BIOSYNTHETIC PATHWAYS, RECOMBINANT CELLS, AND METHODS

CROSS-REFERENCE TO RELATED APPLICATION

This application claims priority to U.S. Provisional Patent Application Serial No. 61/652,505, filed May 29, 2012, which is incorporated herein by reference.

SUMMARY

This disclosure describes, in one aspect, a recombinant cell modified to exhibit increased biosynthesis of an ester compared to a wild-type control. The recombinant cell may be a eukaryotic cell or a prokaryotic cell. In some cases, the microbial cell may be photosynthetic. In some cases, the microbial cell may be cellulolytic. In some embodiments, the recombinant cell can exhibit an increase in conversion of an organic acid to an acyl-CoA compared to a wild-type control, an increase in conversion of ketoacids to an acyl-CoA compared to a wild-type control, an increase in conversion of an aldehyde to an organic acid compared to a wild-type control, an increase in conversion of an aldehyde to an alcohol compared to a wild-type control, or an increase in combining an acyl-CoA with an alcohol to form an ester compared to a wild-type control.

In another aspect, this disclosure describes a method that generally includes incubating a recombinant cell modified to exhibit increased biosynthesis of an ester compared to a wild-type control in medium that includes a carbon source under conditions effective for the recombinant cell to produce an ester, wherein the carbon source comprises one or more of: glucose, pyruvate, ketovaline, CO_2, cellulose, xylose, sucrose, arabinose, or glycerol.

In another aspect, this disclosure describes a method that generally includes introducing into a host cell a heterologous polynucleotide encoding at least one polypeptide that catalyzes a step in converting a carbon source to an ester, wherein the at least one polynucleotide is operably linked to a promoter so that the modified host cell catalyzes conversion of the carbon source to an ester. In some embodiments, the carbon source can include one or more of: glucose, pyruvate, ketovaline, CO_2, cellulose, xylose, sucrose, arabinose, or glycerol. In some embodiments, the host cell can be a eukaryotic cell. In other

embodiments, the host cell can be a prokaryotic cell. In some embodiments, the host cell can be photosynthetic. In some embodiments, the host cell can be cellulolytic.

The above summary of the present invention is not intended to describe each disclosed embodiment or every implementation of the present invention. The description that follows more particularly exemplifies illustrative embodiments. In several places throughout the application, guidance is provided through lists of examples, which examples can be used in various combinations. In each instance, the recited list serves only as a representative group and should not be interpreted as an exclusive list.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. (a) Proposed artificial biosynthetic pathway to esters. (b) Example molecules. (c) Advantages of ester approach to fuels and chemicals.

FIG. 2. An exemplary synthetic pathway to ester isobutyl-isobutyrate. Two independent pathways can lead to the production of isobutyryl-CoA.

FIG. 3. (a) Plasmids and (b) gas chromatography data result showing biosynthesis of isobutyl isobutyrate.

FIG. 4. Synthetic pathways for the production of isobutyl acetate (IBAC) and isoamyl acetate (IVAC). The engineered steps of the pathways are shown in the box. NADPH-dependent enzymes are indicated with a dotted circle and key enzyme acyltransferase are indicated with dotted rectangles. Abbreviation: PDC (pyruvate dehydrogenase complex), AAT (alcohol acyltransferase); other enzymes and are specified in FIG. 5.

FIG. 5. Synthetic operons for (a) isobutyl acetate (IBAC) (b) isoamyl acetate (IVAC) production. Abbreviation: AAT (alcohol acyltransferase).

FIG. 6. Fermentation results with the introduction of five candidate acyltransferases (AAT) for (a) isobutyl acetate production and (b) isoamyl acetate production. Error bars indicate standard deviation. These five AATs and their natural substrates are shown as in Table 3.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

In the description of exemplary embodiments that follow, certain metabolic enzymes, and the natural source of those enzymes, are specified. These are merely examples

of suitable enzymes and suitable sources of the specified enzymes. Alternative enzymes with similar catalytic activities are possible, as are homologs that are obtainable from different microbial species or strains. Accordingly, the exemplary embodiments described herein should not be construed as limiting the scope of the microbes or methods that are reflected in the claims. The search for renewable resources to replace petroleum is a significant challenge facing science, industry, and society. Biosynthesis can provide a sustainable supply of fuels and chemicals from biomass resources. Factors that can influence the viability of a fermentation process include, for example, feedstock availability, fermentation performance (e.g., yield, titer, productivity), and the cost of recovering the fermentation product. While great advances have been made in feedstock development, current fermentation approaches to the production of alcohols or organic acids is not ideal. First, alcohols and organic acids can be very toxic to cells, which can limit the concentration to which these products can accumulate in a fermentation culture before they have a deleterious effect on the viability of the microbes in the culture. Second, alcohols and acids tend to be very soluble in aqueous media (e.g., culture media) and therefore can require an energy-intensive distillation purification scheme to recover these products from an aqueous fermentation medium. As a result, while higher alcohols such as, for example, butanol can offer advantages as fuels compared to, for example, ethanol, it is difficult for higher alcohols to compete with ethanol as a commercially viable biofuel because of the high purification cost from low fermentation titers (<20 g/L). Third, fermentation to produce organic acids often involves adding a base to the fermentation in order to neutralize the pH of the medium in which the organic acid accumulates. The recovery of the organic acid often involves subsequent addition of sulfuric acid and disposal of salts, each of which can involve significant cost.

To provide a general solution, we have developed an ester platform for the production of alcohols, organic acids, or other biofuels. As shown in FIG. 1(a), one embodiment of this approach has three components: 1) a metabolic pathway for the biosynthesis of carboxylic acids and then acyl-CoAs; 2) a parallel metabolic pathway for the biosynthesis of alcohols; and 3) an engineered pathway for the production of esters from acyl-CoAs and alcohols. The successful implementation of this platform has enabled the bio-based production of esters. In some alternative embodiments, the approach may include a metabolic pathway for the biosynthesis of carboxylic acids (and then acyl-CoAs) and an

engineered pathway for the production of esters from the biosynthesized acyl-CoAs and alcohols provided as a co-reactant (e.g., in the culture medium). In other alternative embodimetns, the approach can include a metabolic pathway for the biosynthesis of alcohols and an engineered pathway for the production of esters from the biosynthesized alcohol and acyl-CoAs provided as a co-reactant (e.g., in the culture medium).

An ester produced by using our platform technology may be used as a biofuel, an industrial chemical, or a raw material for the production of other compounds. For example, esters can be readily hydrolyzed to make alcohols and organic acids. In principle, this approach can be used to manufacture any alcohol and/or organic acid from an appropriate ester produced by a microbe engineered according to our platform. Several exemplary organic acids and alcohols are listed in Fig. 1(b). Exemplary organic acid products include, for example, acetate, isobutyrate, 3-hydroxypropionate, butyrate, lactate, methacrylate, acrylate, and isopentanoate. Exemplary alcohol products include, for example, ethanol, methanol, butanol, isobutanol, propanol, isopropanol, pentanol, isopentanol, hexanol, heptanol, and octanol. The combination of any of these acids with any of these alcohols could generate an ester metabolite.

An ester produced as described herein can be used as a biofuel. Esters, in general, can provide certain advantages over, for example, ethanol as a fuel. As shown in Table 1, ester fuels have similar energy density to higher alcohols such as, for example, isobutanol and isopentanol. Esters also can exhibit less solubility in water compared to corresponding alcohol compounds, allowing one to recover an ester from aqueous medium using phase separation rather than distillation. As a result, recovering esters can be simpler, more efficient, and less costly than recovering alcohols from fermentations. While fatty acids and alkanes also have very low water solubility, long chain fatty acids typically are not efficiently secreted to the extracellular milieu and fuels prepared from these compounds may not perform well at low temperatures because they may be prone to gelling.

Bioproduction of esters can produce higher theoretical yields than bioproduction of higher alcohols, alkanes, and fatty acids. In *E. coli*, for example, isobutanol accumulation can reach approximately 22 g/L without *in situ* recovery during fermentation (Baez et al., Appl. Microbiol. Biotechnol. 2011, 90 (5), 1681-1690). In contrast, we can produce 90 g/L isobutyrate, which is comparable to fermentation of lactate (Wang et al., Proc. Natl. Acad. Sci. USA. 2011, 108 (47), 18920-18925) or succinate (Lin et al., Metab. Eng. 2005, 7 (2),

116-127), two of the most promising renewable chemicals under commercial production. Also, C5 isovalerate can accumulate to 32 g/L, much higher than isopentanol (4.4 g/L) (Connor et al., Appl. Microbiol. Biotechnol. 2010, 86 (4), 1155-1164) and fatty acid (4.5 g/L) (Liu et al., Metab. Eng. 2010, 12 (4), 378-386). Finally, esters are not toxic to cells, allowing one to observe higher accumulations in fermentation broths compared to other compounds.

Table 1. Comparison of biosynthesis profile, physical properties, and fuel properties of various compounds.

Fuel	Energy density (MJ/L)	Theoretical yield (g/g glucose)	Titer (g/L)	Solubility (g/L)
Ethanol	21	0.51	200	miscible
Fatty acid	33	0.36	4.5	insoluble
Farnesene	31	0.29	104	insoluble
Isobutanol	26	0.41	22	85
Isopentanol	27	0.33	4.4	27
Isobutyric acid	x	0.49	90	200
Isovaleric acid	x	0.38	32	25
Ethyl acetate	19	0.49		83
Ethyl isobutyrate	25	0.43		3.2
Ethyl isovalerate	26	0.36		2
isobutyl isobutyrate	27	0.40		0.5
isovaleryl isovalerate	29	0.32		insoluble
Gasoline	32			
Jet fuel	35			
Diesel	39			

FIG. 2 shows an exemplary, generalized engineered pathway for producing an exemplary ester compound, isobutyl-isobutyrate. To catalyze the esterification enzymatically, a carboxylic acid is activated to an acyl-CoA. Then, the acyl-CoA can react with an alcohol to produce an esters. The esterification reaction is catalyzed by an acyltransferase (FIG. 2). We have engineered two ester-producing strains of *E. coli*, Ester strain 1 and Ester strain 2, each of which employs an independent pathway for the generation of the acyl-CoA intermediate. One pathway to producing an acyl-CoA converts isobutyrate into isobutyryl-CoA by an acyl-CoA synthetase (Acs). We cloned FadDx from *Pseudomonas putida*, an exemplary acyl-CoA synthetase, to catalyze the production of the acyl-CoA in this manner (Ester strain 1, shown in FIG. 2 as "Pathway II"). Another pathway

to acyl-CoA is to employ branched-chain keto acid dehydrogenase complex BKDH from *Pseudomonas putida*. We employed this strategy in a separate strain (Ester strain 2, shown in FIG. 2 as "Pathway I").

We then cloned benzoyl-coenzyme A (CoA):benzyl alcohol benzoyl transferase (BEBT, or LuxE) from *Clarkia breweri* (D'Auria et al., Plant Physiol. 2002, 130(1):466) into both Ester strain 1 and Ester strain 2.

According to gas chromatography analysis, 3.5 mg/L isobutyl isobutyrate was obtained during shake flask fermentations for Ester 1 strain and 200 mg/L for Ester 2 strain. Without LuxE, no isobutyl isobutyrate was detected in the fermentation broth.

This embodiment establishes a basic platform in which microbes can be engineered to produce an ester compound. The particular enzymes we have used are merely exemplary, establishing that the platform can be effective for biosynthesis of ester compounds. One can use any suitable combination of acyl-CoA-generating enzymes—either acyl-CoA synthetase or branched-chain keto acid dehydrogenase complex, BKDH—and acyltransferase to produce a desired ester product from a given feedstock. Exemplary acyl-CoA synthetases that may be used in our platform include, for example, those reflected in any one of SEQ ID NO:5-28, regardless of the enzyme's common name or native substrate. Certain exemplary acyl-CoA synthetases are listed in Table 2. Exemplary branched-chain keto acid dehydrogenase complex enzymes that may be used in our platform include, for example, any one or more of the amino acid sequences reflected in SEQ ID NO:29 and 78-80, regardless of the enzyme's common name or native function. Certain exemplary branched-chain keto acid dehydrogenase complex enzymes are listed in Table 2. Exemplary acyltransferases that may be used in our platform include, for example, those reflected in any one of SEQ ID NO:30-77, regardless of the enzyme's common name or native function. Certain exemplary acyltransferases include, for example, those listed in Table 2.

Table 2. Exemplary alternative acyl-CoA synthetases and acyl-transferases

Common Name	Organism	Encoding gene	Accession No.	Native Substrate	Comment	SEQ ID NO
Exemplary Acyl-CoA synthetases						
Acyl-CoA synthetase	*P. Putida*	*Acs*	NP_746598.1	aliphatic acids	Synthesizes isobutyl isobutyrate	5
Acyl-CoA synthetase	*S. cerevisiae*	*Faa2P*	NP_010931.1	medium chain acids	Activate C4-C22 substrates	11
Acyl-CoA synthetase	*S. cerevisiae*	*Acs1p*	NP_009347.1	acetate	Activate propionate	17
Acyl-activating enzyme 11	*A. thaliana*	*AAE11*	AAP03024.1	Fatty acids	Activate C4-C8 acids	23
Branched-chain alpha-keto acid dehydrogenase comlex enzymes						
branched-chain alpha-keto acid dehydrogenase	*P. putida* KT2440	*bkdA1*	NP_746515.1	Branched-chain alpha-keto acids	Activate C4-C6 keto acids	78
branched-chain alpha-keto acid dehydrogenase	*P. putida* KT2440	*bkdA2*	NP_746516.1	Branched-chain alpha-keto acids	Activate C4-C6 keto acids	79
branched-chain alpha-keto acid dehydrogenase	*P. putida* KT2440	*bkdB*	NP_746517.1	Branched-chain alpha-keto acids	Activate C4-C6 keto acids	80
branched-chain alpha-keto acid dehydrogenase	*P. putida* KT2440	*lpdV*	NP_746518.1	Branched-chain alpha-keto acids	Activate C4-C6 keto acids	29
Exemplary Acyltransferases						
Acyl-transferase	*S. cerevisiae*	*EEB1*	NP_015230.1	acyl-CoA & ethanol	Produce ethyl esters	30
benzyl alcohol benzoyl transferase	*C. breweri*	*BEBT (luxE)*	Q8GT21.1	benzoyl CoA & benzyl alcohol	Synthesize isobutyl isobutyrate in our preliminary study	36
alcohol acyl-transferases	*C. melo*	*CmAAT3*	AAW51125.1	acetyl CoA & benzyl alcohol	Accept a broad range of acyl-CoA and alcohols	42
benzyl alcohol benzoyl transferase	*P. hybrida*	*BPBT*	AAT68601.1	benzoyl CoA & phenylethanol	Accept a broad range of acyl-CoA and alcohols	48
alcohol acyl transferase	*M. domestica*	MpAAT1	AAU14879.2	alcohol	Produce medium-chain aliphatic volatile esters	54
alcohol *acyltransferase*	Fragaria spp. and hybrids	*SAAT*	AAG13130.1	medium-chain aliphatic alcohols	Produce butyl butyrate	60
alcohol acetyltransferase	*S. cerevisiae*	*ATF1*	EGA72844.1	alcohol	Produce acetyl acetate	66
alcohol acetyltransferase	*S. cerevisiae*	*ATF2*		alcohol	Produce acetyl acetate	72

FIG. 4 illustrates an alternative embodiment of our platform for ester biosynthesis. In this embodiment, isobutyl acetate (IBAC) and/or isoamyl acetate (IVAC, banana oil) may be produced by a microbe in which the native valine biosynthetic pathway is modified. Acetyl-CoA is natively and readily available in, for example, *E. coli.* as a component of the TCA cycle. To produce either IBAC and IVAC, the microbe is first constructed to overexpress AlsS and IlvD to promote biosynthesis of 2-ketoisovalerate. The microbe also is constructed to express Kivd and Yqhd, which together can convert 2-ketoisovalerate to isobutanol, which can be esterified to isobutyl acetate in a reaction catalyzed by an acyltransferase. To produce isoamyl acetate, the microbe may be constructed to further express the "+1" pathway (LeuABCD), which can elongate 2-ketoisovalerate by one carbon to form 2-keto-4-methylvalerate. In these embodiments, the combination of KivD and Yqhd can convert 2-keto-4-methylvalerate to isopentanol, which can be esterified to isoamyl acetate by an acyltransferase.

We characterized five exemplary alcohol acyltransferases (AAT), LuxE, ATF1, ATF2, BPBT, and SAAT (as shown in Table 3). Each was cloned and transformed into *E. coli* strain BW25113 for analysis.

Table 3. Exemplary alcohol acyltransferases (AAT) in medium-chain esters biosynthesis.

