hydroxyacyl-CoA → An α-functionalized enoyl-CoA	4.2.1.17; 4.2.1.119	enoyl-CoA hydratase	*E. coli* fadB	NP_418288.1
				E. coli fadJ	NP_416843.1
				E. coli paaF	NP_415911.1
				P. putida fadB	AAK18167.2
				P. putida fadB1x	AAK18173.1
				Aceinetobacter sp. ADP1 dcaE	CAG68535.1
				Clostridium acetobutylicum crt	AAA95967.1
				Aeromonas caviae phaJ	O32472.1
			3-hydroxyacyl-[acyl-carrier-protein] dehydratase	*E. coli* fabA	NP_415474.1
				E. coli fabZ	NP_414722.1
α-functionalized enoyl-CoA → α-functionalized acyl-CoA	 An α-functionalized enoyl-CoA → An α-functionalized acyl-CoA	1.3.1.44	enoyl-CoA reductase	*Euglena gracillis* TER	Q5EU90.1
				Treponema denticola TER	4GGO_A
				Clostridium acetobutylicum TER	4EUH_A
			enoyl-[acyl-carrier-protein] reductase	*E. coli* fabI	NP_415804.1
				Enterococcus faecalis fabK	NP_816503.1
				bacillus subtilis fabL	KFK80655.1
				Vibrio cholerae fabV	ABX38717.1
			acyl-CoA dehydrogenase	*E. coli* fadE	NP_414756.2
				E. coli ydiO	NP_416210.4

TABLE 4

Termination Pathways

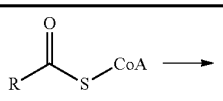
Reaction	Illustration	EC Numbers	Enzyme names	Source organism and gene name	Protein Accession Numbers
Acyl-CoA → carboxylic acid	 An acyl-CoA → A carboxylic acid	3.1.2.-	Thioesterase	*E. coli* tesA	NP_415027.1
				E. coli tesB	NP_414986.1
				E. coli yciA	NP_415769.1
				E. coli fadM	NP_414977.1
				E. coli ydiI	NP_416201.1
				E. coli ybgC	NP_415264.1

TABLE 4-continued

Termination Pathways

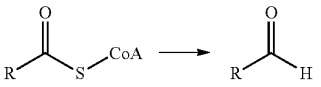
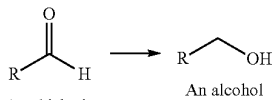
Reaction	Illustration	EC Numbers	Enzyme names	Source organism and gene name	Protein Accession Numbers
				E. coli paaI	NP_415914.1
				Mus musculus acot8	P58137.1
				Lycopersicon hirsutum f *glabratum* mks2	ADK38536.1
				Alcanivorax borkumensis tesB2	YP_692749.1
				Fibrobacter succinogenes Fs2108	YP_005822012.1
				Prevotella ruminicola Pr655	YP_003574018.1
				Prevotella ruminicola Pr1687	YP_003574982.1
		2.8.3-	CoA transferase	*E. coli* atoD	NP_416725.1
				E. coli atoA	NP_416726.1
				E. coli scpC	NP_417395.1
				Clostridium kluyveri cat1	AAA92346.1
				Clostridium kluyveri cat2	AAA92344.1
				Clostridium acetobutylicum ctfAB	NP_149326.1, NP_149327.1
				Pseudomonas putida pcaIJ	NP_746081.1 NP_746082.1
				Megasphaera elsdenii pct	WP_014015705.1
				Acidaminococcus fermentans gctAB	CAA57199.1 CAA57200.1
				Acetobacter aceti aarC	AGG68319.1
				E. coli ydiF	NP_416209.1
		2.3.1.-; 2.7.2.1; 2.7.2.15	Phosphotransacylase + Carboxylate kinase	*Clostridium acetobutylicum* ptb	NP_349676.1
				Enterococcus faecalis ptb	AAD55374.1
				Salmonella enterica pduL	AAD39011.1
				Clostridium acetobutylicum buk	AAK81015.1
				Enterococcus faecalis buk	AAD55375.1
				Salmonella enterica pduW	AAD39021.1
Acyl-CoA → Aldehyde	 An acyl-CoA An aldehyde	1.2.1.10	Aldehyde forming CoA reductase	*Acinetobacter calcoaceticus* acr1	AAC45217.1
				Acinetobacter sp Strain M-1 acrM	BAB85476.1
				Clostridium beijerinckii ald	AAT66436.1
				E. coli eutE	NP_416950.1
				Salmonella enterica eutE	AAA80209.1
				Marinobacter aquaeolei VT8 maqu_2507	YP_959769.1
				E. coli mhpF	NP_414885.1
				Clostridium kluyveri sucD	EDK35023.1
Aldehyde → Alcohol	 An aldehyde An alcohol	1.1.1.-	Alcohol dehydrogenase	*E. coli* betA	NP_414845.1
				E. coli dkgA	NP_417485.4
				E. coli eutG	NP_416948.4
				E. coli fucO	NP_417279.2
				E. coli ucpA	NP_416921.4
				E. coli yahK	NP_414859.1
				E. coli ybbO	NP_415026.1
				E. coli ybdH	NP_415132.1

