Biotechnological synthesis process of organic compounds with the aid of an alkL gene product

Field of the invention

Subject matter of the invention is a biotechnological process for the production of organic compounds with the aid of at least one alkL gene product.

Prior art

Fatty acids and their derivatives are currently obtained exclusively from vegetable and animal oils or fats. This has a number of disadvantages:
As a consequence of the BSE crisis, animal fats in particular are virtually no longer accepted by the customer as raw materials. Vegetable oils which contain short- and medium-chain fatty acids are either not readily available or are produced in tropical regions. Here, the sustainability of the production is open to question in many cases because it may be the case that rainforest is destroyed so as to make the cropping areas available.
Furthermore, vegetable and animal oils and fats have fatty acid spectra which are specific for the raw material in question, but fixed. The consequence is a coupled production, which may determine the price of a particular fatty acid species. Finally, many of the vegetable oils are simultaneously also foodstuffs so that, under certain circumstances, competition may emerge between the use as a feed stock substance and the use as a foodstuff.

This is why there is a search for alternative sources and production pathways for fatty acids, and, as a result, a great deal of research effort is currently being invested into the production of fatty acids in, for example, algae, but also in particular in recombinant microorganisms such as, for example, yeasts and bacteria.

Although a series of technologies are being developed for the production of fatty-acid-based fuels and chemicals from renewable raw materials, in particular carbohydrates, the yields achieved are too low for a meaningful commercial utilization.

The problem of the invention was to provide a more productive biological process for the production of organic compounds.

Description of the invention

Surprisingly, it has been found that the coexpression of an alkL gene product in the producing microorganism, which coexpression is described hereinbelow, is capable of solving the problem of the invention.

Subject matter of the present invention, therefore, are microorganisms which synthesize organic substances and which express alkL at a higher level.

A further subject matter of the invention is the use of the abovementioned microorganisms for the production of organic substances, and a process for producing organic substances using the microorganisms.

An advantage of the present invention is that the product inhibition in the production process can be reduced greatly.

A further advantage is that the space-time yield and the carbon yield of the process are increased in comparison with microorganisms which express no, or less, alkL.

Yet another advantage of the present invention is that the product concentration in the culture supernatant is increased so as to facilitate efficient work-up.

Unless otherwise specified, all percentages stated (%) are percent by mass.

The invention comprises methods for generating recombinant microbial cells which are capable of producing organic substances, such as carboxylic acids and carboxylic acid derivatives, such as, for example, carboxylic acid esters, alkanes, alkan-1-ols, alkan-1-als, alkan-1-amines and 1-alkenes, from unrelated carbon sources.

The present invention therefore comprises a microorganism which includes a first genetic modification so that it is capable of forming more organic substance from at least one simple carbon source in comparison with its wild type, characterized in that the microorganism includes a second genetic modification so that it forms more alkL gene product in comparison with its wild type.

In the context of the present invention, the expression "first genetic modification" is understood as meaning at least one genetic modification of the microorganism in which one or more genes have been modified, i.e. increased or reduced, in their expression in comparison with the wild-type strain.

In the context of the present invention, the expression "simple carbon source" is understood as meaning carbon sources in which, in the carbon skeleton, at least one C-C bond must be broken and/or at least one carbon atom of the simple carbon source must form at least one new bond with at least one carbon atom of another molecule so as to arrive at the carbon skeleton of the "organic substance of which more is formed".

In the context of the present invention, the expression "alkL gene product" is understood as meaning proteins which meet at least one of the following two conditions:

1.) the protein is identified as a member of the superfamily of the OmpW proteins (Protein family 3922 in the Conserved Domain Database (CDD) of the National Centre for Biotechnology Information (NCBI)), this assignment being made by an alignment of the amino acid sequence of the protein with the database entries present in the NCBI CDD that had been deposited by 22.03.2010, using the standard search parameters, an E value less than 0.01 and using the algorithm "blastp 2.2.23+",

2.) in a search for conserved protein domains contained in the amino acid sequence of interest in the NCBI CDD (Version 2.20) by means of RPS-BLAST, the presence of the conserved domain "OmpW, Outer membrane protein W" (COG3047) with an E value less than 1×10^{-5} is obtained (a domain hit).

Preferred organic substances of the present invention are those which have more than one, in particular 3 to 36, preferably 6 to 24, in particular 10 to 18 carbon atoms. The organic substances may be linear, branched, saturated or unsaturated and optionally substituted by other groups.

It is preferred in accordance with the invention that the organic substance is selected from the group comprising, preferably consisting of,

carboxylic acids, in particular having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,

carboxylic acid esters, in particular having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms in the carboxylic acid moiety, in which the alcohol

component is derived from methanol, ethanol or other primary alcohols having 3-18 carbon atoms, in particular from methanol and ethanol,
alkanes having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,
alkenes having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,
monohydric alcohols having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,
aldehydes having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,
monovalent amines having 3 to 34, preferably having 6 to 22, especially preferably having 6 to 18, carbon atoms,
and substituted compounds of the above group members, in particular those which carry, as further substituents, one or more hydroxyl, amine, keto, carboxyl, methyl, ethyl, cyclopropyl or epoxy functions, with unsubstituted ones being preferred.
Especially preferred are the organic substances fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alkanes and alkenes, in particular 1-alkenes, where the esters in the abovementioned compounds are preferably those in which the alcohol component is derived from methanol, ethanol or other primary alcohols having 3-18 carbon atoms, in particular from methanol and ethanol.
The organic substances are especially preferably selected from among fatty acids and fatty acid esters in which the fatty acid component is selected from the group consisting of formic acid, acetic acid, propionic acid, butyric acid, valeric acid, caproic acid, oenanthic acid, caprylic acid, pelargonic acid, capric acid, lauric acid, myristic acid, pentadecanoic acid, palmitic acid, margaric acid, stearic acid, nonadecanoic acid, arachidic acid, behenic acid, lignoceric acid, cerotic acid, montanic acid, melissic acid, undecylenic acid, myristoleic acid, palmitoleic acid, petroselic acid, oleic acid, elaidic acid, vaccenic acid, gadoleic acid, eicosenoic acid, cetoleic acid, erucic acid, nervonic acid, pelargonic acid, linoleic acid, α-linolenic acid, γ-linolenic acid, calendulic acid, punicic acid, α-elaeostearic acid, β-elaeostearic acid, arachidonic acid, timnodonic acid, clupanodonic acid, cervonic acid, vernolic acid, ricinoleic acid
and

their derivatives in the form of corresponding alkan-1-als, alkan-1-ols, alkan-1-amines and, in the case of unsaturated fatty acids, such as, for example, palmitoleic acid, oleic acid, linoleic acid, α-linolenic acid, γ-linolenic acid, also alken-1-als, alken-1-ols, alken-1-amines, and alkanes and alkenes prepared from the abovementioned fatty acids by enzymatic reduction and decarbonylation, and alkenes, in particular 1-alkenes, prepared from the abovementioned fatty acids by enzymatic decarboxylation, if appropriate having further, nonterminal double bonds. In this context, the expression "corresponding alkane/alkene-1 compounds" is understood as meaning that the carboxyl group of the fatty acid in question is replaced by a -COH, a $-CH_2OH$ or a $-CH_2NH_2$.

If, in the context of the present invention, the following text will describe enzymatic activities which catalyse reactions in which alkanoic acids, alkan-1-als, alkan-1-ols or alkan-1-amines are involved either directly or indirectly, it shall be assumed that alkanoic acids, alkan-1-als, alkan-1-ols or alkan-1-amines which additionally have one or more nonterminal double bonds are, as a rule, included in the abovementioned enzymatic activity.

Carbohydrates such as, for example, glucose, sucrose, arabinose, xylose, lactose, fructose, maltose, molasses, starch, cellulose and hemicellulose, but also glycerol or very simple organic molecules such as CO_2, CO or synthesis gas may be employed as the carbon source.

It is preferred in accordance with the invention that, owing to the good genetic accessibility, microorganisms are employed which are selected from the group of the bacteria, especially from the group containing, preferably consisting of, *Magnetococcus, Mariprofundus, Acetobacter, Acidiphilium, Afipia, Ahrensia, Asticcacaulis, Aurantimonas, Azorhizobium, Azospirillum, Bartonella, tribocorum, Beijerinckia, Bradyrhizobium, Brevundimonas, subvibrioides, Brucella, Caulobacter, Chelativorans, Citreicella, Citromicrobium, Dinoroseobacter, Erythrobacter, Fulvimarina, Gluconacetobacter, Granulibacter, Hirschia, Hoeflea, Hyphomicrobium, Hyphomonas, Ketogulonicigenium, Labrenzia, Loktanella, Magnetospirillum, Maricaulis, Maritimibacter, Mesorhizobium, Methylobacterium, Methylocystis, Methylosinus, Nitrobacter, Novosphingobium, Oceanibulbus, Oceanicaulis, Oceanicola, Ochrobactrum, Octadecabacter, Oligotropha, Paracoccus, Parvibaculum, Parvularcula, Pelagibaca, Phaeobacter, Phenylobacterium, Polymorphum, Pseudovibrio, Rhodobacter, Rhodomicrobium, Rhodopseudomonas, Rhodospirillum, Roseibium, Roseobacter,*

Roseomonas, Roseovarius, Ruegeria, Sagittula, Silicibacter, Sphingobium, Sphingomonas, Sphingopyxis, Starkeya, Sulfitobacter, Thalassiobium, Xanthobacter, Zymomonas, Agrobacterium, Rhizobium, Sinorhizobium, Anaplasma, Ehrlichia, Neorickettsia, Orientia, Rickettsia, Wolbachia, Bordetella, Burkholderia, Cupriavidus, taiwanensis, Lautropia, Limnobacter, Polynucleobacter, Ralstonia, Chromobacterium, Eikenella, corrodens, Basfia, Kingella, Laribacter, Lutiella, Neisseria, Simonsiella, Achromobacter, Acidovorax, Alicycliphilus, Aromatoleum, Azoarcus, Comamonas, Dechloromonas, Delftia, Gallionella, Herbaspirillum, Herminiimonas, Hylemonella, Janthinobacterium, Leptothrix, Methylibium, Methylobacillus, Methylophilales, Methyloversatilis, Methylovorus, Nitrosomonas, Nitrosospira, Oxalobacter, Parasutterella, Polaromonas, Polaromonas, Pusillimonas, Rhodoferax, Rubrivivax, Sideroxydans, Sutterella, wadsworthensis, Taylorella, Thauera, Thiobacillus, Thiomonas, Variovorax, Verminephrobacter, Anaeromyxobacter, Bdellovibrio, bacteriovorus, Bilophila, Desulfarculus, Desulfatibacillum, Desulfobacca, Desulfobacterium, Desulfobulbus, Desulfococcus, Desulfohalobium, Desulfitobacterium, Desulfomicrobium, Desulfonatronospira, Desulfotalea, Desulfovibrio, Desulfuromonas, Geobacter, Haliangium, Hippea, Lawsonia, Myxococcus, Pelobacter, Plesiocystis, Sorangium, Stigmatella, Syntrophobacter, Syntrophus, Arcobacter, Caminibacter, Campylobacter, Helicobacter, Nitratifractor, Nitratiruptor, Sulfuricurvum, Sulfurimonas, Sulfurospirillum, Sulfurovum, Wolinella, Buchnera, Blochmannia, Hamiltonella, Regiella, Riesia, Citrobacter, Cronobacter, Dickeya, Edwardsiella, Enterobacter, Erwinia, Escherichia, Klebsiella, Pantoea, Pectobacterium, Proteus, Providencia, Rahnella, Salmonella, Serratia, Shigella, Sodalis, Wigglesworthia, Glossina, Xenorhabdus, Yersinia, Acidithiobacillus, Acinetobacter, Aeromonas, Alcanivorax, Alkalilimnicola, Allochromatium, Alteromonadales, Alteromonas, Baumannia, Beggiatoa, Bermanella, Carsonella, Ruthia, Vesicomyosocius, Cardiobacterium, Chromohalobacter, Colwellia, Congregibacter, Coxiella, Dichelobacter, Endoriftia, Enhydrobacter, Ferrimonas, Francisella, Glaciecola, Hahella, Halomonas, Halorhodospira, Halothiobacillus, Idiomarina, Kangiella, Legionella, Marinobacter, Marinomonas, Methylobacter, Methylococcus, Methylomicrobium, Methylophaga, Moraxella, Moritella, Neptuniibacter, Nitrococcus, Pseudoalteromonas, Psychrobacter, Psychromonas, Reinekea, Rickettsiella, Saccharophagus, Shewanella, Succinatimonas, Teredinibacter, Thioalkalimicrobium, Thioalkalivibrio, Thiomicrospira, Tolumonas, Vibrionales, Actinobacillus, Aggregatibacter, Gallibacterium, Haemophilus, Histophilus, Mannheimia, Pasteurella, Azotobacter, Cellvibrio, Pseudomonas, Aliivibrio, Grimontia, Photobacterium, Photobacterium,

Vibrio, Pseudoxanthomonas, Stenotrophomonas, Xanthomonas, Xylella, Borrelia, Brachyspira, Leptospira, Spirochaeta, Treponema, Hodgkinia, Puniceispirillum, Liberibacter, Pelagibacter, Odyssella, Accumulibacter, in particular
E. coli, *Pseudomonas sp.*, *Pseudomonas fluorescens*, *Pseudomonas putida*, *Pseudomonas stutzeri*,, *Acinetobacter* sp., *Burkholderia* sp., *Burkholderia thailandensis*, cyanobacteria, *Klebsiella* sp., *Klebsiella oxytoca*, *Salmonella sp.*, *Rhizobium sp.* and *Rhizobium meliloti*, with *E. coli* being especially preferred.

Preferred alkL gene products which are present in the microorganisms according to the invention are characterized in that the production of the alkL gene product in the native host is induced by dicyclopropyl ketone; in this context, it is additionally preferred that the alkL gene is expressed as part of a group of genes, for example in a regulon, such as, for example, in an operon.

alkL gene products which are present in the microorganisms according to the invention are preferably encoded by alkL genes of organisms selected from the group of the Gram-negative bacteria, in particular the group containing, preferably consisting of, *Pseudomonas* sp., *Azotobacter* sp., *Desulfitobacterium* sp., *Burkholderia* sp., preferably *Burkholderia cepacia*, *Xanthomonas* sp., *Rhodobacter* sp., *Ralstonia* sp., *Delftia* sp. and *Rickettsia* sp., *Oceanicaulis* sp., *Caulobacter* sp., *Marinobacter* sp. and *Rhodopseudomonas* sp., preferably *Pseudomonas putida*, *Oceanicaulis alexandrii*, *Marinobacter aquaeolei*, in particular *Pseudomonas putida* GPo1 and P1, *Oceanicaulis alexandrii* HTCC2633, *Caulobacter* sp. K31 and *Marinobacter aquaeolei* VT8.

In this context, very especially preferred alkL gene products are encoded by the alkL genes from *Pseudomonas putida* GPo1 and P1, which are shown by SEQ ID No. 1 and SEQ ID No. 29, and proteins with the polypeptide sequence SEQ ID No. 2, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33 or with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, particularly up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33 by deletion, insertion, substitution or a combination thereof and which products still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90% of the activity of the protein with the respective reference sequence

SEQ ID No. 2, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, more precisely in a system as described in the exemplary embodiments, in which system glucose is reacted in an *E. coli* cell to give palmitoleic acid. A method of choice for determining the synthesis rate can be found in the exemplary embodiments.

The definition of the units here is the definition customary in enzyme kinetics: 1 unit of biocatalyst reacts 1 µmol of substrate in one minute to form the product.

1 U = 1 µmol/min

Modifications of amino acid residues of a given polypeptide sequence that do not lead to any substantial changes of the properties and function of the given polypeptide are known to the skilled worker. For instance, some amino acids, for example, can frequently be exchanged for one another without problem; examples of such suitable amino acid substitutions are: Ala for Ser; Arg for Lys; Asn for Gln or His; Asp for Glu; Cys for Ser; Gln for Asn; Glu for Asp; Gly for Pro; His for Asn or Gln; Ile for Leu or Val; Leu for Met or Val; Lys for Arg or Gln or Glu; Met for Leu or Ile; Phe for Met or Leu or Tyr; Ser for Thr; Thr for Ser; Trp for Tyr; Tyr for Trp or Phe; Val for Ile or Leu. Likewise, it is known that modifications, especially at the N- or C-terminus of a polypeptide in the form of, for example, amino acid insertions or deletions, will frequently have no substantial effect on the function of the polypeptide.

First genetic modification for the synthesis of carboxylic acids, carboxylic acid esters and other carboxylic acid derivatives from a simple carbon source

According to the invention, the microorganisms include a first genetic modification so that they are capable of forming more organic substance, in particular carboxylic acids and carboxylic acid derivatives, from at least one simple carbon source in comparison with their wild type.

In this context, it is preferred in accordance with the invention that the first genetic modification is an activity of at least one of the enzymes selected from the group

E_i acyl-ACP (Acyl Carrier Protein) thioesterase, preferably from EC 3.1.2.14 or EC 3.1.2.22, which catalyses the hydrolysis of an acyl-acyl carrier protein thioester,

E_{ii} acyl-CoA (Coenzyme A) thioesterase, preferably from EC 3.1.2.2, EC 3.1.2.18, EC 3.1.2.19, EC 3.1.2.20 or EC 3.1.2.22, which catalyses the hydrolysis of an acyl-coenzyme A thioester,

E_{iib} acyl-CoA (Coenzyme A): ACP (Acyl Carrier Protein) transacylase, which preferably catalyses a reaction in which a CoA thioester is converted into an ACP thioester,

E_{iii} polyketide synthase, which catalyses a reaction which participates in the synthesis of carboxylic acids and carboxylic acid esters, and

E_{iv} hexanoic acid synthase, a specialized fatty acid synthase of the FAS-I type, which catalyses the synthesis of hexanoic acid from two molecules malonyl-coenzyme A and one molecule acetyl-coenzyme A

which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

What will now be said on increasing the enzymatic activity in cells applies not only to the increase of the activity of the enzyme E_i to E_{iv}, but also to all of the enzymes mentioned thereafter, whose activity may optionally be increased, and to an increased alkL gene product formation.

The expression "increased activity of an enzyme" as used hereinabove and in what will be said hereinbelow in the context of the present invention is preferably understood as meaning an increased intracellular activity; this statement also applies to an increased alkl gene product formation.

In principle, an increase of the enzymatic activity can be achieved by increasing the number of copies of the gene sequence or of the gene sequences which encode the enzyme, using a strong promoter, modifying the codon usage of the gene, increasing in various ways the half-life of the mRNA or of the enzyme, modifying the regulation of expression of the gene or using a gene or allele which encodes a corresponding enzyme with an increased activity, and optionally combining these measures. Microorganisms which are genetically modified in accordance with the invention are generated for example by transformation, transduction, conjugation or a

combination of these methods using a vector which contains the desired gene, an allele of this gene or parts thereof, and a promoter which makes possible the expression of the gene. Heterologous expression is made possible, in particular, by integrating the gene or the alleles into the chromosome of the cell or a vector which replicates extrachromosomally.

An overview over the possibilities of increasing the enzymatic activity in cells with pyruvate carboxylase as example can be found in DE-A-100 31 999, which is herewith incorporated by reference and whose disclosure regarding the possibilities of increasing the enzymatic activity in cells forms part of the disclosure of the present invention.

The expression of the abovementioned, and all hereinafter mentioned, enzymes and/or genes can be detected in the gel with the aid of one- and two-dimensional protein gel separation followed by optical identification of the protein concentration using suitable evaluation software. If the increase of an enzymatic activity is based exclusively on an increase of the expression of the gene in question, the quantification of the increase of the enzymatic activity can be determined in a simple manner by a comparison of the one- or two-dimensional protein separations between the wild type and the genetically modified cell. A customary method for preparing the protein gels in the case of bacteria and for identifying the proteins is the procedure described by Hermann et al. (Electrophoresis, 22: 1712-23 (2001). The protein concentration can likewise be analysed by Western blot hybridization with an antibody which is specific for the protein to be detected (Sambrook et al., Molecular Cloning: a laboratory manual, 2nd Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. USA, 1989) followed by optical evaluation with suitable software for determining the concentration (Lohaus and Meyer (1989) Biospektrum, 5: 32-39; Lottspeich (1999), Angewandte Chemie 111: 2630-2647). This is also always the method of choice when potential products of the reaction catalysed by the enzymatic activity to be determined can be metabolized rapidly in the microorganism or else when the activity in the wild type itself is too low to be able to sufficiently determine the enzymatic activity to be determined with the aid of the product formation.

Using the above-described methods, it can also be determined whether an observed microorganism forms more alkL gene product in comparison with its wild type.

The accession numbers mentioned in the context of the present invention correspond to the ProteinBank database entries of the NCBI dated 26.07.2011; as a rule, the version number of the entry is identified here by ".number", such as, for example, ".1".

Specific enzymes E_i

The reaction catalysed by E_i differs from the reaction catalysed by E_{ii} only in that an acyl-coenzyme A thioester is hydrolyse in place of an acyl-acyl carrier protein thioester. It is obvious that many of the enzymes E_i mentioned can, due to the significant secondary activity, also be employed as E_{ii}, and vice versa.