Gene	Enzyme	Native Function	Organism
luxE	Benzyl alcohol O-benzoyltransferase	Uses benzoyl-CoA and benzyl alcohol to make benzyl benzoate	*C. breweri*
ATF1	Alcohol acetyltransferase	Acetate ester production	*S. cerevisiae*
ATF2	Alcohol acetyltransferase	Acetate ester production	*S. cerevisiae*
BPBT	Benzyl alcohol O-benzoyltransferase	Uses benzoyl-CoA and benzyl alcohol to make benzyl benzoate	*P. hybrida*
SAAT	Strawberry alcohol acetyltransferase	Uses aliphatic medium-chain alcohols and broad ranges of acyl-CoA to make esters	*Strawberry*

Three synthetic operons were constructed for gene expression to produce isobutyl acetate and isoamyl acetate (FIG. 5). All the plasmids were constructed to be under the regulation of $P_L$lacO1 promoter. To produce isobutyl acetate, the first operon included four coding regions on a medium copy plasmid carrying kanamycin resistance marker in a transcriptional order *ilvC-ilvD-alsS-AAT*, with the *ATT* position being occupied by the coding region of one of the five exemplary acyltransferases (AAT) being analyzed. (FIG. 5(a)). The second operon included two coding regions on a high copy plasmid with an ampicillin resistance maker in a transcriptional order *kivd-yqhD*. For the synthesis of isoamyl acetate, the coding regions of *leuA*, *leuB*, *leuC*, and *leuD* involved in leucine biosynthesis were introduced in the first medium copy plasmid between *alsS* and *AAT*, and the same second high copy plasmid was used. (FIG. 5(b)).

We assessed the effect of each of the five exemplary acyltransferases on the production titers for isobutyl acetate and isoamyl acetate. Coding regions for ATF1 and ATF2 were amplified by PCR from *S. cerevisiae* genomic DNA. Coding regions for LuxE, BPBT, and SAAT were artificially synthesized by annealing based connection of oligonucleotides. Recombinant strains were constructed with the synthetic operons as shown in FIG. 2.

Shake flask fermentations and products analyses were carried as described in Example 2 and three independent colonies were streaked for inoculation to get standard deviation. All strains were identical except for the alcohol acyltransferase that was expressed. Therefore, with the same fermentation conditions, the strain with the highest production titer of the target compound would have the most active alcohol acyltransfersase. The activity here represents the combined effects of kinetic parameters and protein expression levels.

FIG. 6(a) provides data for isobutyl acetate production. ATF1 produced the highest titer (2.14 ± 0.17 g/L). ATF2 produced a titer of 1.69 ± 0.46 g/L. FIG. 6(b) shows data for the production of isoamyl acetate and reveals a similar trend. ATF1 and ATF2 produced the highest production titers.

Coding regions for any heterologous enzyme introduced into a host cell can be PCR amplified from the genomic DNA of a native host if commercially available (e.g., from

American Type Culture Collection). Otherwise, one can artificially synthesize a coding region by PCR assembly using multiple primers. A synthetic coding region can be codon optimized for expression in a host cell such as, for example, *E. coli* or *S. cerevisiae*. Cells transformed with plasmids harboring the coding region for a heterologous enzyme can be cultured in medium that includes carboxylic acid and/or alcohol precursors.

Thus, in one aspect, the invention provides recombinant microbial cell modified to exhibit increased biosynthesis of an ester compared to a wild-type control. In some cases, the wild-type control may be unable to produce ester and, therefore, an increase in the biosynthesis of an ester may reflect any measurable biosynthesis of the ester. In certain embodiments, an increase in the biosynthesis of an ester can include biosynthesis sufficient for a culture of the microbial cell to accumulate the ester to a predetermine concentration.

The predetermined concentration may be any predetermined concentration of the product suitable for a given application. Thus, a predetermined concentration may be, for example, a concentration of at least 3 mg/L such as, for example, at least 10 mg/L, at least 100 mg/L, at least 200 mg/L, at least 500 mg/L, at least 1.0 g/L, at least 2.0 g/L, at least 3.0 g/L, at least 4.0 g/L, at least 5.0 g/L, at least 6.0 g/L, at least 7.0 g/L, at least 8.0 g/L, at least 9.0 g/L, at least 10 g/L, at least 20 g/L, at least 50 g/L, at least 100 g/L, or at least 200 g/L.

The recombinant cell can be, or be derived from, any suitable microbe including, for example, a prokaryotic microbe or a eukaryotic microbe. As used herein, the term "or derived from" in connection with a microbe simply allows for the "host cell" to possess one or more genetic modifications before being further modified to exhibit the indicated increased biosynthetic activity. Thus, the term "recombinant cell" encompasses a "host cell" that may contain nucleic acid material from more than one species before being modified to exhibit the indicated biosynthetic activity.

In some embodiments, the host cell may be selected to possess one or more natural physiological activities. For example, the host cell may be photosynthetic (e.g., cyanobacteria) or may be cellulolytic (e.g., *Clostridium cellulolyticum*).

In some embodiments, the recombinant cell may be, or be derived from, a eukaryotic microbe such as, for example, a fungal cell. In some of these embodiments, the fungal cell may be, or be derived from, a member of the Saccharomycetaceae family such as, for example, *Saccharomyces cerevisiae*, *Candida rugosa*, or *Candida albicans*.

In other embodiments, the recombinant cell may be, or be derived from, a prokaryotic microbe such as, for example, a bacterium. In some of these embodiments, the bacterium may be a member of the phylum Protobacteria. Exemplary members of the phylum Protobacteria include, for example, members of the Enterobacteriaceae family (e.g., *Escherichia coli*) and, for example, members of the Pseudomonaceae family (e.g., *Pseudomonas putida*). In other cases, the bacterium may be a member of the phylum Firmicutes. Exemplary members of the phylum Firmicutes include, for example, members of the Bacillaceae family (e.g., *Bacillus subtilis*), members of the Clostridiaceae family (e.g., *Clostridium cellulolyticum*) and, for example, members of the Streptococcaceae family (e.g., *Lactococcus lactis*). In other cases, the bacterium may be a member of the phylum Cyanobacteria.

In some embodiments, the increased biosynthesis of an ester compared to a wild-type control can include one or more of the following: an increase in conversion of an organic acid to an acyl-CoA compared to a wild-type control, an increase in conversion of ketoacids to an acyl-CoA compared to a wild-type control, an increase in conversion of an aldehyde to an organic acid compared to a wild-type control, an increase in conversion of an aldehyde to an alcohol compared to a wild-type control, or an increase in combining an acyl-CoA with an alcohol to form an ester compared to a wild-type control. The particular acyl-CoA synthetase, branched-chain keto acid dehydrogenase (BKDH) complex enzyme(s), and/or acyltransferase can be selected based on one or more criteria such as, for example, the metabolic substrate in the designed pathway, the available feedstock, and/or the efficiency at which the enzyme is expressed in the host microbe.

In other embodiments, the increased biosynthesis of an ester compared to a wild-type control can include one or more of the following: an increase in conversion of 2-ketoisovalerate to isobutyraldehyde, and increase in conversion of isobutyraldehyde to isobutanol, an increase in synthesis of isobutyl acetate from isobutanol and an acyl-CoA, an increase in elongation of 2-ketoisovalerate to 2-keto-4-methylvalerate, an increase in conversion of 2-keto-4-methylvalerate to isovaleraldehyde, an increase in conversion of isovaleraldehyde to isopentanol, or an increase in synthesis of isoamyl acetate from isopentanol and an acyl-CoA.

In some cases, increased biosynthesis of an ester compared to a wild-type control can include a decrease in catalytic activity of one or more enzymes such as, for example, an

esterase and/or a lipase that can otherwise divert an intermediate of the designed pathway to an alternative pathway that does not result in biosynthesis of the desired ester.

As used herein, the terms "activity" with regard to particular enzyme refers to the ability of a polypeptide, regardless of its common name or native function, to catalyze the conversion of the enzyme's substrate to a product, regardless of whether the "activity" is less than, equal to, or greater than the native activity of the identified enzyme. Methods for measuring the biosynthetic activities of cells and enzymatic activities of acyl-CoA synthetase and acyltransferase are routine and well known to those of ordinary skill in the art. In the context of a genetically-modified cell, the term "activity" refers to the ability of the genetically-modified cell to synthesize an identified product compound, regardless of whether the "activity" is less than, equal to, or greater than the native activity of a wild-type strain of the cell.

As used herein, an increase in catalytic activity of an enzyme or an increase in the biosynthetic activity of a genetically-modified cell can be quantitatively measured and described as a percentage of the catalytic activity of an appropriate wild-type control. The catalytic activity exhibited by a genetically-modified polypeptide or the biosynthetic activity of a genetically-modified cell can be, for example, at least 110%, at least 125%, at least 150%, at least 175%, at least 200% (two-fold), at least 250%, at least 300% (three-fold), at least 400% (four-fold), at least 500% (five-fold), at least 600% (six-fold), at least 700% (seven-fold), at least 800% (eight-fold), at least 900% (nine-fold), at least 1000% (10-fold), at least 2000% (20-fold), at least 3000% (30-fold), at least 4000% (40-fold), at least 5000% (50-fold), at least 6000% (60-fold), at least 7000% (70-fold), at least 8000% (80-fold), at least 9000% (90-fold), at least 10,000% (100-fold), or at least 100,000% (1000-fold) of the activity of an appropriate wild-type control.

Alternatively, an increase in catalytic activity may be expressed as at an increase in k_{cat} such as, for example, at least a two-fold increase, at least a three-fold increase, at least a four-fold increase, at least a five-fold increase, at least a six-fold increase, at least a seven-fold increase, at least an eight-fold increase, at least a nine-fold increase, at least a 10-fold increase, at least a 15-fold increase, or at least a 20-fold increase in the k_{cat} value of the enzymatic conversion.

An increase in catalytic activity also may be expressed in terms of a decrease in K_m such as, for example, at least a two-fold decrease, at least a three-fold decrease, at least a

four-fold decrease, at least a five-fold decrease, at least a six-fold decrease, at least a seven-fold decrease, at least an eight-fold decrease, at least a nine-fold decrease, at least a 10-fold decrease, at least a 15-fold decrease, or at least a 20-fold decrease in the K_m value of the enzymatic conversion.

A decrease in catalytic activity of an enzyme or an increase in the biosynthetic activity of a genetically-modified cell can be quantitatively measured and described as a percentage of the catalytic activity of an appropriate wild-type control. The catalytic activity exhibited by a genetically-modified polypeptide or the biosynthetic activity of a genetically-modified cell can be, for example, no more than 95%, no more than 90%, no more than 85%, no more than 80%, no more than 75%, no more than 70%, no more than 65%, no more than 60%, no more than 55%, no more than 50%, no more than 45%, no more than 40%, no more than 35%, no more than 30%, no more than 25%, no more than 20%, no more than 15%, no more than 10%, no more than 5%, no more than 4%, no more than 3%, no more than 2%, no more than 1% of the activity, or 0% of the activity of a suitable wild-type control.

Alternatively, a decrease in catalytic activity can be expressed as a decrease in k_{cat} such as, for example, at least a two-fold decrease, at least a three-fold decrease, at least a four-fold decrease, at least a five-fold decrease, at least a six-fold decrease, at least a seven-fold decrease, at least an eight-fold decrease, at least a nine-fold decrease, at least a 10-fold decrease, at least a 15-fold decrease, or at least a 20-fold decrease in the k_{cat} value of the enzymatic conversion.

A decrease in catalytic activity also may be expressed in terms of an increase in K_m such as, for example, an increase in K_m of at least two-fold, at least three-fold, at least four-fold, at least five-fold, at least six-fold, at least seven-fold, at least an eight-fold, at least nine-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 30-fold, at least 35-fold, at least 40-fold, at least 45-fold, at least 50-fold, at least 75-fold, at least 100-fold, at least 150-fold, at least 200-fold, at least 230-fold, at least 250-fold, at least 300-fold, at least 350-fold, or at least 400-fold.

Thus, in another aspect, we describe herein methods for biosynthesis of an ester. The ester may be any desired ester. As noted above, the ester may be used as a biofuel, an industrial chemical, or a raw material for the production of other compounds. Our approach can be used to prepare an ester from combining any organic acid—e.g., the exemplary

organic acids identified in FIG. 1(b)—with any alcohol—e.g., the exemplary alcohols identified in FIG. 1(b). The combination of any of these acids and any of these alcohols could generate an ester metabolite. In various applications, the organic acid, the alcohol, or both may be synthesized by the cell. In some of these embodiments, the cell may be genetically modified to promote the biosynthesis of the organic acid or the alcohol. Also in various applications, the organic acid or the alcohol may be provided in culture medium so that its biosynthesis is unnecessary to produce the ester.

In some cases, the ester can be an ester having no more than 12 carbon atoms (C12) such as, for example, a C11 ester, a C10 ester, a C9 ester, a C8 ester, a C7 ester, a C6 ester, a C5 ester, a C4 ester, or a C3 ester. In other cases, the ester can be an ester having any number of carbons and a predetermined degree of branching. The degree of branching may be characterized by the number of branched carbons and/or the length of one or more—or, cumulatively, all—of the branches. As used herein, branching refers to the number of carbons that are covalently bound to at least three other carbons. In certain specific embodiments, the ester can be, for example, isobutyl isobutyrate, isovaleryl isovalerate, or ethyl lactate.

Generally, the methods include incubating a recombinant cell as described herein in medium that includes a carbon source under conditions effective for the recombinant cell to produce the ester. Thus, the carbon source can include one or more of: glucose, pyruvate, or ketovaline. In addition, the carbon sources for cell growth can be CO_2, cellulose, glucose, xylose, sucrose, arabinose, glycerol, alginate, glucarate, galacturonate, etc. as long as the related carbon assimilation pathways are introduced in the engineered microbe. Also, the carbon source can include the organic acid—or a metabolic precursor of the organic acid—to be activated to produced the desired ester. In the exemplary pathway shown in FIG. 2, the organic acid is isobutyric acid. In other pathways in which the ester is formed from a different organic acid, the different organic acid may be a component of the culture medium. Similarly, the carbon source can include the alcohol—or a metabolic precursor of the alcohol—from which the desired ester is synthesized. In the exemplary pathway shown in FIG. 2, the alcohol is isobutanol and metabolic precursors include, for example, isobutyraldehyde and ketovaline. In pathways in which the ester is formed from a different alcohol, the different alcohol and/or precursors to the different alcohol may be components of the culture medium.

As noted above, the ester may be the desired end product or may be used as a precursor to produce another compound. In some cases, the ester may be hydrolyzed to the alcohol and organic acid from which it was biosynthesized. In this way, one can use the platform described herein to produce greater amounts of an alcohol or organic acid than can be accumulated if the alcohol and/or organic acid is the fermentation end product. The ester may be biosynthesized and recovered from aqueous culture by phase separation—a process that can be simpler, more efficient, and/or less costly than recovery of an alcohol and/or an organic acid form an aqueous medium by, for example, distillation. The recovered ester can be hydrolyzed in a controlled volume of water, in most cases without any additional enzymatic or activating treatment, to yield the constituent alcohol and organic acid.

In yet another aspect, we describe herein methods for introducing a heterologous polynucleotide into cell so that the host cell exhibits an increased ability to convert a carbon source to an ester. The heterologous polynucleotide can encode a polypeptide operably linked to a promoter so that the modified cell catalyzes conversion of the carbon source to an ester. In some of these embodiments, the carbon source can include one or more of glucose, pyruvate, ketovaline, and organic acid (or precursor thereof), or an alcohol (or precursor thereof). The host cells for such methods can include, for example, any of the microbial species identified above with regard to the recombinant cells described herein.

As used in the preceding description, the term "and/or" means one or all of the listed elements or a combination of any two or more of the listed elements; the term "comprises" and variations thereof do not have a limiting meaning where these terms appear in the description and claims; unless otherwise specified, "a," "an," "the," and "at least one" are used interchangeably and mean one or more than one; and the recitations of numerical ranges by endpoints include all numbers subsumed within that range (e.g., 1 to 5 includes 1, 1.5, 2, 2.75, 3, 3.80, 4, 5, etc.).

In the preceding description, particular embodiments may be described in isolation for clarity. Unless otherwise expressly specified that the features of a particular embodiment are incompatible with the features of another embodiment, certain embodiment can include a combination of compatible features described herein in connection with one or more embodiments.

For any method disclosed herein that includes discrete steps, the steps may be conducted in any feasible order. And, as appropriate, any combination of two or more steps may be conducted simultaneously.

The present invention is illustrated by the following examples. It is to be understood that the particular examples, materials, amounts, and procedures are to be interpreted broadly in accordance with the scope and spirit of the invention as set forth herein.