TABLE 4-continued

Termination Pathways

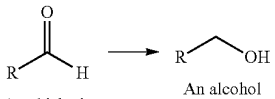
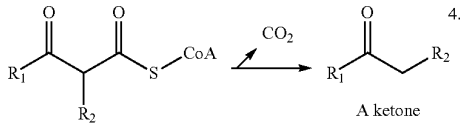
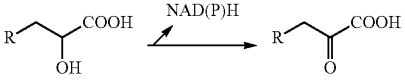
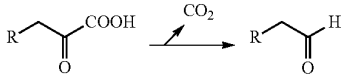
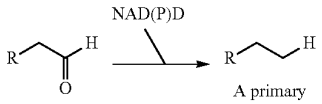
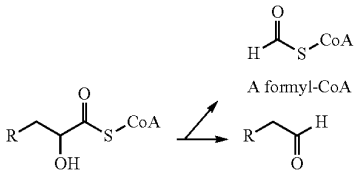
Reaction	Illustration	EC Numbers	Enzyme names	Source organism and gene name	Protein Accession Numbers
				E. coli yiaY	YP_026233.1
				E. coli yjgB	NP_418690.4
				Marinobacter aquaeolei VT8 maqu_2507	YP_959769.1
				Saccharomyces cerevisiae ADH6	Q04894.1
				Clostridium kluyveri 4hbD	EDK35022.1
				Acinetobacter sp. SE19 chnD	AAG10028.1
Aldehyde → Amine	 An aldehyde An alcohol	2.6.1.-	Transaminase	*Arbidopsis thaliana* At3g22200	NP_001189947.1
				Alcaligenes denitrificans AptA	AAP92672.1
				Bordetella bronchiseptica BB0869	WP_015041039.1
				Bordetella parapertussis BPP0784	WP_010927683.1
				brucella menlitensis BAWG_0478	EEW88370.1
				Burkholderia pseudomallei BP1026B_I0669	AFI65333.1
				Chromobacterium violaceum CV2025	AAQ59697.1
				Oceanicola granulosus OG2516_07293	WP_007254984.1
				Paracoccus denitrificans PD1222 Pden_3984	ABL72050.1
				Pseudogulbenkiania ferrooxidans ω-TA	WP_008952788.1
				Pseudomonas putida ω-TA	P28269.1
				Ralstonia solanacearum ω-TA	YP_002258353.1
				Rhizobium meliloti SMc01534	NP_386510.1
				Vibrio fluvialis ω-TA	AEA39183.1
				Mus musculus abaT	AAH58521.1
				Flavobacterium lutescens lat	BAB13756.1
				Streptomyces clavuligerus lat	AAB39833.1
				E. coli gabT	YP_490877.1
				E. coli puuE	NP_415818.1
				E. coli ygjG	NP_417544.5
β-keto acid → ketone	 An α-functionalized β-keto acid A ketone	4.1.1.56;	β-keto acid decarboxylase	*Lycopersicon hirsutum* f *glabratum* mks1	ADK38535.1
				Clostridium acetobutylicum adc	AAA63761.1

TABLE 5

Enzymes of derivatization of 2-hydroxy acid to primary alcohol

Reaction	Illustration	EC Numbers	Enzyme names	Source organism and gene name	Accession Numbers
2-hydroxy acid → α-keto acid	 A 2-hydroxy acid An α-keto acid	1.1.1-	Keto-dehydrogenase	*Clostridium beijerinckii* adh *E. coli* serA *Gordonia* sp. TY-5 adh1 *Gordonia* sp. TY-5 adh2 *Gordonia* sp. TY-5 adh3 *Rhodoccoccus ruber* adh-A *Acidaminococcus fermentans* hgdH *E. coli* ldhA *E. coli* lldD *E. coli* leuB	AAA23199.2 NP_417388.1 BAD03962.1 BAD03964.1 BAD03961.1 WP_043801412.1 ADB47349.1 NP_415898.1 NP_418062.1 NP_414615.4
α-keto acid → primary aldehyde	 An α-keto acid A primary aldehyde	4.1.1.1	a-keto acid decarboxylase	*Lactococcus lactis* kivd *Saccharomyces cerevisiae* PDC1 *S. cerevisiae* PDC5 *S. cerevisiae* PDC6 *S. cerevisiae* ARO10 *S. cerevisiae* THI3 *Zymomonas mobilis* pdc	AIS03677.1 CAA97573.1 CAA97705.1 CAA97089.1 NP_010668.3 CAA98646.1 ADK13058.1
Primary aldehyde → Primary alcohol	 A primary aldehyde A primary alcohol	1.1.1.-	alcohol dehydrogenase	*E. coli* betA *E. coli* dkgA *E. coli* eutG *E. coli* fucO *E. coli* ucpA *E. coli* yahK *E. coli* ybbO *E. coli* ybdH *E. coli* yiaY *E. coli* yjgB *Saccharomyces cerevisiae* ADH6 *Clostridium kluyveri* 4hbD *Acinetobacter* sp. SE19 chnD	NP_414845.1 NP_417485.4 NP_416948.4 NP_417279.2 NP_416921.4 NP_414859.1 NP_415026.1 NP_415132.1 YP_026233.1 NP_418690.4 Q04894.1 EDK35022.1 AAG10028.1
2-hydroxyacyl-CoA → primary aldehyde + formyl-CoA	 A formyl-CoA A 2-hydroxyacyl-CoA A primary aldehyde	4.1.-.-	2-hydroxyacyl-CoA Lyase	*Homo sapiens* hacl1 *Rattus norvegicus* hacl1 *Dictyostelium discoideum* hacl1 *Mus musculus* hacl1	Q9UJ83 Q8CHM7 Q54DA9 Q9QXE0

[0086] All strains used in this study are listed in Table 6. Gene deletions were performed using P1 phage transduction with single-gene knockout mutants from the National BioResource Project (NIG, Japan) as the specific deletion donor. The λDE3 prophage, carrying the T7 RNA polymerase gene and lacIq, was integrated into the chromosome through λDE3 lysogenization kit (Novagen, Darmstadt, Germany). All strains were stored in 32.5% glycerol stocks at −80° C. Plates were prepared using LB medium containing 1.5% agar, and appropriate antibiotics were included at the following concentrations: ampicillin (100 μg/mL), spectinomycin (50 μg/mL), kanamycin (50 μg/mL), and chloramphenicol (34 μg/mL).

[0087] All plasmids used in this study and oligonucleotides used in their construction are listed in Tables 6 and 7. Plasmid based gene overexpression was achieved by cloning the desired gene(s) into either pETDuet-1 or pCDFDuet-1 (Novagen, Darmstadt, Germany) digested with appropriate restriction enzymes using In-Fusion PCR cloning technology (Clontech Laboratories, Inc., Mountain View, Calif.). Cloning inserts were created via PCR of ORFs of interest from their respective genomic or codon-optimized DNA with Phusion polymerase (Thermo Scientific, Waltham, Mass.). *E. coli* genes were obtained from genomic DNA, while heterologous genes were synthesized by GenScript (Piscataway, N.J.) or GeneArt (Life Technologies, Carlsbad,

Calif.) with codon optimization except for bktB, phaB1, and pct, which were amplified from genomic DNA or cDNA of their source organisms. The resulting In-Fusion products were used to transform *E. coli* Stellar cells (Clontech Laboratories, Inc., Mountain View, Calif.) and PCR identified clones were confirmed by DNA sequencing.