In cells which are preferred in accordance with the invention, the enzyme E_i is an enzyme which comprises sequences selected from among:
AAC72881.1, ABB71579.1, CAC19934.1, AAC49180.1 (encoded by SEQ ID No.: 10), AAC49783.1, AAC49179.1, CAB60830.1, ABB71581.1, AAC49269.1, CAC19933.1, CAA54060.1, AAC72882.1, Q39513.1, AAC49784.1, ABO38558.1, ABO38555.1, ABO38556.1, ABO38554.1, ADB79568.1, ADB79569.1, ACQ57188.1, ACQ57189.1, ABK96561.1, ACQ63293.1, ACQ57190.1, Q9SQI3.1, ABU96744.1, ABC47311.1, XP_002324962.1, AAD01982.1, AAB51525.1, ACV40757.1, XP_002309244.1, CBI28125.3, ABD91726.1, XP_002284850.1, XP_002309243.1, XP_002515564.1, ACR56792.1, ACR56793.1, XP_002892461.1, ABI18986.1, NP_172327.1, CAA85387.1, CAA85388.1, ADA79524.1, ACR56795.1, ACR56794.1, CAN81819.1, ACF17654.1, AAB71729.1, ABH11710.1, ACQ57187.1, AAX51637.1, AAB88824.1, AAQ08202.1, AAB71731.1, AAX51636.1, CAC80370.1, CAC80371.1, AAG43858.1, ABD83939.1, AAD42220.2, AAG43860.1, AAG43861.1, AAG43857.1, AAL15645.1, AAB71730.1, NP_001068400.1, EAY86877.1, NP_001056776.1, XP_002436457.1, NP_001149963.1, ACN27901.1, EAY99617.1, ABL85052.1, XP_002437226.1, NP_001151366.1, ACF88154.1, NP_001147887.1, XP_002453522.1, BAJ99650.1, EAZ37535.1, EAZ01545.1, AAN17328.1, EAY86884.1, EEE57469.1, Q41635.1, AAM09524.1, Q39473.1, NP_001057985.1, AAC49001.1, XP_001752161.1, XP_001770108.1, XP_001784994.1, XP_002318751.1, NP_001047567.1, XP_002322277.1, XP_002299627.1, XP_002511148.1, CBI15695.3, XP_002299629.1, XP_002280321.1, CAN60643.1, XP_002459731.1, XP_002975500.1, XP_002962077.1, XP_001773771.1, NP_001151014.1, XP_002317894.1, XP_002971008.1, XP_001774723.1, XP_002280147.1, XP_002526311.1, XP_002517525.1, XP_001764527.1, ABI20759.1,

BAD73184.1, XP_002987091.1, XP_002985480.1, CBI26947.3, ABI20760.1, XP_002303055.1, XP_002885681.1, ADH03021.1, XP_002532744.1, EAY74210.1, EEC84846.1, EEE54649.1, AAG35064.1, AAC49002.1, CAD32683.1, ACF78226.1, BAJ96402.1, XP_002462626.1, NP_001130099.1, XP_002462625.1, ABX82799.3, Q42712.1, NP_193041.1, AAB51524.1, NP_189147.1, ABR18461.1, XP_002863277.1, AAC72883.1, AAA33019.1, CBI40881.3, XP_002262721.1, AAB51523.1, NP_001063601.1, ADB79567.1, AAL77443.1, AAL77445.1, AAQ08223.1, AAL79361.1, CAA52070.1, AAA33020.1, CAA52069.1, XP_001785304.1, CAC39106.1, XP_002992591.1, XP_002968049.1, XP_001770737.1, XP_001752563.1, AAG43859.1, XP_002978911.1, XP_002977790.1, ACB29661.1, XP_002314829.1, XP_002991471.1, EAZ45287.1, XP_002986974.1, EEC73687.1, XP_002312421.1, ACJ84621.1, NP_001150707.1, AAD28187.1, XP_001759159.1, XP_001757193.1, XP_002322077.1, ABE01139.1, XP_002447294.1, AAX54515.1, AAD33870.1, AEM72521.1

in particular

AAC72881.1, ABB71579.1, CAC19934.1, AAC49180.1 (encoded by SEQ ID No.: 10), AAC49783.1, AAC49179.1, CAB60830.1, ABB71581.1, AAC49269.1 (encoded by SEQ ID No.: 8), CAC19933.1, CAA54060.1, AAC72882.1, Q39513.1 (encoded by SEQ ID No.: 9), AAC49784.1, AAC72883.1, Q41635.1, AAC49001.1 (encoded by SEQ ID No.: 37), AEM72521.1 (encoded by SEQ ID No.: 35)

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of the dodecanoyl-ACP thioester.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow, which include a first genetic modification within the meaning of the invention, are employed as the starting point by being provided with the second genetic modification and, if appropriate, with at least one further genetic modification within the meaning of the invention.

WO2010063031 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more microbial oil from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0007] to [0008], [0092] to [0100], [0135] to [0136], [0181] to [0186] and [0204] to [0213] and in the exemplary embodiments 4 to 8. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0012] to [0013], [0155], [0160] to [0163], [0185] to [0190] and [0197] to [0199], Figure 12, the exemplary embodiments 4 to 8 and Table 3.

WO2010063032 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more microbial oil from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0007] to [0008], [0092] to [0100], [0135] to [0136], [0181] to [0186] and [0204] to [0213] and in the exemplary embodiments 4 to 8. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0012] to [0013], [0155], [0160] to [0163], [0185] to [0190] and [0197] to [0199], Figure 12, the exemplary embodiments 4 to 8 and Table 3.

WO2011003034 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular adipic acid, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 3, second section, to page 7, first section, page 20, second section, to page 22, second section, and on page 156 to page 166, fifth section, and in Claims 1 to 100. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on page 35, third section, and page 36, first section.

WO2011008565 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids, alkan-1-als, alkan-1-ols, alkanes and fatty acid esters, from at least one simple carbon source in

comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0018] to [0024] and [0086] to [0102] and in the exemplary embodiments 2, 4, 7, 9 and 10. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0009] to [0018] and [0073] to [0082], Figures 1 to 3 and 7, Table 4, the exemplary embodiments 1 to 10 and Claims 1 to 5 and 11 to 13.

WO2009076559 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids, alkan-1-ols, alkanes or alkenes, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0013] to [0051] and [0064] to [00111] and in Claims 1 to 10. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1, sections [0021], [0024] to [0030] and [0064] to [00111] and Figure 6.

WO2010017245 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0011] to [0015] and [00114] to [00134], in the exemplary embodiment 3 and in Claims 1 to 2 and 9 to 11. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Tables 1, 2 and 3, sections [0080] to [00112] and Claims 3 to 8.

WO2010127318 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular biodiesel equivalents and other fatty acid derivatives, mainly fatty acid ethyl esters, fatty acid esters, wax esters, alkan-1-ols and alkan-1-als, from at least one simple carbon source in comparison with their wild type and which are preferably employed in accordance with the invention, in particular on pages 1 to 9 and 11 to 16, exemplary embodiments 1, 2 and 4, Figures 1A to 1E and Claims 23 to 43, 62 to 79 and 101 to 120. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on pages 17, 19 to 23.

WO2008100251 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed in accordance with the invention, in particular

on pages 4 to 7 and 45 to 46, Figures 1A to 1E and Claims 9 to 13. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on pages 4 to 5 and 45 to 46.

WO2007136762 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, hydrocarbons and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 2 to 4 and 17 to 18, Table 7, Figures 2 to 4, exemplary embodiments 2 to 8 and Claims 13 and 35. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on pages 17 to 18, in Tables 1, 7, 8 and 10 and in Figure 10.

WO2008113041 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, hydrocarbons, aliphatic ketones and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 35 to 41 and 64 to 67, Figure 2, exemplary embodiments 6 and 10 and Claims 7 and 36. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Figure 7 and exemplary embodiments 6 and 10.

WO2010126891 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0034] to [0091], [0195] to [0222] and [0245] to [0250], Figures 3 to 5 and the exemplary embodiments 1 to 5. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0245] to [0250], Table 1 and exemplary embodiments 1 to 5.

WO2010118410 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters and wax esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0022] to [0043], [0158] to [0197], Figures 1 to 4, exemplary embodiments 3 and 5 to 8 and Claims 1 to

53 and 82 to 100. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0158] to [0197], Table 1, Figures 3 and 4 and exemplary embodiments 3 and 5 to 8.

WO2010118409 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters and wax esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0134] to [0154], Figures 1 to 3 and 6 and exemplary embodiment 3. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0134] to [0154], Figures 3 and 6 and the exemplary embodiment 3.

WO2010075483 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids, fatty acid methyl esters, fatty acid ethyl esters, alkan-1-ols, fatty alkyl acetates, alkan-1-als, fatty amines, fatty amides, fatty sulphates, fatty ethers, ketones, alkanes, internal and terminal olefins, dicarboxylic acids, α,ω-dicarboxylic acids and α,ω-diols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0061] to [0090] and [0287] to [0367], Figures 1, 4 and 5, exemplary embodiments 1 to 38 and Claims 18 to 26. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0012] to [0060], Tables 7, 17, 26 and 27, Figures 1, 44 to 47 and 55 to 59, exemplary embodiments 1 to 38 and Claims 1 to 17.

WO2010062480 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0022] to [0174] and [0296] to [0330], exemplary embodiments 3 and 5 to 8 and Claims 17 and 24. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0022] to [0174], Table 1 and exemplary embodiments 3 and 5 to 8.

WO2010042664 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular alkan-1-als, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0022] to [0143] and

[0241] to [0275], exemplary embodiment 2 and Claims 3 and 9. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1, Figure 5 and exemplary embodiment 2.

WO2011008535 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular carboxylic acids, hydroxycarboxylic acids and their lactones, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0024] to [0032] and [0138] to [0158] and Figure 13.

WO2010022090 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters and wax esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0022] to [0143] and [0238] to [0275], Figures 3 to 5, the exemplary embodiment 2 and Claims 5, 15, 16 and 36. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1, Figure 6 and exemplary embodiment 2.

WO2009140695 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hydrocarbons, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0214] to [0248] and exemplary embodiments 22 to 24. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1, Figure 40 and exemplary embodiments 22 to 24.

WO2010021711 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters and wax esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0009] to [0020] and [0257] to [0317], Figures 3 to 5 and 19, exemplary embodiments 2 to 24 and Claims 4, 5 and 30. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 3, Figure 6 and exemplary embodiments 2 to 24.

WO2009085278 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular olefins, from

at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0188] to [0192] and Figure 10. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1 and Figure 10.

WO2011019858 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0023], [0064] to [0074] and [0091] to [0099], exemplary embodiments 1 to 13, Figure 1 and Claim 8. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0085] to [0090], exemplary embodiments 1 to 13 and Table 1.

WO2009009391 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0010] to [0019] and [0191] to [0299], Figures 3 to 5, exemplary embodiments 2, 4 to 6, 9 to 14, 17 and 19 and Claims 16, 39, 44 and 55 to 59. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0010] to [0019] and [0191] to [0299], Figure 9 and exemplary embodiments 2, 4 to 6, 9 to 14, 17 and 19.

WO2008151149 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more microbial oil from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0009], [0015] to [0033], [0053], [0071], [0174] to [0191], [0274] and [0396], Claims 53 to 114, 188 to 206 and 344 to 355 and Tables 1 to 3. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 5.

WO2008147781 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hydrocarbons, olefins and aliphatic ketones, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0147] to [0156], exemplary embodiments 1 to 3, 8, 9 and 14 and Claims

65 to 71. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in exemplary embodiments 1 to 3, 8, 9 and 14.

WO2008119082 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, triglycerides, biodiesel, gasoline, jet fuel and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 3 to 5, 8 to 10 and 40 to 77, in Figures 4 and 5, exemplary embodiments 2 to 5 and 8 to 18 and Claims 3 to 39 and 152 to 153. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1, Figure 1, exemplary embodiments 2 to 5 and 8 to 18 and Claims 124 to 134 and 138 to 141.

WO2010135624 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0067] to [0083] and [0095] to [0098]. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in sections [0067] to [0083] and [0095] to [0098].

Zheng Z, Gong Q, Liu T, Deng Y, Chen JC and Chen GQ. (Thioesterase II of *Escherichia coli* plays an important role in 3-hydroxydecanoic acid production. Appl Environ Microbiol. 2004. 70(7):3807-13) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 3808 to 3810 and 3012 and Table 1, 3 and 4. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on pages 3807 and in Table 2.

Steen EJ, Kang Y, Bokinsky G, Hu Z, Schirmer A, McClure A, Del Cardayre SB and Keasling JD (*Microbial production of fatty-acid-derived fuels and chemicals from plant biomass*. Nature. 2010. 463(7280):559-62) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 559,

third section, to page 559, first section. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in supplementary Table 1.

Lennen RM, Braden DJ, West RA, Dumesic JA and Pfleger BF (*A process for microbial hydrocarbon synthesis: Overproduction of fatty acids in Escherichia coli and catalytic conversion to alkanes*. Biotechnol Bioeng. 2010. 106(2):193-202) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 193, first section, page 194, first and second section, page 195, second section to page 197, second section, page 198, second section to page 199, third section. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on page 193, first section, page 194, first and second section, page 196, second section, and in supplementary material.

Liu T, Vora H and Khosla C. (Quantitative analysis and engineering of fatty acid biosynthesis in E. coli. Metab Eng. 2010 Jul;12(4):378-86.) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections 2.2 and 3.1 and in Table 1 and 2. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in Table 1.

Yuan L, Voelker TA and Hawkins DJ. (*Modification of the substrate specificity of an acyl-acyl carrier protein thioesterase by protein engineering*. Proc Natl Acad Sci U S A. 1995 Nov 7;92(23):10639-43) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 10641, fourth section, and in Figure 2 and Table 1. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on page 10639, first section, page 10640, second, third and last section, page 10641, second and third section, and in Figure 1 and Table 1 and 2.

Lu X, Vora H and Khosla C. (*Overproduction of free fatty acids in E. coli: implications for biodiesel production*. Metab Eng. 2008. 10(6):333-9.) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention in particular on page 334, second section, sections 2.2, 2.3 and 3 (first to fourth section) and in Table 1. The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular in section 2.2.

Liu X, Sheng J and Curtiss IIII R. (*Fatty acid production in genetically modified cyanobacteria*. Proc Natl Acad Sci U S A. 2011. 108(17):6899-904) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 6899, fourth and last section, page 6900, first to penultimate section, and in Table S1 of the "Supporting Information". The document also describes enzymes E_i which are preferred according to the invention and their sequences, in particular on page 6899, sixth and last section.

Specific enzymes E_{ii}

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow, which include a first genetic modification within the meaning of the invention, are employed as the starting point by being provided with the second genetic modification and, if appropriate, with at least one further genetic modification within the meaning of the invention.

Steen EJ, Kang Y, Bokinsky G, Hu Z, Schirmer A, McClure A, Del Cardayre SB and Keasling JD (*Microbial production of fatty-acid-derived fuels and chemicals from plant biomass*. Nature. 2010. 463(7280):559-62) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their

wild type and which are preferably employed according to the invention, in particular on page 559, third section, to page 559, first section. The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular in supplementary Table 1.

Lennen RM, Braden DJ, West RA, Dumesic JA and Pfleger BF (*A process for microbial hydrocarbon synthesis: Overproduction of fatty acids in Escherichia coli and catalytic conversion to alkanes*. Biotechnol Bioeng. 2010. 106(2):193-202) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 193, first section, page 194, first and second section, page 195, second section to page 197, second section, page 198, second section to page 199, third section. The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular on page 193, first section, page 194, first and second section, page 196, second section, and in supplementary material.

Liu T, Vora H and Khosla C. *(Quantitative analysis and engineering of fatty acid biosynthesis in E. coli.* Metab Eng. 2010 Jul;12(4):378-86.) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections 2.2 and 3.1 and in Table 1 and 2. The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular in Table 1.

Yuan L, Voelker TA and Hawkins DJ. (*Modification of the substrate specificity of an acyl-acyl carrier protein thioesterase by protein engineering*. Proc Natl Acad Sci U S A. 1995 Nov 7;92(23):10639-43) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 10641, fourth section, and in Figure 2 and Table 1. The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular on page 10639, first

section, page 10640, second, third and last section, page 10641, second and third section, and in Figure 1 and Table 1 and 2.

Lu X, Vora H and Khosla C. (*Overproduction of free fatty acids in E. coli: implications for biodiesel production*. Metab Eng. 2008. 10(6):333-9.) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention in particular on page 334, second section, sections 2.2, 2.3 and 3 (first to fourth section) and in Table 1. The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular in section 2.2.

Liu X, Sheng J and Curtiss IIII R. (*Fatty acid production in genetically modified cyanobacteria.* Proc Natl Acad Sci U S A. 2011. 108(17):6899-904) describe microorganisms which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid esters, in particular fatty acids and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 6899, fourth and last section, page 6900, first to penultimate section, and in Table S1 of the "Supporting Information". The document also describes enzymes E_{ii} which are preferred according to the invention and their sequences, in particular on page 6899, sixth and last section.

Specific enzymes E_{iii}

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow, which include a first genetic modification within the meaning of the invention, are employed as the starting point by being provided with the second genetic modification and, if appropriate, with at least one further genetic modification within the meaning of the invention.

WO2009121066 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular dicarboxylic acids, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in Claims 8 to 14. The document

also describes enzymes E_{iii} which are preferred according to the invention and their sequences, in particular in sections [00026] to [0054], in exemplary embodiments 1 to 6, Figures 4 to 10 and Claims 1 to 7.

WO2009134899 A1 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular carboxylic acids, hydroxycarboxylic acids and their lactones, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0079] to [0082], exemplary embodiment 1 and Claim 20. The document also describes enzymes E_{iii} which are preferred according to the invention and their sequences, in particular in sections [0009] to [0010] and [0044] to [0078], exemplary embodiment 1, Figures 1 and 5 to 8 and Claims 15 to 17 and 19.

Specific enzymes E_{iv}

In cells which are preferred according to the invention, the enzyme E_{iv} is one which comprises sequences selected from among:

AAS90071.1, XP_002379948.1, AAS90024.1, XP_001821514.2, BAE59512.1, AAL99898.1, AAS90001.1, AAS90049.1, XP_001911518.1, ACH72901.1, XP_681084.1, AAC49198.1, EFW18013.1, XP_003070494.1, XP_001241401.1, XP_002384449.1, XP_001827206.1, XP_002836001.1, XP_001393196.1, XP_660984.1, XP_001395284.1, XP_002148677.1, XP_001827151.2, BAE66018.1, XP_001217254.1, CAK40139.1, XP_001393516.2, XP_002477829.1, XP_002146311.1, XP_002340042.1, XP_002544942.1, CBF87553.1, XP_002149766.1, 2UV8_A, XP_682676.1, CBX98966.1, XP_002560069.1, XP_001273102.1, P15368.1, XP_001273530.1, CBX99714.1, AAB41493.1, XP_001823764.1, XP_001388458.1, XP_748738.1, EDP53207.1, XP_001259179.1, XP_001825741.2, BAE64608.1, XP_001213437.1, XP_002377327.1, XP_002152724.1, EFZ04065.1, XP_001792784.1, EGP89632.1, XP_001407660.1, EFQ31023.1, XP_003040066.1, 2UV9_A, XP_002486436.1, XP_001585982.1, EFY87204.1, XP_002620504.1, XP_003295647.1, EEQ86108.1, XP_001938586.1, XP_001547465.1, XP_001906653.1, XP_001402457.2, CAK40502.1, XP_002568116.1, XP_003230922.1, XP_001647236.1, XP_385497.1, EGD94294.1, EGE05134.1, XP_002849847.1, XP_003015737.1, EFX06093.1, XP_003019052.1,

EEH03423.1, XP_001942351.1, EGC45478.1, XP_002556020.1, XP_003011025.1, CAY86729.1, EDN60916.1, EGA84463.1, EGA56454.1, EEU05652.1, NP_015093.1, XP_003231214.1, XP_445956.1, EGA60201.1, XP_003349949.1, XP_003070417.1, XP_001241314.1, EGR48038.1, XP_002615278.1, EFW15042.1, EGO59647.1, XP_452914.1, XP_962466.1, XP_001537327.1, XP_002796517.1, XP_003305240.1, XP_002543037.1, XP_002499262.1, NP_985412.2, XP_003019770.1, EFW96269.1, XP_002843350.1, EEH43965.1, XP_457388.1, XP_001799391.1, EEH21370.1, BAD08376.1, XP_001486434.1, BAF79876.1, EFY90998.1, XP_001939431.1, EER44845.1, EFZ02060.1, XP_001386834.2, XP_501096.1, XP_003299758.1, XP_002419391.1, XP_002490414.1, ACZ66251.1, XP_002548204.1, P43098.1, XP_002176039.1, XP_002479407.1, EEQ44526.1, AAA34601.1, XP_001791764.1, XP_003009337.1, BAA11913.1, NP_593823.1, BAB62031.1, BAB62032.1, BAB62030.1, 2PFF_A, XP_380212.1, ADN94478.1, EGF83443.1, XP_681149.1, EGG00662.1, ADN94479.1, ABC94883.1, XP_571099.1, EFY94095.1, EFW39589.1, XP_003194430.1, XP_003031600.1, XP_001836417.1, XP_001880844.1, XP_762607.1, EGN98830.1, EGO24420.1, ACD87451.1, XP_003328630.1, XP_002997955.1, CCA25392.1, XP_002901724.1, EFY86381.1, XP_002901728.1, ADN97213.1, XP_759118.1, XP_003325251.1, XP_003169619.1, XP_002555446.1, ABJ98780.1, XP_723161.1, EDZ68993.1, XP_001526334.1, XP_001223165.1, YP_889015.1, AAO43178.1, YP_001702252.1, XP_003026305.1, YP_003659808.1, ZP_08155637.1, ZP_04749666.1, ZP_08022190.1, YP_004007770.1, YP_954908.1, YP_004522637.1, YP_640811.1, ZP_04448562.1, NP_301868.1, ZP_06851996.1, YP_003273140.1, YP_001071929.1, YP_001133797.1, YP_004076455.1, YP_701403.1, ZP_03324816.1, YP_002778327.1, ZP_02028077.1, YP_909119.1, YP_880884.1, YP_002767320.1, NP_961266.1, ZP_07457010.1, ZP_08206945.1, ZP_02917151.1, ZP_04387794.1, YP_003359863.1, EGO39886.1, ABE96385.1, ZP_05228143.1, ZP_06522069.1, EGL13180.1, ZP_06976698.1, YP_001852225.1, ZP_06596502.1, YP_907384.1, ZP_06518033.1, AEF27803.1, YP_003374392.1, ZP_07485570.1, NP_217040.1, ZP_03742148.1, NP_856198.1, YP_004724192.1, NP_337093.1, AEJ51135.1, ZP_05765008.1, YP_004745991.1, AEJ47516.1, ZP_06927266.1, ZP_03646962.1, AEF31807.1, YP_003939358.1, YP_003971698.1, YP_003986333.1, ZP_05750911.1, ADD61451.1, ZP_07942485.1, YP_004209716.1, YP_004221489.1, AEI96705.1, NP_696693.1, AEG82252.1, YP_004001156.1, ZP_03976473.1, ZP_04663991.1, ZP_00121397.1, YP_003662064.1,