EXAMPLES

Example 1

Plasmid construction

BKDH enzyme complex coding regions and fadDX were amplified from *Pseudomonas Putida* KT2440 genomic DNA with primers bkdh_ecofwd (TgcatcgaattcAGGAGAAATT AACTatgAACGAGTACGCCC CCCTGCGTTTGC, SEQ ID NO:1) and bkdh_hindrev (Tgcatc aagcttTCAGATATGCAAGGCGTGGCCCAG, SEQ ID NO:2), fadDXsalI-F (tgtacggtat taatgtcgac AGGAGAAATTAACTATGCTTCAACTCCAAAAACAAGAAAC, SEQ ID NO:3) and fadDXbam-R (TGATCATGCGCCATAGTTAATTTCTCCTGGATCCTTAGACGC TGGCAGGGGTGGCCTGTT, SEQ ID NO:4), respectively. The PCR product of BKDH was then digestion with EcoRI and HindIII, and inserted into pZE12 to make pIBA16. To construct plasmid pESTER1, the coding region of BEBT from *Clarkia breweri* was synthesized by DNAworks (Hoover and Lubkowski, Nucleic Acids Res 2002, 30 (10), e43), and then the linear plasmid of pIBA7 was obtained after XbaI digestion. Finally, the plasmid of pESTER1 was formed after combination of fadDX, BEBT, and linear pIBA7 by as described in Gibson et al., Nat Meth 2009, 6(5):343-345. The BEBT coding region, digested with Acc65I and HindIII, was inserted into the corresponding site of pZS plasmid, to form plasmid pESTER2.

Fermentation results

E. coli host BW25113 was used for fermentation. One strain Ester 1 was BW25113 transformed with pIBA1 (International Patent Publication No. WO 2012/109534) and

pESTER1, and the other strain Ester 2 was BW25113transformed with pIBA1, pIBA16 and pESTER2.

Overnight cultures incubated in LB medium were diluted 25-fold into 5 mL M9 medium supplemented with 0.5% yeast extract and 4% glucose in 125-mL conical flasks. Antibiotics were added appropriately (ampicillin 100 mg/L and kanamycin 25 mg/L). 0.1 mM isopropyl-b-D-thiogalactoside (IPTG) was added to induce protein expression. The culture medium was buffered by adding 0.5 g $CaCO_3$. Cultures were placed in a 30°C shaker (250 rpm) and incubated for 48 hours. Fermentation products were quantified by HPLC or GC analysis. Results are shown in FIG. 2(b).

Example 2

Acyltransferases LuxE, ATF1, ATF2, BPBT, and SAAT were amplified from *Clarkia breweri* with primers:

luxEalsS-F (gaaaacgaaagctctctaa GCTGAGCAGG AGAAATTAAC TATGGCGCAT GATCAGAGCCT, SEQ ID NO:81) and

luxEvec-R (agcctttcgttttatttgatgcctctaga GCTCAGCTTA CAGGCTGCTC TGGGTGAAATG, SEQ ID NO:82) from *S. cerevisiae*;

ATF1alsS-F (cgaaagctctctaa GCTGAGCAGG AGAAATTAAC TATGAATGAA ATCGATGAGAAAAATC, SEQ ID NO:83) and

ATF1vec-R (agcctttcgttttatttgatgcctctaga GCTCAGCTTA AGGGCCTAAA AGGAGAGCTTT, SEQ ID NO:84) from *S. cerevisiae*;

ATF2alsS-F (cgaaagctctctaa GCTGAGCAGG AGAAATTAAC TATGGAAGAT ATAGAAGGAT ACGAAC, SEQ ID NO:85) and

ATF2vec-R (cctttcgttttatttgatgcctctaga GCTCAGCTTA AAGCGACGCA AATTCGCCGA TGG, SEQ ID NO:86) from *P. hybrida*;

BPBTalsS-F (aaacgaaagctctctaa GCTGAGCAGG AGAAATTAAC TATGGACAGC AAACAGAGCA GCG, SEQ ID NO:87) and

BPBTvec-R (cctttcgttttatttgatgcctctaga GCTCAGCTTA AAGCGCTGGG GTGATGAACG CAT, SEQ ID NO:88) from Strawberry; and

SAATalsS-F (aaacgaaagctctctaa GCTGAGCAGG AGAAATTAAC TATGGAGAAA ATAGAAGTGA GCA, SEQ ID NO:89) and

SAATvec-R (cctttcgttttatttgatgcctctaga GCTCAGCTTA GATCAGCGTC TTTGGACTCG CCA,, SEQ ID NO:90) from Strawberry.

The different acyltransferases were ligated with BlpI digested plasmids of pIBA1 (International Patent Publication No. WO 2012/109534) and pIVC1 (Xiong et al. *Sci Rep* 2012, 2:311) as described in Gibson et al., Nat Meth 2009, 6(5):343-345, to form plasmids of pZA-ilvD-alsS-LuxE, pZA-ilvD-alsS-ATF1, pZA-ilvD-alsS-ATF2, pZA-ilvD-alsS-BTBT, pZA-ilvD-alsS-SAAT, pZA-leuABCD-ilvD-alsS-LuxE, pZA-leuABCD-ilvD-alsS-ATF1, pZA-leuABCD-ilvD-alsS-ATF2, pZA-leuABCD-ilvD-alsS-BTBT and pZA-leuABCD-ilvD-alsS-SAAT, respectively. To construct plasmid of pZE-KivD-yqhD, yqhD was PCR amplified with primers yqhDSphI-F (GGGCCCgcatgc AGGAGAAATT AACTATGAAC AACTTTAATC TGCACACCCC, SEQ ID NO:91) and yqhDXbaI-R (GGGCCCtctaga TTAGCGGGCG GCTTCGTATA TACGGC, SEQ ID NO:92), and then replaced the padA of plasmid pIBA7 (International Patent Publication No. WO 2012/109534) to form pZE-KivD-yqhD.

Fermentation results

Shake flask fermentations were carried out for the recombinant strains. Cells were inoculated in test tubes overnight and 200 μL cells were transferred into 10 mL of fermentation medium in a 150-mL screw-cap conical flask. Fermentation medium consisted of 20 g/L glucose in M9 minimum medium (5 g/L yeast extract) supplemented with thiamine (10 mg/L), ampicillin (100 μg/mL), kanamycin (25 μg mL), and 0.5 g calcium carbonate for neutralization. Protein expression was induced by addition of 0.1 mM isopropyl-β-D-1-thiogalactoside (IPTG). Flasks were sealed with Parafilm before fermentations started to create a micor-aerobic environment. Samples were collected after incubation at 30°C on a rotary shaker (250 r.p.m.) for 48 hours. The produced medium-chain ester compounds were quantified by GC-FID (gas chromatography-flame ionization detector) analysis. Their byproducts and remaining glucose were identified by HPLC-RID (high-performance liquid chromatography-refractive index detector) analysis. Results are shown in FIG. 6.

The complete disclosure of all patents, patent applications, and publications, and electronically available material (including, for instance, nucleotide sequence submissions in, e.g., GenBank and RefSeq, and amino acid sequence submissions in, e.g., SwissProt,

PIR, PRF, PDB, and translations from annotated coding regions in GenBank and RefSeq) cited herein are incorporated by reference in their entirety. In the event that any inconsistency exists between the disclosure of the present application and the disclosure(s) of any document incorporated herein by reference, the disclosure of the present application shall govern. The foregoing detailed description and examples have been given for clarity of understanding only. No unnecessary limitations are to be understood therefrom. The invention is not limited to the exact details shown and described, for variations obvious to one skilled in the art will be included within the invention defined by the claims.

Unless otherwise indicated, all numbers expressing quantities of components, molecular weights, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about." Accordingly, unless otherwise indicated to the contrary, the numerical parameters set forth in the specification and claims are approximations that may vary depending upon the desired properties sought to be obtained by the present invention. At the very least, and not as an attempt to limit the doctrine of equivalents to the scope of the claims, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques.

Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the invention are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. All numerical values, however, inherently contain a range necessarily resulting from the standard deviation found in their respective testing measurements.

All headings are for the convenience of the reader and should not be used to limit the meaning of the text that follows the heading, unless so specified.

Sequence Listing Free Text

SEQ ID NO:1

Tgcatc gaattc AGGAGAAATT AACTatg AACGAGTACGCCC CCCTGCGTTTGC

SEQ ID NO:2

Tgcatc aagctt TCAGATATGCAAGGCGTGGC CCAG

SEQ ID NO:3

tgtacggtat taatgtcgac AGGAGAAATT AACTATGCTT CAACTCCAAA AACAAGAAAC

SEQ ID NO:4

TGATCATGCGCCATAGTTAATTTCTCCTGGATCCTTAGACGC

TGGCAGGGGTGGCCTGTT

SEQ ID NO:5

GI:26991173, Protein name: acetyl-CoA synthetase ACS_[Pseudomonas putida KT2440]

```
        1 msaaplypvr pevaattltd eatykamyqq svinpdgfwr eqaqridwik
pftkvkqtsf
       61 ddhhvdikwf adgtlnvssn cldrhleerg dqlaiiwegd dpsehrnity
relheqvckf
      121 analrgqdvh rgdvvtiymp mipeavvaml acarigaihs vvfggfspea
lagriidcks
      181 kvvitadegv rggrrtplka nvdlaltnpe tssvqkiivc krtggdiawh
qhrdiwyedl
      241 mkvasshcap kemgaeealf ilytsgstgk pkgvlhttgg ylvyaalthe
rvfdyrpgev
      301 ywctadvgwv tghsyivygp langattllf egvpnypdit rvskivdkhk
vnilytapta
      361 irammaegqa avegadgssl rllgsvgepi npeawnwyyk tvgkercpiv
dtwwqtetgg
      421 ilisplpgat glkpgsatrp ffgvvpalvd nlgnlidgaa egnlvildsw
pgqsrslygd
      481 hdrfvdtyfk tfrgmyftgd garrdedgyy witgrvddvl nvsghrmgta
eiesamvahs
      541 kvaeaavvgv phdikgqgiy vyvtlnagie aseqlrlelk nwvrkeigpi
aspdviqwap
      601 glpktrsgki mrrilrkiat geydalgdis tladpgvvqh lidthkamnl asa
```

SEQ ID NO: 6

GI:260770658, Protein name: acetyl-CoA synthetase [Vibrio furnissii CIP 102972]

```
        1 mseahiypvk enikahthad detylamyqq svsdpegfws ehgkivdwmk
pftqvkhtsf
       61 dtghvdirwf edgtlnvsan cidrhlaerg ddvaiiwegd dpaddktltf
nelhrdvcrf
      121 snalkaqgvr kgdvvclymp mvpeaavaml actrigavht vvfggfspea
lagriidsds
      181 kvvitadegv rggravplkk nvdealtnpe vktiskvivf krtggevawh
ehrdvwwhda
      241 vaaasdvcpp eemnaedplf ilytsgstgk pkgvlhttgg ylvyatmtfk
yvfdyqpget
      301 fwctadvgwi tghtyliygp lsngaktilf egvpnypsta rmsevvdkhq
vnilytapta
      361 iralmakgde avkgtsrssl rimgsvgepi npeawewyyk tignekspiv
dtwwqtetgg
      421 ilitplpgat alkpgsatrp ffgvqpalvd nmgevidgaa egnlvildsw
pgqmrtvygd
      481 herfeqtyfs tfkgmyftgd garrdedgyy witgrvddvl nvsghrmgta
eiesalvafd
      541 kiaeaavvgv phdikgqaiy ayitlndgvy psaelhkevk dwvrkeigpi
atpdvlhwtd
      601 alpktrsgki mrrilrkiat gdtgnlgdts tladpsvvdk liaekaqlv
```

SEQ ID NO:7
GI:167623628, Protein name: acetyl-CoA synthetase [Shewanella halifaxensis HAW-EB4]

```
        1 mstqslykvp seiaanalvn deqykkmyqe sivnpegfwr ehgnridwik
pftkvkktsf
       61 ddhnlfikwf ydgtlnasan cldrhlenna dklaiiwegd dakdqrtlty
gqlhtqvckf
      121 analrsqgvr rgdvvtiymp mvpeaavaml acarigaihs vvfggfspds
iasrvidgns
      181 kvvitadegv ragriiplka nidealshpd vncvekvivm krtggdinwv
egrdiwwdsl
      241 mdtasehcia eemgaedplf llytsgstgn pkgvlhttgg ymvyaamthe
yvfdykenev
      301 ywctadvgwi tghsymvygp langatvlih egvpnypspa rlgemvdrhk
vnilytaptl
      361 iralmaegke qfagfdgssl rimgsvgepi npeawrwynd vighekcpiv
dtwwqtetgg
      421 ilisplpgat dtkpgsatrp ffgvqpalvd nmgnivdgas egnlvildsw
pgqmrtvfgd
      481 hdrfvltyfk tfrgmyftgd gakrdedgyy witgrvddvi nvsghrlgta
evesalvahe
      541 fvaeaavvgy phdikgqgiy ayvtltkgsv eteelrqelr qwvrkeigal
atpdliqwag
      601 glpktrsgki mrrflrkiaa nevsnlgdss tladpavidt lietrlnrse
```

SEQ ID NO:8
GI:330830937, Protein name: acetyl-CoA synthetase [Aeromonas veronii B565]

```
        1 mstqslykvp seiaanalvn deqykkmyqe sivnpegfwr ehgnridwik
pftkvkktsf
       61 ddhnlfikwf ydgtlnasan cldrhlenna dklaiiwegd dakdqrtlty
gqlhtqvckf
```

121 analrsqgvr rgdvvtiymp mvpeaavaml acarigaihs vvfggfspds iasrvidgns
181 kvvitadegv ragriiplka nidealshpd vncvekvivm krtggdinwv egrdiwwdsl
241 mdtasehcia eemgaedplf llytsgstgn pkgvlhttgg ymvyaamthe yvfdykenev
301 ywctadvgwi tghsymvygp langatvlih egvpnypspa rlgemvdrhk vnilytaptl
361 iralmaegke qfagfdgssl rimgsvgepi npeawrwynd vighekcpiv dtwwqtetgg
421 ilisplpgat dtkpgsatrp ffgvqpalvd nmgnivdgas egnlvildsw pgqmrtvfgd
481 hdrfvltyfk tfrgmyftgd gakrdedgyy witgrvddvi nvsghrlgta evesalvahe
541 fvaeaavvgy phdikgqgiy ayvtltkgsv eteelrqelr qwvrkeigal atpdliqwag
601 glpktrsgki mrrflrkiaa nevsnlgdss tladpavidt lietrlnrse

SEQ ID NO:9
GI:209696237, Protein name: acetyl-CoA synthetase [Aliivibrio salmonicida LFI1238]

1 msdihvypvn qdiaknahad edkyremyqq svinpegfwr ehgqivdwmt pytkvkntsf
61 dtghvdikwf edgelnvsan cidrhlaarg devaiiwegd dpqddasitf nelheqvckf
121 snalksqgvr kgdvvciymp mvaeaaiaml actrigavht vvfggfspea lagrivdsda
181 kvvitadegv rggrtvplkk nvddalnnpe vttiekvvvf qrtgndidwn eerdvwwhea
241 tavasahcep eamnaedplf ilytsgstgk pkgvlhttgg ylvyaamtfk yifdyqegev
301 fwctadvgwi tghtyliygp langaktilf egvpnypsts rmsevvdkhn vnilytapta
361 iralmahgnd avegtsrssl rvmgsvgepi npeawewyyn tigdarcpiv dtwwqtetgg
421 ilisplpgat alkpgsatrp ffgvqpalvd nmgnliegaa dgnlvitdsw pgqmrtiygd
481 hdrfeqtyfs tfkgmyftsd garrdedgyy witgrvddvl nvsghrmgta evesalvsfs
541 kiaeaaivgv phdikgqaiy ayitlnsgey psaelhkevk dwvrkeigpi atpdflhwtd
601 slpktrsgki mrrilrkiat gdtsnlgdts tladpsvvnk lieeqrkia

SEQ ID NO:10
GI:54310469, Protein name: acetyl-CoA synthetase [Photobacterium profundum SS9]

1 msevhvypvn qeiaatahvn deqyremyqq svinpegfwr ehgqivdwik pftkvkhtsf
61 dtghvsvkwf edgtlnvsan cidrhlatrg dqpaiiwegd dptddatfty nelheqvckf
121 snalksqgvr kgdvvclymp mvaeaaiaml actrigavht ivfggfspea lagrivdsna

181 klvitadegv ragravplkk nvddalankn vtsiekvivl krtggnvewh serdvwwhea
241 tavasshcep eemnaedplf ilytsgstgk pkgvlhttgg ylvyatmtfk yvfdyqegdv
301 ywctadvgwi tghsylvygp langattvlf egvpnypsts rmsevvdkhn vsilytapta
361 iralmakgte aikgtsrssl rimgsvgepi npeawewyhh tigdsrcpiv dtwwqtetgg
421 ilitplpgat alkpgsatrp ffgvqpaivd nmgnilegva egnlvmvdsw pgqmrtlwgd
481 herfeqtyfs tfqgmyftgd garrdedgyy witgrvddvl nisghrmgta eiesalvafd
541 kiaeaaivgv phdikgqaiy ayitlndgei psaelhkevk dwvrkeigpi atpdflhwtd
601 alpktrsgki mrrilrkiat gdtgslgdts tladpsvvdk liaekqtil

SEQ ID NO:11
GI:6320852, Protein name: acetyl-CoA synthetase Faa2p[*S. cerevisiae*]