TABLE 6

Strains and plasmids used in this study.

Strain/plasmid	Genotype
E. coli Strains	
MG1655	F-λ-ilvG-rfb-50 rph-1
JC01	MG1655 ΔldhA::FRT ΔpoxB::FRT Δpta::FRT ΔadhE::FRT ΔfrdA::FRT
JC01(DE3)	JC01 with DE3, a λ prophage carrying the T7 RNA polymerase gene and lacI^q
JST06	JC01 ΔyciA:FRT ΔybgC::FRT Δydil::FRT ΔtesA::FRT ΔfadM::FRT ΔtesB::FRT
JST06(DE3)	JST06 with DE3, a λ prophage carrying the T7 RNA polymerase gene and lacI^q
MG1655(DE3)	MG1655 with DE3, a λ prophage carrying the T7 RNA polymerase gene and lacI^q
MG1655(DE3) ΔglcD	MG1655(DE3) ΔglcD::FRT
BL21(DE3)	F- ompT gal dcm lon hsdS$_B$($r_B^- m_B^-$) λ(DE3 [lacI lacUV5-T7 gene 1 ind1 sam7 nin5]) [malB$^+$]$_{K\text{-}12}$(λ^S)
S. cerevisiae strains	
INVSc1	MATa his3D1 leu2 trp1-289 ura3-52 MAT his3D1 leu2 trp1-289 ura3-52
Plasmids	
pETDuet	ColE1(pBR322) ori, lacI, T7lac,
pETDuet-P1-fadB2x-fadB1x	ColE1 ori; Amp^R; P$_{T7lac\text{-}1}$: fadB2x-fadB1x
pETDuet-P1-fadB2x-fadB1x-P2-ydil	ColE1 ori; Amp^R; P$_{T7lac\text{-}1}$: fadB2x-fadB1x P$_{T7lac\text{-}2}$: ydil
pETDuet-P1- bktB-phaB1	ColE1 ori; Amp^R; P$_{T7lac\text{-}1}$: bktB-phaB1
pETDuet-P1- bktB-phaB1-P2-phaJ	ColE1 ori; Amp^R; P$_{T7lac\text{-}1}$: bktB-phaB1 P$_{T7lac\text{-}2}$: phaJ
pCDFDuet-1	CloDF13 ori, lacI, T7lac, Strep^R
pCDFDuet-P1-pct-fadAx	CloDF13 ori; Strep^R; P$_{T7lac\text{-}1}$: pct-fadAx
pCDFDuet-P1-pct-fadAx-P2-fabI	CloDF13 ori; Strep^R; P$_{T7lac\text{-}1}$: pct-fadAx P$_{T7lac\text{-}2}$: fabI
pCDFDuet-P1-pct-P2-tdTer	CloDF13 ori; Strep^R; P$_{T7lac\text{-}1}$: pct P$_{T7lac\text{-}2}$: tdTer
pCDFDuet-1-P1-ntH6-HACL1	CloDF13 ori; Strep^R; P$_{T7lac\text{-}1}$: ntHis6-HACL1
pYE260-HACL1	ColE1 ori; Amp^R; P$_{GAL1}$: ntHis6-HACL1

TABLE 7

Oligonucleotides used in this study for plasmid constructions

Name	Sequence
pct-f1	5'-AGGAGATATACCATGAGAAAAGTAGAAATCATTAC-3'
pct-r1	5'-CGCCGAGCTCGAATTCTTATTTTTTCAGTCCCATGGGAC-3'
fabI-f1	5'-AAGGAGATATACATATGGGTTTTCTTTCCGGTAAG-3'
fabI-r1	5'-TTGAGATCTGCCATATGTTATTTCAGTTCGAGTTCGTTC-3'
fadAx-f1	5'-GAAAAAATAAGAATTTAAGGAGGAATAAACC ATGACCCTGGCAAATGATCC-3'
fadAx-r1	5'-CGCCGAGCTCGAATTCTTAATACAGACATTCAACTGCC-3'
fadB2x-f1	5'-AGGAGATATACCATGCATATCGCCAACAAACAC-3'
fadB2x-r1	5'-CGCCGAGCTCGAATTCTTATTTTGCTGCCATGCGCAG-3'
fadB1x-f1	5'-AGCAAAATAAGAATTTAAGGAGGAATAAACC ATGGCCTTTGAAACCATTCTG-3'
fadB1x-r1	5'-CGCCGAGCTCGAATTCTTAGCGATCTTTAAACTGTGC-3'
ydil-f1	5'-AAGGAGATATACATATGATATGGAAACGGAAAATCAC-3'
ydil-r1	5'-TTGAGATCTGCCATATGTCACAAAATGGCGGTCGTC-3'

TABLE 7-continued

Oligonucleotides used in this study for plasmid constructions

Name	Sequence
bktB-f1	5'-AGGAGATATACCATGATGACGCGTGAAGTGGTAGT-3'
bktB-r1	5'-CGCCGAGCTCGAATTCTCAGATACGCTCGAAGATGG-3'
phaB1-f1	5'-GCGTATCTGAGAATTAGGAGGCTCTCT ATGACTCAGCGCATTGCGTA
phaB1-r1	5'-CGCCGAGCTCGAATTCTCAGCCCATGTGCAGGCC-3'
phaJ-f1	5'-AAGGAGATATACATATGTCGGCACAAAGCCTG-3'
phaJ-r1	5'-TTGAGATCTGCCATATGTTACGGCAGTTTCACCACC-3'
HACL1-f1	5'-GCCAGGATCCGAATTctATGCCGGACAGCAACTTC-3'
HACL1-r1	5'-CGCCGAGCTCGAATTcTTACATATTGCTACGGGTCAGC-3'

[0088] Fermentation medium and conditions: The minimal medium designed by Neidhardt et al. with 125 mM MOPS and Na_2HPO_4 in place of K_2HPO_4 (1.48 mM for fermentations in flasks; 2.8 mM for fermentations in bioreactors), supplemented with 20 g/L glycerol, 10 g/L tryptone, 5 g/L yeast extract, 100 μM $FeSO_4$, 5 mM calcium pantothenate, 5 mM $(NH_4)_2SO_4$, and 30 mM NH_4Cl was used for all fermentations unless otherwise stated. Neutralized 20 mM glycolic acid or propionic acid was supplemented as needed. Antibiotics (50 mg/mL carbenicillin and 50 mg/mL spectinomycin) were included when appropriate. All chemicals were obtained from Fisher Scientific Co. (Pittsburg, Pa.) and Sigma-Aldrich Co. (St. Louis, Mo.).