YP_003646283.1, YP_004630447.1, YP_002323720.1, YP_002835610.1, YP_117466.1, ZP_02963252.1, ADC85342.1, NP_940183.1, NP_739002.1, ZP_06755645.1, ADL21513.1, YP_003784047.1, ADL11108.1, ZP_06608499.1, ZP_07967121.1, ZP_05966223.1, ZP_08682531.1, ZP_03918327.1, ZP_07879655.1, ZP_03972703.1, ZP_06162645.1, ZP_06837277.1, ZP_07990916.1, ZP_03394081.1, CAA46024.1, YP_004760934.1, ZP_06751771.1, ZP_03934033.1, NP_601696.1, BAB99888.1, YP_001139316.1, ZP_03926457.1, NP_737523.1, ZP_02044858.1, ZP_07404023.1, ZP_03709883.1, XP_002388648.1, ZP_07402466.1, ZP_03710807.1, ZP_08294093.1, ZP_08232611.1, XP_682514.1, ZP_06837028.1, YP_001137826.1, CAA61087.1, ZP_06043461.1, YP_002833817.1, YP_225128.1, NP_600065.1, ABU23831.1, ZP_07716892.1, ZP_03935133.1, ZP_02549600.1, ZP_05215994.1, YP_004494858.1, XP_001526333.1, AAS90085.1, XP_002379947.1, AAS90025.1, XP_001821515.1, AAL99899.1, AAS90002.1, AAS90050.1, XP_001911517.1, ACH72900.1, XP_681083.1, AAC49199.1, XP_003070495.1, XP_001241402.1, EFW18012.1, CBX98970.1, EEH03422.1, EEQ86107.1, EGC45479.1, XP_002620503.1, XP_001537328.1, XP_002796516.1, 2UVA_G, EEH43966.1, DAA05950.1, EGR47893.1, XP_003070418.1, XP_001241316.1, XP_001827193.1, XP_002384436.1, XP_682677.1, XP_002486435.1, EGP88608.1, EDP53206.1, XP_001259180.1, EEH21369.1, XP_002543038.1, XP_748739.1, XP_003015735.1, EGE05135.1, XP_002152723.1, XP_002560068.1, XP_001273529.1, XP_003230923.1, EFX05327.1, XP_003019051.1, XP_001585981.1, XP_361644.2, XP_001223166.1, XP_003349948.1, XP_002380737.1, AAB41494.1, XP_001823765.1, XP_962465.1, EGO59648.1, XP_001906652.1, XP_003039864.1, XP_001213436.1, XP_385498.1, XP_003295646.1, EFQ31022.1, XP_002849848.1, XP_002148679.1, CBX99715.1, XP_002149767.1, EFY87205.1, EFZ04064.1, XP_002340041.1, EGD94295.1, XP_001938587.1, CAK45758.1, XP_001792785.1, XP_001393189.2, XP_003169620.1, XP_001547461.1, XP_001217253.1, XP_001939430.1, BAA92930.1, Q92215.1, EDK38075.2, EFW97345.1, XP_002495511.1, XP_451653.1, XP_500912.1, CAA42211.1, XP_001486502.1, XP_002477835.1, XP_445436.1, NP_594370.1, XP_001827152.2, BAE66019.1, BAA36384.1, BAB62141.1, XP_003299759.1, XP_002553365.1, XP_002489642.1, 2UV8_G, XP_457311.1, CAY80909.1, XP_001395285.1, EGA61562.1, EDN60099.1, EDV12927.1, NP_012739.1, XP_002616181.1, XP_002420328.1, XP_001524822.1, XP_002550943.1, XP_001386364.2, NP_984945.2, 227846, AAB59310.1, XP_001646561.1, XP_716877.1, XP_001836417.1, XP_002146312.1, P34731.1, EGO24420.1,

XP_002544941.1, EFZ02054.1, XP_002175228.1, XP_001393490.2, XP_003031600.1, XP_002479408.1, XP_002568119.1, XP_001825735.2, XP_002377320.1, EGN98830.1, ACD87451.1, XP_001880844.1, XP_571100.1, ABC94882.1, XP_775164.1, BAE64602.1, EFY90992.1, XP_003194424.1, XP_001273103.1, XP_681142.1, XP_003011020.1, AAA34602.1, XP_003231209.1, XP_003019765.1, ADN94478.1, EEQ46070.1, XP_001799393.1, CAK40504.1, AAM75418.1, ADN94479.1, XP_002843356.1, CAA27616.1, XP_380213.1, ADN97213.1, XP_759118.1, XP_762607.1, CAK49094.1, EER44843.1, XP_003009335.1, XP_002997955.1, XP_002901724.1, CCA25392.1, CAK36856.1, XP_001388457.2, ABO37974.1, ABJ98780.1, XP_660985.1, EDZ71063.1, XP_001402459.2, XP_001791765.1, XP_003324647.1, EGG10429.1, EFW15039.1, XP_002384390.1, XP_003031976.1, EDZ71062.1, EFW39589.1, ACZ80683.1, XP_002901728.1, XP_003328630.1, XP_681125.1, XP_003325251.1,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{iv} is generally understood in particular as meaning the conversion into hexanoic acid of two molecules malonyl-coenzyme A and one molecule acetyl-coenzyme A.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow, which include a first genetic modification within the meaning of the invention, are employed as the starting point by being provided with the second genetic modification and, if appropriate, with at least one further genetic modification within the meaning of the invention.

WO2011003034 A2 describes microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hexanoic acid, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 2 to 3, page 5, third section, in exemplary embodiments 1 to 4, 7 to 9 and 12 to 14 and Claims 1 to 100. The document also describes enzymes E_{iv} which are preferred according to the invention and their sequences, in particular on page 5 and in exemplary embodiment 3.

Hitchman TS, Schmidt EW, Trail F, Rarick MD, Linz JE and Townsend CA. (*Hexanoate synthase, a specialized type I fatty acid synthase in aflatoxin B1 biosynthesis.* Bioorg Chem. 2001. 29(5):293-307) describe microorganisms which include a first genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hexanoic acid, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on page 296, penultimate section to page 298, second section. The document also describes enzymes E_{iv} which are preferred according to the invention and their sequences, in particular on page 299, fourth section, to page 302, first section.

In the context of the first genetic modification, it may be beneficial to employ, in place of the enzyme E_i, a combination of the activity increase in comparison with that of the wild type of an enzyme E_{ii} paired with that of an enzyme E_{iib}, which catalyses a reaction in which a CoA thioester is converted into an ACP thioester.

Such enzymes E_{iib} are known as acyl-CoA (Coenzyme A):ACP (Acyl Carrier Protein) transacylases. Preferred enzymes E_{iib} are selected from among XP_003402554.1, YP_002908243.1, YP_001778804.1, YP_001670627.1, YP_004703658.1, YP_001747923.1, YP_004348703.1, YP_004352505.1, YP_004379169.1, ADR61731.1, YP_001269622.1, YP_001186851.1, YP_004659609.1, YP_003519049.1, YP_001811696.1, YP_004616040.1, NP_252697.1, NP_252169.1, NP_249421.1, ZP_06456665.1, ZP_01167071.1, ZP_08557569.1, ZP_08554397.1, YP_001157914.1, YP_004475334.1, EGM20156.1, BAK10182.1, YP_347066.1, Q9KJH8.1, YP_002987902.1, ZP_03794633.1, ZP_03627777.1, YP_004434330.1, NP_743567.1, ZP_03456835.1, ZP_07911512.1, ZP_07264431.1, ZP_02265387.2, ZP_03456013.1, ZP_07577798.1, ZP_08429367.1,

YP_004055319.1, YP_004053883.1, YP_275219.1, YP_276116.1, YP_003882762.1, EGH97259.1, EGH95622.1, EGH90852.1, EGH85976.1, EGH81248.1, EGH79586.1, EGH79549.1, EGH73565.1, EGH66549.1, EGH64812.1, EGH58099.1, EGH54896.1, EGH50352.1, EGH43364.1, EGH41593.1, EGH29888.1, EGH29417.1, EGH22392.1, EGH22129.1, EGH11618.1, EGH10011.1, ZP_04589662.1, CCA60711.1, YP_003004716.1, BAK16630.1, YP_003264146.1, YP_371314.1, YP_439272.1, NP_762892.1, ADW02533.1, YP_003291774.1, EGC99875.1, ZP_08139631.1, YP_003333890.1, EGC08366.1, YP_080427.1, YP_258557.1, YP_001985016.1, YP_002875182.1, YP_002871082.1, YP_237050.1, YP_236199.1, NP_794008.1, NP_793082.1, YP_609790.1, EFW81598.1, EFW79804.1, ZP_07261632.1, ZP_07229875.1, ZP_06458504.1, ZP_05640568.1, ZP_03399268.1, ZP_03398232.1, ZP_08004496.1, ZP_06876938.1, ZP_03227482.1, ZP_02511781.1, ZP_02503964.1, ZP_02477255.1, ZP_02466678.1, ZP_02465791.1, ZP_02461688.1, ZP_02417235.1, ZP_02414413.1, ZP_02408727.1, ZP_02376540.1, ZP_02358949.1, ZP_07778021.1, ZP_07774051.1, ZP_07795409.1, ZP_07089008.1, YP_776393.1, ZP_07684652.1, ZP_06640022.1, ZP_03054335.1, ZP_02907621.1, ZP_02891475.1, ZP_01862226.1, ZP_01769192.1, ZP_01367441.1, ZP_01366930.1, ZP_01364106.1, ZP_01312991.1, ZP_01173135.1, ZP_07005523.1, ZP_04955702.1, ZP_04943305.1, ZP_04936014.1, ZP_04932415.1, ZP_04930223.1, ZP_04905334.1, ZP_04893870.1, ZP_04893165.1, ZP_04892059.1, ZP_04884056.1, YP_002438575.1, YP_002234939.1, YP_001488024.1, YP_001346487.1, YP_001350135.1, YP_001347031.1, YP_990329.1, YP_860279.1, YP_789111.1, YP_792557.1, YP_623139.1, YP_175644.1, YP_111362.1, YP_110557.1, YP_105231.1, NP_937516.1, AAU44816.1, AAA25978.1, XP_002721010.1, AAK81868.1, AAK71350.1, AAK71349.1, ZP_06499968.1, ZP_06498781.1, YP_003472045.1, ACA03779.1, ABL84756.1, AAQ16175.1, AAT51302.1, AAT51199.1, ZP_05639386.1, ACH70299.1, ACA60824.1, BAB32432.1,

in particular

AAK81868.1, NP_743567.1, AAK71349.1, YP_001269622.1, ADR61731.1, AAU44816.1, AAQ16175.1, YP_001670627.1, ACH70299.1, Q9KJH8.1, YP_004703658.1, ZP_08139631.1, YP_609790.1, YP_001747923.1, YP_258557.1, YP_347066.1, YP_002871082.1, YP_004352505.1, ACA60824.1, ZP_07774051.1, BAB32432.1, ZP_05640568.1, EGH58099.1, EGH64812.1, EGH11618.1, ZP_06456665.1, YP_276116.1, EFW81598.1, EGH95622.1, EGH22129.1, NP_794008.1, ZP_03399268.1, ZP_07264431.1, EGH73565.1, YP_237050.1,

ZP_06498781.1, EGH29888.1, EGH79586.1, EGH50352.1, YP_792557.1, YP_001350135.1, ZP_01364106.1, ZP_04932415.1, NP_249421.1, YP_004379169.1, ACA03779.1, YP_001186851.1, YP_004475334.1, ZP_04589662.1, ZP_03398232.1, EGH10011.1, ZP_07229875.1, ZP_05639386.1, EGH66549.1, YP_275219.1, ZP_07005523.1, EFW79804.1, ZP_06458504.1, EGH85976.1, YP_236199.1, EGH43364.1, ZP_07261632.1, ZP_06499968.1, EGH29417.1, EGH54896.1, EGH22392.1, EGH97259.1, NP_793082.1, EGH90852.1, EGH41593.1, NP_252169.1, ZP_01366930.1, YP_001347031.1, ZP_07778021.1, YP_002875182.1, AAA25978.1, ABL84756.1, EGH81248.1, ZP_07795409.1
and especially preferably AAU44816.1, NP_743567.1, YP_001269622.1, ADR61731.1, AAK71349.1, YP_001670627.1, AAK81868.1, AAQ16175.1, Q9KJH8.1, ACH70299.1, YP_004703658.1, ZP_08139631.1, YP_609790.1, YP_001747923.1, AAK71350.1,
and
proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{iib} is generally understood in particular as meaning the conversion of dodecanoyl-CoA thioester into dodecanoyl-ACP thioester.

Third genetic modification for the production of carboxylic acid esters from a simple carbon source

It is advantageous in particular for the production of carboxylic acid esters when the microorganism additionally includes a third genetic modification which comprises an activity of

at least one of the enzymes E_{iib}, E_v, E_{vi} or E_{vii} which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

In this context, it is preferred according to the invention that this genetic modification is an activity of at least one of the enzymes selected from the group

E_{iib} acyl-CoA (Coenzyme A):ACP (Acyl Carrier Protein) transacylase, which converts an ACP thioester into a CoA thioester or a CoA thioester into an ACP thioester,

E_v wax ester synthase or alcohol O-acyltransferase, preferably of EC 2.3.1.75 or EC 2.3.1.84, which catalyses the synthesis of an ester from an acyl-coenzyme A thioester or an ACP thioester and an alcohol,

E_{va} fatty acid *O*-methyl transferase, preferably of EC 2.1.1.15, which catalyses the synthesis of a fatty acid methyl ester from a fatty acid and S-adenosylmethionine,

E_{vi} acyl-CoA (Coenzyme A) synthetase, preferably of EC 6.2.1.3, which catalyses the synthesis of an acyl-coenzyme A thioester, and

E_{vii} acyl thioesterase, preferably of EC 3.1.2.2, EC 3.1.2.4, EC 3.1.2.18, EC 3.1.2.19, EC 3.1.2.20 or EC 3.1.2.22, which catalyses the conversion of an acyl thioester with an alcohol to give a carboxylic acid ester,

which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

In this context, it is especially preferred that the third genetic modification comprises combinations of the increased activities of the enzymes selected from among E_v, E_{va}, E_{vii}, $E_{va}E_{vii}$, E_vE_{vi}, $E_{vi}E_{vii}$, $E_{vi}E_{vii}E_{iib}$.

Preferred enzymes E_{iib} in connection with the third genetic modification correspond to the enzymes E_{iib} which have been emphasized above as being preferred in connection with the first genetic modification.

Specific enzymes E_v

In cells which are preferred according to the invention, the enzyme E_v is one which comprises sequences selected from among:

NP_808414.2, NP_001178653.1, XP_003272721.1, XP_002720111.1, NP_001002254.1, XP_529027.1, XP_002831804.1, BAC28882.1, XP_549056.2, XP_002918053.1, XP_001085075.1, XP_002763005.1, XP_002700092.1, XP_599558.4, EDL95940.1, XP_001496780.1, CAD89267.1, EFB28125.1,
YP_004747160.1, YP_004746900.1, YP_004746665.1, YP_004746558.1, YP_004746531.1, YP_004746530.1, YP_004745948.1, YP_004745222.1, YP_004744358.1, YP_004743710.1, YP_002492297.1, AEK40846.1, YP_001847685.1, YP_001712672.1, YP_001706290.1, YP_004724737.1, YP_004723134.1, AEJ51098.1, AEJ48174.1, AEJ47480.1, YP_004392630.1, YP_004099725.1, YP_003912033.1, YP_003652731.1, YP_003301387.1, YP_003298139.1, YP_001509672.1, YP_001505948.1, YP_001432486.1, YP_001432432.1, YP_924893.1, YP_923981.1, YP_922869.1, YP_922597.1, YP_922419.1, ZP_08629145.1, ZP_08628906.1, YP_001380027.1, YP_001280731.1, YP_001280730.1, YP_888966.1, YP_890540.1, YP_888236.1, YP_888223.1, YP_888574.1, YP_884705.1, YP_889488.1, YP_886248.1, YP_882534.1, YP_881069.1, YP_881444.1, YP_883472.1, YP_879642.1, YP_884073.1, YP_880917.1, YP_882201.1, YP_879422.1, YP_707862.1, YP_707847.1, YP_707633.1, YP_707572.1, YP_707571.1, YP_706785.1, YP_706267.1, YP_705586.1, YP_705294.1, YP_702929.1, YP_701572.1, YP_700576.1, YP_700081.1, YP_700033.1, YP_700018.1, YP_700017.1, YP_699999.1, CCB78299.1, CCB78283.1, CCB72233.1, YP_004663601.1, YP_004525283.1, YP_004524901.1, YP_004524237.1, YP_004524223.1, YP_004523752.1, YP_004522677.1, YP_004521797.1, YP_004521441.1, YP_004020500.1, YP_004014348.1, EGO40684.1, EGO38684.1, EGO38655.1, EGO37244.1, EGO36970.1, EGO36701.1, YP_003951335.1, YP_003812176.1, YP_003811992.1, YP_003810691.1, YP_003810418.1, YP_003809501.1, ZP_08574204.1, CCA19760.1, XP_002900672.1, ZP_06414567.1, ZP_06413635.1, ZP_06411773.1, ZP_06411772.1, ZP_06271823.1, ZP_05620754.1, ZP_05360001.1, ZP_04752019.1, ZP_04751943.1, ZP_04750965.1, ZP_04750465.1, ZP_04750453.1, ZP_04750228.1, ZP_04750091.1, ZP_04749363.1, ZP_04749348.1, ZP_04749293.1, ZP_04749287.1, ZP_04749022.1, ZP_04748677.1, ZP_04747379.1, ZP_04747377.1, ZP_04747348.1, ZP_04747282.1, ZP_04747159.1, ZP_04747093.1, ZP_04746958.1, ZP_04717323.1, ZP_04684258.1, ZP_04386203.1, ZP_04385082.1, ZP_04384030.1, ZP_04384029.1, ZP_03534755.1, ZP_01115502.1, ZP_01102322.1, YP_004583872.1, YP_004583323.1, YP_004573656.1, YP_004571392.1, YP_003513699.1, ZP_08553011.1, ZP_08552672.1, YP_003467054.1, YP_003572597.1,

YP_579515.1, YP_001136465.1, YP_001136231.1, YP_001135959.1, YP_001135349.1, YP_001133828.1, YP_001133806.1, YP_001133693.1, YP_001133270.1, YP_001132329.1, YP_001131721.1, YP_001131631.1, YP_001073715.1, YP_001073143.1, YP_001072388.1, YP_001072036.1, YP_001071893.1, YP_001071814.1, YP_001071689.1, YP_001070856.1, YP_001069682.1, YP_001069164.1, YP_001068496.1, YP_939377.1, YP_642242.1, YP_641664.1, YP_641419.1, YP_640919.1, YP_640783.1, YP_640704.1, YP_640572.1, YP_640571.1, YP_640494.1, YP_639709.1, YP_639198.1, YP_638523.1, YP_638030.1, YP_637968.1, YP_637380.1, YP_446603.1, NP_001185377.1, NP_200151.2, NP_568547.1, NP_197641.1, NP_200150.1, NP_197139.1, NP_190490.1, NP_190488.1, NP_177356.1, YP_004495408.1, YP_004495023.1, YP_004494197.1, YP_004494168.1, YP_004493973.1, YP_004493936.1, YP_004493628.1, YP_004493589.1, YP_004493509.1, YP_004493477.1, YP_004493462.1, YP_004492352.1, YP_004492155.1, YP_004492039.1, YP_004491716.1, YP_004491715.1, YP_004491501.1, YP_003375642.1, YP_003411203.1, YP_003410436.1, YP_003395271.1, YP_003395089.1, YP_003393635.1, YP_003384208.1, YP_003379551.1, ZP_04388235.1, YP_002134168.1, ZP_01900421.1, ZP_01900085.1, ZP_01899829.1, ZP_01898741.1, BAK05274.1, BAJ93623.1, BAJ97841.1, BAK08349.1, BAJ93204.1, BAJ92722.1, BAK06983.1, BAJ86545.1, BAK02325.1, BAJ85619.1, BAJ84892.1, ZP_05218281.1, ZP_05218149.1, ZP_05217310.1, ZP_05216978.1, ZP_05216447.1, ZP_05216446.1, ZP_05216025.1, ZP_05214687.1, ZP_08476543.1, ZP_04749239.1, YP_823060.1, ADP99639.1, ADP98951.1, ADP98855.1, ADP98710.1, ADP96265.1, ZP_08461736.1, ZP_08461735.1, ZP_07608690.1, YP_045555.1 (encoded by SEQ ID No.: 19), YP_872243.1, YP_004009106.1, YP_004008736.1, YP_004008003.1, YP_004007600.1, YP_004006799.1, YP_004006436.1, YP_004006072.1, YP_004005008.1, YP_003486913.1, NP_301898.1, ZP_08434757.1, YP_004079491.1, YP_004078785.1, YP_004077880.1, YP_004076486.1, YP_004076464.1, YP_004076350.1, YP_004075391.1, YP_004074864.1, ZP_01103855.1, YP_465274.1, ZP_08403393.1, ZP_08402717.1, ZP_08402716.1, YP_004427559.1, YP_001277083.1, YP_001276783.1, YP_524767.1, YP_522739.1, YP_521788.1, YP_004335162.1, YP_004333708.1, YP_004332973.1, YP_004332349.1, YP_004157731.1, YP_004224204.1, YP_003275673.1, YP_003275371.1, YP_003274979.1, YP_003274924.1, YP_003274705.1, YP_956544.1, YP_955502.1, YP_955007.1, YP_954887.1, YP_954886.1, YP_954859.1, YP_954399.1, YP_953715.1, YP_953073.1, YP_952592.1, YP_951909.1, YP_951298.1, YP_951083.1, ZP_08287899.1, ZP_08272356.1,