1 maapdyaltd liesdprfes lktrlagytk gsdeyieely sqlpltsypr yktflkkqav
61 aisnpdneag fssiyrssls senlvscvdk nlrtaydhfm fsarrwpqrd clgsrpidka
121 tgtweetfrf esystvskrc hnigsgilsl vntkrkrple andfvvails hnnpewiltd
181 lacqaysltn talyetlgpn tseyilnlte apilifaksn myhvlkmvpd mkfvntlvcm
241 delthdelrm lnesllpvkc nslnekitff sleqveqvgc fnkipaippt pdslytisft
301 sgttglpkgv emshrniasg iafafstfri ppdkrnqqly dmcflplahi fermviaydl
361 aigfgigflh kpdptvlved lkilkpyava lvpriltrfe agiknaldks tvqrnvanti
421 ldsksarfta rggpdksimn flvyhrvlid kirdslglsn nsfiitgsap iskdtllflr
481 saldigirqg ygltetfagv clsepfekdv gscgaigisa ecrlksvpem gyhadkdlkg
541 elqirgpqvf eryfknpnet skavdqdgwf stgdvafidg kgrisvidrv knffklahge
601 yiapekieni ylsscpyitq ifvfgdplkt flvgivgvdv daaqpilaak hpevktwtke
661 vlvenlnrnk klrkeflnki nkctdglqgf eklhnikvgl epltleddvv tptfkikrak
721 askffkdtld qlyaegslvk tekl

SEQ ID NO:12
GI:255717016, Protein name: acetyl-CoA synthetase [Lachancea thermotolerans]

1 mskqdgyisl selietdkrf qnlreelavy dknskeylsn lisklpltnh vsyrqflkeq
61 avslesskkh gyspvfrssl speclvsnvh prlstffelf nfsverfpdn dclgqrsqdr
121 vtghwgqhye fesyreiqer sqnlgsgimt vvnlkrkrrf gsndfivsfl stnrkewvis

181 dlacqgyslg ntalyetlgl dtseyilnvt espvlilske niyrvmemvp klphlstivc
241 mdelsdlela qlngpllpqh tnskgerisi lnfrqverig asnkvplipp tpdslytisf
301 tsgttgtpkg vqmkqshvaa avafvlstlr mprlkhrsqa ydlcflplah iferqivafd
361 lssgtaigfl hkpdpsvlve dlkllkpdvf psvpriltkf eagiknslqn gdgsavtknv
421 astilnkrle rtthhggkdh silntvvfhr vlidkirssl glenldvvit gsapisndtl
481 lfmksaldcg vrqgygltet fagiclsear erdsgtcggm avttecrlrs ipemgydaeh
541 dlkgevqlrg sqvfrgyykn pqetsralge dgwystgdvg fidskgrlsi idrvknffkl
601 aqgeyiapek iesvylsscp yltqisvhgd slqtflvavi glelditapi ihkkipelrg
661 fsgkdlvdei nksrahrkal ivlinsfieg lqgfekihnl yvgieplkvt ddtitptlkv
721 kranaakhfr kilenlyeeg slikvekl

SEQ ID NO:13
GI:45187925, Protein name: acetyl-CoA synthetase [Ashbya gossypii ATCC 10895]

1 msnetevnry pgmgpislve virtdarfae lwkrlslfqq gsvefykely dnmplfagmd
61 gmalsapvpg sgkkgyspvf rnvlvpegkl lsaidegvdt gyhvfklsar mypdnhclgm
121 raydeatgkw ldeyrwetys qverraenlg agllsvvnvk rskpldtndf ivammsansk
181 ewvltdlacq tfslvntaly etlgpntsey imnltespvv vvskpnllri falasklral
241 ntivimddmd lqevdrlasl lpvtknakge tisvltlrqv ekigelnnia pippspdsfh
301 tisftsgtts lpkgvqlthr aycaalafac shvrcepnkq ryalcllplt hiyqrqmtgl
361 nlmhafgigf lhkpnpdlfi eamcvlrpam vslvprvltk leagiknsiq gadvstfkrk
421 laktvidakd krfsavsgpd dsymnrfiyr kifvdkirdk lgftnvplvt tgsapispet
481 lrfiqcamdi gilqgyglte tfggnflsvp yetdcgscgp pamttevrlr dvpgmsynae
541 kdhmgevvvr sqqqferyyk mpektaevld kdgwfstgdv gyidkkgrlf itdrvknifk
601 lsqgeyiape kvencylssc pfitqifvhg nslnnylvgv vgidvvpfka ildsrtskws
661 klpleevipt inkdpalkql tlkiinsfvt aelqgfekig nlyadvepls vdgetltptf
721 kvkrevctkv fkdilsslyd eghilkagkl

SEQ ID NO:14
GI:380351855, Protein name: acetyl-CoA synthetase [Candida orthopsilosis]

1 maslfnekpe hiwktitesf pldqsvtsra lplpnsevpg fspiyrnays qkelktvpyp

61 gittlhdtfe lsvannghkr alghrvkkad gsfgeyvwqd yktvqqrrnn lgsgiffvlq
121 nnpyktdsea hkklkydpls ddsfvltifa hnrpewvlad vtstaysitn talydtlgpd
181 tskyilnlte cpiilcskdk vkslvelkeq npeelsnlic lvsmddltte davlknychd
241 hnislfdykq veklgeinpl apippkpetk fsitftsgtt ganpkgvllt hetavagitf
301 vysgitlpra davfysflpl ahiyerqgih faltygaaig fpqgpspltl lediqvlepd
361 ylalvprvlt kleagikaqt inndekpilk slftkaintk lalqsnpane ntnpshllyd
421 rvlgllrkkl gmknlkiims gsapispetl kflkaslntg vgqgygmset fagvmasstf
481 etdasscgpi svttecktrd lpamgytskd eggprgellv rgpqifleyy knpeetaksf
541 dedgwfytgd varidsktgr tyiidrvknf fklaqgeyvt perientyls cfpyiaqlfv
601 hgdslrthlv gvvgvdpasi tqyikqrhge titdaadlvr ffqdpkrkre llvdmnaslg
661 nklqgfeklh nievdvepls veknlitptm kikrpictky fkdtldklye egslirndkl

SEQ ID NO:15
GI:126136683,Protein name: acetyl-CoA synthetase [Scheffersomyces stipitis CBS 6054]

1 mslfqedpkn ihnfiraslp ldpkklcesv plpysekpgy savyrnkysv dglitrphps
61 latlfdlhev aarsqpdspc fgvrhkqadg tygpyqwiny qevydrkvhf gsgvffilqn
121 npyrtnspvh qkihydpqat espfvlsifs anraewvttd macsayslts talydslgaq
181 tskyilsste spivvsskdk lksliklkae dpetlsnlit lvsmdpldpk tdealvkyan
241 dnritlfdfd qvlklgeink lpqippkpet iytisftsgt tganpkgvll thanavcavt
301 fcysnitlpe sptvycflpl ahiyermsis falsmcaaig fpqspspltl mddikhlrph
361 flnlvprvyt kleaalkaqt fnsdkpiiks lfsaainkkm elqavedgaq gkhivydqvv
421 qllrkkigfd rliavttgsa pispetlkfi kaslntgmsq gygltesfag vctslkyean
481 pgscgaisit temrlrevpe mnyhahdkgg prgelmlrgp qifreyfknp eetakaidse
541 gwfatgdiar idatngnriy iidrvknffk laqgeyitpe kientylsqf pfiqqlyvhg
601 dplkthlvai vgldpatvds yikrkfndil snqddivdff rnpkhrlall edmnssvggl
661 lqgyerihni kvdfnpltie dnvitptlki krpiavkffk edfdalyeeg slikpdahkl

SEQ ID NO:16
GI:294656605, Protein name: acetyl-CoA synthetase [Debaryomyces hansenii CBS767]

```
        1 mtssdvydhg dspyvfkpsk tpasqlirdh lplpekmfkd svslpgteke gysaiyrnkm
       61 fpgrlkealt peldtyyrlf knsvltfgdk sclayrkydy vnkksaddys
fltyrevdem
      121 kqrygsgfly llqnnpfkns ekfeshrkid nhvkdyknfd isdmsfvati
ysanrmewvl
      181 sdlmcssysi tntalydtlg adtseyilqt tqspvviatk ehvmdivnlk
ekypeklehv
      241 isivcldpld lknetslsae dqalvtacks hritlvdinq vmkvgeifpt
pelppspetl
      301 ytisftsgtt gahpkgvlls qkictagvtf vltqlpripd arsfsflpla
hiferqvcaf
      361 glscgncigf pqnggtpltl iedlklfkpn ymcnvprvft kyeaaiksat
vdhptstfkr
      421 gifdkvistk iqaqekydga dgshlvydrl flssirkafg fdnmefivtg
sapispstvk
      481 flkatlcvgm pqgygstesf agfaigipye aepgscgsvg vtvemklrel
pamgynlddp
      541 egprgelllr gpqifkqyfh neeetkksfd degwfhtgdv arfsknngrl
fiidrvknff
      601 klsqgeyvtp ekvenkylss ssilnqlyvh gdslrhflvg ivgidpegav
nflvekckvs
      661 ksqlssseqi lneinkkenr ellvayinsr isnqlsgfek lhniyvefep
lrldrdvvta
      721 tqklkrpvaf kffkpqidvm ydegslvkgp kl
```

SEQ ID NO:17
GI:6319264, Protein name: Acs1p [Saccharomyces cerevisiae S288c]

```
        1 mspsavqssk leeqsseidk lkakmsqsaa taqqkkehey ehltsvkivp
qrpisdrlqp
       61 aiathysphl dglqdyqrlh kesiedpakf fgskatqfln wskpfdkvfi
pdpktgrpsf
      121 qnnawflngq lnacyncvdr halktpnkka iifegdepgq gysitykell
eevcqvaqvl
      181 tysmgvrkgd tvavympmvp eaiitllais rigaihsvvf agfssnslrd
rindgdskvv
      241 ittdesnrgg kvietkrivd dalretpgvr hvlvyrktnn psvafhaprd
ldwatekkky
      301 ktyypctpvd sedplflyt sgstgapkgv qhstagyllg alltmrytfd
thqedvffta
      361 gdigwitght yvvygpllyg catlvfegtp aypnysrywd iidehkvtqf
yvaptalrll
      421 kragdsyien hslkslrclg svgepiaaev wewysekigk neipivdtyw
qtesgshlvt
      481 plaggvtpmk pgsasfpffg idavvldpnt geelntshae gvlavkaawp
sfartiwknh
      541 dryldtylnp ypgyyftgdg aakdkdgyiw ilgrvddvvn vsghrlstae
ieaaiiedpi
      601 vaecavvgfn ddltgqavaa fvvlknkssw statddelqd ikkhlvftvr
kdigpfaapk
      661 liilvddlpk trsgkimrri lrkilagesd qlgdvstlsn pgivrhlids vkl
```

SEQ ID NO:18
GI:254579411, Protein name: ZYRO0C00682p [Zygosaccharomyces rouxii]

1 mtvnyvyagm wrnlfpesic rlrdkrkehi pysmspstta tgtsptggti gdlkarlvha
61 aerentspat tnnvstekdh eaetntpttd ydhlisvhtv qqkpithrlq selschycph
121 isgfreyekl yresidqpse ffgnkarqfl nwfkdfdqvf ipdprtgkps lnnnawflng
181 qtnacyncvd rhaletpdkp aiiyetdepg qgytltysel leqvcqlaqv lrysmgvrkg
241 dtvavympmi pqavislmai arigaihsvv fagfscnslr drindadshv vittdetkrg
301 gkivetkriv ddalketpgv snvlvyrrtn nprvprqvsr dldwdgelrk ykgycpcepv
361 dsehplflly tsgstgtpkg vqhstagyll salltmrysf dthredvfft agdvgwitgh
421 tyvvygplly gcttlvfegt payptyaryw diidqykvtq fyvaptalrl lkragdsfie
481 ghslqslral gtvgepiaae vwewysekig knelpivdty wqtesgshml tpmaggvtpm
541 kpgsagfpfi gidscildpt tgqeltkplv egvlavrcgw psfartiwkd hdrfldtylk
601 pypgyyftgd gaardkdgyi wilgrvddvv nisghrlsta eiesavldda ivaecavvgf
661 nddltgqava afvvlknkss wstaseeell dikkhlilav rkdigpfaap klivlvddlp
721 ktrsgkimrr ilrkilagec dqlgdvstls npgvvrhlid svkl

SEQ ID NO:19
GI:45188280, Protein name: ADR408Wp [Ashbya gossypii ATCC 10895]

1 mvtsagvgha eynngadvqh adyahltsvg qveqkplggr lgalaeyykp nvasmeeyra
61 mhaqsitdpa afygerarty vdwfrpfdav flpgpdgrps fdnnawfvng qlnacynlvd
121 rhaartpdkv aiiyeadepg egysltyrel laqvckvaqv lqysmgvrkg dtvavympmi
181 pqalvtllai srigaihsvv fagfssnslr drindarsev vvttdeskrg gkiietkriv
241 ddaiketpql rkvlvykrtc npsvsyvadr dldwdtevkk yksycpcepv dsehplflly
301 tsgstgapkg vqhstagyll qaylsmlysf dvhsddifft agdigwitgh tyvvygplfs
361 gcttvvfegt paypsysryw diidkysvtq fyvaptalrl lkragdsyvd gyslrtlrsl
421 gtvgepiaae vwewyytvig kreipvidty wqtesgahlv tplaggstpm kpgsasfpff
481 gidlaildpq tgeellgpnv egvlavkqpw psftrtiwnn hdryldtyln pykgyyfagd
541 gaardsqgfi wilgrvddvv nvsghrlsta eveaaiiqes mvaecavvgf adeltgqaia
601 afvvlkqkss wntaserelq eikkhlilsv rrdigpfaap klivlvddlp ktrsgkimrr
661 ilrkilagea dqlgdvstls npgivkhlie svkf

SEQ ID NO:20
GI:3139035, Protein name: acetyl-CoA synthetase [Kluyveromyces lactis]

```
        1 mksnasaaaa dqiktheyeh ltsvpivqpl pitdrlssea aqkykpnlpg
gfeeykslhk
       61 eslenpakfy heraqllnwf kpydqvfipd tegkptfenn awftngqlna
cynlvdrhaf
      121 tqpnkvaily eadepgqgys ltyaelleqv ckvaqilqys mnvkkgdtva
vympmipqal
      181 itllaitrig aihsvvfagf ssnslrdrin daysktvitt deskrggkti
etkrivdeal
      241 kdtpqvtnvl vfkrthneni kyipgrdldw deevkkyksy tpcepvdseh
plfllytsgs
      301 tgapkgvqhs tagyllqall smkytfdiqn ddifftagdi gwitghtycv
ygpllqgctt
      361 lvfegtpayp nfsryweivd kyqvtqfyva ptalrllkra gdsftegfsl
kslrslgsvg
      421 epiaaevwew ysekigknel pivdtywqte sgshlvtpla ggatpmkpga
aafpffgidl
      481 avldpttgie qtgehaegvl aikrpwpsfa rtiwknndrf ldtylkpypg
yyftgdgvar
      541 dkdgffwilg rvddvvnvsg hrlstaeiea aiieddmvae cavvgfndel
tgqavaafvv
      601 lknkssltaa seselqdikk hliitvrkdi gpfaapkliv lvddlpktrs
gkimrrilrk
      661 ilagesdqla tsphyptlvs lst
```

SEQ ID NO:21
GI:320580699, Protein name: Acetyl-coA synthetase isoform [Ogataea parapolymorpha DL-1]

```
        1 mpekhleneh lmreralepp agflerhpsk pylssldeyk kmyeesirdp
gsffggmaeq
       61 hlswfkpftv pkvpnapflk dnngepsawf vdgelnacyn cvdrwaiknp
dkpaiiyead
      121 epdqgeiity gellkqvckv sqvllnlgvk kgdtvavylp mipeaivtlm
aivrigaihs
      181 vvfagfssgs lrdrindans kvvittdesk rggkiietkk ivddallacp
qvtnvlvykr
      241 tgnshipwte grdlwwheev kkypsyypat pvsaedtlfl lytsgstgkp
kgiqhstagy
      301 llgallttky vfdvhpedil ftagdvgwit ghsyvvygpl lngattvvfe
gtpaypnysr
      361 yweivdkykv tqfyvaptal rllkragesy iepyslqslr vlgsvgepia
kdvwewynah
      421 igrgkahicd tywqtesgsh litplagvtp tkpgsaslpf fgidpaiidp
vsgkelegne
      481 vegvlairss wpsmartiwr dysrfldtyl rpyhgyyfsg dgaardkdgf
ywilgrvddv
      541 vnvsghrlst aeieaalieh smvaesavvg fpdeltgsav aafvslknrs
iedpsaikke
      601 liltvrkeig pfaapklill vndlpktrsg kimrrilrki lsgeedqlgd
tstlsnpqvv
      661 shlievvkak
```