[0089] Unless otherwise stated, fermentations were performed in 25 mL Pyrex Erlenmeyer flasks (narrow mouth/heavy duty rim, Corning Inc., Corning, N.Y.) filled with 20 mL fermentation medium and sealed with foam plugs filling the necks. A single colony of the desired strain was cultivated overnight (14-16 h) in LB medium with appropriate antibiotics and used as the inoculum (1%). After inoculation, flasks were incubated in a NBS 124 Benchtop Incubator Shaker (New Brunswick Scientific Co., Inc., Edison, N.J.) at 200 rpm and 37° C., except fermentations supplemented with phenylacetic acid or isobutyric acid in which the temperature was 30° C. When optical density (550 nm, OD550) reached ~0.3-0.5, 5 μM isopropyl β-d-1-thiogalactopyranoside (IPTG) was added for plasmid based gene expression in all cases except the following: 1 μM IPTG was used for adipic acid production from glycerol without succinic acid supplementation and 10 μM IPTG was used during production of ω-phenylalkanoic acids. For induction of controlled chromosomal expression constructs, 0.1 mM cumate and 15 ng/mL anhydrotetracycline were also added when appropriate. Flasks were then incubated under the same conditions for 48 h post-induction unless otherwise stated.

[0090] Additional fermentations were conducted in a Six-Fors multi-fermentation system (Infors HT, Bottmingen, Switzerland) with an air flow rate of 2 N L/hr, independent control of temperature (37° C.), pH (controlled at 7.0 with NaOH and H_2SO_4), and stirrer speed (720 rpm). Tiglic acid fermentations used the previously described fermentation media with 30 g/L glycerol, the inclusion of 5 μM sodium selenite, and 5 μM IPTG. Propionic acid (20 mM) was added at 0, 24, and 48 h. Pre-cultures were grown in 25 mL flasks as described above, incubated for 4 h post-induction, and used for inoculation as described above.

[0091] Fermentations with glycolyl-CoA as a primer were conducted in 250 mL Erlenmeyer Flasks filled with 50 mL LB media supplemented with 10 g/L glucose and appropriate antibiotics. The cultivation of inoculum was same as above but 2% inoculation was used. After inoculation, cells were cultivated at 30° C. and 250 rpm in a NBS 124 Benchtop Incubator Shaker until an optical density of ~0.8 was reached, at which point IPTG (0.1 mM) and neutralized glycolic acid (40 mM) were added. Flasks were then incubated under the same conditions for 96 h post induction.

[0092] GC sample preparation: Sample preparation was conducted as follows: 2 mL culture supernatant samples were transferred to 5 mL glass vials (Fisher Scientific Co., Fair Lawn, N.J., USA) and 80 μL of 50% H_2SO_4 and 340 μL of 30% NaCl solution were added for pH and ionic strength adjustment, respectively. Tridecanoic acid (final concentration 50 mg/L) was added as internal standard and 2 mL of hexane-MTBE (1:1) added for extraction. The bottles were sealed with Teflonlined septa (Fisher Scientific Co., Fair Lawn, N.J., USA), secured with caps, and rotated at 60 rpm for 120 min. The samples were then centrifuged for 2 min at 2,375×g to separate the aqueous and organic layers. 1 mL of the dry organic layer was transferred into a 2 mL borosilicate glass vial, dried under N_2, and re-suspended in 100 μL of pyridine. After vortexing, 100 μL of BSTFA (N, O-bis (trimethylsilyl)trifluoroacetamide) was added, the samples were heated at 70° C. for 30 min, dried under N_2 and re-suspended in 1 mL hexane for analysis.

[0093] GC-MS metabolite identification: Except identifications of 2,3-dihydroxybutyric acid, metabolite identification was conducted via GC-MS in an Agilent 7890A GC system (Agilent Technologies, Santa Clara, Calif.), equipped with a 5975C inert XL mass selective detector (Agilent) and Rxi-5Sil column (0.25 mm internal diameter, 0.10 mm film thickness, 30 m length; Restek, Bellefonte, Pa.). The sample injection amount was 2 mL with 40:1 split ratio. The injector and detector were maintained at 280° C. The column temperature was held initially at 35° C. for 1 min and increased to 200° C. at the rate of 6° C./min, then to 270° C. at the rate of 30° C./min. That final temperature was maintained for 1

min before cooling back to initial temperature. The carrier gas was helium (2.6 mL/min, Matheson Tri-Gas, Longmont, Colo.).

[0094] Identification of 2,3-dihydroxybyturic acid was conducted by the Baylor College of Medicine Analyte Center (bcm.edu/research/centers/analyte, Houston, Tex.). An Agilent 6890 GC system (Agilent Technologies, Santa Clara, Calif.), equipped with a 5973 mass selective detector (Agilent Technologies) and HP-5ms column (Agilent Technologies) was used. Sample extraction was conducted using Agilent Chem Elut liquid extraction columns (Agilent Technologies) according to manufacturer protocols.

[0095] HPLC metabolite quantification: The concentration of products were determined via ion-exclusion HPLC using a Shimadzu Prominence SIL 20 system (Shimadzu Scientific Instruments, Inc., Columbia, Md.) equipped with an HPX-87H organic acid column (Bio-Rad, Hercules, Calif.) with operating conditions to optimize peak separation (0.3 ml/min flow rate, 30 mM H_2SO_4 mobile phase, column temperature 42° C.).