ZP_08270967.1, CCA60099.1, CCA56737.1, YP_983728.1, YP_550833.1, YP_549124.1, YP_121795.1, YP_120815.1, YP_118589.1, YP_117783.1, YP_117375.1, YP_003646883.1, YP_003646055.1, YP_003645661.1, EGE49469.1, ZP_08234310.1, CBZ53121.1, YP_004010866.1, EGE24961.1, EGE18726.1, EGE15701.1, EGE12950.1, EGE10026.1, EGB03968.1, ZP_08206563.1, ZP_08205089.1, ZP_08204958.1, ZP_08204416.1, ZP_08203326.1, YP_714381.1, YP_713817.1, YP_694462.1 (encoded by SEQ ID No.: 67), YP_693524.1, YP_003341775.1, YP_003339587.1, ZP_08197177.1, ADW01905.1, YP_004242683.1, ZP_07484742.2, ZP_07441979.2, ZP_07441978.2, ZP_07437333.2, ZP_06960424.1, ZP_06801236.1, ZP_06799517.1, ZP_05769718.1, ZP_05768326.1, ZP_05767970.1, ZP_05766272.1, ZP_05763839.1, YP_003204265.1, YP_003203570.1, YP_003200768.1, YP_003134884.1, YP_003134608.1, ZP_05140320.1, NP_001140997.1, EEE64643.1, EEE55448.1, EEE32548.1, ZP_03534756.1, ZP_03533653.1, ZP_03531929.1, EEC71274.1, EAY98969.1, EAY75974.1, EAY75973.1, ADZ24988.1, ZP_08157247.1, ZP_08156660.1, ZP_08156249.1, ZP_08153292.1, ZP_08152876.1, ZP_08152662.1, YP_002946672.1, YP_960669.1, YP_960629.1, YP_960328.1, YP_958134.1, YP_957462.1, YP_001022272.1, ZP_08123690.1, ZP_08120547.1, ZP_08119498.1, EGB29195.1, EGB27143.1, YP_003770089.1, YP_003769971.1, YP_003764703.1, YP_003764513.1, YP_003103950.1, YP_003168536.1, YP_003168331.1, YP_003166844.1, CAJ88696.1, NP_769520.1, YP_001141853.1, YP_001108534.1, YP_001106516.1, YP_907824.1, YP_907344.1, YP_906945.1, YP_906856.1, YP_906855.1, YP_906831.1, YP_906494.1, YP_906243.1, YP_905962.1, YP_905765.1, YP_905343.1, YP_905239.1, YP_325796.1, YP_130413.1, NP_625255.1, NP_624462.1, NP_338129.1, NP_338004.1, NP_337859.1, NP_337740.1, NP_337694.1, NP_336266.1, NP_335919.1, NP_335351.1, NP_334638.1, NP_218257.1, NP_218251.1, NP_217997.1, NP_217888.1, NP_217751.1, NP_217750.1, NP_217646.1, NP_217604.1, NP_217603.1, NP_217000.1, NP_216801.1, NP_216276.1, NP_215941.1, NP_215410.1, NP_214735.1, ZP_04661667.1, EFW44815.1, EFW44455.1, ZP_08024634.1, ZP_08024620.1, ZP_08023777.1, ZP_08023597.1, YP_002784032.1, YP_002783585.1, YP_002782904.1, YP_002782647.1, YP_002780099.1, YP_002779887.1, YP_002778497.1, YP_002777657.1, YP_002777402.1, ZP_07966321.1, ZP_07944768.1, CBI21867.3, CBI40547.3, CBI40544.3, CBI40540.3, CBI40536.3, CBI40534.3, CBI40533.3, CBI32385.3, ZP_05765756.1, ZP_05765643.1, ZP_05765597.1, ZP_05765596.1, YP_001705267.1, YP_001704692.1, YP_001704281.1, YP_001702654.1, YP_001701260.1,

ZP_05770434.1, ZP_05766274.1, ZP_05762133.1, ZP_05762130.1, ZP_01101223.1, YP_481580.1, YP_979623.1, YP_979196.1, ZP_07414300.2, ZP_03537340.1, ZP_03537339.1, ZP_03536772.1, ZP_03536404.1, ZP_03433478.1, ZP_03430367.1, ZP_03430260.1, ZP_03429345.1, ZP_03428583.1, ZP_03426905.1, ZP_03426458.1, ZP_03426456.1, ZP_03426455.1, ZP_03425014.1, ZP_03424082.1, ZP_03421649.1, ZP_03419291.1, ZP_03418394.1, ZP_03417976.1, ZP_03414875.1, ZP_06952098.1, ZP_05528769.1, ZP_05527907.1, ZP_05227984.1, ZP_05227897.1, ZP_05227653.1, ZP_05227585.1, ZP_05227420.1, ZP_05227202.1, ZP_05226387.1, ZP_05226386.1, ZP_05225355.1, ZP_05225200.1, ZP_05223431.1, ZP_05223402.1, ZP_04697793.1, ZP_02550609.1, ZP_02548969.1, EEE25493.1, ABO13188.2, ZP_07205208.1, YP_589436.1, BAJ33896.1, ZP_07718107.1, ZP_07717513.1, ZP_07717390.1, ZP_07716424.1, ZP_04384387.1, ZP_07376578.1, ZP_06871097.1, ZP_06852444.1, ZP_06852442.1, ZP_06852283.1, ZP_06852150.1, ZP_06852032.1, ZP_06850980.1, ZP_06850766.1, ZP_06850644.1, ZP_06849846.1, ZP_06849446.1, ZP_06849265.1, ZP_06848894.1, ZP_06848550.1, ZP_06847321.1, ZP_06847245.1, ZP_06728640.1, ZP_06155537.1, ZP_03822106.1, ZP_03822105.1, ZP_03264909.1, ZP_01915979.1, ZP_01914209.1, ZP_01909198.1, ZP_01895985.1, ZP_01893763.1, ZP_01893601.1, ZP_01893547.1, ZP_01864269.1, ZP_01736818.1, ZP_01693481.1, ZP_01626518.1, ZP_01616172.1, ZP_01461648.1, ZP_01439861.1, ZP_01311414.1, ZP_01222733.1, ZP_01038993.1, ZP_00997001.1, ZP_06533596.1, ZP_07308012.1, ZP_07282351.1, ZP_07282257.1, ZP_07278697.1, ZP_07277986.1, ZP_07277799.1, ZP_07011797.1, ZP_06913634.1, ZP_06711075.1, ZP_06575037.1, ZP_06523715.1, ZP_06522644.1, ZP_06520408.1, ZP_06518751.1, ZP_06514733.1, ZP_06511304.1, ZP_06510466.1, ZP_06509700.1, ZP_06504004.1, ZP_06452618.1, ZP_06451687.1, ZP_06450049.1, ZP_06444722.1, ZP_06443996.1, ZP_06443677.1, ZP_06438510.1, ZP_06435077.1, ZP_06434554.1, ZP_06432969.1, ZP_06431341.1, ZP_06430915.1, ZP_05129423.1, ZP_05127637.1, ZP_05126217.1, ZP_05096686.1, ZP_05095013.1, ZP_05094400.1, ZP_05093434.1, ZP_05043539.1, ZP_05041631.1, ZP_04959394.1, ZP_04956551.1, ZP_01052702.1, YP_437020.1, YP_436128.1, YP_432512.1, YP_432391.1, ZP_06072118.1, ZP_06069021.1, ZP_06065092.1, ZP_06062254.1, YP_003032200.1, YP_003030813.1, YP_002766854.1, YP_002766842.1, YP_002766292.1, YP_002765623.1, YP_002765076.1, YP_002764977.1, YP_002764976.1, YP_002764693.1, YP_002764633.1, YP_002646305.1, YP_002646304.1,

YP_001853537.1, YP_001853530.1, YP_001853214.1, YP_001852100.1, YP_001851711.1, YP_001851686.1, YP_001851684.1, YP_001851611.1, YP_001851610.1, YP_001851579.1, YP_001850950.1, YP_001850935.1, YP_001850900.1, YP_001850899.1, YP_001850378.1, YP_001849911.1, YP_001849825.1, YP_001849624.1, YP_001849470.1, YP_001848848.1, YP_001848784.1, YP_001822237.1, YP_001289190.1, YP_001289078.1, YP_001288434.1, YP_001287727.1, YP_001286168.1, YP_001085790.1, YP_856793.1, YP_629387.1, YP_615587.1, YP_615252.1, YP_457389.1, YP_263530.1, NP_962591.1, NP_962411.1, NP_962281.1, NP_961234.1, NP_960903.1, NP_960387.1, NP_960090.1, NP_959281.1, NP_959065.1, NP_857403.1, NP_857149.1, NP_857148.1, NP_857047.1, NP_856907.1, NP_856759.1, NP_856156.1, NP_855443.1, NP_855112.1, NP_853892.1, NP_828432.1, NP_603766.1, XP_003081224.1, YP_003778608.1, YP_003730939.1, XP_003059244.1, ADI13131.1, XP_002992800.1, XP_002963877.1, XP_001419779.1, XP_002988280.1, XP_002987493.1, CBH32551.1, CBH32550.1, CBH19575.1, CBH19574.1, YP_003627553.1, XP_002879777.1, XP_002877657.1, XP_002877655.1, XP_002873570.1, XP_002871716.1, XP_002870738.1, XP_002868506.1, XP_002865972.1, XP_002864239.1, XP_002862308.1, ZP_05823139.1, NP_001043877.1, ZP_06693274.1, ZP_06058985.1, NP_001044374.1, XP_002835451.1, XP_002787542.1, XP_002785958.1, XP_002785645.1, XP_002783220.1, XP_002774061.1, XP_002767852.1, XP_002766051.1, XP_002765456.1, XP_002765455.1, XP_002677788.1, XP_002671612.1, XP_002736281.1, CBA31373.1, XP_002184474.1, XP_002325936.1, XP_002323705.1, XP_002325937.1, XP_002323911.1, XP_002323706.1, XP_002328965.1, XP_002318416.1, XP_002310400.1, ACY38597.1, ACY38596.1, ACY38595.1, ACY38594.1, ACY38593.1, ACY38592.1, ACY38591.1, ACY38590.1, ACX81315.1, ACX81314.1, XP_001868729.1, XP_001847517.1, XP_001847515.1, XP_002502575.1, ACU20370.1, ACU18073.1, XP_002523348.1, XP_002516707.1, XP_002429016.1, BAH89673.1, XP_002440221.1, XP_002459294.1, XP_002458560.1, XP_320167.4, XP_001780431.1, XP_002364905.1, XP_002263196.1, XP_002263137.1, XP_002263409.1, XP_002263252.1, XP_002268615.1, XP_002278404.1, XP_002274522.1, XP_002282418.1, XP_001633379.1, XP_001632267.1, XP_001632004.1, XP_001622638.1, XP_002155609.1, XP_759225.1, XP_002152406.1, XP_001914129.1, XP_001738032.1, XP_001731626.1, XP_001209859.1, CAN79451.1, CAN78449.1, CAN72806.1, CAN71951.1, CAN71950.1, CAN76656.1, CAN62907.1, AAZ08051.1, ABO21022.1, ABO21021.1, ABO21020.1, ABJ96321.1, BAF01088.1, XP_758106.1, BAC42871.1, BAB09801.1,

BAB09102.1, in particular YP_045555.1 (encoded by SEQ ID No.: 19), YP_694462.1 (encoded by SEQ ID No.: 67) and NP_808414.2.

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_v is generally understood in particular as meaning the conversion of dodecanoyl-CoA thioester and/or dodecanoyl-ACP thioester with methanol into dodecanoyl methyl ester.

If the enzyme E_v is an alcohol O-acyltransferase of EC 2.3.1.84, it is preferred that they are selected from among:

EGA72844.1, NP_015022.1, S69991, AAP72991.1, EDN63695.1, BAA05552.1, AAP72992.1, S69992, AAP72995.1, XP_002552712.1, XP_001646876.1, XP_002551954.1, EGA82692.1, EDN61766.1, EGA86689.1, EGA74966.1, AAU09735.1, NP_011693.1, XP_445666.1, BAA13067.1, AAP72993.1, EGA62172.1, XP_455762.1, EGA58658.1,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used

(units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_v is generally understood in particular as meaning the conversion of dodecanoyl-CoA thioester with methanol into dodecanoyl methyl ester.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow featuring a third genetic modification within the meaning of the invention are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.
WO2007136762 A2 describes microorganisms which include a third genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, hydrocarbons and alkan-1-ols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 2 to 4 and 21 to 24, Figures 2 to 4, exemplary embodiments 1, 2 and 5 to 7 and Claims 1, 2, 5, 6, 9 to 27 and 33. The document also describes enzymes E_v which are preferred according to the invention and their sequences, in particular on pages 21 to 24, in Table 10 and Figure 10.

Specific enzymes E_{va}

In cells which are preferred according to the invention, the enzyme E_{va} is one which comprises sequences selected from among YP_001851637.1 (encoded by SEQ ID No.: 114) and proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, particularly preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst,

that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{va} is generally understood in particular as meaning the conversion of lauric acid and S-adenosylmethionine to lauric acid methyl ester and S-adenosylhomocysteine.

Specific Enzymes E_{vi}

In cells which are preferred according to the invention, the enzyme E_{vi} is one which comprises sequences selected from among YP_001724804.1 (encoded by SEQ ID No.: 18)
and
proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{vi} is generally understood in particular as meaning the synthesis of dodecanoyl-CoA thioester.

Specific enzymes E_{vii}

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms listed hereinbelow featuring a third genetic modification within the meaning of the invention are employed as starting point by being equipped with a first and

second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2010075483 A2 describes microorganisms which include a third genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids, fatty acid methyl esters, fatty acid ethyl esters, fatty alcohols, fatty alkyl acetates, fatty aldehydes, fatty amines, fatty amides, fatty sulphates, fatty ethers, ketones, alkanes, internal and terminal olefins, dicarboxylic acids, α,ω-dicarboxylic acids and α,ω-diols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0061] to [0090] and [0287] to [0367], Figures 1, 4 and 5, exemplary embodiments 1 to 38 and Claims 18 to 26. The document also describes enzymes E_{vii} which are preferred according to the invention and their sequences, in particular in sections [0012] to [0060], Tables 7, 17, 26 and 27, Figures 1, 44 to 47 and 55 to 59, exemplary embodiments 1 to 38 and Claims 1 to 17.

Fourth genetic modification for the production of alkan-1-ols, alkan-1-als, alkan-1-amines, alkanes, olefins, alken-1-als, alken-1-ols and alken-1-amines from a simple carbon source

In the event that the production of alkan-1-ols, alkan-1-als, alkan-1-amines and olefins is desired, it may be advantageous to suitably enzymatically reduce, aminate, decarboxylate or decarbonylate the corresponding carboxylic acids or carboxylic acid esters.

To this end, microorganisms which are preferred according to the invention include a fourth genetic modification which comprises an activity of at least one of the following, selected from the group

E_{iib} acyl-CoA (Coenzyme A):ACP (Acyl Carrier Protein) transacylase, which converts an ACP thioester into a CoA thioester or a CoA thioester into an ACP thioester,

E_{vi} acyl-CoA (Coenzyme A) synthetase, preferably of EC 6.2.1.3, which catalyses the synthesis of an acyl-coenzyme A thioester,

E_{viii} acyl-CoA (Coenzyme A) reductase, preferably of EC 1.2.1.42 or EC 1.2.1.50, which preferably catalyses the reduction of an acyl-coenzyme A thioester to give the corresponding alkan-1-al or alkan-1-ol,

E_{ix} fatty acid reductase (also fatty aldehyde dehydrogenase or arylaldehyde oxidoreductase), preferably of EC 1.2.1.3, EC 1.2.1.20 or EC 1.2.1.48, which preferably catalyses the reduction of an alkanoic acid to give the corresponding alkan-1-al,

E_x acyl-ACP (Acyl Carrier Protein) reductase, preferably of EC 1.2.1.80, which catalyses the reduction of an acyl-ACP thioester to give the corresponding alkan-1-al or alkan-1-ol,

E_{xi} cytochrome P450 fatty acid decarboxylase, which catalyses the conversion of an alkanoic acid with n carbon atoms into a corresponding terminal olefin with n-1 carbon atoms, in particular of dodecanoic acid to undec-10-enoic acid,

E_{xii} alkan-1-al decarbonylase, which catalyses the conversion of an alkan-1-al (n carbon atoms) into a corresponding alkane (n-1 carbon atoms), and

E_{xiii} alkan-1-al transaminase, which catalyses the conversion of an alkan-1-al into a corresponding alkan-1-amine,

which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

In this context, it is especially preferred that the fourth genetic modification comprises combinations of increased activities of the enzymes selected from among E_{ix}, E_x, E_{xi}, $E_{vi}E_{viii}$, $E_{vi}E_xE_{iib}$, $E_{viii}E_{xii}$, $E_{viii}E_{xiii}$, $E_{ix}E_{xii}$, $E_{ix}E_{xiii}$, E_xE_{xii}, E_xE_{xiii}, $E_{vi}E_{viii}E_{xii}$, $E_{vi}E_{viii}E_{xiii}$, $E_xE_{xii}E_{vi}E_{iib}$ and $E_xE_{xiii}E_{vi}E_{iib}$.

Preferred enzymes E_{iib} in connection with the fourth genetic modification correspond to the enzymes E_{iib} emphasized above as being preferred in the context of the first and third genetic modification.

Preferred enzymes E_{vi} in connection with the fourth genetic modification correspond to the enzymes E_{vi} emphasized above as being preferred in the context of the third genetic modification.

Specific enzymes E_{viii}

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms including a fourth genetic modification within the meaning of the invention listed hereinbelow are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2011008565 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acids, fatty aldehydes, fatty alcohols, alkanes and fatty acid esters, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0021], [0103] to [0106], [0108] and [0129]. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0104] to [0106] and [0108] and [0129] and exemplary embodiment 11.

WO2008151149 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more microbial oil in comparison with their wild type from at least one simple carbon source and which are preferably employed according to the invention, in particular in sections [0009], [0015] to [0037], [0053], [0071], [0171], [0174] to [0191], [0274] and [0396], Claims 53 to 114, 188 to 206 and 344 to 355 and Tables 1 to 3. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0255] to [0261] and [0269] and Tables 6 and 7.

WO2007136762 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, hydrocarbons and fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 2 to 4 and 19 to 20, Figures 2 to 4, exemplary embodiments 2 to 7 and Claims 4, 8 to 27 and 33. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular on pages 19 to 20, in Table 10 and Figure 10.

WO2011019858 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0015] to [0020],

[0064] to [0074], [0085] to [0086] and [0092] to [0099], exemplary embodiments 1 to 13, Figure 1 and Claims 1 to 14. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0004] to [0007] and [0075] to [0080] and exemplary embodiments 1 to 13.

WO2009140695 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hydrocarbons, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention in particular in sections [0031] to [0040], [0051] and [0214] to [0233], exemplary embodiments 5 to 24 and 28 to 30, Table 1, Figure 40, and Claims 29 to 30. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0023] to [0030], [0056], [0066] to [0069] and [0193] to [0208], Table 1, Figure 39, exemplary embodiments 5 to 24 and 28 to 30 and Claims 69 to 74.

WO2011008535 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular carboxylic acids, hydroxycarboxylic acids and their lactones from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0023] to [0024] and [0133] to [0158], Figure 13, Claims 39 and 45 to 47 and exemplary embodiments 1 to 5. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0017] to [0022], [0084] to [0132], Figures 2 to 12, Claims 31 to 37 and 40 to 44 and exemplary embodiments 1 to 5.

WO2010063031 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more microbial oil from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0007], [0092] to [0100], [0181] to [0183] and [0199] to [0213]. The document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0191] to [0194] and Tables 4 and 5.

WO2010063032 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more microbial oil from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0007], [0092] to [0100], [0181] to [0183] and [0199] to [0213]. The

document also describes enzymes E_{viii} which are preferred according to the invention and their sequences, in particular in sections [0191] to [0194] and Tables 4 and 5.

Specific enzymes E_{ix}

In cells which are preferred according to the invention, the enzyme E_{ix} is one which comprises sequences selected from among YP_887275.1 (encoded by SEQ ID No. 117), ABI83656.1 (encoded by SEQ ID No.: 122), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, particularly preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight) [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{ix} is generally understood in particular as meaning the synthesis of lauryl aldehyde, NADP, AMP and 2 P_i from lauric acid, ATP, NADPH and H^+.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms including a fourth genetic modification within the meaning of the invention listed hereinbelow are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2011019858 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0004] to [0008], [0064] to [0074], [0085] to [0086], [0095] to [0099]. The document also describes enzymes E_{ix}

which are preferred according to the invention and their sequences, in particular in sections [0008] to [0009], [0074] and [0081] to [0082] and exemplary embodiments 1 to 13.
WO2010135624 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular carboxylic acids, hydroxycarboxylic acids and their lactones, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0005], [0067] to [0085] and [0092] to [0102], Claims 13 to 17 and exemplary embodiments 1 to 4. The document also describes enzymes E_{ix} which are preferred according to the invention and their sequences, in particular in sections [0005] to [0006] and [0086] to [0090], Figures 3 to 7, Claim 28 and exemplary embodiments 1 to 4.
WO2010062480 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0022] to [0174] and [0292] to [0316], exemplary embodiments 1 and 3 to 8, Figure 9 and Claims 17 and 24. The document also describes enzymes E_{ix} which are preferred according to the invention and their sequences, in particular in sections [0019] to [0032] and [0263] to [0286], Table 1, Figures 6 to 8 and exemplary embodiments 1 and 3 to 8.
WO201042664 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0236] to [0261], exemplary embodiment 2, Figure 1 and 5 and Claim 25. The document also describes enzymes E_{ix} which are preferred according to the invention and their sequences, in particular in sections [0211] to [0233], Figures 2 to 4 and exemplary embodiments 1 to 2.

Specific enzymes E_x

In cells which are preferred according to the invention, the enzyme E_x is one which comprises sequences selected from among BAB85476.1 (encoded by SEQ ID No. 77), YP_047869.1

(encoded by SEQ ID No. 79 or 81), YP_959486.1 (encoded by SEQ ID No. 83), YP_959769.1 (encoded by SEQ ID No. 139), B9TSP7.1 (encoded by SEQ ID No. 141), and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, particularly preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_x is generally understood in particular as meaning the synthesis of lauryl alcohol and $NAD(P)^+$ from lauryl-ACP, NAD(P)H and H^+.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms including a fourth genetic modification within the meaning of the invention listed hereinbelow are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2007136762 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty acid esters, wax esters, hydrocarbons and fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular on pages 2 to 4 and 19 to 20, Figures 2 to 4, exemplary embodiments 2 to 7 and Claims 4, 8 to 27 and 33. The document also describes enzymes E_x which are preferred according to the invention and their sequences, in particular on pages 19 to 20, in Table 10 and Figure 10.

WO2011019858 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0015] to [0020],

[0064] to [0074], [0085] to [0086] and [0092] to [0099], exemplary embodiments 1 to 13, Figure 1 and Claims 1 to 14. The document also describes enzymes E_x which are preferred according to the invention and their sequences, in particular in sections [0004] to [0007] and [0075] to [0080] and exemplary embodiments 1 to 13.