SEQ ID NO:22
GI:190348910,Protein name: acetyl-coenzyme A synthetase 1 [Meyerozyma guilliermondii ATCC 6260]

```
        1 mpestdhldh ekmldppkgf ferstskpnl asldeykkly kqsiedpatf
fgnaaksfld
       61 wdrpfdytrf pvdpkddfkn gdipswfing qlnasynavd rwamknpekp
aiiyeadevn
      121 egrtitygel lkdvsklaat ltnlgvkkgd svavylpmip eaivtllaiv
rigalhsvvf
      181 agfsstslrd riidadsriv itadeskrgg ktietkkivd dalkecphvr
nvlvfkrtgn
      241 shvpfsagrd lwwhdelqky gpyfppvpvn sedplflyt sgstgkpkgv
qhntagyllg
      301 almtakytfd lheediifta gdvgwitght yvvygpllcg attvvfegtp
aypdysrywd
      361 vvdkykvnqf yvaptalrll kragtkyvek hdlsslrvlg svgepiaaev
whwyndnigr
      421 gkahivdtyw qtesgshllt plagvtptkp gsaslpffgi darildpvsg
kdlvdnnveg
      481 vlcvksawps itrgiyhdya ryietylkpy pnhyfsgdga ardkdgffwi
lgrvddvvnv
      541 sghrlstaei eaaliehelv gesavvgyad eltgqavaay vslksnvevd
dleaikkeli
      601 ltvrkeigpf aapklillvd dlpktrsgki mrrilrkvla geedqlgdis
tlsnpqvvsq
      661 vievvkasrk
```

SEQ ID NO:23
GI:29893231, Protein name: acyl-activating enzyme 11 –AAE11[Arabidopsis thaliana]

```
        1 mdnlvlcean nvpltpitfl krasecypnr tsiiygqtrf twpqtydrcc
rlaasllsln
       61 itrndvvsil apnvpamyem hfsvpmtgav lnpintrlda ktiaiilrha
epkilfvdye
      121 fapliqevlr liptdqsqah priilineid sttkpfskel dyeglirkge
ptpsssasmf
      181 rvhnehdpis lnytsgttad pkgvvishrg aylsalssii gwemgifpvy
lwtlpmfhcn
      241 gwthtwsvaa rggtnvcirh vtapeiykni elhgvthmsc vptvfrflle
gsrtdqspks
      301 spvqvltggs sppavlikkv eqlgfhvmhg yglteatgpv lfcewqdewn
klpehqqmel
      361 qqrqgvrnlt ladvdvkntk tlesvprdgk tmgeivikgs slmkgylknp
katseafkhg
      421 wlntgdigvi hpdgyveikd rskdiiisgg enissievek vlymyqqvle
aavvamphpl
      481 wgetpcafvv lkkgdeesvt segdlikycr enmphfmcpk kvvffqelpk
nsngkilksk
      541 lrdiakalvv reddagskkv hqrsiehvss rl
```

SEQ ID NO:24
GI:29893229, Protein name: acyl-activating enzyme 12 [Arabidopsis thaliana]

```
        1 mdnlalcean nvpltpitfl krasecypnr tsiiygktrf twpqtydrcc
rlaaslisln
       61 igkndvvsvv apntpamyem hfavpmagav lnpintrlda tsiaailrha
kpkilfidrs
      121 feplareilq llssedsnln lpvifiheid fpkrvssees dyecliqrge
ptpsllarmf
      181 ciqdehdpis lnytsgttad pkgvvishrg aylstlsaii gwemgtcpvy
lwtlpmfhcn
      241 gwtftwgtaa rggtsvcmrh vtapeiykni emhnvthmcc vptvfnillk
gnsldlshrs
      301 gpvhvltggs pppaalvkkv qrlgfqvmha yglteatgpv lfcewqdewn
rlpenqqmel
      361 karqglsilg ltevdvrnke tqesvprdgk tmgeivmkgs simkgylknp
katyeafkhg
      421 wlnsgdvgvi hpdghveikd rskdiiisgg enissveven iiykypkvle
tavvamphpt
      481 wgetpcafvv lekgetnned redklvtker dlieycrenl phfmcprkvv
fldelpkngn
      541 gkilkpklrd iakglvaede vnvrskvqrp vehftsrl
```

SEQ ID NO:25
GI:224065064, Protein name: acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]

```
        1 mdqllkcdan yvpltpitfl kranavyanr tsviyegtrf twsqtyercc
rladslrsln
       61 vgkndvvsvl apnipavyem hfavpmagav lntinirlda kniatilshs
gakvffvdyq
      121 ykelaskals fldgavpsii aciddidtpt gvqfgqleye qlvqrgnpgy
tgelvqdewd
      181 pialnytsgt tsapkgvvys hrgaylssls lilgwemgna pvylwslpmf
hcngwtftwg
      241 vaarggtnvc irntsakdmy hniaehavth mccapivfnv llearpherr
eitspveilt
      301 ggapppasll qdierlgfhv thayglteat gpalvcewqk kwnklpqqdq
aklkarqgis
      361 iltladadvk dldtmvsvpr dgktmgeivl rgssimkgyf kdpeatskaf
rngwfatgdv
      421 gvihpdgyle ikdrskdvii sggenissve lesvlyrhpr vleaavvamp
hpkwgespca
      481 fisvkknsng dtndvkesdi iayckknlph ftvpkrvefm aelpktstgk
iqkfqlrala
      541 qnfvvneilp skkinghsqp sasgrvntev teyaqgheqv lalsrl
```

SEQ ID NO:26
GI:226508754, Protein name: acyl-activating enzyme 11 [Zea mays]

```
        1 mdqlpkrpan yvplspvgfl pranavygdr tsviyrgvrf twrqtyarcr
rlasallslg
```

```
        61 vvrrgdvvsv lapnvpamye mhfavpmaga vlntintrld aaavatilrh
sgaklffvdy
       121 dyvrlasdal rlldaadvpl vaviddihsp tgarlgeley eallahgdpd
adlpplqdew
       181 davtlsytsg ttsapkgvvy shrgaylstt slllqwgvpa epvylwtlpm
fhcngwtftw
       241 gmaarggvnv cirdarpadi yraiarhrvt hmccapvvfs illdgdgdsd
gaarqlqapv
       301 hvltggappp aallerveri gfnvthaygl teatgpalac ewrdqwdrlp
lperarlkar
       361 qgvsvlslad advknadtml svprdgrtvg eivlrgssvm kgylnnpean
esafragwfl
       421 tgdvgvvhpd gyieikdrsk dviisggeni cskeleevlf rhpavadaav
vamphprwge
       481 tpcafvvprd kaavlsegdv lafcskrmar fmvpkkvevv galprnalgk
vekvklreaa
       541 rklaptvaaa qkpkaktttv ggrrdgqpva hvmavsrl
```

SEQ ID NO:27
GI:357491641, Protein name: 2-succinylbenzoate-CoA ligase [Medicago truncatula]

```
         1 mnqltrnqan staltpltfl eraatvygns isiiynntsf twsqthkrcl
qlasslsslg
        61 iqkgdvvsvl spntpamyel hfsvpmsgai lnnlnfrldh ktlsvllihs
esklifvdil
       121 slsltlnals lfptniqqpk lvlimdetla phqipplpkn vniintyegl
vakgdpyfkw
       181 irpdsewdpi tlnytsgtts spkgvvhchr atfivsldsl idwsvpvqpv
flwtlpmfhs
       241 ngwsypwama avgginictr rtdaptiytl ieshgvthmc aapvvlnmls
nfnkteplkk
       301 pvhvltggss pptailtrae rlgfevshgf gmtevigviv scawkrewdr
fpatekarmk
       361 arqgvrkvgv aevdvvgptg esvkndgvtv geivvkgacv mlgyfkdeia
tsqcikkngw
       421 fytgdvavmh edgyleikdr skdliisgge nmssvevegv lymhsavkea
avvarpddfw
       481 getpcgfvsl kdelkkndip tdneikefck eklphfmmpk tivfmkelpk
tstgkvqkhv
       541 lrkvakkmgs lslpppprli sri
```

SEQ ID NO:28
GI:149375957, Protein name: acyl-CoA synthase [Marinobacter algicola DG893]

```
         1 mnsifdkgle ptdannatlt pldflartas vypeypavih gatrrnwqqt yercrrlasa
        61 ladrgvgkgd tvaamlpnip pmlechfgip mlgavlnaln trldakaiaf mlehgeakvl
       121 iadrefgdvi neavgmldnp pqvidvndpe fsgagtqvsd ldydafvasg dpafdwqmpa
       181 dewdaislcy tsgttgnpkg vvyhhrgaye namgnqavws mgmhpvylwt lpmfhcngwc
       241 fpwtitafag thvclrkvep ekilqliseh kvshmcgapi vlntllgase aakssfshtv
       301 qamtagaapp akvieaienm gfrvthvygl tevygpvtvc awksewddlp vedrarikar
       361 qgvryhtlag mmvgdpetme avpkdgntig eiflrgntvm kgylknpkat eeafrggwfh
       421 tgdlavwhad gyaeikdrlk diiisggeni stievedvly rhpdileaav varpdekwge
       481 tpcafvtlkp eagevseddi iafcrermak fkvpktivfs elpktstgki qkfvlrddak
       541 kl
```

SEQ ID NO:29
GI:26991093, Protein name: lpdV gene product [Pseudomonas putida KT2440]

```
        1 mqqiiqttll iigggpggyv aairagqlgi ptvlvegqal ggtclnigci
pskalihvae
       61 qfhqasrfte psplgisvas prldigqsvt wkdgivdrlt tgvaallkkh
gvkvvhgwak
      121 vldgkqvevd gqriqcehll latgsssvel pmlplggpvi sstealapkt
lpqhlvvvgg
      181 gyiglelgia yrklgaqvsv vearerilpt ydseltapva eslkklgial
hlghsvegye
      241 ngcllasdgk ggqlrleadq vlvavgrrpr tkgfnlecld lkmngaaiai
derchtsmhn
      301 vwaigdvage pmlahramaq gemvaeiiag karrfeptai aavcftdpev
vvvgktpeqa
      361 sqqgldciva qfpfaangra msleskgfv rvvarrdnhl ivgwqavgva
vselstafaq
      421 slemgacled vagtihahpt lgeavqeaal ralghalhi
```

SEQ ID NO:30,
GI:6325162, Protein name: Eeb1p [Saccharomyces cerevisiae S288c]

```
        1 mfrsgyyptv tpshwgyngt vkhvlgekgt kslafrdskr qiplhefvtk
hvptlkdgan
       61 frlnslftg ylqtlylsag dfskkfqvfy greiikfsdg gvctadwvmp
eweqtyslna
      121 ekasfnekqf sndekathpk gwprlhprtr ylsseelekc hskgysyplv
vvlhglaggs
      181 hepliralse dlskvgdgkf qvvvlnargc srskvttrri ftalhtgdvr
eflnhqkalf
      241 pqrkiyavgt sfgaamltny lgeegdncpl naavalsnpw dfvhtwdkla
hdwwsnhifs
      301 rtltqfltrt vkvnmnelqv penfevshkp tvekpvfyty trenlekaek
ftdilefdnl
      361 ftapsmglpd gltyyrkass inrlpnikip tliinatddp vtgenvipyk
qarenpcvll
      421 cetdlgghla yldnesnswl tkqaaeflgs fdelvl
```

SEQ ID NO:31
GI:207340567, Protein name: YPL095Cp-like protein [Saccharomyces cerevisiae AWRI1631]

```
        1 mfrsgyyptv tpshwgyngt vkhvlgekgt rslafrdskr qiplhefvtk
hvptlkdgan
       61 frlnslftg ylqtlylsag dfskkfqvfy greiikfsdg gvctadwvmp
eweqtyslna
      121 ekasfnekqf sndekathpk gwprlhprtr ylsseelekc hskgysyplv
vvlhglaggs
      181 hepliralse dlskvgdgkf qvvvlnargc srskvttrri ftalhtgdvr
eflnhqkalf
      241 pqrkiyavgt sfgaamltny lgeegdncpl naavalsnpw dfvhtwdkla
hdwwsnhifs
      301 rtltqfltrt vkvnmnelqv penfevshkp tvekpsfiri pekiwkrlkn lqty
```

SEQ ID NO:32
GI:255715549, Protein name: KLTH0E13310p [Lachancea thermotolerans]

```
        1 mplpifnpfh wgyhgtieqv snpngtvalt lkdekkpvqf sdfvsreipg
lkdkakfevn
       61 pllftgylqt lylggadfsk sfpvyygrei vkfsdggict adwvmkswks
kygadtssfk
      121 tdeqathpen wprlhprtrf leesekkdvh nsekplvvvl hglaggshep
iirsltqdls
      181 nagdskfdvv vlncrgcars kittrklfya vftsdirefi arekarhpsr
kiyavgfsfg
      241 atmlghylge egekapieaa sflcnpwdly qsalkmnqdw wsrnlfskni
aqflirlvkv
      301 nikelefkeg dvmpaepasl ehpsfcvfts knlrkarefg staefdnlft
apclgfdnam
      361 dyykacgsih qlpnikvpsl iinskddpvv gedsipykca kesdnlvlcv
sdlgghlafl
      421 dkkynswats kiaaffdkfe elvq
```

SEQ ID NO:33
GI:254584546, Protein name: ZYRO0F14740p [Zygosaccharomyces rouxii]

```
        1 msnlpiinpf hwgsrgtlkh tsapsgttkl tlnhdktkid fqhfvsqyvp
alkdgskfkl
       61 nnflftgilq tmylsgadyt kwfpvfygre ilelsdggvc tvdnvmvswe
ekyqlrqnsg
      121 sfnklefekd ekdthpqnwp rlqartrylt akelaevhgd qrplvvvlhg
laggshetii
      181 rsltsklski dggkfqvavl ncrgcarski tnkklfsafq tgdlkeylar
eksrnpnrki
      241 yavgfsfgas llanylgetg sesnltaavt lccpwdfllc aekmkkdyws
knlfskaitq
      301 flvrlvkvnm gelespegsk pefqpdienp clymctksnl eraksftqml
efdgtftaps
      361 mgfssaeeyy ragsainnlh kvqvptliin stddpiidas sipysqvkmn
pnllllatdl
      421 gghlayldet wdswmnthia sffstfdefl v
```

SEQ ID NO:34
GI:45185426, Protein name: ABR194Cp [Ashbya gossypii ATCC 10895]

```
        1 mglptfaprs wgyrgtithr pheeglvklp lkdkekepvt lsdllnehvp
elkdgarfyl
       61 hpylyngilq tmylygadfs qqykpfygre ivsysdggvs tadwamrewd
dlyaapegyn
      121 kekfdadaak thpenwprlq pntrfldeee lakipkdtrp livvahglag
gsheniiral
      181 vtellsvgng qfnvvvlnsr gcarskiank klfsafhtmd irefinreha
rqperkiygl
      241 gfsfgsvifg nylgeegdks plsgavccag pwdmfasskm lnddfwisrl
fgknlvkhls
```

301 rllhvnrkel eydgskgddv edasptnpas hiftkenlar astmactrdf dnfftapalg
361 fknandyyka aspvnivgki rvptllinal ddpmvgaegf lpieklrsnk hillcttdig
421 ghlayldkny tpwmagrvae flskmdtlva

SEQ ID NO:35
GI:294659670, Protein name: DEHA2G12430p [Debaryomyces hansenii CBS767]

1 mvfpwgfrsn vkihqsnsdk sidlplrnge ktikyadfik delpiideke klwlnpllfn
61 gllqtlyyss anlshkfqvy ygreiftyed ggvcsidhvi pqpenteefk alhdktlpeg
121 wpklhprsry fsneeleqvn spsegsqstk picvvlhgla ggsheplirn laeylstgkn
181 enkwdtlvin srgccrtkit ngklftalst gdihevlvel kkrnpnrpiy tvgfsfgaai
241 lanylaeikd dtmitaaclv gcpwdlidsa yhiekswsgs ylfnpaltsf lnklvknnft
301 elnhhnpelf neenlkrgmk qtktwqfdsv ytchtigysn pfeyyrdasp vnriskihtp
361 tlilnstddp avgvrlpwme vennphlcmv etdlgghlgy vqssgkfwcv qlveeffakf
421 delias

SEQ ID NO:36
GI:75150384, Protein name: Benzoyl coenzyme A:benzyl alcohol benzoyl transferase[Clarkia breweri]

1 mahdqslsfe vcrrkpelir pakqtphefk klsdvedqeg lrfqipviqf ykhnnesmqe
61 rdpvqvireg iaralvyyyp fagrlrevdg rklvvectge gvmfieadad vtleqfgdal
121 qppfpcfdql lfdvpgsggi ldsplliqv trlkcgsfif alrlnhtmad aagivlfmka
181 vgemargaat pstlpvwdrh ilnarvppqv tfnhreyeev kgtiftpfdd lahrsfffgs
241 teisamrkqi pphlrscstt ievltaclwr crtlaikpnp deevrmiciv narskfnppl
301 pdgyygnafa ipaavttagk lcnnplgfal elirkakrev teeymhsvad lmvatgrphf
361 tvvntylvsd vtragfgevd fgwgeavygg pakggvgvip gvtsfyiplr nrqgekgivl
421 piclpsaame ifaealnntl ngkeieiakh ftqssl