[0096] In vitro enzyme assay: Purified HACL1 was tested for its native catabolic activity by assessing its ability to cleave 2-hydroxyhexadecanoyl-CoA to pentadecanal and formyl-CoA. Enzyme assays were performed in 50 mM tris-HCl pH 7.5, 0.8 mM $MgCl_2$, 0.02 mM TPP, 6.6 μM BSA, and 0.3 mM 2-hydroxyhexadecanoyl-CoA. The assay mixtures were incubated for one hour at 37° C., after which the presence of pentadecanal was assessed by extraction with hexane and analysis by GC-FID.

[0097] 2-hydroxyhexadecanoyl-CoA was prepared by the n-hydroxysuccinimide method. In summary, the n-hydroxysuccinimide ester of 2-hydroxyhexadecanoic acid is prepared by reacting n-hydroxysuccinimide with the acid in the presence of dicyclohexylcarbodiimide. The product was filtered and purified by recrystallization from methanol to give pure n-hydroxysuccinimide ester of 2-hydroxyhexadecanoic acid. The ester was reacted with CoA-SH in presence of thioglycolic acid to give 2-hydroxyhexadecanoyl-CoA. The 2-hydroxyhexadecanoyl-CoA was purified precipitation using perchloric acid, filtration, and washing the filtrate with perchloric acid, diethyl ether, and acetone.

[0098] For specific activity assays (reported in μmol substrate/mg protein/min) these supernatant fractions were utilized and protein concentration was established using the Bradford Reagent (Thermo Sci.) using BSA as the protein standard.

[0099] Enzyme purification: A plasmid containing the codon optimized gene encoding human HIS-tagged HACL1 was constructed as described. The resulting construct was transformed into *S. cerevisiae* InvSC1 (Life Tech.). The resulting strain was cultured in 50 mL of SC-URA media containing 2% glucose at 30° C. for 24 hours. The cells were pelleted and the required amount of cells were used to inoculate a 250 mL culture volume of SC-URA media containing 0.2% galactose, 1 mM $MgCl_2$, and 0.1 mM thiamine to 0.4 OD600. After 20 hours incubation with shaking at 30° C., the cells were pelleted and saved.

[0100] When needed, the cell pellets were resuspended to an OD600 of approximately 100 in a buffer containing 50 mM potassium phosphate pH 7.4, 0.1 mM thiamine pyrophosphate, 1 mM $MgCl_2$, 0.5 mM AEBSF, 10 mM imidazole, and 250 units of Benzonase nuclease. To the cell suspension, approximately equal volumes of 425-600 μm glass beads were added. Cells were broken in four cycles of 30 seconds of vortexing at 3000 rpm followed by 30 seconds on ice. The glass beads and cell debris were pelleted by centrifugation and supernatant containing the cell extract was collected. The HIS-tagged HACL1 was purified from the cell extract using Talon Metal Affinity Resin as described above, with the only modification being the resin bed volume and all subsequent washes were halved. The eluate was collected in two 500 μL fractions.

[0101] Expression and purification of the desired protein can be confirmed by running cell pellet sample and eluate on SDS-PAGE.

[0102] We demonstrated several cases of the iterative system can synthesize alpha-functionalized small molecules through the use of alpha-functionalized forms of acetyl-CoA as the extender unit. One case used of propionyl-CoA as the extender unit. To implement this, *P. putida* FadAx (thiolase), FadB2x (HACD), FadB1x (ECH), and *E. coli* FabI (ECR) were used with Pct for activation of exogenous propionic acid. Expression in JC01(DE3) resulted in the production of 2-methylbutyric acid (75 mg/L) and tiglic acid (573 mg/L) (FIG. **5**), representing products of acid-forming endogenous termination enzymes at the acyl-CoA and enoyl-CoA pathway nodes.

[0103] Interestingly, 2-methylpentanoic acid (49 mg/L) and (E)-2-methyl-2-pentenoic acid (84 mg/L) were also synthesized, as the result of propionyl-CoA serving as both the primer and the extender unit. Products resulting from non-functionalized extender units (acetyl-CoA) with acetyl-CoA or propionyl-CoA priming were also observed, demonstrating the nonspecific activity of the thiolase (and subsequent β-reduction enzymes). This represents a potential area for further improvement through the selection and engineering of a thiolase with maximal specificity for the desired condensation. Additional alpha-functionalization was demonstrated with glycolyl-CoA (i.e. α-hydroxylated acetyl-CoA) as the extender unit, which with acetyl-CoA priming supported the synthesis of 2,3-dihydroxybutyric acid (FIG. **11**).

[0104] The ability of the alpha-functionalization system to support high product titers was investigated by improving tiglic acid production. Omission of ECR and manipulation of the termination pathway through deletion of native thioesterases and controlled overexpression of YdiI, a thioesterase previously shown to act effectively on α, β-unsaturated enoyl-CoAs, resulted in further improvement, from 573 mg/L to 1.39 g/L (FIG. **7**). When a controlled bioreactor with a higher initial glycerol concentration was used, tiglic acid production increased to 3.79 g/L (11.6% mol/mol glycerol) (FIG. **8**).

[0105] The host strains and plasmids used for production of above products are summarized in Table 8.