WO2009140695 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hydrocarbons, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0031] to [0040], [0051] and [0214] to [0233], exemplary embodiments 5 to 24 and 28 to 30, Table 1, Figure 40, and Claims 29 to 30. The document also describes enzymes E_x which are preferred according to the invention and their sequences, in particular in sections [0023] to [0030], [0056], [0066] to [0069] and [0193] to [0208], Table 1, Figure 39, exemplary embodiments 5 to 24 and 28 to 30 and Claims 69 to 74.

WO2011008535 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular carboxylic acids, hydroxycarboxylic acids and their lactones, from at least one simple carbon source in comparison with their wild type and which are preferably employed according to the invention, in particular in sections [0023] to [0024] and [0133] to [0158], Figure 13, Claims 39 and 45 to 47 and exemplary embodiments 1 to 5. The document also describes enzymes E_x which are preferred according to the invention and their sequences, in particular in sections [0017] to [0022], [0084] to [0132], Figures 2 to 12, Claims 31 to 37 and 40 to 44 and exemplary embodiments 1 to 5.

Specific enzymes E_{xi}

In cells which are preferred according to the invention, the enzyme E_{xi} is one which comprises sequences selected from among ADW41779.1 (encoded by SEQ ID No. 168) and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, particularly preferably 80%, in particular more than 90%, of the activity of the protein with the

corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context the determination of the activity of the enzyme E_{xiii} is generally understood in particular as meaning the reaction of sodium palmitate with hydrogen peroxide to form pentadecene, CO_2 and water.

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms including a fourth genetic modification within the meaning of the invention listed hereinbelow are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2009085278 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular olefins, from at least one simple carbon source in comparison with their wild type and which are preferred according to the invention, in particular in sections [0033] to [0048], [0056] to [0063] and [0188] to [0202], Figure 10, Table 8, exemplary embodiments 5 to 18 and Claims 28 to 51 and 188 to 195. The document also describes enzymes E_{xi} which are preferred according to the invention and their sequences, in particular in sections [0021] to [0032], [0051] to [0055], [0081] to [0084] and [0160] to [0183], Table 8, exemplary embodiments 5 to 18, Claims 1 to 25 and Figures 3, 7 and 9.

Specific enzymes E_{xii}

Microorganisms which are preferred according to the invention are those which are obtained when the microorganisms including a fourth genetic modification within the meaning of the invention listed hereinbelow are employed as starting point by being equipped with a first and second genetic modification and, if appropriate, at least one further genetic modification within the meaning of the invention.

WO2009140695 A1 describes microorganisms which include a fourth genetic modification so that they are capable of forming more fatty acids and fatty acid derivatives, in particular hydrocarbons, from at least one simple carbon source in comparison with their wild type and which are preferred according to the invention, in particular in sections [0031] to [0040], [0051] and [0214] to [0233], exemplary embodiments 5 to 24 and 28 to 30, Table 1, Figure 40, and Claims 29 to 30. The document also describes enzymes E_{xii} which are preferred according to the invention and their sequences, in particular in sections [0023] to [0030], [0056], [0066] to [0069] and [0193] to [0208], Table 1, Figure 38, exemplary embodiments 5 to 24 and 28 to 30 and Claims 69 to 74.

WO2008151149 A2 describes microorganisms which include a fourth genetic modification so that they are capable of forming more microbial oil, from at least one simple carbon source in comparison with their wild type and which are preferred according to the invention, in particular in sections [0009], [0015] to [0037], [0053], [0071], [0171], [0174] to [0191], [0274] and [0396], Claims 53 to 114, 188 to 206 and 344 to 355 and Tables 1 to 3. The document also describes enzymes E_{xii} which are preferred according to the invention and their sequences, in particular in Table 8.

Specific enzymes E_{xiii}

The enzyme E_{xiii} is preferably according to the invention an ω-transaminase of EC 2.6.1.-. Preferred enzymes E_{xiii} are selected from the group:
3HMU_A, AAD41041.1, AAK15486.1, ABE03917.1, ADR60699.1, ADR61066.1, ADR62525.1, AEL07495.1, CAZ86955.1, EFW82310.1, EFW87681.1, EGC99983.1, EGD03176.1, EGE58369.1, EGH06681.1, EGH08331.1, EGH24301.1, EGH32343.1, EGH46412.1, EGH55033.1, EGH62152.1, EGH67339.1, EGH70821.1, EGH71404.1, EGH78772.1, EGH85312.1, EGH97105.1, EGP57596.1, NP_102850.1, NP_106560.1, NP_248912.1, NP_248990.1, NP_354026.2, NP_421926.1, NP_637699.1, NP_642792.1, NP_744329.1, NP_744732.1, NP_747283.1, NP_795039.1, NP_901695.1 (encoded by SEQ ID No. 132), XP_002943905.1, YP_001021095.1, YP_001059677.1, YP_001061726.1, YP_001066961.1, YP_001074671.1, YP_001120907.1, YP_001140117.1, YP_001170616.1, YP_001185848.1, YP_001188121.1, YP_001233688.1, YP_001268866.1, YP_001270391.1, YP_001345703.1,

YP_001412573.1, YP_001417624.1, YP_001526058.1, YP_001579295.1, YP_001581170.1, YP_001668026.1, YP_001669478.1, YP_001671460.1, YP_001685569.1, YP_001747156.1, YP_001749732.1, YP_001765463.1, YP_001766294.1, YP_001790770.1, YP_001808775.1, YP_001809596.1, YP_001859758.1, YP_001888405.1, YP_001903233.1, YP_001977571.1, YP_002229759.1, YP_002231363.1, YP_002280472.1, YP_002297678.1, YP_002543874.1, YP_002549011.1, YP_002796201.1, YP_002801960.1, YP_002875335.1, YP_002897523.1, YP_002912290.1, YP_002974935.1, YP_003060891.1, YP_003264235.1, YP_003552364.1, YP_003578319.1, YP_003591946.1, YP_003607814.1, YP_003641922.1, YP_003674025.1, YP_003692877.1, YP_003755112.1, YP_003896973.1, YP_003907026.1, YP_003912421.1, YP_004086766.1, YP_004142571.1, YP_004147141.1, YP_004228105.1, YP_004278247.1, YP_004305252.1, YP_004356916.1, YP_004361407.1, YP_004378186.1, YP_004379856.1, YP_004390782.1, YP_004472442.1, YP_004590892.1, YP_004612414.1, YP_004676537.1, YP_004693233.1, YP_004701580.1, YP_004701637.1, YP_004704442.1, YP_108931.1, YP_110490.1, YP_168667.1, YP_237931.1, YP_260624.1, YP_262985.1, YP_271307.1, YP_276987.1, YP_334171.1, YP_337172.1, YP_350660.1, YP_351134.1, YP_364386.1, YP_366340.1, YP_369710.1, YP_370582.1, YP_426342.1, YP_440141.1, YP_442361.1, YP_468848.1, YP_521636.1, YP_554363.1, YP_608454.1, YP_610700.1, YP_614980.1, YP_622254.1, YP_625753.1, YP_680590.1, YP_751687.1, YP_767071.1, YP_774090.1, YP_774932.1, YP_788372.1, YP_858562.1, YP_928515.1, YP_983084.1, YP_995622.1, ZP_00948889.1, ZP_00954344.1, ZP_00959736.1, ZP_00998881.1, ZP_01011725.1, ZP_01037109.1, ZP_01058030.1, ZP_01076707.1, ZP_01103959.1, ZP_01167926.1, ZP_01224713.1, ZP_01442907.1, ZP_01446892.1, ZP_01550953.1, ZP_01625518.1, ZP_01745731.1, ZP_01750280.1, ZP_01754305.1, ZP_01763880.1, ZP_01769626.1, ZP_01865961.1, ZP_01881393.1, ZP_01901558.1, ZP_02145337.1, ZP_02151268.1, ZP_02152332.1, ZP_02167267.1, ZP_02190082.1, ZP_02242934.1, ZP_02360937.1, ZP_02367056.1, ZP_02385477.1, ZP_02456487.1, ZP_02883670.1, ZP_03263915.1, ZP_03263990.1, ZP_03400081.1, ZP_03452573.1, ZP_03456092.1, ZP_03517291.1, ZP_03529055.1, ZP_03571515.1, ZP_03572809.1, ZP_03587785.1, ZP_03588560.1, ZP_03697266.1, ZP_03697962.1, ZP_04521092.1, ZP_04590693.1, ZP_04890914.1, ZP_04891982.1, ZP_04893793.1, ZP_04902131.1, ZP_04905327.1, ZP_04941068.1, ZP_04944536.1, ZP_04945255.1, ZP_04959332.1, ZP_04964181.1, ZP_05053721.1, ZP_05063588.1, ZP_05073059.1, ZP_05077806.1, ZP_05082750.1, ZP_05091128.1,

ZP_05095488.1, ZP_05101701.1, ZP_05116783.1, ZP_05121836.1, ZP_05127756.1, ZP_05637806.1, ZP_05742087.1, ZP_05783548.1, ZP_05786246.1, ZP_05843149.1, ZP_05945960.1, ZP_06459045.1, ZP_06487195.1, ZP_06492453.1, ZP_06493162.1, ZP_06703644.1, ZP_06731146.1, ZP_06839371.1, ZP_07007312.1, ZP_07266194.1, ZP_07374050.1, ZP_07662787.1, ZP_07778196.1, ZP_07797983.1, ZP_08099459.1, ZP_08138203.1, ZP_08141719.1, ZP_08142973.1, ZP_08177102.1, ZP_08185821.1, ZP_08186468.1, ZP_08208888.1, ZP_08266590.1, ZP_08402041.1, ZP_08406891.1, ZP_08522175.1, ZP_08527488.1, ZP_08631252.1, ZP_08636687.1,
in particular NP_901695.1 (encoded by SEQ ID No. 132), ZP_03697266.1, AAD41041.1, YP_002796201.1, ZP_03697962.1, YP_001859758.1, YP_002229759.1, YP_001120907.1, YP_110490.1, ZP_04964181.1, YP_774932.1, YP_001766294.1, YP_001581170.1, YP_622254.1, ZP_03588560.1, YP_001809596.1, YP_370582.1, ZP_03572809.1, NP_248990.1, YP_001888405.1, ZP_04905327.1, YP_001061726.1, YP_001668026.1, ZP_01750280.1, ZP_07778196.1, EGH71404.1, NP_744329.1, YP_004147141.1, ADR61066.1, ZP_05783548.1, YP_004701637.1, YP_366340.1, YP_003264235.1, EGD03176.1, YP_001268866.1, ZP_01901558.1, ZP_05121836.1, YP_003692877.1, ZP_03517291.1, YP_002974935.1, YP_001668026.1, ADR61066.1, NP_744329.1, YP_001268866.1, YP_004701637.1, ZP_08142973.1, ADR62525.1, YP_610700.1, NP_747283.1, ADR62525.1, YP_001270391.1, YP_004704442.1, YP_610700.1, YP_001747156.1, ZP_08138203.1, ZP_07266194.1, EGH70821.1, YP_351134.1, EGH32343.1, EGH08331.1, EGH67339.1, YP_001668026.1, YP_004701637.1, YP_237931.1, ZP_03400081.1, ZP_05116783.1, ZP_01550953.1, ZP_07662787.1, YP_928515.1, YP_788372.1, YP_001021095.1, ZP_07797983.1, YP_003578319.1, YP_004305252.1, NP_248912.1, ZP_08636687.1, YP_003912421.1, YP_751687.1, ZP_08142973.1, YP_271307.1, ZP_05082750.1, YP_001417624.1, YP_353455.1,
and especially preferably NP_901695.1 (encoded by SEQ ID No. 132), YP_353455.1, and
proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with

the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{xiii} is generally understood in particular as meaning the conversion of ω-oxo lauric acid and/or its methyl ester to give ω-amino lauric acid and/or its methyl ester.

E_{xiv}, auxiliary enzyme for E_{xiii}

For an increased activity of the enzyme E_{xiii}, it may be beneficial to employ, in place of the enzyme E_{xiii} alone, the combination of an enzyme E_{xiii} paired with an enzyme E_{xiv}, which catalyses the conversion of an α-keto carboxylic acid to an amino acid, the enzyme E_{xiv} is preferably an amino acid dehydrogenase, such as, for example, serine dehydrogenases, aspartate dehydrogenases, phenylalanine dehydrogenases and glutamate dehydrogenases, especially preferably an alanine dehydrogenase of EC 1.4.1.1.
Such preferred alanine dehydrogenases are selected from among EGR93259.1, YP_004743277.1, YP_004741620.1, YP_004737294.1, YP_002509853.1, YP_002492255.1, YP_002489845.1, YP_002481919.1, YP_001819330.1, YP_004728333.1, ZP_08670930.1, YP_004672392.1, YP_004467026.1, YP_004326214.1, YP_002349951.1, YP_001674437.1, YP_003921585.1, YP_001699731.1, YP_004720756.1, YP_004719515.1, EGQ22316.1, EGQ21760.1, YP_004689232.1, YP_004698526.1, YP_004694875.1, EGP67576.1, YP_001832691.1, YP_001760857.1, AEJ53875.1, AEJ42949.1, YP_004392931.1, YP_004404798.1, YP_004374160.1, YP_004303162.1, YP_004196134.1, YP_004178581.1, YP_004163857.1, YP_004161555.1, YP_004099081.1, YP_004101986.1, YP_004042336.1, YP_003994181.1, YP_003966543.1, YP_003913256.1, YP_003825828.1, YP_003806106.1, YP_003686355.1, YP_003678575.1, YP_003654745.1, YP_003651439.1, YP_003637111.1, YP_003631815.1, YP_003300711.1, YP_002886396.1, ZP_03493991.1, YP_001890813.1, YP_001888849.1, YP_001554753.1, YP_001529018.1, YP_001528954.1, YP_001502090.1, YP_001412833.1, YP_001363812.1, YP_923679.1, NP_440110.1,

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and especially preferably NP_391071.1.
and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, to be more precise in a system in which pyruvate is converted into alanine.

Fifth genetic modification for suppressing the degradation of carboxylic acids and carboxylic acid derivatives

Furthermore preferred according to the invention are microorganisms which include a fifth genetic modification which comprises an activity of at least one of the enzymes selected from the group

E_a acyl-CoA synthetase, preferably of EC 6.2.1.3, which catalyses the synthesis of an acyl-coenzyme A thioester,

E_b acyl-CoA dehydrogenase, preferably of EC 1.3.99.-, EC 1.3.99.3 or EC 1.3.99.13, which catalyses the oxidation of an acyl-coenzyme A thioester to give the corresponding enoyl-coenzyme A thioester,

E_c acyl-CoA oxidase, preferably of EC 1.3.3.6, which catalyses the oxidation of an acyl-coenzyme A thioester to give the corresponding enoyl-coenzyme A thioester,

E_d enoyl-CoA hydratase, preferably of EC 4.2.1.17 or EC 4.2.1.74, which catalyses the hydratization of an enoyl-coenzyme A thioester to give the corresponding 3-hydroxyacyl-coenzyme A thioester,

E_e 3-hydroxyacyl-CoA dehydrogenase, preferably of EC 1.1.1.35 or EC 1.1.1.211, which catalyses the oxidation of a 3-hydroxyacyl-coenzyme A thioester to give the corresponding 3-oxoacyl-coenzyme A thioester, and

E_f acetyl-CoA acyltransferase, preferably of EC 2.3.1.16, which catalyses the transfer of an acetyl residue from a 3-oxoacyl-coenzyme A thioester to coenzyme A and thus generates an acyl-coenzyme A thioester which is shortened by two carbon atoms,

which is reduced in comparison with the enzymatic activity of the wild type of the microorganism.

The technical effect of this is that the drain of the carboxylic acids and carboxylic acid derivatives formed in larger amounts due to the first genetic modification, but also of those formed in larger amounts due to the second, third and fourth genetic modification, is prevented.

The wording "activity which is reduced in comparison with its wild type" is preferably understood as meaning an activity which is reduced by at least 50%, especially preferably by at least 90%, more preferably by at least 99.9%, even more preferably by at least 99.99% and most preferably by at least 99.999%, based on the wild type activity. The wording "reduced activity" also comprises no detectable activity ("zero activity"). The reduction of the activity of a specific enzyme can be effected for example by the targeted mutation or by other means known to a person skilled in the art for reducing the activity of a specific enzyme. Other methods of reducing enzymatic activities in microorganisms are known to a person skilled in the art. Methods of choice here are, in particular, molecular-biological techniques. Information on the modification and reduction of protein expressions and reduced enzymatic activity which these entail specifically for *Candida,* in particular for interrupting specific genes, can be found by the skilled worker in WO91/006660 and WO03/100013.

Microorganisms which are preferred according to the invention are characterized in that the reduction of the enzymatic activity is achieved by modifying a gene comprising a nucleic acid sequence encoding the abovementioned enzymes, the modification being selected from the group comprising, preferably composed of, insertion of foreign DNA into the gene, deletion of at

least parts of the gene, point mutations in the gene sequence, RNA interference (siRNA), antisense RNA or modification (insertion, deletion or point mutations) of regulatory sequences which flank the gene. In this context, foreign DNA is understood as meaning any DNA sequence which is "foreign" to the gene (but not the organism). In this context it is especially preferred that the gene is interrupted by inserting a selection marker gene, the foreign DNA thus being a selection marker gene, where the insertion has preferably been effected by homologous recombination into the gene locus. In this context, it may be advantageous to extend the selection marker gene by further functionalities which, in turn, make possible a subsequent removal from the gene. This may be achieved for example by recombination systems which are foreign to the organism, such as a Cre/loxP system or FRT (Flippase Recognition Target) system or by the homologous recombination system which belongs to the organism.
The reduction of the activity of the microorganism according to the invention in comparison with its wild type is determined by abovementioned methods for determining the activity using cell numbers/concentrations which are as equal as possible, the cells having been grown under identical conditions such as, for example, medium, gas supply, agitation.

Specific enzymes E_a

In cells which are preferred according to the invention, the enzyme E_a is one which comprises the sequence NP_416319.1 (SEQ ID No.: 18)

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of

the determination of the activity of the enzyme E_a is generally understood in particular as meaning the synthesis of dodecanoyl-CoA thioester.

Specific enzymes E_b

Furthermore, it is preferred according to the invention that the enzyme E_b in the cells according to the invention is one which comprises sequences selected from among:
YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), ZP_08341828.1, YP_002291517.1, ZP_08393771.1, EFW53921.1, YP_003227327.1, YP_001461409.1, AEG35025.1, YP_002385739.1, EGJ00024.1, ZP_08352177.1, ZP_03070250.1, ZP_08367389.1, EGM63466.1, CBI99746.1, ZP_06660773.1, ZP_08372569.1, YP_309282.2, YP_001879017.1, YP_003497883.1, ACI71032.1, YP_002406464.1, EGB79412.1, EFZ76765.1, ZP_07145000.1, ZP_07151031.1, AAZ87047.1, EFZ56676.1, ZP_06656148.1, EGB35012.1, EGB71054.1, EFW49392.1, ZP_07183316.1, YP_002396328.1, YP_002327805.1, ZP_03027602.1, AAG54546.1, YP_001742341.1, ZP_04538240.1, EFX12717.1, ACI71029.1, NP_285938.2, ZP_03064986.1, ZP_07120505.1, YP_539295.2, ZP_03049609.1, ZP_06652178.1, AAP15817.1, NP_706224.3, ABI99723.1, EGB60663.1, EFW71911.1, EGH38574.1, YP_668186.1, EGK29152.1, EGC05203.1, ZP_02801146.2, YP_687886.1, ZP_08346491.1, EGJ94671.1, EGC94003.1, ZP_08362542.1, YP_002381459.1, AAN78852.1, NP_752308.2, ZP_07173894.1, ZP_08357265.1, ZP_08382276.1, ZP_02902298.1, ZP_04560694.1, ZP_06354226.1, CBY94356.1, NP_459307.1, EGE28353.1, ZP_04657138.1, YP_002225434.1, YP_002635948.1, YP_151638.1, ZP_02663643.1, NP_454921.1, YP_004729161.1, YP_215297.1, YP_001454506.1, YP_001571699.1, YP_003363866.1, EGK30199.1, EGJ91900.1, EGK28208.1, ZP_08497358.1, CBK85993.1, YP_003611563.1, YP_004592567.1, YP_003441061.1, YP_002240296.1, YP_002917946.1, ZP_06549304.1, ZP_06017126.1, YP_001333918.1, AAM28523.1, ZP_08305363.1, YP_001439185.1, EGL74026.1, YP_001175495.1, ZP_05968792.1, YP_003209204.1, YP_003943022.1, YP_004499335.1, ZP_06191708.1, YP_001477183.1, ZP_07951567.1, YP_003740265.1, NP_668276.1, ZP_04637564.1, ZP_04631714.1, CBY26031.1, YP_004297237.1, YP_001007400.1, ZP_04625511.1, YP_069424.1, ZP_04616432.1, ZP_04639135.1, YP_001871363.1, ZP_04620883.1, ZP_06636999.1, ZP_07377275.1,