SEQ ID NO:37
GI:49798480, Protein name: benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Petunia x hybrida]

1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi nfyrkdssmg

61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal

SEQ ID NO:38
GI:1171577, Protein name: hsr201 [Nicotiana tabacum]

1 mdskqsselv ftvrrqkpel iapakptpre tkflsdiddq eglrfqipvi
qfyhkdssmg
61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada
dvtleqfgde
121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
181 avgemarggs apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip
lddmvhksff
241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc
ivnarsrfnp
301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv
adlmvlkgrp
361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip
fknkkgengi
421 vvpiclpgfa metfvkeldg mlkvdaplvn snyaiirpal

SEQ ID NO:39
GI:84578877, Protein name: benzoyl CoA benzoic acid benzoyltransferase [Verbena x hybrida]

1 maqnntlltf tvrrnepeli apakptprel kplsdiddqe glrfqipviq
fyrhdpkmrn
61 knparvirea lakvlvfyyp fagrlkegpa kklmvdcsge gvlfieaead
vtlnqfgdal
121 qppfpcleel lydvpgsggv ldsplliqv trllcggfif alrlnhtmsd
apglvqfmta
181 lgemaqgapr psilpvwqre llfarvqphv tcthheydev kdtkgtiipl
ddmahrsfff
241 gptevaalrr fvpsslqkcs tfevltaclw rcrtialkpd peeemriici
vnarakfnpp
301 lpkgyygngf afpvaisrag dlstkplgha lklvmqakna vndeymrslt
dlmvikgrph
361 ftvvrsylvs dvtragfdav dfgwgnaayg gpakggvgai pgvasfyipf
tnhkgetgiv
421 lpiclpnaam etfvkelnnm lakgnndqvl kehnynvlsr l

SEQ ID NO:40
GI:254771941, Protein name: alcohol acyltransferase [Vasconcellea cundinamarcensis]

```
        1 maekasslmf nvrrhepeli tpakptprei kllsdiddqd glrfqvpiiq
fyknnssmqg
       61 knpakiiksa laetlvhyyp lagrlregfg rklmvectge gilfieadad
vtlhefgddl
      121 pppfpclvel lydvpgssgi idtpllliqv trlkcggfif alrlnhtmsd
asglvqfmta
      181 vgemargqrs lsiqpvwerh llnardpprv thihheyddl edtkgtiipl
ddmvhrsfff
      241 gpsemaairr lvpahfhrst tsevltaylw rcytialqpd peeemrvicv
vnsrtklnpp
      301 lptgfygngi afpaaisqak kicenpfgyt lqlvkqtkvd vteeymrsaa
dlmamkgrph
      361 ftvvrrymvs dvtragfglv dfgwgrpepv yggpakggvg pipgvtsffv
pfknrkgekg
      421 ivvptclptp amerfaklmn eilqnqllvs aeenksvfiv sai
```

SEQ ID NO:41
GI:161089458,Protein name: acyltransferase [Vanda hybrid cultivar]

```
        1 masstlhfsv rrrppqlvap asptprelkr lsdiddqegl rfqipviqfy
rhepamagqn
       61 pasvirdala rtlvfyypfa grlregagkk lfvdctgegv lfieaeadvk
lkdfgdalhp
      121 pfpcleellf dvdgssavln tpllliqvtl lscggfilal rlnhtmsdap
glvqlmtavg
      181 elargsssps vipvwrrell earpspapff phpeyeqvpd tegtitpldn
tahrsfifgp
      241 reisilrsrl psqlrgasst fdiltacvwr srtralqpad pkenfriici
vnirgrinpp
      301 lpsgfygnaf glpvaiatag elcsrpldya velvkraksq vsgdylhsva
dymvmkgrph
      361 ftvvrtyvis dltragfgdv dfgwgkpvyg gpakggvgvs pgvfnffipf
vnasgekgiv
      421 vpiclpppam rrfvaeiqsl lsaqsal
```

SEQ ID NO:42
GI:57471999, Protein name: putative alcohol acyl-transferases CmAAT3 [Cucumis melo]

```
        1 masslvfqvq rsqpqlipps dptphefkql sdiddqeglr fqipviqfyr
hdprmagtdp
       61 arvikeaiak alvfyypfag rlregpgrkl fvectgegvm fieadadvsl
eqfgdalqpp
      121 fpcleeplfd vpnssgvldc pllliqvtrl kcggfifalr lnhtmsdasg
lvqfmmavge
      181 margatapsv rpvwqralln ardppkvtch hreydevvdt kgtiipldam
ahrsfffgps
      241 eisairkalp shlrqcssfe vltaclwrfr tislqpdpee evrvlcivns
rskfnpplpt
```

```
      301 gyygnafafp valttagklc qnplgyalel vrkakadvte dymksvadlm
vikgrphftv
      361 vrtylvsdvt ragfedvdfg wgkamyggpa kggvgaipgv asfyipfknk
kgergilvpl
      421 clpapamerf vkeldallka gktidgvdnk kplfiasal
```

SEQ ID NO:43
GI:49798480, Protein name: benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:44
GI:75150383, Protein name: Benzoyl coenzyme A:benzyl alcohol benzoyl transferase [Nicotiana tabacum]

```
        1 mdskqsselv ftvrrqkpel iapakptpre ikflsdiddq eglrfqipvi
qfyhkdssmg
       61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada
dvtleqfgde
      121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargas apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip
lddmvhksff
      241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc
ivnarsrfnp
      301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv
adlmvlkgrp
      361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip
fknkkgengi
      421 vvpiclpgfa metfvkeldg mlkvdapldn snyaiirpal
```

SEQ ID NO:45
GI:224144897, Protein name: predicted protein [Populus trichocarpa]

```
        1 masspasllf kvhrrepeli kpakptphef kllsdiddqe glrfhipvmq
fyrnnpsmqg
```

```
       61 kdpvkiirea laktlvfyyp fagrlregpn rklmvectge gilfieadad
vtleqfgdal
      121 qppfpcleel lfdvpgssgv lncpllliqv trlkcggflf alrlnhtmsd
avglvqfmaa
      181 vgemargana psvpavwerq vlnasdpprv tcthreyeev adtkgtiipl
ddmahrsfff
      241 gpsemsalrk fvpphlshcs tfeiltaclw kcrtialqpd pteemrilci
vnarekfnpp
      301 lprgyygngf afpvavatae elsknpfgya lelvrkakad vteeymrsvs
slmvikgrph
      361 ftvvraylvs dlrragfeev dfgwgnaiyg gaakggvgai pgvasfyipf
tnkkgengvv
      421 vpfclpapam erfvkeldgm lkddqtvsaq tkskfivssl
```

SEQ ID NO:46
GI:356500043, Protein name: PREDICTED: benzyl alcohol O-benzoyltransferase-like [Glycine max]

```
       1 mdtslvftvr rseaeliapa kptprevkll sdiddqdglr fqipviqfyr
hdpsmagkdp
      61 vdvirkavak tlvfyypfag rlreglgrkl mvdctgegvl fieadadvtl
kqfgdalqpp
     121 fpcweellyd vpgsqgvlnt pllliqvtrl kcggfilavr lnhtmsdaag
lvqfmsalge
     181 iargrqepsi ppvwrrelln ardpprvtct hreyehvpdt kgtiipldhm
ahrsfffgps
     241 evaairslip qtdqrcsnfe vltaclwrcr tialqpdkde evrilcivna
rskfdpplps
     301 gyygnafafp vavttagklc dnplgyalel vrkakadvte eymhsvadlm
vtkgrphftv
     361 vrsylvsdvt ragfgniefg wgkavyggpa kggvgaipgv asfyipfkna
kgeeglvipv
     421 clpseamerf qkeldcvlnh hivqpsaiap nsrfivssl
```

SEQ ID NO:47
GI:133874202, Protein name: putative acyltransferase [Clitoria ternatea]

```
       1 matstssssl mfqvqkreae liapakptpr evkllsdidd qeglrfqipv
iqfyrynetm
      61 agkdpvevir kalaktlvfy ypfagrlreg pgrklmvdct gegvlfieah
advtlqqfgd
     121 slqppfpgld hllynlpnsd gvlnspllli qvtrlkcggf ilalrlnhtm
sdaaglvqfm
     181 savgeiargm eepsippvwr rellnarnpp kvtcthreye qvpdskgtii
plddmahrsf
     241 ffgpaeisai rrlipaqqqr qcsnfeilta clwrcrtial qpdsdeevri
lcivnargkf
     301 npplpagyyg nafafpvavt tagklcgnpl gyalelvrka kgdvseeymh
sladlmvtkg
     361 rphftvvrsy lvsdvtragf gdvdfgwgkp vyggpakggv gaipgvasfy
ipfrnskgee
     421 glvipvclps qamdrfvrel dtilnhhlqp ppksplvlss l
```

SEQ ID NO:48
GI:49798480, Protein name: benzyl alcohol benzoyl transferase(BPBT) [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:49
GI:1171577, Protein name: hsr201 [Nicotiana tabacum]

```
        1 mdskqsselv ftvrrqkpel iapakptpre tkflsdiddq eglrfqipvi
qfyhkdssmg
       61 rkdpvkvikk aiaetlvfyy pfagrlregn grklmvdctg egimfveada
dvtleqfgde
      121 lqppfpclee llydvpdsag vlncpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemarggs apsilpvwcr ellnarnppq vtcthheyde vrdtkgtiip
lddmvhksff
      241 fgpsevsalr rfvphhlrkc stfelltavl wrcrtmslkp dpeeevralc
ivnarsrfnp
      301 plptgyygna fafpvavtta aklsknplgy alelvkktks dvteeymksv
adlmvlkgrp
      361 hftvvrtflv sdvtrggfge vdfgwgkavy ggpakggvga ipgvasfyip
fknkkgengi
      421 vvpiclpgfa metfvkeldg mlkvdaplvn snyaiirpal
```

SEQ ID NO:50
GI:57471999, Protein name: putative alcohol acyl-transferases [Cucumis melo]

```
        1 masslvfqvq rsqpqlipps dptphefkql sdiddqeglr fqipviqfyr
hdprmagtdp
       61 arvikeaiak alvfyypfag rlregpgrkl fvectgegvm fieadadvsl
eqfgdalqpp
      121 fpcleeplfd vpnssgvldc pllliqvtrl kcggfifalr lnhtmsdasg
lvqfmmavge
      181 margatapsv rpvwqralln ardppkvtch hreydevvdt kgtiipllddm
ahrsfffgps
      241 eisairkalp shlrqcssfe vltaclwrfr tislqpdpee evrvlcivns
rskfnpplpt
```

301 gyygnafafp valttagklc qnplgyalel vrkakadvte dymksvadlm vikgrphftv
361 vrtylvsdvt ragfedvdfg wgkamyggpa kggvgaipgv asfyipfknk kgergilvpl
421 clpapamerf vkeldallka gktidgvdnk kplfiasal

SEQ ID NO:51
GI:133874202, Protein name: putative acyltransferase [Clitoria ternatea]

1 matstssssl mfqvqkreae liapakptpr evkllsdidd qeglrfqipv iqfyrynetm
61 agkdpvevir kalaktlvfy ypfagrlreg pgrklmvdct gegvlfieah advtlqqfgd
121 slqppfpgld hllynlpnsd gvlnspllli qvtrlkcggf ilalrlnhtm sdaaglvqfm
181 savgeiargm eepsippvwr rellnarnpp kvtcthreye qvpdskgtii plddmahrsf
241 ffgpaeisai rrlipaqqqr qcsnfeilta clwrcrtial qpdsdeevri lcivnargkf
301 npplpagyyg nafafpvavt tagklcgnpl gyalelvrka kgdvseeymh sladlmvtkg
361 rphftvvrsy lvsdvtragf gdvdfgwgkp vyggpakggv gaipgvasfy ipfrnskgee
421 glvipvclps qamdrfvrel dtilnhhlqp ppksplvlss l

SEQ ID NO:52
GI:224144897, Protein name: predicted protein [Populus trichocarpa]

1 masspasllf kvhrrepeli kpakptphef kllsdiddqe glrfhipvmq fyrnnpsmqg
61 kdpvkiirea laktlvfyyp fagrlregpn rklmvectge gilfieadad vtleqfgdal
121 qppfpcleel lfdvpgssgv lncpllliqv trlkcggflf alrlnhtmsd avglvqfmaa
181 vgemargana psvpavwerq vlnasdpprv tcthreyeev adtkgtiipl ddmahrsfff
241 gpsemsalrk fvpphlshcs tfeiltaclw kcrtialqpd pteemrilci vnarekfnpp
301 lprgyygngf afpvavatae elsknpfgya lelvrkakad vteeymrsvs slmvikgrph
361 ftvvraylvs dlrragfeev dfgwgnaiyg gaakggvgai pgvasfyipf tnkkgengvv
421 vpfclpapam erfvkeldgm lkddqtvsaq tkskfivssl

SEQ ID NO:53
GI:225454593, Protein name: benzyl alcohol O-benzoyltransferase [Vitis vinifera]

1 mapppslvfs vrrskpelva pakptphefk plsdiddqeg lrfqipviqf ykkvpsmhgr
61 dpakvikdav aralvfyypf agrlreeagr klvvectgeg ivfieadadv tleqfgdalq

121 ppfpgleeli ydapgsggvl nsplliqvt rlqcggfifg lrlnhtmsda aglvqfmsav
181 gemargasap sippvwrrdl lnardpprvt rthheydeva dtkgtiipld dmehrsfffg
241 ptefaalrrl lsphlrtcst felltaclwr crtialrpdp eeevrvlciv narsrlqppl
301 pagyygnvfg fpvalssagk lcrnpleyal dlvkgaknsv dqeymksvad lmvstgrrhf
361 tvvrsylvsd ltragfgdvd fgwgkavygg aakggvgaip gvasfyipfr nhkgedgivv
421 pfclpaaame ifvkelnsll keehplpsnk sstfiisal

SEQ ID NO:54
GI:52139953, Protein name: alcohol acyl transferase (MpAAT1) [Malus x domestica]

1 mmsfsvlqvk rlqpelitpa kstpqetkfl sdiddqeslr vqipiimcyk dnpslnknrn
61 pvkaireals ralvyyypla grlregpnrk lvvdcngegi lfveasadvt leqlgdkilp
121 pcplleefly nfpgsdgiid cpllliqvtc ltcggfilal rlnhtmcdaa glllfltaia
181 emargahaps ilpvwerell fardppritc ahheyedvig hsdgsyassn qsnmvqrsfy
241 fgakemrvlr kqipphlist cstfdlitac lwkcrtlaln inpkeavrvs civnargkhn
301 nvrlplgyyg nafafpaais kaeplcknpl gyalelvkka katmneeylr svadllvlrg
361 rpqysstgsy livsdntrvg fgdvnfgwgq pvfagpvkal dlisfyvqhk nntedgilvp
421 mclpssamer fqqeleritq epkedicnnl rstsq

SEQ ID NO:55
GI:44887628, Protein name: alcohol acyl transferase [Pyrus communis]

1 mmslsvlqvk rlqpelitpa kptpqetkfl sdiddqeglr fqlpvimcyk dnpslnknrn
61 pikvikeals ralvyyypla grlregpnrk lmvncngegi lfveasadvt leqlgdkilp
121 pcplleeflf nfpgsdgiig cplllvqvtc ltcggfilal rlnhtmcdat gllmfltait
181 emgrgadaps ilpvwerell fardppritc ahyeyedvid hsdgsyafsn qsnmvqrsfy
241 fgakemrvlr kqipphlist cstfdlitac lwkcrtlvlk inpkqavrvs civnargkhn
301 nvhiplgyyg nafafpaavs kaeplcknpl gyalelvkka katmneeylr svadllvlrg
361 rpqysstgsy livsdntrag fgdvnfgwgq pvfagpakal dlisfyvqhk nniedgilvp
421 mclpssamer fqqeleritt gt

SEQ ID NO:56
GI:147801410, Protein name: hypothetical protein VITISV_042062 [Vitis vinifera]

```
        1 masswsplvf svkrcapefv rptnltprev kqlsdiddqe glrfqipvim
fypnnplmkg
       61 kdpvkvirea lgkalvyyyp fagrliegdn rklmvdctge gvlfieadad
ttlenlgdai
      121 qpmcpcfeel lydvpgsggi lgspliliqv trlrcggfif alrlnhtmsd
algliqflna
      181 isemaqglsv psllpiwere llnarnppri trihheyeev tnnkgtlmam
dennlvhrsf
      241 ffgpkeiral rnrlpaslga cstfevltay vwrcrtiafa vdpdevvris
clinmrgkrg
      301 fdlppgyygn afvypasitk agmlcknple yairllkkak aemsqeyiks
vadlmvikgr
      361 psftqpgnyf vsdvtragfg evnfgwgkpv ygglaralsi isfctrfrns
kgeegnvipi
      421 clpppvmerf eqelkrmtke aepvrliksm l
```