TABLE 8

Host strains and plasmids enabling alpha-functionalized small molecule synthesis with listed primer/extender unit combinations

Host strain	Plasmid 1	Plasmid 2	Primer	Extender unit	Product
JC01(DE3)	pETDuet-P1-fadB2x-fadB1x	pCDFDuet-P1-pct-fadAx-P2-fabI	Acetyl-CoA	Propionyl-CoA	2-methylbutyric acid Tiglic acid

TABLE 8-continued

Host strains and plasmids enabling alpha-functionalized small molecule synthesis with listed primer/extender unit combinations

Host strain	Plasmid 1	Plasmid 2	Primer	Extender unit	Product
			Propionyl-CoA	Propionyl-CoA	2-methylpentanoic acid (E)-2-methyl-2-pentenoic acid
JC01(DE3)	pETDuet-P1-fadB2x-fadB1x	pCDFDuet-P1-pct-fadAx	Acetyl-CoA	Propionyl-CoA	Tiglic acid
JST06(DE3)	pETDuet-P1-fadB2x-fadB1x	pCDFDuet-P1-pct-fadAx	Acetyl-CoA	Propionyl-CoA	N.A.
JST06(DE3)	pETDuet-P1-fadB2x-fadB1x-P2-ydil	pCDFDuet-P1-pct-fadAx	Acetyl-CoA	Propionyl-CoA	Tiglic acid
Acetyl-CoA	Glycolyl-CoA	2,3-dihydroxybutyric acid	Acetyl-CoA	Glycolyl-CoA	2,3-dihydroxybutyric acid

[0106] We also successfully expressed *Homo sapiens* 2-hydroxyacyl-CoA lyase HACL1 in *Saccharomyces cerevisiae* and *Escherichia coli* (FIGS. **14** and **16**), and confirmed its activity of degradation of 2-hydroxyhexadecanoyl-CoA to pentadecanal (FIGS. **17-18**). This provides the potential of combination of 2-hydroxyacyl-CoA lyase with proposed iterative platform using alpha-hydroxylated glycolyl-CoA as the extender unit for the synthesis of primary alcohols.

[0107] We believe that, pathway and process optimization, in line with industrial biotechnology approaches, can further improve performance for a specific target product, as the underlying carbon and energy efficiency enables the feasibility of further advancing product titer, rate, and yield. Important areas include generating and balancing pools of priming and extender units and optimization of required pathway enzymes for a given target product. The former can exploit previously developed pathways for primers and extender units, whereas the latter includes identifying and engineering enzymes that may be flux limiting due to suboptimal enzyme specificity or activity. These approaches will be continually aided by developments in protein and metabolic engineering and synthetic and systems biology.

[0108] The above experiments are repeated in *Bacillus subtilis*. The same genes can be used, especially since *Bacillus* has no significant codon bias. A protease-deficient strain like WB800N is preferably used for greater stability of heterologous protein. The *E. coli—B. subtilis* shuttle vector pMTLBS72 exhibiting full structural stability can be used to move the genes easily to a more suitable vector for *Bacillus*. Alternatively, two vectors pHT01 and pHT43 allow high-level expression of recombinant proteins within the cytoplasm. As yet another alternative, plasmids using the theta-mode of replication such as those derived from the natural plasmids pAMβ1 and pBS72 can be used. Several other suitable expression systems are available. Since the FAS genes are ubiquitous, the invention is predicted to function in *Bacillus*.

[0109] The above experiments are repeated in yeast. The same genes can be used, but it may be preferred to accommodate codon bias. Several yeast *E. coli* shuttle vectors are available for ease of the experiments. Since the FAS genes are ubiquitous, the invention is predicted to function in yeast, especially since yeasts are already available with exogenous functional TE genes and the reverse beta oxidation pathway has also been made to run in yeast.

[0110] Each of the following is incorporated by reference herein in its entirety for all purposes:

[0111] US20130316413 Reverse beta oxidation pathway

[0112] 62/140,628 BIOCONVERSION OF SHORT-CHAIN HYDROCARBONS TO FUELS AND CHEMICALS, Mar. 31, 2015

[0113] WO2015112988 TYPE II FATTY ACID SYNTHESIS ENZYMES IN REVERSE BETA-OXIDATION, Jan. 26, 2015 and 61/932,057, Jan. 27, 2014.

[0114] 62/069,850 SYNTHETIC PATHWAY FOR BIOSYNTHESIS FROM 1-CARBON COMPOUNDS, Oct. 29, 2014

[0115] 61/531/911, Sep. 7, 2011; 61/440,192, Feb. 7, 2011, US20140273110, WO2013036812 Functionalized carboxylic acids and alcohols by reverse fatty acid oxidation

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alized small molecules in bacteria using non-decarboxylative Claisen condensation reactions. *Nat. Biotechnol.* 34 (5): doi:10.1038/nbt.3505.

[0125] The following claims are provided to add additional clarity to this disclosure. Future applications claiming priority to this application may or may not include the following claims, and may include claims broader, narrower, or entirely different from the following claims. Further, any detail from any claim may be combined with any other detail from another claim, even if not yet so combined.

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1-36) (cancel)

37) A genetically engineered microorganism comprising means for:

a) an overexpressed activation enzyme(s) able to produce an alpha-functionalized CoA thioester extender unit, wherein said activation enzyme(s) is selected from:
   i) an acyl-CoA synthase which converts the alpha-functionalized CoA thioester extender unit from an alpha-functionalized acid;
   ii) an acyl-CoA transferase which converts the alpha-functionalized CoA thioester extender unit from said alpha-functionalized acid;
   iii) a phosphotransacylase and a carboxylate kinase which converts the alpha-functionalized CoA thioester extender unit from said alpha-functionalized acid; or
   iv) other one or more enzyme(s) that allows production of said alpha-functionalized CoA thioester extender unit from a carbon source without said alpha-functionalized acid;

b) an overexpressed activation enzyme(s) able to produce an acyl-CoA primer, wherein said activation enzyme is selected from:
   i) an acyl-CoA synthase which converts the acyl-CoA primer from its acid form;
   ii) an acyl-CoA transferase which converts the acyl-CoA primer from said acid form;
   iii) a phosphotransacylase and a carboxylate kinase which converts the acyl-CoA primer from said acid form; or,
   iv) other one or more enzymes that allows production of the acyl-CoA primer from the carbon source without said acid form;

c) an overexpressed thiolase enzyme that catalyzes a condensation of said acyl-CoA primer with said alpha-functionalized CoA thioester extender unit to form an alpha-functionalized β-ketoacyl-CoA;

d) an overexpressed 3-hydroxyacyl-CoA dehydrogenase or 3-oxoacyl-[acyl-carrier-protein] reductase enzyme that catalyzes a reduction of said alpha-functionalized β-ketoacyl-CoA to produce an alpha-functionalized β-hydroxyacyl-CoA;