YP_003929932.1, YP_001722031.1, ZP_04614013.1, ZP_04628476.1, YP_003713213.1, YP_003530236.1, CBX79727.1, YP_004114694.1, YP_001908526.1, ADP11689.1, YP_002649711.1, YP_003469212.1, YP_003519171.1, YP_051564.1, ZP_03833764.1, ZP_03827249.1, NP_928504.1, YP_004211704.1, ZP_07681706.1, YP_003018849.1, YP_003260788.1, YP_003042091.1, ZP_05973896.1, ZP_03317495.1, ZP_02958330.2, EFW60358.1, EGI98786.1, ZP_06127315.2, YP_002150121.1, ZP_03842196.1, YP_003884303.1, YP_003003248.1, YP_003334792.1, ZP_03379559.1, CBA73629.1, YP_002986552.1, ZP_06538530.1, ZP_01258771.1, ZP_04921840.1, ZP_06180371.1, ZP_08308836.1, ZP_06174994.1, YP_001446380.1, ZP_01237449.1, ZP_01161468.1, ZP_01222040.1, ZP_06038476.1, ZP_05925639.1, ZP_06154677.1, ZP_02195704.1, ZP_01989646.1, ZP_01868523.1, YP_131060.1, ZP_05722161.1, ZP_05716057.1, NP_798668.1, EGF45205.1, ZP_05120764.1, EGR07881.1, ZP_08100412.1, ZP_04919383.1, ZP_06054287.1, YP_002156761.1, YP_205315.2, ZP_04961417.1, ZP_06050299.1, ZP_08103013.1, ZP_01949008.1, NP_231862.1, AEA79156.1, ZP_06081122.1, ZP_04418155.1, YP_001217747.1, ZP_04413631.1, NP_935312.1, ZP_01977990.1, NP_760770.1, YP_004188005.1, YP_002810906.1, ZP_05884155.1, ZP_05946273.1, ZP_01065180.1, ZP_01815735.1, YP_002417909.1, YP_002263750.1, YP_856109.1, ZP_07744057.1, ZP_08520214.1, ZP_06034047.1, YP_004565576.1, ZP_05881167.1, ZP_00991316.1, YP_734276.1, ADT86286.1, YP_001142550.1, YP_869958.1, ZP_08566610.1, ZP_05876732.1, YP_001366225.1, YP_001094233.1, ADV54653.1, YP_963612.1, YP_738268.1, YP_001502248.1, YP_004391846.1, YP_002311644.1, YP_002358241.1, YP_001050670.1, ZP_07390237.1, YP_001674114.1, YP_001554497.1, NP_718122.1, YP_001760976.1, YP_927745.1, YP_562771.1, YP_003557130.1, ZP_02159449.1, YP_003913548.1, YP_001473736.1, YP_750554.1, ZP_01897495.1, YP_268985.1, ZP_01042474.1, ZP_08570996.1, YP_004427315.1, ZP_07010199.1, YP_156047.1, ZP_07097521.1, YP_004467113.1, ZP_01614110.1, YP_340459.1, YP_004434754.1, YP_662062.1, YP_004068195.1, ZP_08409704.1, ZP_08622396.1, ZP_01135962.1, ZP_03560927.1, ZP_04716612.1, EGB41427.1, EGP48304.1, EFV84045.1, ZP_08505249.1, ZP_06688896.1, YP_003980530.1, YP_003168652.1, YP_003146346.1, YP_001250478.1, YP_095752.1, YP_124009.1, CBW99992.1, YP_284763.1, YP_127029.1, YP_746940.1, ZP_07663653.1, ZP_03349444.1, YP_002354470.1, YP_004145615.1, YP_003524477.1, ZP_03698069.1, YP_003376672.1, ZP_06188282.1, EFW81359.1,

EGH83675.1, EGH67821.1, EFW83732.1, YP_273865.1, NP_902393.1, ZP_06457469.1, EGH99235.1, ZP_03397893.1, ZP_07004262.1, ZP_06732661.1, ZP_07263971.1, EGH75297.1, NP_888341.1, EGH31566.1, EGH45251.1, NP_643363.1, EGH24154.1, EGH92666.1, EGH73945.1, EGH12424.1, NP_793629.1, ZP_06705890.1, YP_234714.1, EGH62932.1, EGH52925.1, ZP_01126966.1, NP_841588.1, ZP_05109483.1, YP_003847638.1, YP_004294524.1, ZP_02244088.1, NP_884586.1, ZP_08176463.1, ZP_04588788.1, YP_450732.1, ZP_08185386.1, YP_001914265.1, YP_003527565.1, YP_004696148.1, NP_638218.1, ZP_05046817.1, YP_343737.1, ZP_07652844.1, YP_004227922.1, YP_364921.1, YP_001632020.1, NP_744048.1, YP_001898007.1, YP_003145987.1, YP_558241.1, YP_410795.1, YP_001895310.1, YP_002980410.1, ZP_06841648.1, YP_258889.1, YP_931967.1, YP_003760619.1, YP_002029446.1, YP_004474743.1, YP_158312.1, YP_004380764.1, YP_001973352.1, CBJ39115.1, YP_349912.1, YP_003753442.1, ZP_05135288.1, YP_004700980.1, YP_927690.1, YP_001269130.1, YP_742956.1, ADR61321.1, YP_001347709.1, YP_004355482.1, YP_003907207.1, NP_251505.1, ZP_04929120.1, NP_518658.1, YP_002871500.1, ZP_01451059.1, EGM21899.1, YP_001187411.1, ZP_08570514.1, ZP_07794119.1, YP_004391835.1, YP_002256385.1, ZP_07774414.1, YP_855885.1, YP_563120.1, YP_001172167.1, YP_004713921.1, ZP_08138366.1, AEA83572.1, YP_003746704.1, ZP_08521441.1, ZP_05061205.1, YP_001667709.1, YP_750573.1, YP_607261.1, ZP_05118288.1, YP_002311716.1, NP_718079.1, YP_003777020.1, ZP_06052248.1, ZP_00943163.1, ZP_08309312.1, AEG70141.1, YP_001748377.1, YP_001857928.1, YP_001094176.1, YP_003604813.1, ZP_01947893.1,

in particular

EFW81359.1, EGH83675.1, EGH67821.1, EFW83732.1, YP_273865.1, ZP_06457469.1, EGH99235.1, ZP_03397893.1, ZP_07004262.1, ZP_07263971.1, EGH75297.1, EGH31566.1, EGH45251.1, EGH24154.1, EGH92666.1, EGH73945.1, EGH12424.1, NP_793629.1, YP_234714.1, EGH62932.1, EGH52925.1, ZP_04588788.1, NP_744048.1, YP_258889.1, YP_004474743.1, YP_004380764.1, YP_349912.1, YP_004700980.1, YP_001269130.1, ADR61321.1, YP_001347709.1, YP_004355482.1, NP_251505.1, ZP_04929120.1, YP_002871500.1, EGM21899.1, YP_001187411.1, ZP_07794119.1, ZP_07774414.1, YP_001172167.1, YP_004713921.1, ZP_08138366.1, AEA83572.1, YP_001667709.1, YP_607261.1, YP_001748377.1, YP_260045.1, YP_002873091.1, ZP_07775826.1,

CAC34855.1, EGH11916.1, ZP_05641615.1, ZP_06480669.1, ZP_06480668.1, ZP_05641616.1, ZP_06492823.1, ZP_06492821.1, EGH11920.1, EGH25319.1, ZP_06492824.1, ADX52254.1, YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), ZP_08341828.1, YP_002291517.1, YP_003227327.1, YP_001461409.1, AEG35025.1, YP_002385739.1, ZP_08352177.1, ZP_03070250.1, ZP_08367389.1, CBI99746.1, ZP_06660773.1, ZP_08372569.1, YP_003497883.1, ACI71032.1, YP_002406464.1, EGB79412.1, EFZ76765.1, ZP_07145000.1, ZP_07151031.1, EFZ56676.1, ZP_06656148.1, EGB35012.1, EGB71054.1, ZP_07183316.1, YP_002396328.1, YP_002327805.1, ZP_03027602.1, AAG54546.1, YP_001742341.1, ABE05764.1, EFX12717.1, ACI71029.1, NP_285938.2, ZP_07120505.1, YP_539295.2, ZP_03049609.1, ZP_06652178.1, ABI99723.1, EGB60663.1, EFW71911.1, EGH38574.1, YP_668186.1, ZP_02801146.2, ZP_08346491.1, ZP_08362542.1, AAN78852.1, NP_752308.2, ZP_07173894.1, ZP_08357265.1, ZP_08382276.1, AAM28523.1, ZP_07097521.1, EGB41427.1, EGB41426.1, BAA07583.1, ZP_07100038.1, CAX20347.1

and especially preferably

NP_744048.1, YP_004700980.1, YP_001269130.1, ADR61321.1, YP_001667709.1, YP_001748377.1, YP_258889.1, YP_349912.1, YP_002871500.1, ZP_07774414.1, YP_260045.1, YP_002873091.1, ZP_07775826.1, CAC34855.1, YP_001172167.1, YP_004713921.1, AEA83572.1, YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), BAA07583.1, ZP_07594808.1,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of

the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to give 2-dodecenoyl-CoA thioester.

Specific enzymes E_c

Furthermore, it is preferred according to the invention that the enzyme E_c in the cells according to the invention is one which comprises sequences selected from among:
YP_003571780.1, YP_445820.1, YP_634556.1, YP_004665862.1, ZP_01461690.1, YP_921666.1, YP_002778910.1, ZP_08550394.1, YP_003384289.1, YP_001195727.1, YP_702012.1, ZP_04384437.1, YP_002765110.1, ZP_04996322.1, ZP_08195144.1, ZP_04700546.1, YP_954595.1, YP_004736804.1, ADW07059.1, YP_001827916.1, ZP_04691466.1, YP_001109453.1, ZP_08240125.1, YP_003272226.1, YP_004053469.1, ZP_06272176.1, YP_004491616.1, YP_001133991.1, YP_001071715.1, YP_290295.1, YP_003193744.1, YP_001704317.1, YP_004008413.1, YP_004655806.1, YP_640598.1, ZP_08153802.1, ZP_00995173.1, ZP_05225674.1, YP_888747.1, YP_003114111.1, YP_004522832.1, ZP_06848773.1, ZP_08203814.1, YP_001851901.1, EGO40578.1, YP_003134974.1, ZP_07282448.1, YP_003770185.1, YP_881295.1, YP_004336131.1, NP_961035.1, YP_004164861.1, YP_003681133.1, ZP_04749633.1, ZP_07718288.1, ZP_01201898.1, YP_004223976.1, YP_118690.1, YP_905275.1, BAE47462.1, YP_831622.1, YP_003407476.1, ZP_01129477.1, YP_003645654.1, YP_004454693.1, YP_002487953.1, YP_004084231.1, YP_003836912.1, YP_004241154.1, ZP_07706098.1, YP_001855531.1, ZP_08124588.1, YP_947882.1, BAE47461.1, YP_003327670.1, YP_001363757.1, YP_004601796.1, YP_001625220.1, YP_003638017.1, ZP_06501585.1, YP_004404736.1, YP_062974.1, YP_002957230.1, YP_003316209.1, YP_003149881.1, YP_001221553.1, YP_003162313.1, ZP_03978917.1, YP_001708860.1, ZP_05912043.1, ZP_06806059.1, YP_003155732.1, YP_002835700.1, YP_003916799.1, ZP_03936415.1, ZP_07090640.1, ZP_08516453.1, AAB97825.1, YP_004541029.1, YP_004606508.1, YP_001801238.1, ZP_07989876.1, YP_004761186.1, YP_002883572.1, ZP_08023616.1, ZP_05847263.1, YP_251740.1, ZP_03394212.1, YP_001107648.1, YP_002872770.1, YP_001821654.1, ZP_08233739.1, AAD12170.1, ZP_08215859.1, AAD40800.1, ZP_05005905.1, ADW07311.1, YP_348592.1, NP_824883.1, NP_627459.1, YP_001828149.1, ZP_05525554.1,

ZP_08240364.1, ZP_07299658.1, ZP_06582153.1, ZP_06921827.1, ZP_04703961.1, BAJ27090.1, ZP_06592678.1, ZP_04691265.1, YP_001751500.1, BAJ31579.1, preferably YP_003571780.1, YP_445820.1, YP_634556.1, YP_004665862.1, ZP_01461690.1, YP_921666.1, YP_002778910.1, ZP_08550394.1, YP_003384289.1, YP_001195727.1, YP_702012.1, ZP_04384437.1, YP_002765110.1, ZP_04996322.1, ZP_08195144.1, ZP_04700546.1, YP_954595.1, YP_004736804.1, ADW07059.1, YP_001827916.1, ZP_04691466.1, YP_001109453.1, ZP_08240125.1, YP_003272226.1, YP_004053469.1, ZP_06272176.1, YP_004491616.1, YP_001133991.1, YP_001071715.1, YP_290295.1, YP_003193744.1, YP_001704317.1, YP_004008413.1, YP_004655806.1, YP_640598.1, ZP_08153802.1, ZP_00995173.1, ZP_05225674.1, YP_888747.1, YP_003114111.1, YP_004522832.1, ZP_06848773.1, ZP_08203814.1, YP_001851901.1, EGO40578.1, YP_003134974.1, ZP_07282448.1, YP_003770185.1, YP_881295.1, YP_004336131.1, NP_961035.1, YP_004164861.1, YP_003681133.1, ZP_04749633.1, ZP_07718288.1, ZP_01201898.1, YP_004223976.1, YP_118690.1, YP_905275.1, BAE47462.1, YP_831622.1, YP_003407476.1, ZP_01129477.1, YP_003645654.1, YP_004454693.1, YP_002487953.1, YP_004084231.1, YP_003836912.1, YP_004241154.1, ZP_07706098.1, YP_001855531.1, ZP_08124588.1, YP_947882.1, BAE47461.1, YP_003327670.1, YP_001363757.1, YP_004601796.1, YP_001625220.1, YP_003638017.1, ZP_06501585.1, YP_004404736.1, YP_062974.1, YP_002957230.1, YP_003316209.1, YP_003149881.1, YP_001221553.1, YP_003162313.1, ZP_03978917.1, YP_001708860.1, ZP_05912043.1, ZP_06806059.1, YP_003155732.1, YP_002835700.1, YP_003916799.1, ZP_03936415.1, ZP_07090640.1, ZP_08516453.1, AAB97825.1, YP_004541029.1, YP_004606508.1, YP_001801238.1, ZP_07989876.1, YP_004761186.1, YP_002883572.1, ZP_08023616.1, ZP_05847263.1, YP_251740.1,

and especially preferably YP_002835700.1, ZP_03936415.1, BAE47461.1, YP_001801238.1, ZP_03978917.1, ZP_03394212.1, ZP_05847263.1, ZP_08516453.1, YP_004606508.1, YP_251740.1, ZP_07090640.1, ZP_07989876.1, YP_004761186.1,

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with

the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_c is generally understood in particular as meaning oxidation of dodecanoyl-CoA thioester to give 2-dodecenoyl-CoA thioester.

Specific enzymes E_d and E_e

Furthermore, it is preferred according to the invention that the enzyme E_d or E_e in the cells according to the invention is one which comprises sequences selected from among: ZP_07164313.1, NP_418288.1, YP_003231641.1, EGM59778.1, EFZ53307.1, AAA23750.1, ZP_07192215.1, YP_001460638.1, YP_001727088.1, EGK16564.1, ZP_08380619.1, ZP_07136310.1, CAB40809.1, NP_839030.1, ZP_07690617.1, EGC97039.1, ZP_07103516.1, ZP_03027888.1, ZP_07121980.1, YP_002414996.1, EGP22873.1, EGJ82677.1, EGB59499.1, ZP_07118761.1, YP_002409078.1, YP_002295407.1, EGE62412.1, EGB69560.1, ZP_06655948.1, ZP_06664574.1, ZP_03070699.1, ZP_07145404.1, ZP_08376058.1, EGB85466.1, ZP_07189176.1, ZP_02999920.1, ZP_08356523.1, ZP_06659936.1, ZP_07139396.1, YP_001746178.1, YP_002384700.1, ZP_07098889.1, CBG37051.1, ZP_04873109.1, CBJ03626.1, ZP_08366395.1, ZP_03066301.1, BAI57243.1, YP_001465330.1, YP_405325.1, NP_312801.1, EGI89589.1, EGC09628.1, EFW73050.1, ZP_07221474.1, EGB39932.1, EFW72281.1, ZP_07154547.1, YP_002331616.1, EGB76756.1, EFZ75005.1, ZP_07449248.1, NP_756652.2, ZP_04006347.1, NP_290476.1, EGH36687.1, YP_671920.1, ZP_08350773.1, EGC05062.1, ZP_07174622.1, CAP78309.1, ZP_08361145.1, YP_002400350.1, ZP_08386169.1, EFU60028.1, ZP_02904283.1, YP_859447.1, YP_543379.2, NP_462868.1, ZP_02663494.1, ACY91152.1, ZP_03221347.1, YP_001591071.1, YP_002639596.1, EFY10009.1, ZP_04656823.1, ZP_03213459.1, ZP_02701437.1, ZP_02347126.1, YP_002217909.1, ZP_02658976.1, YP_002245833.1, YP_002228260.1, YP_001451793.1, EGE35935.1, YP_002047992.1, ZP_02834645.1, ZP_02669606.1, YP_001572623.1, ZP_03075319.1, YP_002148908.1, YP_004591813.1,

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in particular

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and especially preferably

NP_744285.1, YP_004701152.1, ADR61111.1, YP_001268914.1, YP_001667915.1, ABP88736.1, YP_001748526.1, Q9AHY3.2, YP_004713990.1, YP_001172246.1, AEA83639.1, AEA82038.1, YP_001170648.1, YP_004712521.1, YP_002871195.1, YP_349607.1, YP_259059.1, ZP_07774142.1, NP_418288.1, NP_416843.1, ZP_07593201.1, ZP_07590743.1,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference

protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_d and E_e is generally understood in particular as meaning conversion of 2-dodecenoyl-CoA thioester into 3-oxododecanoyl-CoA thioester.

Specific enzymes E_f

Furthermore, it is preferred according to the invention that the enzyme E_f in the cells according to the invention is one which comprises sequences selected from among: YP_026272.1, YP_002389323.1, EGB30581.1, YP_001460637.1, YP_001727089.1, CAB40810.1, EGK16565.1, NP_709649.1, YP_001882545.1, ZP_08356522.1, ZP_06664573.1, AAA67642.1, ADA76222.1, EGK17812.1, YP_405326.1, YP_003236969.1, ZP_06659935.1, YP_410143.1, NP_290475.1, ZP_03027945.1, EFZ59092.1, YP_002295406.1, CBG37050.1, EGP22872.1, EGE62411.1, EGC97040.1, ZP_05435276.1, YP_002400349.1, EGB59498.1, EFW54756.1, ZP_08361144.1, YP_001465329.1, YP_002384701.1, YP_002409079.1, ZP_06655947.1, YP_002414995.1, EGB69559.1, YP_859446.1, EGC05061.1, ZP_02904263.1, ZP_08386168.1, YP_543378.1, ZP_08366394.1, ZP_03066325.1, YP_001746177.1, ZP_07154548.1, ZP_03070708.1, NP_756651.1, YP_312775.1, YP_671919.1, YP_002331615.1, YP_003367348.1, ZP_07449249.1, ZP_04558440.1, ZP_06354347.1, YP_001451792.1, YP_004732312.1, ZP_06938722.1, NP_457770.1, ZP_02834646.1, ZP_02658975.1, ZP_03221210.1, EFY10008.1, YP_001591070.1, YP_218866.1, YP_003943710.1, ZP_03086141.1, ZP_03163187.1, ZP_08495783.1, EGE35936.1, YP_003615423.1, YP_002228261.1, YP_002148907.1, ZP_05970963.1, YP_002241092.1, YP_004591812.1, YP_001178656.1, ZP_08302761.1, YP_002917175.1, YP_001337974.1, Q9F0Y6.1, ZP_06014072.1, YP_001439748.1, YP_003208639.1, 3GOA_A, YP_003739634.1, ZP_06192593.1, YP_001906199.1, YP_001476498.1, YP_003019596.1, YP_003261566.1, ZP_03831341.1, ZP_07380062.1, YP_048334.1, YP_003933022.1, ZP_07953301.1, YP_004114075.1, YP_002647269.1, ADP11111.1, ZP_03827988.1, ZP_06638308.1, YP_004214865.1, YP_003518495.1,

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in particular

YP_790159.1, ZP_06877967.1, NP_251703.1, EGH66370.1, EGH10832.1, YP_349606.1, YP_236359.1, ZP_07263340.1, EGH95844.1, NP_793296.1, 1WDK_C, P28790.2, YP_259060.1, ZP_04587908.1, EGH45981.1, ZP_07774144.1, EGH84449.1, YP_275369.1, ZP_07005686.1, YP_001172247.1, YP_004352962.1, ACP17922.1, YP_002871196.1, ZP_08142929.1, YP_004701153.1, YP_001667916.1, YP_001268913.1, Q93Q11.1, Q9R9W0.1, NP_744286.1, YP_001187077.1, YP_609234.1, YP_004379417.1, YP_004474975.1, ABP88737.1, EGH76239.1, EGH29725.1, ZP_06499584.1, YP_001749490.1, ABF82237.1, YP_004713534.1, CAD76924.1, YP_608369.1, AEA83130.1, YP_001171793.1, YP_788379.1, CAE45106.1, NP_248919.1, YP_001348923.1, ZP_07797976.1, YP_001747677.1, NP_250427.1, AAR83740.1, YP_001668851.1, ZP_06495825.1, YP_004379898.1, EGH60624.1, ZP_04933402.1, YP_001345710.1, Q8VPF1.1, YP_004473788.1, EGH77345.1, EGH44350.1, YP_001188713.1, YP_004380648.1, YP_001188079.1, ZP_08142248.1, YP_004703691.1, ZP_04936650.1, YP_606872.1, YP_610092.1, ADR61907.1, ZP_04934614.1, ZP_07262554.1, YP_001747891.1, Q51956.1, YP_002871766.1, NP_746745.1, YP_001267798.1, YP_004703877.1, EGH73771.1, EGH61062.1, YP_233920.1, YP_258448.1, YP_004702122.1, ZP_03398400.1,