SEQ ID NO:57
GI:49798480, Protein name: benzyl alcohol benzoyl transferase [Petunia x hybrida]

```
        1 mdskqsselv ftvrrqepel iapakptpre tkflsdiddq eglrfqipvi
nfyrkdssmg
       61 gkdpvevikk aiaetlvfyy pfagrlregn drklmvdctg egvmfveana
dvtleefgde
      121 lqppfpclee llydvpgsag vlhcpllliq vtrlrcggfi falrlnhtms
dapglvqfmt
      181 avgemargat apstlpvwcr ellnarnppq vtcthheyee vpdtkgtlip
lddmvhrsff
      241 fgptevsalr rfvpphlhnc stfevltaal wrcrtisikp dpeeevrvlc
ivnarsrfnp
      301 qlpsgyygna fafpvavtta eklcknplgy alelvkktks dvteeymksv
adlmvikgrp
      361 hftvvrtylv sdvtragfge vdfgwgkavy ggpakggvga ipgvasfyip
frnkkgengi
      421 vvpiclpgfa mekfvkelds mlkgdaqldn kkyafitpal
```

SEQ ID NO:58
GI:158828372, Protein name: alcohol acyl transferase [Citrus sinensis]

```
        1 mvftfsqgll vtrkapeliv perptprevk qisdiddqes lrfqipllff
ykndpspsmq
       61 grdpvkvire aiskalvfyy plagrlkegy nrklmvecna egvlfieada
nftleqlrdd
      121 vqppcpylnq liydvpgseg ilgcpllliq vtrltcggfi fairfnhtmc
dafglvqflk
      181 aiedmarger sptlfpiwqr lilnarnppq vtcihheyde intnevpsdn
mahksfffsl
      241 kgikalrnql pfqlkdcstf elllaflwkc rtialklqpe eiakvccivn
vrgksyemdi
      301 ppgyygnaft fsavcskaeq lcknpigyav elvkkakaqm neeyirsaad
lmvikgrrik
      361 fstrgnfivs dlrnvglgdv dfgwgkpiya gtagavavis fftkyqnkng
epgilvpicl
      421 pqsamerlqe elkglmiqgs aedlcninqt qifskl
```

SEQ ID NO:59
GI:255552914, Protein name: Taxadien-5-alpha-ol O-acetyltransferase, putative [Ricinus communis]

```
      1 malppppftf avrrsppeli vparptprel kkvsdiddqe glrfqisfvm fyrslpsmkg
     61 rdpveiirka lsealvfyyp fagrliegpn rklivdcnge gilfieadad
itieqlgdsm
    121 qppcpcieel lydvpgssgi igcpllliqi trlacggfvf avrlnhvmsd
svglakffka
    181 tgeiakgacm pslfpvwqre ilsarnppqv thkleeyeei khtddksilt
ldspdmvqra
    241 fffgpkemrs lrrqlpshlr ncssfemlaa clwrcrtiaf dippnevvrl
scimnvrgkk
    301 glqlpdgycg nsfifpavls raehlcknpl gyavelvrks kskmseeyir
stidlmeikg
    361 rphyvtawnl llvdmshvgl advdfgwgnp vyfgptgsfp nismfsrfkn
skgengfvvp
    421 mwlprtvmek fqdeflkmte esaenlndar rqriistl
```

SEQ ID NO:60
GI:10121328, Protein name: alcohol acyltransferase (SAAT) [Fragaria x ananassa]

```
      1 mekievsins khtikpstss tplqpykltl ldqltppayv pivffypitd
hdfnlpqtla
     61 dlrqalsetl tlyyplsgrv knnlyiddfe egvpylearv ncdmtdflrl
rkieclnefv
    121 pikpfsmeai sderypllgv qvnvfdsgia igvsvshkli dggtadcflk
swgavfrgcr
    181 eniihpslse aallfpprdd lpekyvdqme alwfagkkva trrfvfgvka
issiqdeaks
    241 esvpkpsrvh avtgflwkhl iaasraltsg ttstrlsiaa qavnlrtrmn
metvldnatg
    301 nlfwwaqail elshttpeis dlklcdlvnl lngsvkqcng dyfetfkgke
gygrmceyld
    361 fqrtmssmep apdiylfssw tnffnpldfg wgrtswigva gkiesasckf
iilvptqcgs
    421 gieawvnlee ekmamleqdp hflalaspkt li
```

SEQ ID NO:61
GI:374498907, Protein name: alcohol acyl-transferase [Rosa rugosa]

```
      1 mekievsiis rdtikpsaas sslhpyklsi idqftpttyf pviffypitd
pvfnlpqtlt
     61 dlkitvsqtl tlyyplsgri knnlyiddfe agipylearv nchmidflrl
pkiewlnefv
    121 piapyrketi sellpllgiq vnifdsgiai gvsfshkind getancflks
wvaifrgyrn
    181 kiihpnlsqa allfpsrddl sekyvammer wwfgekkvvt rrfvfdtkai
salqhegkse
    241 yvpkpsrvqa ltgflwkhql aatralssgt strfslaiqa vnlrsrmnmk
ttldnaigni
```

301 flwapaflel nyttpessdh klcdlvnllk esvkeynsdy letlkgekgy ggmcdwldlm
361 degssiepal eiysfsswtr mfdqvdfgwg kpfwigvtgk vqttytnstv lvetqcengi
421 eawvtldqkr mamleqdpqf lafasptpgi smassvgid

SEQ ID NO:62
GI:255585363, Protein name: Anthranilate N-benzoyltransferase protein, putative [Ricinus communis]

1 mvtkmqvdii srevikpssp tihhykpfkf plfsqltptt yspviffypt tkpnlnitqt
61 lihlkktlae tltlyypfsg rvvdnlsidh fdegvpffia rvtglvlsdf lknpeielln
121 gflpykpftk etdkgvpqma fqvnvfscgg ivigwssshk lvdgptgaaf ihawatmsrt
181 gslsdvikpn cdeasiffpp rnpfpeehls lmeslwftkg nyiskrfvfd skaiaslrvk
241 argegnekkn mpsrvealsc fiwkccmaas raasgtpkps ilveavnlrt rtkppmskvs
301 igdifwwata vadpslhnke lhelatllde aialydsdym eslqgedgfe tmseycnqlr
361 glfsieepdi faftswsrlg iydmdfgfgn pfwigilgkv gpafrnltvf letrdgkgie
421 awitldeerm allerdpefl anaspnprfs sl

SEQ ID NO:63
GI:380863876, Protein name: BAHD acyltransferase [Erythroxylum coca]

1 mevhivsret vkpsspatlt kkpyklslfd qltpgtytpt iffypknrpn sdttqvlarl
61 krslsetlds yfflsgrtrd nrfidcfdeg vpffeasvsv glsdflkhhe hewlnrlvay
121 rpytkealds pllsiqvsvf acggivigts ashklidalt gsfilktwaa mfrgdvsdgi
181 spqideasmy fptrdsfpqn hlslmeslwf teanyvtrrf vfgaksisai kemakskpes
241 kqsriealsc fiwkhcmsas kavsgspqvs ilveavnlrt rttppmssss igdlfwwata
301 asnnddtkst elpelanllk eaielydtdf tkslqgnegd eaiyqyceql eglfslekpd
361 ifaftswcyv gftklnfgwg epiwvgtvgk agpafrnltv fietrdgkgi eawitldqkr
421 msvlehdpqf lafaslnpki ssl

SEQ ID NO:64
GI:255577416, Protein name: Anthranilate N-benzoyltransferase protein, putative [Ricinus communis]

1 mevhivsrem mkpsspaikh qkpyklclld qltpttyipi iffypmnnlf tkstlahlke

61 slvktlnfyy pfsgrakdnl yidrfeegvp ffeakvncsm syflkhyete slsnlfipsh
121 pfskeidmsi alvavqvsmf tcggiavglc lshklidaat assfvttwas fcrgdpknvi
181 qpdfeqpstf fpsstslpqn ylslmeriwf vkanyitkrf vfdakaiaal rvkakaklea
241 eptriatlsc fiwkcsmaas raisgapkps ilveavnlrq ktkppmkdss tgnlfwwava
301 lasptdtnst elnelvsmls eaiavyksdy thslqgengl kimseyceql egmfsleepd
361 ifgftswskm pvtrpnfgwg epfwvglmak agpefrnftv fidtkdgkgi eawitldear
421 mailqrdpef lafaspnpki ssl

SEQ ID NO:65
GI:359492333, Protein name: PREDICTED: vinorine synthase-like [Vitis vinifera]

1 mevtiisret ikpssptphh lrafklslld qlvpccytqv llfylidgfh gqsietshis
61 trlkdslset lthfyplags igddelqidc ndegvpyfea rvdcnlsefl qepelellnq
121 ffpcdplntp pmaklhlami qvnifnrggi aigvclshki adgvsisafl kawaaiargc
181 feeypsfeak slfpqneslp qdysmvlgkc lirtgkcvtk rvvfdasaia alkakasvdc
241 trvevvsafi wkramaaakq klgfqrssil thavnlrkkt ilslpessmg nlfwiaiteg
301 rvddeaeldl lvdktrkais kiscdfakkl qgeegfavaf ehvkevkaaf eedgvdfygf
361 sswckfevye gdfgwgrpiw vssfsgkgsv yknliffmdt rcgngieewv tldeeelgil
421 ecdpeflsfg smdpsplkla hfgqv

SEQ ID NO:66
GI:323331427, Protein name: Atf1p [Saccharomyces cerevisiae AWRI796]

1 mdlwkrlfea nptkirdkki knghfisitn tinlsalmne ideknqapvq qeclkemiqn
61 gharrmgsve dlyvalnrqn lyrnfctyge lsdyctrdql tlalreiclk nptllhivlp
121 trwpnhenyy rsseyysrph pvhdyisvlq elklsgvvln eqpeysavmk qileefknsk
181 gsytakifkl tttltipyfg ptgpswrlic lpeehtekwk kfifvsnhcm sdgrssihff
241 hdlrdelnni ktppkkldyi fkyeedyqll rklpepiekv idfrppylfi pksllsgfiy
301 nhlrfsskgv cmrmddvekt ddvvteiini sptefqaika niksniqgkc titpflhvcw
361 fvslhrwgkf fkplnfewlt difipadcrs qlpdddemrq myryganvgf idftpwisef
421 dmndnkenfw pliehyhevi sealrnkkhl hglgfniqgf vqkyvnidkv mcdraigkrr
481 ggtllsnvgl fnqleepdak ysicdlafgq fqgswhqafs lgvcstnvkg mnivvastkn
541 vvgsqeslee lcsiykalll gp

SEQ ID NO:67
GI:34485580, Protein name: lager alcohol acetyltransferase I [Saccharomyces pastorianus]

```
        1 meteesqfss itkiinpktl mntysektsl vqdeclvkmi qnghsrrmgs
vedlyaalnr
       61 qklyrnfsty selndyctkd qlalalrnic lknptllhiv lparwpdhkk
yylsseyysq
      121 prpkhdyisv lpelkldgvi lneqpehnal mkqileefan sngsytakif
klttaltipy
      181 tgptsptwrl iclpeeddtn kwkkfifvsn hcmcdgrssi hffqdlrdel
nniktlpkkl
      241 dyifeyekdy qllrklpepi enmidfrppy lfipksllsg fiyshlrfss
kgvctrmdei
      301 eksdeivtei inispsefqk irtkiklnip gkctitpfle vcwfvtlhkw
gkffkplkfe
      361 wltdvfipad crsllpedee vramyrygan vgfvdftpwi skfnmndske
nfwpliahyh
      421 evisgaikdk khlnglgfni qslvqkyvni dkvmrdralg ksrggtllsn
vgmfhqseet
      481 ehkyrirdla fgqfqgswhq afslgvsstn vkgmniliss tknvvgsqel
leelcamyka
      541 lllnp
```

SEQ ID NO:68
GI:365758173, Protein name: Atf1p [Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7]

```
        1 miqngharrm gsvedlyval nrqnlyrnfs ayaelsdycs kdqltlalrn
iclknptllh
       61 ivlptrwpdh enyylsseyy shphpkhdyi svlpelkldg viineqpeng
kivrqileef
      121 rnsngtynak ifklttalti pyfgptspnw rliclpeeht dkwkkfifvs
nhcmsdgrss
      181 ihffhdlrae lndiktppkk ldylfkyend yqllrklpep iekvidfrpp
ylfipkslls
      241 gfiynhlrfa srgictrmdd meksddvvae iitispselq eirtkiksni
qgkctltpfl
      301 qvcwfvslhq wgkffkplnf ewltdifipa dcrpqlpdde evrqmyryga
nvgfvdftpw
      361 icesnmnenk enfwpliehy hqvisgalrd nkhlhglgln iqgfvqkyvn
idkamcdrai
      421 gkarggtlls nvgmfkqlds sncnysiktw llgnfkghgt khfhwvfvrl m
```

SEQ ID NO:69
GI:255712859, Protein name: KLTH0C11440p [Lachancea thermotolerans]

```
        1 mdslkergha rplghlenyf sitqrqklya nfsmycelsk pcspkqlaya
lrsiclqnpi
       61 lvhqvlpkhw pnhleyyasd eflaqptlqh edmrlldnvl lsdivmneqe
eygtvvseai
```

121 eefsqnggqy skkifdiiad iripygdplk pnwrllcfpe gesnlwrkfi yitnhcssdg
181 rsaanlmrdl seqlnhvpet lpdsdiifny ssdyeglrkl pdpienridy kppisyllql
241 lsssyvrdyl gyyskgplvt ridevgenkt yysyflnfsa eqmktikqkl ksrlpgctmt
301 pflqacwlts myksgrvfsk smrewffdvv itmntaqmlp ddpelrsmyk ygsnvggtry
361 nylissfnvg edkdafwslv dyyqgvfnsa mekkhylfpl galmldslre ksnmdkvimd
421 dllgkprqgv ilsnvgyfqq kketdgyyvr dlvfaqslgs lrhtfvcnsc ttdvggmniv
481 acaaqgsvas ehdwadvcel fkeqtlal

SEQ ID NO:70
GI:156847986, Protein name: hypothetical protein Kpol_2002p89 [Vanderwaltozyma polyspora DSM 70294]

1 meeyapfitq elvdrgharr mgqlenyfal lqrqnlyknf nvygeinepi dkfqlgtafr
61 qmllkypilm hvivprkyph heeyyasdey lnnpqpindy ikvmenidle dillnsqpey
121 eaivgklldq yksdgykytn rmieiigdis ipicdqtkpn wrllclptke sdkkwhafvy
181 isnhcaadgm tsmnffhdiv nglndksset vtevngrmnl vnyakdhkni skfpkpiter
241 veyrpslsql pkfmigniar tklnykspca ltttvdkvdm qtfdyilnft neevgkirkh
301 ikanthngvt ltpflqtclf vtlyqfgtif qktllewgld svlpvnarky lpedaelrds
361 ykygsnvggi hyfnlissfn ikndeaetfw slvdyyhany qkayhngdtf vgfgllmsdf
421 ivknknvdkl ikedyvnqkr ggvilsnlgf fpqdtrneyy lndlifaqtf gsmkftfgls
481 lcstnvngln igisvvrdaf ndretfekfc khyketiinf anl

SEQ ID NO:71
GI:255711342, Protein name: KLTH0B03806p [Lachancea thermotolerans]

1 mttsqadtkl eelekrghar rlgnlenyfa lgqrqdlysn fgmfceldra csenelaeal
61 rgmcleypll lhtvlekkea qdvnfyqtse ylskpwpqhd yirvlqrvrf advllndqee
121 yaeivnaalk efasnggqys sevfelinkv ripychnsrp nwrimcfpee gnaqsrewrk
181 illlsnhcss dgmssanffh dlqdhlnnlp pslpqadvif dysqdhetlg klpapietqi
241 syvgpksyfa qlvgnqvlre yfgyksptpp iprvnepggn dfysyflkit psevaavkkk
301 lknkldpsct ltpffqacwf aalyksgivf sksfsqqlsn imvamntaql lpedkqlkkq
361 yryganvggs hynyqissfn vadkpeafwk lvryyqdvfv dakrkkhfly plgalmidsi

421 yktknidlav tnsilgksrl gtmlsnvgyf pqkaratvgg fhiqdlifaq ttgsfrftfd
481 inlcatdigg lnitacvaeg alptredwkk lcelfktiil es

SEQ ID NO:72
GI:6321616, Protein name: Atf2p [Saccharomyces cerevisiae S288c]

1 mediegyeph itqelidrgh arrmghleny favlsrqkmy snftvyaeln kgvnkrqlml
61 vlkvllqkys tlahtiipkh yphheayyss eeylskpfpq hdfikvishl efddlimnnq
121 peyrevmeki seqfkkddfk vtnrlielis pviiplgnpk rpnwrliclp gkdtdgfetw
181 knfvyvtnhc gsdgvsgsnf fkdlallfck ieekgfdyde efiedqviid ydrdyteisk
241 lpkpitdrid ykpaltslpk ffltttfiyeh cnfktssest ltaryspssn anasynyllh
301 fstkqveqir aqikknvhdg ctltpfiqac flvalyrldk lftkslleyg fdvaipsnar
361 rflpndeelr dsykygsnvg gshyayliss fdipegdndk fwslveyyyd rflesydngd
421 hliglgvlql dfivenknid sllansylhq qrggaiisnt glvsqdttkp yyvrdlifsq
481 sagalrfafg lnvcstnvng mnmdmsvvqg tlrdrgewes fcklfyqtig efasl