e) an overexpressed enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydratase, or 3-hydroxyacyl-[acyl-carrier-protein] dehydratase enzyme that catalyzes a dehydration of said alpha-functionalized β-hydroxyacyl-CoA to an alpha-functionalized trans-enoyl-CoA;

f) an overexpressed acyl-CoA dehydrogenase, trans-enoyl-CoA reductase, or enoyl-[acyl-carrier-protein] reductase enzyme that catalyzes a reduction of said alpha-functionalized trans-enoyl-CoA to an alpha-functionalized acyl-CoA;

g) iterations of steps b to e, wherein said iteration is achieved by utilizing an alpha-functionalized acyl-CoA-thioester product generated in step e of the last turn as a primer or an extender unit of step c in a next cycle of iteration;

h) an overexpressed termination enzyme(s) able to use a substrate selected from the group consisting alpha-functionalized β-ketoacyl-CoA-thioester products generated in step b, alpha-functionalized β-hydroxyacyl-CoA-thioester products generated in step c, alpha-functionalized trans-enoyl-CoA-thioester products generated in step d, and alpha-functionalized acyl-CoA-thioester products generated in step e, wherein said termination enzyme(s) is selected from:
   i) the group consisting of a thioesterase, or an acyl-CoA transferase, or a phosphotransacylase and a carboxylate kinase catalyzing a conversion of a CoA moiety of said substrate to a carboxylic acid group;
   ii) an aldehyde-forming acyl-CoA reductase catalyzing a conversion of said CoA moiety of said substrate to an aldehyde and an alcohol dehydrogenase catalyzing the conversion of said aldehyde to an alcohol;

iii) an aldehyde-forming acyl-CoA reductase catalyzing a conversion of the CoA moiety of said substrate to an aldehyde and a transaminase catalyzing the conversion of said aldehyde to an amine;

i) optionally reduced expressions of fermentation genes leading to reduced production of lactate, acetate, ethanol and succinate; and

wherein said microorganism has an iterative carbon elongation pathway beginning with said acyl-CoA thioester primer and said alpha-functionalized CoA thioester extender unit and running in a biosynthetic direction.

38) The microorganism of claim **37**, wherein said an alpha-functionalized CoA thioester extender unit is an acyl CoA thioester whose alpha group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, and halogenated acyl group.

39) The microorganism of claim **37**, wherein said alpha-functionalized acid is supplemented in a media containing said microorganisms, or said acid form of said acyl-CoA primer is supplemented in said media, or both are supplemented in said media.

40) The microorganism of claim **37**, wherein said microorganism produces a product selected from the group consisting of β-keto acids, β-keto alcohols, β-keto amines, β-hydroxy acids, 1,3-diols, β-hydroxy amines, Δ^2-fatty acids, Δ^2-fatty alcohols, Δ^2-amines, fatty acids, alcohols and amines, whose alpha group is selected from the group consisting of hydrogen, alkyl group, hydroxyl group, carboxyl group, aryl group, halogen, amino group, hydroxyacyl group, carboxyacyl group, aminoacyl group, ketoacyl group, and halogenated acyl group.

41) The microorganism of claim **37**, wherein:

a) said overexpressed acyl-CoA synthase is encoded by a gene(s) selected from the group consisting of *E. coli* sucC, *E. coli* sucD, *E. coli* paaK, *E. coli* prpE, *E. coli* menE, *E. coli* fadK, *E. coli* fadD, *Penicillium chrysogenum* phl, *Salmonella typhimurium* LT2 prpE, *Bacillus subtilis* bioW, *Cupriavidus basilensis* hmfD, *Rhodopseudomonas palustris* badA, *R. palustris* hbaA, *Pseudomonas aeruginosa* PAO1 pqsA, and *Arabidopsis thaliana* 4cl; and

b) said overexpressed acyl-CoA transferase is encoded by a gene(s) selected from the group consisting of *E. coli* atoD, *E. coli* scpC, *E. coli* ydiF, *E. coli* atoA, *E. coli* atoD, *Clostridium acetobutylicum* ctfA, *C. acetobutylicum* ctfB, *Clostridium kluyveri* cat2, *C. kluyveri* cat1, *P. putida* pcaI, *P. putida* pcaJ, *Megasphaera elsdenii* pct, *Acidaminococcus fermentans* gctA, *Acidaminococcus fermentans* gctB, and *Acetobacter aceti* aarC.

42) The microorganism of claim **37**, wherein:

a) said overexpressed thiolase is encoded by a gene(s) selected from the group consisting of *E. coli* atoB, *E. coli* yqeF, *E. coli* fadA, *E. coli* fadI, *Ralstonia eutropha* bktB, *Pseudomonas* sp. B13 catF, *E coli* paaJ, *Rhodococcus opacus* pcaF, *Pseudomonas putida* pcaF, *Streptomyces* sp. pcaF, *P. putida* fadAx, *P. putida* fadA, *Ralstonia eutropha* phaA, *Acinetobacter* sp. ADP1 dcaF, *Clostridium acetobutylicum* thlA, and *Clostridium acetobutylicum* thlB;

b) said overexpressed 3-hydroxyacyl-CoA dehydrogenase or 3-oxoacyl-[acyl-carrier-protein] reductase is encoded by a gene(s) selected from the group consisting of *E. coli* fabG, *E. coli* fadB, *E. coli* fadJ, *E. coli* paaH, *P. putida* fadB, *P. putida* fadB2x, *Acinetobacter* sp. ADP1 dcaH, *Ralstonia eutrophus* phaB, and *Clostridium acetobutylicum* hbd; and

c) said acyl-CoA dehydrogenase, trans-enoyl-CoA reductase, or enoyl-[acyl-carrier-protein] reductase is encoded by a gene(s) selected from the group consisting of *E. coli* fadE, *E. coli* ydiO, *Euglena gracilis* TER, *Treponema denticola* TER, *Clostridium acetobutylicum* TER, *E. coli* fabI, *Enterococcus faecalis* fabK, *Bacillus subtilis* fabL, and *Vibrio cholerea* fabV.