YP_002439726.1, EGH66881.1, YP_004352451.1, YP_001189077.1, YP_237079.1, NP_745423.1, ZP_08139209.1, NP_251630.1, EGH73592.1, ZP_04934925.1, YP_001186637.1, EGH11975.1, YP_276147.1, YP_790233.1, YP_002440908.1, YP_001172996.1, ZP_06878044.1, ZP_07797009.1, EGH21143.1, ZP_06461447.1, ZP_07794257.1, NP_794063.1, ZP_01365347.1, ZP_04928407.1, AAC24332.1, ZP_04929241.1, YP_001670661.1, NP_250691.1, YP_004381309.1, YP_004714773.1, YP_791238.1, YP_001269802.1, ZP_06879064.1, YP_001670851.1, ZP_06498740.1, YP_004381943.1, YP_004378973.1, EGH79619.1, YP_347001.1, YP_347471.1, YP_002874183.1, ZP_07774002.1, ADR60119.1, NP_743536.1, YP_001269653.1, ZP_06482365.1, ADI95330.1, ZP_07003619.1, BAB96553.1, ZP_07777009.1, ABA10831.1, YP_273131.1, YP_259428.1, EFW86233.1, EGH85840.1, ZP_07774597.1, EGH54613.1, YP_004353129.1, YP_002871014.1, YP_001171232.1, EGH67454.1, EFW82139.1, ZP_04590526.1, EGH58132.1, EGH06629.1, EGH99157.1, ZP_05638078.1, NP_790796.1, AEE59172.1, YP_026272.1, YP_002389323.1, EGB30581.1, YP_001460637.1, YP_001727089.1, CAB40810.1, ZP_03049054.1, ZP_08356522.1, ZP_06664573.1, AAA67642.1, YP_003236969.1, ZP_06659935.1, NP_290475.1, ZP_03027945.1, EFZ59092.1, YP_002295406.1, CBG37050.1, EGP22872.1, EGE62411.1, YP_002400349.1, EGB59498.1, ZP_08361144.1, YP_001465329.1, YP_002409079.1, ZP_06655947.1, YP_002414995.1, EGB69559.1, YP_859446.1, ZP_08386168.1, YP_543378.1, ZP_08366394.1, YP_001746177.1, ZP_07154548.1, ZP_03070708.1, NP_756651.1, YP_671919.1, YP_002331615.1, ZP_07449249.1, ZP_06938722.1, ZP_03086141.1, ZP_07189177.1, ZP_07136312.1, EFZ47010.1, ZP_07136311.1, EFZ47009.1, ZP_03026937.1, EGB73439.1, EGP25245.1, ZP_03026966.1, YP_001462757.1, CAP76727.1, YP_670163.1,

and especially preferably

YP_026272.1, AAA67642.1, ZP_07593202.1, YP_004701153.1, YP_001667916.1, YP_001268913.1, Q9R9W0.1, NP_744286.1, ABP88737.1, YP_001749490.1, YP_001747677.1, YP_001668851.1, YP_004703691.1, ADR61907.1, YP_001747891.1, Q51956.1, NP_746745.1, YP_001267798.1, YP_004703877.1, YP_004702122.1, NP_745423.1, AAC24332.1, YP_001670661.1, YP_001269802.1, YP_001670851.1, ADR60119.1, NP_743536.1, YP_001269653.1, ADI95330.1, BAB96553.1, YP_001172247.1, YP_004713534.1, AEA83130.1, YP_001171793.1, YP_001172996.1, YP_004714773.1, YP_001171232.1, YP_349606.1, YP_259060.1, ZP_07774144.1, YP_002871196.1,

ABF82237.1, YP_002871766.1, YP_258448.1, YP_347001.1, YP_347471.1, YP_002874183.1, ZP_07774002.1, ZP_07777009.1, YP_259428.1, ZP_07774597.1, YP_002871014.1,

AAC72881.1, ABB71579.1, CAC19934.1, AAC49180.1 (encoded by SEQ ID No.: 10), AAC49783.1, AAC49179.1, CAB60830.1, ABB71581.1, AAC49269.1, CAC19933.1, CAA54060.1, AAC72882.1, Q39513.1, AAC49784.1, ABO38558.1, ABO38555.1, ABO38556.1, ABO38554.1, ADB79568.1, ADB79569.1, ACQ57188.1, ACQ57189.1, ABK96561.1, ACQ63293.1, ACQ57190.1, Q9SQI3.1, ABU96744.1, ABC47311.1, XP_002324962.1, AAD01982.1, AAB51525.1, ACV40757.1, XP_002309244.1, CBI28125.3, ABD91726.1, XP_002284850.1, XP_002309243.1, XP_002515564.1, ACR56792.1, ACR56793.1, XP_002892461.1, ABI18986.1, NP_172327.1, CAA85387.1, CAA85388.1, ADA79524.1, ACR56795.1, ACR56794.1, CAN81819.1, ACF17654.1, AAB71729.1, ABH11710.1, ACQ57187.1, AAX51637.1, AAB88824.1, AAQ08202.1, AAB71731.1, AAX51636.1, CAC80370.1, CAC80371.1, AAG43858.1, ABD83939.1, AAD42220.2, AAG43860.1, AAG43861.1, AAG43857.1, AAL15645.1, AAB71730.1, NP_001068400.1, EAY86877.1, NP_001056776.1, XP_002436457.1, NP_001149963.1, ACN27901.1, EAY99617.1, ABL85052.1, XP_002437226.1, NP_001151366.1, ACF88154.1, NP_001147887.1, XP_002453522.1, BAJ99650.1, EAZ37535.1, EAZ01545.1, AAN17328.1, EAY86884.1, EEE57469.1, Q41635.1, AAM09524.1, Q39473.1, NP_001057985.1, AAC49001.1, XP_001752161.1, XP_001770108.1, XP_001784994.1, XP_002318751.1, NP_001047567.1, XP_002322277.1, XP_002299627.1, XP_002511148.1, CBI15695.3, XP_002299629.1, XP_002280321.1, CAN60643.1, XP_002459731.1, XP_002975500.1, XP_002962077.1, XP_001773771.1, NP_001151014.1, XP_002317894.1, XP_002971008.1, XP_001774723.1, XP_002280147.1, XP_002526311.1, XP_002517525.1, XP_001764527.1, ABI20759.1, BAD73184.1, XP_002987091.1, XP_002985480.1, CBI26947.3, ABI20760.1, XP_002303055.1, XP_002885681.1, ADH03021.1, XP_002532744.1, EAY74210.1, EEC84846.1, EEE54649.1, AAG35064.1, AAC49002.1, CAD32683.1, ACF78226.1, BAJ96402.1, XP_002462626.1, NP_001130099.1, XP_002462625.1, ABX82799.3, Q42712.1, NP_193041.1, AAB51524.1, NP_189147.1, ABR18461.1, XP_002863277.1, AAC72883.1, AAA33019.1, CBI40881.3, XP_002262721.1, AAB51523.1, NP_001063601.1, ADB79567.1, AAL77443.1, AAL77445.1, AAQ08223.1, AAL79361.1, CAA52070.1, AAA33020.1, CAA52069.1, XP_001785304.1, CAC39106.1, XP_002992591.1, XP_002968049.1, XP_001770737.1, XP_001752563.1,

AAG43859.1, XP_002978911.1, XP_002977790.1, ACB29661.1, XP_002314829.1, XP_002991471.1, EAZ45287.1, XP_002986974.1, EEC73687.1, XP_002312421.1, ACJ84621.1, NP_001150707.1, AAD28187.1, XP_001759159.1, XP_001757193.1, XP_002322077.1, ABE01139.1, XP_002447294.1, AAX54515.1, AAD33870.1, AAX54514.1, CBI15694.3, XP_002270653.1, AAZ83073.1, CAC14164.1, XP_001753224.1, CBI35766.3, ACU22895.1, BAC43222.1, XP_002965875.1, AAX54516.1, XP_002983123.1, XP_002447046.1, ACL52706.1, CAA06001.1, XP_001772711.1,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_f is generally understood in particular as meaning the reaction of 3-oxododecanoyl-CoA thioester and CoA to give decanoyl-CoA thioester and acetyl-CoA.

Sixth genetic modification for enhancing the acyl-ACP thioester synthesis

According to the invention, the microorganisms include a sixth genetic modification so that they are capable of forming more acyl-ACP thioester from at least one simple carbon source in comparison with their wild type. An overview over correspondingly desirable genetic modifications can be found in Fig. 1 of WO2008119082, section 1 (fatty acid production increase/product production increase).

The technical effect of this is that the formation of carboxylic acids and carboxylic acid derivatives which is increased by the first genetic modification, but also of carboxylic acids and

carboxylic acid derivatives which are formed in larger amounts due to the second, third, fourth or fifth genetic modification, is increased even further.

Preferred microorganisms for the production of alkan-1-ols, alkan-1-als, alkan-1-amines, alkanes, olefins, alken-1-als, alken-1-ols and alken-1-amines

If the microorganisms according to the invention are intended to be used in a process for the production of alkan-1-ols, alkan-1-als, alkan-1-amines, alkanes, alken-1-als, alken-1-ols and alken-1-amines and terminal olefins which optionally contain further double bonds, it may be advantageous that the microorganisms according to the invention include a seventh genetic modification comprising an activity of at least one enzyme E_1 that is reduced in comparison with its wild type, selected from the group:

E_{1a} P450 alkane hydroxylases, which preferably catalyse the following reactions:

reduced haem + alkanoic acid (ester) = oxidized haem + ω-hydroxyalkanoic acid (ester) + H_2O,

2 reduced haem + alkanoic acid (ester) = 2 oxidized haem + ω-oxoalkanoic acid (ester) + 2 H_2O

or

3 reduced haem + alkanoic acid (ester) = alkane monoxygenase + 3 oxidized haem + ω-carboxyalkanoic acid (ester) + 3 H_2O and preferably

component of a reaction system composed of the two enzyme components "cytochrome P450 alkane hydroxylase and NADPH-cytochrome P450 oxidoreductase of EC 1.6.2.4" or component of a reaction system composed of the three enzyme components "cytochrome P450 alkane hydroxylase of the type CYP153, ferredoxin-NAD(P)$^+$ reductases of EC 1.18.1.2 or EC 1.18.1.3 and ferredoxin" and

E_{1b} AlkB alkane hydroxylases of EC 1.14.15.3, which preferably catalyse the following reactions: reduced rubredoxin + alkanoic acid (ester) = oxidized rubredoxin + ω-hydroxy-alkanoic acid (ester) + H_2O,

2 reduced rubredoxins + alkanoic acid (ester) = 2 oxidized rubredoxins + ω-oxoalkanoic acid (ester) + 2 H_2O or

3 reduced rubredoxins + alkanoic acid (ester) = alkane monoxygenase + 3 oxidized rubredoxins + ω-carboxyalkanoic acid (ester) + 3 H_2O and preferably

component of a reaction system composed of the three enzyme components "AlkB alkane hydroxylase of EC 1.14.15.3, AlkT rubredoxin-$NAD(P)^+$ reductase of EC 1.18.1.1 or EC 1.18.1.4 and rubredoxin AlkG",

E_{1c} fatty alcohol oxidases of EC 1.1.3.20, which preferably catalyse at least one of the following irreversible reactions:

alkan-1-ol + O_2 = alkan-1-al + H_2O_2 or

alkan-1-al + O_2 = alkanoic acid + H_2O_2,

E_{1d} AlkJ alcohol dehydrogenases of EC 1.1.99.-, which preferably catalyse at least one of the following reversible reactions:

alkan-1-ol + oxidized acceptor = alkan-1-al + reduced acceptor or

alkan-1-al + oxidized acceptor = alkanoic acid + reduced acceptor,

E_{1e} alcohol dehydrogenases of EC 1.1.1.1 or EC 1.1.1.2, which preferably catalyse at least one of the following reversible reactions:

alkan-1-ol + $NAD(P)^+$ = alkan-1-al + NAD(P)H + H^+ or

alkan-1-al + $NAD(P)^+$ = alkanoic acid + NAD(P)H + H^+ and

E_{1f} aldehyde dehydrogenases of EC 1.2.1.3, EC 1.2.1.4 or EC 1.2.1.5, which preferably catalyse the following reversible reaction:

alkan-1-al + $NAD(P)^+$ = alkanoic acid + NAD(P)H + H^+

It may be advantageous in particular for the production of alkan-1-ols that the microorganisms according to the invention have an activity of at least one enzyme E_{1e} and E_{1f} in comparison with their wild type.

WO2010062480 A2 describes microorganisms which are capable of forming more fatty acids and fatty acid derivatives, in particular fatty alcohols, from at least one simple carbon source in comparison with their wild type, in particular in exemplary embodiments 3, 4, 6 and 7. The document also describes enzymes E_{1e} which are preferred according to the invention and their sequences, in particular in Figure 10 and in exemplary embodiments 2 to 7.

If the microorganisms according to the invention are to be used in a process for the production of alkan-1-ols, alkan-1-als, alkan-1-amines and alkanes, it is especially preferred according to the invention that the activity of such enzymes E_{1a} to E_{1f}, which catalyse the above-described reactions of an alkan-1-al to give the corresponding alkanoic acid, is reduced.

If the microorganisms according to the invention are to be used in a process for the production of alkan-1-als, alkan-1-amines, alkanes and 1-alkenes, it is especially preferred according to the invention that the activity of such enzymes E_{1a} to E_{1e}, which catalyse the above-described conversion of an alkan-1-al to give the corresponding alkan-1-ol, is reduced.

If the microorganisms according to the invention are to be used in a process for the production of alkan-1-ols, it is especially preferred according to the invention that the activity of such enzymes E_{1a} to E_{1e}, which catalyse the above-described conversion of an alkan-1-ol to give the corresponding alkan-1-al, is reduced.

Specific enzymes E_{1a}

P450 alkane hydroxylases E_{1a} which are preferred in this context are selected from among the list
AAO73954.1, AAO73953.1, XP_002546279.1, AAA34353.2, P30607.1, XP_002421627.1, XP_718670.1, CAA39366.1, XP_001527524.1, AAO73955.1, AAO73956.1, XP_002546278.1, EEQ43157.1, XP_718669.1, AAA34354.1, P10615.3, XP_002421628.1, 226487, P16141.3, CAA39367.1, Q9Y757.2, XP_001485567.1, AAO73958.1, XP_001383506.2, XP_460111.2, AAO73959.1, Q12586.1, XP_460112.2, AAO73960.1, Q12589.1, AAO73961.1, XP_460110.2, EEQ43763.1, XP_710174.1, EDK41572.2, XP_001482650.1, CAA75058.1, XP_002548818.1, Q12588.1, XP_002422222.1, XP_001383636.2, XP_001525381.1, XP_002548823.1, P30610.1, AAO73952.1, XP_002548428.1, CAA36197.1, XP_002421126.1, AAA34320.1, P16496.3, P30608.1, P24458.1, XP_717999.1, XP_001383817.1, Q9Y758.1, XP_001482092.1, XP_001383710.2, P30609.1, AAB24479.1, XP_457792.1, XP_001524144.1, XP_457727.2, XP_001525578.1, XP_002616743.1, XP_002614836.1, XP_001525577.1, AAO73957.1, Q12585.1, XP_001386440.2, XP_002616857.1, XP_001483276.1, XP_500402.1, EDK39907.2, XP_500560.1, XP_001211376.1, XP_002560027.1, XP_504857.1, XP_500855.1, XP_504406.1, BAA31433.1, XP_500856.1, XP_501148.1, XP_746567.1, XP_001262425.1, XP_001274843.1, XP_002840588.1, XP_002377641.1, XP_001825995.1, XP_001400739.1, XP_718066.1, CAA35593.1, XP_664735.1, XP_002150795.1, XP_500097.1, XP_002483325.1,

XP_504311.1, XP_500273.1, XP_002548817.1, EDP54484.1, XP_755288.1, XP_001260447.1, EFY97851.1, ACD75398.1, ADK36660.1, XP_001213081.1, XP_002377989.1, XP_001826299.1, XP_001554811.1, XP_501667.1, XP_002148942.1, ADK36662.1, XP_002565827.1, P30611.1, XP_001267871.1, XP_002372373.1, EFY84686.1, P43083.1, XP_001263094.1, XP_002148355.1, XP_002568429.1, XP_001817314.1, Q12587.1, XP_001396435.1, XP_001938589.1, XP_001388497.2, XP_663661.1, XP_003295335.1, XP_002152088.1, XP_001212071.1, Q12573.1, XP_002379858.1, XP_001821592.1, XP_002844341.1, XP_001394678.1, ACD75400.1, BAK03594.1, XP_003170343.1, XP_001265480.1, XP_002550661.1, EDP55514.1, XP_001528842.1, XP_749919.1, XP_001593058.1, P30612.1, EGC48494.1, EEH04429.1, XP_001585586.1, XP_003236182.1, XP_001400199.1, EEQ46951.1, XP_721410.1, EGP87864.1, XP_002380808.1, XP_001792771.1, XP_001208515.1, XP_001216161.1, XP_003071804.1, EFW16963.1, XP_002542118.1, XP_001936677.1, EGD95268.1, XP_003015678.1, XP_501748.1, XP_003169562.1, EFY96492.1, XP_682653.1, XP_002421356.1, CAK43439.1, EFY93677.1, XP_747767.1, XP_001244958.1, XP_003019635.1, XP_002847463.1, EGP83273.1, EGR52487.1, XP_002622526.1, XP_002563618.1, CBX99718.1, XP_001552081.1, XP_003066638.1, XP_003176049.1, ACD75402.1, BAA05145.1, XP_002482834.1, XP_001257501.1, XP_001934574.1, XP_001269972.1, XP_001587438.1, XP_001215856.1, XP_002149824.1, XP_001550556.1, XP_003011982.1, XP_001827121.1, XP_003233566.1, XP_003022481.1, EGR47044.1, EFQ34695.1, XP_003170005.1, BAG09241.1, XP_002796370.1, XP_003019300.1, XP_002563873.1, CAK40654.1, EEH19741.1, XP_003012518.1, EGD95716.1, XP_003239409.1, BAJ04363.1, XP_001537012.1, BAE66393.1, EGP85214.1, XP_002487227.1, AAV66104.1, EGE07669.1, XP_362943.2, XP_003016806.1, EFQ27388.1, XP_002384360.1, XP_002836323.1, XP_001274959.1, EFZ03093.1, XP_661521.1, XP_002849803.1, XP_001589398.1, AAR99474.1, XP_003189427.1, XP_001823699.1, XP_364111.1, XP_001262753.1, EFY86805.1, XP_001390153.2, XP_002384738.1, XP_001941811.1, XP_001220831.1, XP_003296981.1, XP_002480829.1, BAD83681.1, XP_001827526.2, XP_369556.1, CAK38224.1, EFQ26532.1, XP_002562328.1, XP_001904540.1, EGO52476.1, XP_002382002.1, XP_001225874.1, XP_958030.2, XP_002540883.1, XP_001908957.1, XP_001559255.1, XP_364102.1, EDP48064.1, XP_365075.1, XP_381460.1, CBX95930.1, XP_003054099.1, XP_361347.2, XP_002846867.1, XP_001214985.1, EFQ35175.1, XP_002479062.1, XP_001908613.1,

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XP_001589816.1, EEH42702.1, XP_001554577.1, XP_001592850.1, YP_691921.1, CAH59968.1, AAS80270.1, CAH59967.1, ACQ99381.2, YP_003810988.1, YP_957888.1, CBW44755.1, ZP_05042596.1, ZP_01913735.1, ZP_05043097.1, ADQ00145.1, YP_004494060.1, ZP_08206912.1, BAE78452.1, NP_114222.1, ACZ56357.1, YP_640381.1, ZP_04384919.1, ZP_08025219.1, ZP_07715822.1, ZP_06847816.1, YP_001702784.1, AEK27137.1, ZP_07716433.1, ZP_08199554.1, YP_004495520.1, YP_345718.1, ZP_08022914.1, YP_001851443.1, BAG50428.1, YP_001135848.1, BAF95905.1, YP_345695.1, ACP39691.1, ACP39664.1, ACP39635.1, ACP39633.1, ACP39710.1, ACP39698.1, ACP39711.1, BAE47475.1, BAE47474.1, ABW76858.1, ACO50699.1, ACP39643.1, ACP39639.1, ACP39708.1, ACM68663.1, ACP39642.1, ACP39684.1, ACP39636.1, ZP_05095005.1, ACP39652.1, BAE47473.1, ACM68664.1, ACP39646.1, ACP39680.1, ACP39692.1, ACP39675.1, ACP39632.1, ZP_05129284.1, ACP39706.1, ACP39695.1, ACM68665.1, ACP39654.1, ACP39665.1, ACP39649.1, BAE47472.1, ACM68668.1, ACP39676.1, ACP39648.1, ACP39647.1, ZP_01102434.1, ACM68666.1, ACP39641.1, ACM68669.1, ZP_01625037.1, ACP39690.1, ACP39696.1, ACP39697.1, ACP39707.1, ACP39682.1, ACP39650.1, ACP39638.1, ZP_05126641.1, CAH04396.1, ACP39658.1, ZP_01102687.1, ACJ06772.1, YP_001413041.1, YP_552058.1, ADE05601.1, ADI19685.1, BAE47479.1, ZP_01626700.1, ZP_01618279.1, CAH61448.1, YP_001411305.1, YP_003591161.1, ZP_01615522.1, ACM68667.1, ACP39651.1, ZP_05095535.1, ZP_01618489.1, NP_418882.1, ADI19983.1, ACP39677.1, BAE47476.1, ACP39655.1, ACP39656.1, ADI19696.1, BAE47477.1, YP_001413399.1, YP_459878.1, BAE47480.1, BAE47481.1, ACP39653.1, BAE47478.1, YP_001681656.1, ZP_01618281.1, ZP_01627262.1, YP_001413057.1, YP_760740.1, YP_001242466.1, YP_001203574.1, CAH61454.1, YP_002129656.1, YP_001672075.1, ACP39709.1, YP_001990805.1, NP_946959.1, YP_001203575.1, YP_783213.1, YP_003059227.1, YP_004110202.1, ACP39645.1, YP_487538.1, CAH61451.1, YP_570816.1, YP_534107.1, YP_001413223.1, YP_001242465.1, YP_557448.1, ZP_08631162.1, NP_773883.1, ZP_00997728.1

and especially preferably

AAO73954.1, AAO73953.1, XP_002546279.1, AAA34353.2, P30607.1, XP_002421627.1, XP_718670.1, CAA39366.1, AAO73955.1, AAO73956.1, XP_002546278.1, EEQ43157.1, XP_718669.1, AAA34354.1, P10615.3, XP_002421628.1, 226487, P16141.3, CAA39367.1,

AAO73958.1, AAO73959.1, Q12586.1, AAO73960.1, Q12589.1, AAO73961.1, EEQ43763.1, XP_710174.1, CAA75058.1, XP_002548818.1, Q12588.1, XP_002422222.1, XP_002548823.1, P30610.1, AAO73952.1, XP_002548428.1, CAA36197.1, XP_002421126.1, AAA34320.1, P16496.3, P30608.1, P24458.1, XP_717999.1, P30609.1, AAB24479.1, AAO73957.1, Q12585.1, XP_718066.1, CAA35593.1, XP_002548817.1, P30611.1, P43083.1, Q12587.1, Q12573.1, XP_002550661.1, P30612.1, EEQ46951.1, XP_721410.1, XP_002421356.1, BAA05145.1, BAG09241.1, CAC24473.1, BAG09240.1, AAA34334.1, BAA05146.1, XP_500402.1, XP_500560.1, XP_504857.1, XP_500855.1, XP_504406.1, BAA31433.1, XP_500856.1, XP_501148.1, XP_500097.1, XP_504311.1, XP_500273.1, XP_501667.1, XP_501748.1, YP_691921.1, CAH59968.1, AAS80270.1, CAH59967.1, ACQ99381.2, YP_003810988.1, YP_957888.1, CBW44755.1, ZP_05042596.1, ZP_01913735.1, ZP_05043097.1, ADQ00145.1, YP_004494060.1, ZP_08206912.1, BAE78452.1, NP_114222.1, ACZ56357.1, YP_640381.1, ZP_04384919.1, ZP_08025219.1, ZP_07715822.1, ZP_06847816.1, YP_001702784.1, AEK27137.1, ZP_07716433.1, ZP_08199554.1, YP_004495520.1, YP_345718.1, ZP_08022914.1, YP_001851443.1, BAG50428.1, YP_001135848.1, BAF95905.1, YP_345695.1, ACP39691.1, ACP39664.1, ACP39635.1, ACP39633.1, ACP39710.1, ACP39698.1, ACP39711.1, BAE47475.1, BAE47474.1, ABW76858.1, ACO50699.1, ACP39643.1, ACP39639.1, ACP39708.1, ACM68663.1, ACP39642.1, ACP39684.1, ACP39636.1, ZP_05095005.1, ACP39652.1, BAE47473.1, ACM68664.1, ACP39646.1, ACP39680.1, ACP39692.1, ACP39675.1, ACP39632.1, ZP_05129284.1, ACP39706.1, ACP39695.1, ACM68665.1, ACP39654.1, ACP39665.1, ACP39649.1, BAE47472.1, ACM68668.1, ACP39676.1, ACP39648.1, ACP39647.1, ZP_01102434.1, ACM68666.1, ACP39641.1, ACM68669.1, ZP_01625037.1, ACP39690.1, ACP39696.1, ACP39697.1, ACP39707.1, ACP39682.1, ACP39650.1 and ACP39638.1

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst,

that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1a} is generally understood in particular as meaning the conversion of lauric acid and/or its methyl ester into ω-hydroxylauric acid and/or its methyl ester.