SEQ ID NO:73
GI:156847986, Protein name: hypothetical protein Kpol_2002p89 [Vanderwaltozyma polyspora DSM 70294]

1 meeyapfitq elvdrgharr mgqlenyfal lqrqnlyknf nvygeinepi dkfqlgtafr
61 qmllkypilm hvivprkyph heeyyasdey lnnpqpindy ikvmenidle dillnsqpey
121 eaivgklldq yksdgykytn rmieiigdis ipicdqtkpn wrllclptke sdkkwhafvy
181 isnhcaadgm tsmnffhdiv nglndksset vtevngrmnl vnyakdhkni skfpkpiter
241 veyrpslsql pkfmigniar tklnykspca ltttvdkvdm qtfdyilnft neevgkirkh
301 ikanthngvt ltpflqtclf vtlyqfgtif qktllewgld svlpvnarky lpedaelrds
361 ykygsnvggi hyfnlissfn ikndeaetfw slvdyyhany qkayhngdtf vgfgllmsdf
421 ivknknvdkl ikedyvnqkr ggvilsnlgf fpqdtrneyy lndlifaqtf gsmkftfgls
481 lcstnvngln igisvvrdaf ndretfekfc khyketiinf anl

SEQ ID NO:74
GI:50286475, Protein name: hypothetical protein [Candida glabrata CBS 138]

1 mapntksieq pliskakisg kgpdgfaiee sllerghsrr mghlenyfai mqrqklytnf

```
       61 nmygelnkev treqlavair qillrhpimm qaiipkkfpe heeyytsddy
yntpfpendf
      121 lrvitskikl sdiiineqse dygeiidmil seykkngykf daymqelign
ivipignpnk
      181 pnwrllclps aegggaqwkk fvyisnhccs daisavnlfq diaenvslie
qnswavpyad
      241 dvivdyeqdv adiaklpapi terveyrppl sklpkimlvs flktalnfks
daletrcnde
      301 ysgepetsav qmgdvcydsi lnytceevav irdrikhnvh gkctvtpfiq
aaffvamhqs
      361 rkllgqkqgf kewmsewgvd matpsstrry lpedpevrdm ykygsnvggi
hylymisgmk
      421 vereetekfw slveyyhdil lashsngdqt vglgtlmldv ivdkknvdkl
irdeylyqkr
      481 ggvimsnagy fhqdpaqayh vtdlvfgqrp galkfsfgvn vvstniggmn
lnvgmvrrtl
      541 rdraefrefi gildrvirdf tgln
```

SEQ ID NO:75
GI:367002213, Protein name: hypothetical protein TPHA_0E03170 [Tetrapisispora phaffii CBS 4417]

```
       1 mslealsfde ykpyiteeli ergharrmgh lqdyfaiiqr qklynnfniy celnekvnkv
       61 qlshafremf lqypalieyi vpkfypkhea yyrseeylsk pcpihdyirv
lnevnindii
      121 mneqdeyksi ttkisdifvk ndykfsneis emvstikiai cdpkkpnwri
iclpsktsst
      181 ewkdfilvsn hfdsdgtsav nffedltnil skqanvendt ivigndinii
nyskdyklis
      241 klpipiteri sytptlssip kfivgnickt klqytsdggd tpaefvsedp
ltydylinfs
      301 seevakmkkt iknclynsvt ltpfiqacff vamykynkil nlnnwwqwgv
dcalatnarr
      361 llpddpetrd lyrygsnvgg thyfnlisqf ninefeydkf fklvdyyhkn
yqnsyrngde
      421 lvgfgvlfsd liinntnmdk tikddytnhk rggllfsnvg yrnedltkkv
hvnniifsqs
      481 pgcmkftfgl nlistdkcgm nilmngvrgs vksrenfedf crffrktven fakl
```

SEQ ID NO:76
GI:366987729, Protein name: hypothetical protein NCAS_0A06920 [Naumovozyma castellii CBS 4309]

```
       1 mtqdqvtlde ykpyiadeli ergharrmgh lenyfallqr qklytnfsiy
gelnkevkdv
       61 dltralrsii fknpilahti vpkkypdqep fyqseeylna pypehdfikv
lpklslsdil
      121 ineqeefrei vddiltqfke angvitpdim kavayviipi cdpsrpnwrl
frlsptkffy
      181 isnhctsdai sgvnifqdic telsqndeep frddlqifny eedwesfhki
yipitdiiey
      241 rpaltslpki iasalvkgfl nyrnwptelt stndkgipfd fniitftnde
vnsiretvkk
```

```
      301 ynctftpflq acwfvamfnn gkifhmdswr ewgldvaips nsrrfladee
lkdiykygsn
      361 vgglhythli ssfniqldek ekfwdlvqyy qdgytksyen gdhfsglgll
mmdglvkrqn
      421 idkvissdyl hktragvlfs nagffpqdrt qayhvndllf tqsqgamkfs
fglniattni
      481 ggmniainva qgtfddeegi idlsqdfyrn iksfsnia
```

SEQ ID NO:77
GI:372463540, Protein name: hypothetical protein KAFR_0D01730 [Kazachstania africana CBS 2517]

```
        1 mglstkvees vrevqsqsda ssialledpv aeydipqeli drgharrmgh
lenyfamlqr
       61 qelysnfavy lkmnksvsrn dlkhalrevi lensvlahti vpkyypdhea
fyksekylnv
      121 pypkhdfmki lpslsledii indqseytev vnsiidqfvk dngkitnkls
eivsnicipi
      181 ydqsrpnwrl lclpdntdey snfvyisnhc csdgtsginl fqdlvkslng
kkspemtspd
      241 sliynyekdf dkisklpaai tdrvdyrpal wklpqfmlst lgkvffsyks
papvstkinm
      301 skpqpsfhni lnftpdelnk iriaikknac tmtsflqtcl fitlkehgif
anrkwnefgf
      361 ditvpsntrk dlpeelvtsq ykygsnvggl hysflissfi aenfwklcsy
ysavlkqadf
      421 lrplgtimld fvvnkqnids misdsylnkk rggiilsnvg yfeqnddece
ildlmlmqnv
      481 gglnfsyavn icstnlggmn iclsivegtl kdrddfnafc delkttvrqf cdin
```

SEQ ID NO:78
GI:26991090, Protein name: bkdA1 gene product [Pseudomonas putida KT2440]

```
        1 mneyaplrlh vpeptgrpgc qtdfsylrln dagqarkpai dvdaadtadl
syslvrvlde
       61 qgdaqgpwae didpqilrqg mramlktrif dsrmvvaqrq kkmsfymqsl
geeaigsgqa
      121 lalnrtdmcf ptyrqqsilm ardvslvemi cqllsnerdp lkgrqlpimy
svreagffti
      181 sgnlatqfvq avgwamasai kgdtkiasaw igdgataesd fhtaltfahv
yrapvilnvv
      241 nnqwaistfq aiaggesttf agrgvgcgia slrvdgndfv avyaasrwaa
erarrglgps
      301 liewvtyrag phstsddpsk yrpaddwshf plgdpiarlk qhlikighws
eeehqavtae
      361 leaaviaaqk eaeqygtlan ghipsaasmf edvykempdh lrrqrqelgv
```

SEQ ID NO:79
GI:26991091, Protein name: bkdA2 gene product [Pseudomonas putida KT2440]

```
        1 matttmtmiq alrsamdvml erddnvvvyg qdvgyfggvf rcteglqnky
gksrvfdapi
```

```
       61 sesgivgtav gmgayglrpv veiqfadyfy pasdqivsel arlryrsage
fiapltlrmp
      121 cgggiyggqt hsqspeamft qvcglrtvmp snpydakgll iasiecddpv
iflepkrlyn
      181 gpfdghhdrp vtpwskhphs avpdgyytvp ldkaaitrpg ndvtvltygt
tvyvaqvaae
      241 esgvdaevid lrslwpldld tivesvkktg rcvvvheatr tcgfgaelvs
lvqehcfhhl
      301 eapiervtgw dtpyphaqew ayfpgpsrvg aalkkvmev
```

SEQ ID NO:80
GI:26991092, Protein name: bkdB gene product [Pseudomonas putida KT2440]

```
        1 mgthvikmpd igegiaqvel vewfvkvgdi iaedqvvadv mtdkatveip
spvsgkvlal
       61 ggqpgevmav gselirieve gsgnhvdvpq pkpveapaap iaakpepqkd
vkpavyqapa
      121 nheaapivpr qpgdkplasp avrkraldag ielryvhgsg pagrilhedl
dafmskpqsn
      181 agqapdgyak rtdseqvpvi glrrkiaqrm qdakrrvahf syveeidvta
lealrqqlns
      241 khgdsrgklt llpflvralv valrdfpqin atyddeaqii trhgavhvgi
atqgdnglmv
      301 pvlrhaeags lwanageisr lanaarnnka sreelsgsti tltslgalgg
ivstpvvntp
      361 evaivgvnrm verpvvidgq ivvrkmmnls ssfdhrvvdg mdaalfiqav
rglleqpacl
      421 fve
```

SEQ ID NO:81

gaaaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGCGCATGATCAGAGCCT

SEQ ID NO:82

agcctttcgttttatttgatgcctctagaGCTCAGCTTACAGGCTGCTCTGGGTGAAATG

SEQ ID NO:83

cgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGAATGAAATCGATGAGAAAAAT
C

SEQ ID NO:84

agcctttcgttttatttgatgcctctagaGCTCAGCTTAAGGGCCTAAAAGGAGAGCTTT

SEQ ID NO:85
cgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGAAGATATAGAAGGATACGA
AC

SEQ ID NO:86
cctttcgttttatttgatgcctctagaGCTCAGCTTAAAGCGACGCAAATTCGCCGATGG

SEQ ID NO:87
aaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGACAGCAAACAGAGCAGC
G

SEQ ID NO:88
cctttcgttttatttgatgcctctagaGCTCAGCTTAAAGCGCTGGGGTGATGAACGCAT

SEQ ID NO:89
aaacgaaagctctctaaGCTGAGCAGGAGAAATTAACTATGGAGAAAATAGAAGTGAGC
A

SEQ ID NO:90
cctttcgttttatttgatgcctctagaGCTCAGCTTAGATCAGCGTCTTTGGACTCGCCA

SEQ ID NO:91
GGGCCCgcatgcAGGAGAAATTAACTATGAACAACTTTAATCTGCACACCCC

SEQ ID NO:92
GGGCCCtctagaTTAGCGGGCGGCTTCGTATATACGGC

What is claimed is:

1. A recombinant cell modified to exhibit increased biosynthesis of an ester compared to a wild-type control.

2. The recombinant microbial cell of claim 1 wherein the microbial cell is a fungal cell.

3. The recombinant cell of claim 2 wherein the fungal cell is a member of the Saccharomycetaceae family.

4. The recombinant cell of claim 2 wherein the fungal cell is *Saccharomyces cerevisiae*, *Candida rugosa*, or *Candida albicans*.

5. The recombinant cell of claim 1 wherein the microbial cell is a bacterial cell.

6. The recombinant cell of claim 5 wherein the bacterial cell is a member of the phylum Protobacteria.

7. The recombinant cell of claim 6 wherein the bacterial cell is a member of the Enterobacteriaceae family.

8. The recombinant cell of claim 7 wherein the bacterial cell is *Escherichia coli*.

9. The recombinant cell of claim 6 wherein the bacterial cell is a member of the Pseudomonaceae family.

10. The recombinant cell of claim 9 wherein the bacterial cell is *Pseudomonas putida*.

11. The recombinant cell of claim 5 wherein the bacterial cell is a member of the phylum Firmicutes.

12. The recombinant cell of claim 11 wherein the bacterial cell is a member of the Bacillaceae family.

13. The recombinant cell of claim 12 wherein the bacterial cell is *Bacillus subtilis*.

14. The recombinant cell of claim 11 wherein the bacterial cell is a member of the Streptococcaceae family.

15. The recombinant cell of claim 14 wherein the bacterial cell is *Lactococcus lactis*.

16. The recombinant cell of claim 11 wherein the bacterial cell is a member of the Clostridiaceae family.

17. The recombinant cell of claim 16 wherein the bacterial cell is *Clostridium cellulolyticum*.

18. The recombinant cell of claim 5 wherein the bacterial cell is a member of the phylum Cyanobacteria.

19. The recombinant cell of any preceding claim wherein the microbial cell is photosynthetic.

20. The recombinant cell of any preceding claim wherein the microbial cell is cellulolytic.

21. The recombinant cell of any preceeding claim wherein the increased biosynthesis of an ester compared to a wild-type control comprises an increase in production of isobutyl isobutyrate, isovaleryl isovalerate, isobutyl acetate, or isoamyl acetate.

22. The recombinant cell of any preceeding claim wherein the increased biosynthesis of an ester compared to a wild-type control comprises an increase in conversion of an organic acid to an acyl-CoA compared to a wild-type control, an increase in conversion of ketoacids

to an acyl-CoA compared to a wild-type control, an increase in conversion of an aldehyde to an organic acid compared to a wild-type control, an increase in conversion of an aldehyde to an alcohol compared to a wild-type control, or an increase in combining an acyl-CoA with an alcohol to form an ester compared to a wild-type control.

23. The recombinant cell of any one of claims 1-21 wherein the increased biosynthesis of an ester compared to a wild-type control comprises an increase in conversion of 2-ketoisovalerate to isobutyraldehyde, and increase in conversion of isobutyraldehyde to isobutanol, an increase in synthesis of isobutyl acetate from isobutanol and an acyl-CoA, an increase in elongation of 2-ketoisovalerate to 2-keto-4-methylvalerate, an increase in conversion of 2-keto-4-methylvalerate to isovaleraldehyde, an increase in conversion of isovaleraldehyde to isopenatanol, or an increase in synthesis of isoamyl acetate from isopentanol and an acyl-CoA.

24. The recombinant cell of any preceding claim comprising an acyl transferase modified to increase synthesis of a desired ester.

25. The recombinant cell of claim 24 wherein the modified acyl transferase increases synthesis of an ester having more carbons than is produced by the acyl transferase prior to being modified.

26. A method comprising:

incubating a recombinant cell of any one of claims 1-22 in medium that comprises a carbon source under conditions effective for the recombinant cell to produce an ester, wherein the carbon source comprises one or more of: glucose, pyruvate, ketovaline, CO_2, cellulose, xylose, sucrose, arabinose, glycerol, alginate, glucarate, or galacturonate.

27. The method of claim 26 wherein the medium further comprises a carboxylic acid.

28. The method of claim 26 wherein the medium further comprises an alcohol.

29. A method comprising:

introducing into a host cell a heterologous polynucleotide encoding at least one polypeptide that catalyzes a step in converting a carbon source to an ester, wherein the at least one polynucleotide is operably linked to a promoter so that the modified host cell catalyzes conversion of the carbon source to an ester.

30. The method of claim 29 wherein the carbon source comprises one or more of: glucose, pyruvate, ketovaline, CO_2, cellulose, xylose, sucrose, arabinose, glycerol, alginate, glucarate, or galacturonate.

31. The method of claim 29 or claim 30 wherein the host cell is a fungal cell.

32. The method of claim 28 wherein the fungal cell is a member of the Saccharomycetaceae family.

33. The method of claim 32 wherein the fungal cell is *Saccharomyces cerevisiae*, *Candida rugosa*, or *Candida albicans*.

34. The method of any one of claim 29 or claim 27 wherein the host cell is a bacterial cell.

35. The method of claim 34 wherein the bacterial cell is a member of the phylum Protobacteria.

36. The method of claim 35 wherein the bacterial cell is a member of the Enterobacteriaceae family.

37. The method of claim 36 wherein the bacterial cell is *Escherichia coli*.

38. The method of claim 34 wherein the bacterial cell is a member of the Pseudomonaceae family.

39. The method of claim 38 wherein the bacterial cell is *Pseudomonas putida*.

40. The method of claim 34 wherein the bacterial cell is a member of the phylum Firmicutes.

41. The method of claim 40 wherein the bacterial cell is a member of the Bacillaceae family.

42. The method of claim 41 wherein the bacterial cell is *Bacillus subtilis*.

43. The method of claim 40 wherein the bacterial cell is a member of the Streptococcaceae family.

44. The method of claim 43 wherein the bacterial cell is *Lactococcus lactis*.

45. The method of claim 40 wherein the bacterial cell is a member of the Clostridiaceae family.

46. The method of claim 45 wherein the bacterial cell is *Clostridium cellulolyticum*.

47. The method of claim 34 wherein the bacterial cell is a member of the phylum Cyanobacteria.

48. The method of any one of claims 23-47 wherein the host cell is photosynthetic.

49. The method of any one of claims 23-47 wherein the host cell is cellulolytic.