43) The microorganism of claim **37**, wherein said overexpressed thioesterase is encoded by a gene(s) selected from the group consisting of *E. coli* tesA, *E. coli* tesB, *E. coli* yciA, *E. coli* fadM, *E. coli* ydiI, *E. coli* ybgC, *E. coli* paaI, *Mus musculus* acot8, *Alcanivorax borkumensis* tesB2, *Fibrobacter succinogenes* Fs2108, *Prevotella ruminicola* Pr655, *Prevotella ruminicola* Pr1687, and *Lycopersicon hirsutum* f *glabratum* mks2.

44) The microorganism of claim **37**, wherein said overexpressed aldehyde-forming acyl-CoA reductase is encoded by a gene(s) selected from the group consisting of *Acinetobacter calcoaceticus acr*1, *Acinetobacter* sp Strain M-1 acrM, *Clostridium beijerinckii* ald, *E. coli* eutE, *Salmonella enterica* eutE, *E. coli* mhpF, and *Clostridium kluyveri* sucD.

45) The microorganism of claim **37**, wherein said overexpressed alcohol dehydrogenase is encoded by a gene(s) selected from the group consisting of *E. coli* betA, *E. coli* dkgA, *E. coli* eutG, *E. coli* fucO, *E. coli* ucpA, *E. coli* yahK, *E. coli* ybbO, *E. coli* ybdH, *E. coli* yiaY, *E. coli* yjgB, *Saccharomyces cerevisiae* ADH6, *Clostridium kluyveri* 4hbD, and *Acinetobacter* sp. SE19 chnD.

46) The microorganism of claim **37**, wherein said overexpressed transaminase is encoded by a gene(s) selected from the group consisting of *Arabidopsis thaliana* At3g22200, *Alcaligenes denitrificans* aptA, *Bordetella bronchiseptica* BB0869, *Bordetella parapertussis* BPP0784, *Brucella melitensis* BAWG_0478, *Burkholderia pseudomallei* BP1026B_0669, *Chromobacterium violaceum* CV2025, *Oceanicola granulosus* OG_2516_07293, *Paracoccus denitrificans* PD1222 Pden_3984, *Caulobacter crescentus* CC_3143, *Pseudogulbenkiania ferrooxidans* ω-TA, *Pseudomonas putida* ω-TA, *Ralstonia solanacearum* ω-TA, *Rhizobium meliloti* SMc01534, *Vibrio fluvialis* ω-TA, *Bacillus megaterium* SC6394 ω-TA, *Mus musculus* abaT, *Flavobacterium lutescens* lat, *Streptomyces clavuligerus* lat, *E. coli* gabT, *E. coli* puuE, and *E. coli* ygjG.

47) The microorganism of claim **37**, wherein said step g uses alpha-functionalized β-ketoacyl-CoA-thioester products generated in step b as the substrate, and further comprising an overexpressed β-keto acid decarboxylase catalyzing the conversion of the β-keto-acid to a ketone, wherein said overexpressed β-keto acid decarboxylase is encoded by a gene(s) selected from the group consisting of *Clostridium acetobutylicum* adc, and *Lycopersicon hirsutum* f *glabratum* mks1.

48) The microorganism of claim **37**, wherein said termination pathway i) of step h uses alpha-functionalized acyl-CoA-thioester products generated in step b as the substrate, utilizing glycolyl-CoA as the extender unit and further comprising:

a) an overexpressed keto-dehydrogenase catalyzing the conversion of a 2-hydroxy acid to an alpha-keto acid;

b) an overexpressed alpha-keto acid decarboxylase catalyzing the conversion of an alpha-keto acid to a primary aldehyde; and

c) an overexpressed alcohol dehydrogenase catalyzing the conversion of a primary aldehyde to a primary alcohol.

49) The microorganism of claim **43**, wherein said overexpressed keto-dehydrogenase is encoded by a gene(s) selected from the group consisting of *E. coli* ldhA, *E. coli* lldD, *E. coli* leuB, *Clostridium beijerinckii* adh, *Acidaminococcus fermentans* hgdH, *E. coli* serA, *Gordonia* sp. TY-5 adh1, *Gordonia* sp. TY-5 *adh*2, *Gordonia* sp. TY-5 adh3, and *Rhodococcus ruber* adh-A.

50) The microorganism of claim **37**, utilizing glycolyl-CoA as the extender unit and producing a primary alcohol, further comprising:

a) an overexpressed 2-hydroxyacyl-CoA lyase catalyzing the conversion of a 2-hydroxyacyl-CoA, generated from step e of claim **1**, to a primary aldehyde and a formyl-CoA; and

b) an overexpressed alcohol dehydrogenase catalyzing the conversion of a primary aldehyde to a primary alcohol.

51) The microorganism of claim **45**, wherein said overexpressed 2-hydroxyacyl-CoA lyase is encoded by a gene(s) selected from the group consisting *Homo sapiens* hacl 1, *Rattus norvegicus* hacl 1, *Dictyostelium discoideum* hacl 1, and *Mus musculus* hacl1.

52) The microorganism of claim **37**, wherein said reduced expressions of fermentation enzymes are ΔadhE, (Δpta or ΔackA or ΔackApta), ΔpoxB, ΔldhA, and ΔfrdA and less acetate, lactate, ethanol and succinate are thereby produced.

53) The microorganism of claim **37**, comprising the following mutations: fadR, atoC(c), ΔarcA, Δcrp, crp*.

54) A recombinant microorganism, comprising an inducible expression vector or inducible integrated sequences for overexpressing enzymes including 1) a thiolase catalyzing the condensation of an unsubstituted or functionalized acyl-CoA thioester with alpha-functionalized acetyl-CoA; a 2 hydroxyacyl-CoA dehydrogenase, 3) an enoyl-CoA hydratase, 4) an enoyl-CoA reductase and 5) one or more termination enzymes removing a product from a cycle of reactions 1-4.

55) A method of making alpha functionalized products, comprising growing a microorganism of claim **37** in a nutrient broth under conditions such that said enzymes are overexpressed, said microorganism producing an alpha functionalized product using said overexpressed enzymes, and isolating said alpha functionalized product.

56) The method of claim **55**, wherein said nutrient broth is supplemented with said alpha-functionalized acid or said acid form of acyl-CoA primer or both are supplemented.

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