Specific enzymes E_{1b}

AlkB alkane hydroxylases E_{1b} which are preferred according to the invention are selected from among the list
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in particular YP_001185946.1, Q9WWW6.1, YP_957898.1, YP_957728.1, YP_694427.1, BAC98365.1, ZP_00957064.1, CAC86944.1, YP_001672212.1, CAB59525.1, ACH99213.1, ACH99215.1, ACH99216.1, AAK56792.1, ACH99229.1, ACS91348.1, AAP41820.1
and especially preferably YP_001185946.1,
and
proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1b} is generally understood in particular as meaning the conversion of lauric acid and/or its methyl ester into ω-hydroxylauric acid and/or its methyl ester.

Specific enzymes E_{1c}

Eukaryotic fatty alcohol oxidases E_{1c} which are preferred in this context are selected from among the list

AAS46878.1, ACX81419.1, AAS46879.1, CAB75353.1, AAS46880.1, XP_712350.1, XP_002422236.1, XP_712386.1, EEQ43775.1, XP_001525361.1, XP_001386087.1, XP_459506.2, CAB75351.1, CAB75352.1, XP_001385255.2, EDK39369.2, XP_001484086.1, XP_002618046.1, XP_002548766.1, XP_002548765.1, XP_003041566.1, XP_003328562.1, XP_001214264.1, XP_001904377.1, XP_658227.1, XP_001591990.1, XP_753079.1, XP_002569337.1, XP_001268562.1, XP_003348911.1, EGP90120.1, XP_001389382.1, EER37923.1, XP_001264046.1, EGO58212.1, XP_001554225.1, XP_003298648.1, XP_959005.1, XP_002841296.1, XP_001940486.1, EGR52262.1, EEQ89581.1, EGD99881.1, EFQ33355.1, XP_001821106.1, XP_002622231.1, EGG03784.1, EGC44059.1, XP_003018036.1, XP_003011696.1, EFY90752.1, XP_001227812.1, XP_758170.1, XP_001243546.1, XP_002479333.1, XP_003344707.1, EFW14100.1, XP_003071927.1, XP_003171263.1, XP_003051757.1, XP_002147053.1, EEH19591.1, EEH50473.1, XP_001792978.1, XP_387094.1, EFY98644.1, XP_002788971.1, XP_002842592.1, EFX04185.1, XP_003231449.1, XP_001729067.1, CBX94189.1, XP_001413535.1, ACF22878.1, B5WWZ9.1, XP_002994642.1, XP_002269629.1, XP_002519938.1, XP_002982582.1, NP_001047464.1, EEC73620.1, XP_002981110.1, XP_002960521.1, NP_566729.1, XP_001541970.1, XP_002967201.1, BAK00483.1, XP_002182547.1, BAK02336.1, XP_002454190.1, XP_002328753.1, XP_002867943.1, XP_002285334.1, CAC87643.1, CAN71289.1, XP_002454188.1, AAL31049.1, XP_002464494.1, AAL31021.1, YP_117187.1, XP_002543430.1, CAA18625.1, XP_002883430.1, NP_193673.2, XP_002529832.1, XP_001753124.1, NP_001142399.1, ACN27562.1, XP_002464495.1, ACR36691.1, BAJ86655.1, B5WWZ8.1, NP_001148058.1, ABR17814.1, EAY78905.1, NP_194586.1, AAM63097.1, AAK64154.1, NP_001064839.2, XP_002869492.1, XP_002314488.1, AAL31024.1, ZP_06967355.1, AAP54248.2, XP_002311685.1, ACF87929.1, YP_907078.1, EGE07035.1, YP_001849908.1, XP_002464496.1, EEC67160.1, AAL31027.1, XP_001761391.1, XP_002961172.1, XP_002528823.1, XP_002966834.1, NP_001176205.1, XP_001763007.1, XP_002272123.1, XP_002889487.1, XP_003003157.1, NP_285451.1, EGG23219.1, NP_171895.2, YP_003395677.1, Q9ZWB9.1, ACF88407.1, ZP_06413771.1, EEE51131.1, YP_003835264.1, YP_003397164.1, YP_004081922.1, XP_003294587.1, EEE51130.1, YP_003647529.1, YP_003647985.1, CBI29206.3, XP_629786.1,

ZP_07964664.1, EEE57396.1, EEH09589.1, YP_003265796.1, YP_001840752.1, ZP_08620775.1, ACR36076.1, ZP_05043749.1, YP_980677.1, ZP_05043728.1, YP_692894.1, NP_710223.1, EEC67159.1, AAP03110.1, EFA85697.1, YP_691805.1, YP_551012.1, YP_001174466.1, YP_002796294.1, YP_004716331.1, YP_001019547.1, YP_585737.1, AEA86007.1, YP_960830.1, YP_004743970.1, ZP_03431349.1, ZP_06448642.1, ZP_07430351.1, NP_215006.2, ZP_03535393.1, ZP_06801690.1, YP_001849132.1, NP_854165.1, ZP_03427234.1, CBJ27378.1, NP_334920.1, ZP_08571383.1, YP_728161.1, ZP_01896040.1, ZP_03530923.1, YP_551306.1, YP_003167456.1, YP_606070.1, ZP_06850167.1, ADP99095.1, YP_907986.1, ZP_04924166.1, ZP_08139923.1, YP_001270300.1, YP_521830.1, YP_003147410.1, YP_002007173.1, ADR62464.1, YP_004382294.1, NP_747223.1, YP_004687462.1, NP_902159.1, ZP_04936784.1, YP_003914667.1, ZP_01306356.1, ZP_04750553.1, YP_002875279.1, YP_004704374.1, YP_001671392.1, NP_249055.1, ZP_06876360.1, YP_001345853.1, YP_002437969.1, YP_004356853.1, YP_351075.1, CBI23676.3, YP_001189668.1, YP_001528881.1, YP_001613612.1, YP_001747218.1, YP_003393002.1, YP_001365074.1, ZP_07778129.1, ZP_07392715.1, YP_001553329.1, YP_262925.1, YP_751961.1, YP_564183.1, YP_003811876.1, YP_002356821.1, YP_001051828.1, YP_001837525.1, NP_716513.1, ZP_01915079.1, ZP_02156621.1, YP_001184631.1, YP_001475595.1, ZP_05042393.1, YP_962228.1, YP_001612275.1, ADV55625.1, YP_001675797.1, YP_003555260.1, ZP_01075039.1, YP_003812822.1, YP_001503351.1, EFN52938.1, YP_001759063.1, ZP_06503577.1, YP_871025.1, ZP_08564919.1, YP_002310162.1, YP_732875.1, YP_001092722.1, YP_739324.1, XP_002333995.1, NP_085596.1, YP_928870.1, EGD05748.1, NP_443993.1, ZP_08138057.1, ZP_05041587.1, ZP_07011380.1, YP_001612684.1, ZP_07669342.1, ZP_06508361.1, ZP_03423639.1, YP_923293.1, ZP_05061865.1, ZP_08181496.1, YP_559605.1, ZP_06841320.1, ZP_01620712.1, YP_001896340.1, ZP_03276650.1, YP_004303194.1, ZP_08180715.1, ZP_06382740.1, ZP_01034555.1, YP_004604560.1, YP_001020142.1, YP_935375.1, ZP_01546137.1, ZP_07661079.1, YP_001860640.1, ZP_06052841.1, ZP_01881170.1, ZP_05781455.1, YP_932732.1, ZP_08119300.1, YP_004715268.1, ZP_03697402.1, YP_004126957.1, ZP_06703136.1, NP_642445.1, ZP_08273900.1, YP_004524313.1, ZP_01902993.1, YP_001900094.1, AEA84888.1, YP_004690289.1, NP_714358.1, YP_682471.1, YP_003239.1, YP_997465.1, YP_003452130.1, ZP_01739153.1, YP_004219483.1, YP_001761298.1,

ZP_01438251.1, CBI37146.3, ZP_04748383.1, YP_004362245.1, ZP_05912795.1, YP_003390234.1, YP_003122799.1, CCB77579.1, EGB06416.1, ZP_08389346.1, YP_191496.1, ZP_05224727.1, ZP_01125614.1, YP_466287.1, YP_001368620.1, YP_001380256.1, YP_002361951.1, YP_002756103.1, YP_001801399.1, ZP_06847140.1, YP_003200069.1, YP_001940247.1, YP_001584322.1, ZP_04679227.1, YP_002493674.1, YP_002135530.1, YP_004290424.1, YP_001772011.1, ZP_08189046.1, ZP_03423640.1, YP_001834251.1, ZP_01041752.1, YP_001533410.1, YP_269751.1, YP_002432994.1, YP_003694653.1, CAD47896.1, NP_769359.1, YP_004239460.1, YP_004605221.1, YP_001961214.1, YP_001837513.1, YP_004335962.1, YP_004358600.1, ZP_05050026.1, YP_003202983.1, BAD03777.1, ZP_02165013.1, NP_774131.1, YP_432169.1, ZP_05000547.1, YP_001261233.1, XP_002593969.1, XP_002603265.1, YP_003342435.1, ZP_01253183.1, EGO36831.1, YP_001866737.1, YP_001523879.1, YP_133594.1, YP_003768990.1, YP_001237820.1, YP_003133224.1, ZP_01896771.1, ZP_01865125.1, NP_960319.1, YP_826958.1, YP_003326608.1, YP_002219515.1, NP_217926.1, ZP_07441899.2, YP_001208178.1, ADM42038.1, YP_002433510.1, ZP_08274313.1, EGO38668.1, ZP_03393221.1, NP_356358.1, ZP_06055780.1, YP_001684562.1, ZP_08528157.1, BAD03162.1, YP_001800712.1, ACL37106.1, YP_883489.1, ZP_01075202.1, NP_969446.1, ZP_01129577.1, YP_001530285.1, ZP_04746501.1, YP_001341980.1, YP_905003.1, ZP_05218299.1, ZP_08665577.1,

preferably

AAS46878.1, ACX81419.1, AAS46879.1, CAB75353.1, AAS46880.1, XP_712350.1, XP_002422236.1, XP_712386.1, EEQ43775.1, XP_001525361.1, XP_001386087.1, XP_459506.2, CAB75351.1, CAB75352.1, XP_001385255.2, EDK39369.2, XP_001484086.1, XP_002618046.1, XP_002548766.1, XP_002548765.1, XP_003041566.1, XP_001214264.1, XP_001904377.1, XP_658227.1, XP_001591990.1, XP_753079.1, XP_002569337.1, XP_001268562.1, XP_003348911.1, EGP90120.1, XP_001389382.1, EER37923.1, XP_001264046.1, EGO58212.1, XP_001554225.1, XP_003298648.1, XP_959005.1, XP_002841296.1, XP_001940486.1, EGR52262.1, EEQ89581.1, EGD99881.1, EFQ33355.1, XP_001821106.1, XP_002622231.1, EGC44059.1, XP_003018036.1, XP_003011696.1, EFY90752.1, XP_001227812.1, XP_001243546.1, XP_002479333.1, XP_003344707.1, EFW14100.1, XP_003071927.1, XP_003171263.1, XP_003051757.1, XP_002147053.1, EEH19591.1, EEH50473.1, XP_001792978.1, XP_387094.1, EFY98644.1, XP_002788971.1,

XP_002842592.1, EFX04185.1, XP_003231449.1, CBX94189.1, XP_001413535.1, XP_001541970.1, XP_002543430.1, EGE07035.1, XP_003003157.1
and especially preferably
AAS46878.1, ACX81419.1, AAS46879.1, CAB75353.1, AAS46880.1, XP_712350.1, XP_002422236.1, XP_712386.1, EEQ43775.1, CAB75351.1, CAB75352.1, XP_002548766.1, XP_002548765.1,
and
proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1c} is generally understood in particular as meaning the conversion of dodecan-1-ol into dodecan-1-al or dodecan-1-al into dodecanoic acid.

Specific enzymes E_{1d}

Such preferred AlkJ alcohol dehydrogenases are selected from among
Q00593.1, Q9WWW2.1, ZP_00957061.1, YP_957894.1, CAC38030.1, YP_694430.1, YP_957725.1, YP_001672216.1, YP_552061.1, YP_130410.1, ZP_06155535.1, ZP_01222730.1, YP_691907.1, YP_002297804.1, YP_004283522.1, YP_001234383.1, YP_004435031.1, ZP_05110316.1, ZP_05042898.1, YP_004466324.1, ZP_08553549.1, YP_004125220.1, ADI22536.1, ADI18461.1, YP_003810975.1, YP_662346.1, YP_004427557.1, YP_692606.1, ZP_05043291.1, YP_440752.1, ZP_02386160.1, ZP_04763547.1, ZP_02361232.1, YP_003376674.1, ZP_02354055.1, ZP_05085930.1,

ADQ00130.1, YP_003643016.1, ZP_05040520.1, YP_691922.1, AAX23098.1, BAD07371.1, NP_104379.1, YP_002551960.1, YP_003908558.1, YP_987903.1, ZP_05785860.1, YP_004145612.1, YP_004140926.1, CAZ88300.1, ZP_05041901.1, YP_533645.1, ZP_01754259.1, CBA31223.1, YP_587542.1, YP_106852.1, ZP_08402506.1, ZP_05055020.1, ZP_02400829.1, YP_104747.1, ZP_02409412.1, YP_001057269.1, YP_004229837.1, YP_294429.1, YP_001028112.1, ZP_02479747.1, YP_002874799.1, ZP_03541051.1, YP_003606536.1, ZP_02887167.1, YP_001795572.1, YP_487451.1, ACZ62814.1, YP_560809.1, ZP_02167462.1, YP_004482869.1, YP_001581248.1, ZP_07374066.1, YP_001203981.1, ZP_06840259.1, ZP_01915145.1, NP_774525.1, ZP_03561080.1, YP_001208258.1, YP_001897374.1, YP_001413909.1, YP_366469.1, YP_521854.1, YP_004490642.1, YP_003280349.1, ZP_03588744.1, YP_001562229.1, YP_001120981.1, ZP_03574970.1, YP_004234225.1, ZP_02377531.1, ZP_02149954.1, YP_001237360.1, ZP_03266156.1, YP_782821.1, YP_004754039.1, BAB61732.1, ZP_07046388.1, ZP_02145452.1, BAF45123.1, YP_002129953.1, YP_003812439.1, ZP_01055291.1, BAF45124.1, EGH71399.1, ZP_05060389.1, ZP_05090872.1, BAF45126.1, BAB07804.1, ZP_06053464.1, YP_001238278.1, ZP_04944469.1, YP_001171160.1, YP_002984373.1, YP_002237649.1, ZP_08276443.1, BAF98451.1, ZP_05124197.1, YP_568640.1, ZP_05785341.1, NP_769037.1, YP_370657.1, YP_775005.1, ZP_02911119.1, YP_165460.1, ZP_02891796.1, YP_622328.1, ZP_07675057.1, YP_001901188.1, YP_003592183.1, ZP_02361040.1, NP_518244.1, YP_001809673.1, NP_947032.1, YP_001766369.1, YP_002255997.1, ZP_04940241.1, YP_004012032.1, YP_841049.1, YP_002983249.1, YP_003643276.1, YP_003855487.1, YP_003778137.1, ZP_02361104.1, CBA30511.1, ZP_05781295.1, YP_756865.1, ZP_02461782.1, YP_002007988.1, YP_004110133.1, YP_002229680.1, ZP_02386040.1, YP_004684069.1, YP_373268.1, YP_440614.1, NP_421441.1, YP_264896.1, YP_004362617.1, ZP_06053847.1, YP_366538.1, YP_003812285.1, YP_004154520.1, ZP_01901081.1, ZP_02372179.1, ZP_02453559.1, ADP98564.1, YP_003747084.1, ZP_02487888.1, ZP_01768075.1, ZP_02400664.1, YP_106680.1, YP_724753.1, YP_002907583.1, YP_004482470.1, YP_167582.1, YP_270109.1, YP_004362333.1, ZP_02504034.1, YP_003189363.1, YP_973212.1, ZP_00952746.1, YP_459665.1, YP_777218.1, YP_581107.1, ZP_01878091.1, ZP_01057973.1, YP_002913124.1, ZP_01035570.1, YP_001777560.1, YP_552627.1, ZP_02890876.1, YP_587146.1, YP_004141814.1, YP_001685369.1, ZP_05343380.1,

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and especially preferably

Q00593.1, Q9WWW2.1, ZP_00957061.1, YP_957894.1, CAC38030.1, YP_694430.1, YP_957725.1, YP_001672216.1.

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1d} is generally understood in particular as meaning the conversion of dodecan-1-ol into dodecan-1-al or dodecan-1-al into dodecanoic acid.

Specific enzymes E_{1e}

Such preferred alcohol dehydrogenases of EC 1.1.1.1 or EC 1.1.1.2 are selected from among AdhE, AdhP, YjgB, YqhD, GldA, EutG, YiaY, AdhE, AdhP, YhhX, YahK, HdhA, HisD, SerA, Tdh, Ugd, Udg, Gmd, YefA, YbiC, YdfG, YeaU, TtuC, YeiQ, YgbJ, YgcU, YgcT, YgcV, YggP,

YgjR, YliI, YqiB, YzzH, LdhA, GapA, Epd, Dld, GatD, Gcd, GlpA, GlpB, GlpC, GlpD, GpsA and YphC from bacteria, in particular *E. coli*,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1e} is generally understood in particular as meaning the conversion of dodecan-1-al into dodecanoic acid.

Specific enzymes E_{1f}

Such preferred aldehyde dehydrogenases are selected from among Prr, Usg, MhpF, AstD, GdhA, FrmA, Feab, Asd, Sad, PuuE, GabT, YgaW, BetB, PutA, PuuC, FeaB, AldA, Prr, EutA, GabD, AldB, TynA and YneI from bacteria, in particular *E. coli*,

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst

without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{1f} is generally understood in particular as meaning the conversion of dodecan-1-al into dodecanoic acid.

Auxiliary enzymes for E_{1a}

It is preferred according to the invention that, when the activity of an enzyme E_{1a}, a eukaryotic P450 alkane hydroxylase, is reduced, the microorganism according to the invention also has an activity of an NADPH-cytochrome P450 oxidoreductase of EC 1.6.2.4 which is reduced in comparison with its wild type. This has the technical effect of the activity of the eukaryotic P450 alkane hydroxylases is reduced further and the product yields of alkan-1-ols, alkan-1-als, alkan-1-amines, alkanes and terminal olefins are increased.
NADPH-cytochrome P450 oxidoreductases of EC 1.6.2.4 catalyse the following reaction:
oxidized cytochrome P450 + $NADPH^+$ = reduced cytochrome P450 + $NADP^+$ + H^+

It is preferred according to the invention that, when the activity of an enzyme E_{1a}, a prokaryotic P450 alkane hydroxylase, is reduced, the microorganism according to the invention also has an activity of a ferredoxin-$NAD(P)^+$ reductase of EC 1.18.1.2 or EC 1.18.1.3 and/or of a ferredoxin which is reduced in comparison with its wild type. This has the technical effect that the activity of the prokaryotic P450 alkane hydroxylase of the CYP153 type is reduced further and that the product yields of alkan-1-ols, alkan-1-als, alkan-1-amines, alkanes and terminal olefins are increased.
Ferredoxin-$NAD(P)^+$ reductases of EC 1.18.1.2 or EC 1.18.1.3 catalyse the following reaction:
oxidized ferredoxin + NAD(P)H + H^+ = reduced ferredoxin + $NAD(P)^+$ and are preferably encoded by a gene which is located in the immediate vicinity of a gene of an abovementioned prokaryotic P450 alkane hydroxylase of the CYP153 type or of a ferredoxin described in the context of the present invention.
The expression "in the immediate vicinity" means that not more than three other structural genes are located between the genes in question.
Ferredoxins catalyse the following reactions:

alkane hydroxylase + reduced ferredoxin + alkanoic acid (ester) = alkane monoxygenase + oxidized ferredoxin + ω-hydroxyalkanoic acid (ester) + H_2O,
alkane hydroxylase + 2 reduced ferredoxins + alkanoic acid (ester) = alkane hydroxylase + 2 oxidized ferredoxins + ω-oxoalkanoic acid (ester) + 2 H_2O or
alkane hydroxylase + 3 reduced ferredoxins + alkanoic acid (ester) = alkane hydroxylase + 3 oxidized ferredoxins + ω-carboxyalkanoic acid (ester) + 3 H_2O and
are preferably encoded by a gene which is located in the immediate vicinity of a gene of an abovementioned prokaryotic P450 alkane hydroxylase of the CYP153 type or of an abovementioned ferredoxin-NAD(P)$^+$ reductase of EC 1.18.1.2 or EC 1.18.1.3. The expression "in the immediate vicinity" means that not more than three other structural genes are located between the genes in question.
Preferred microorganisms have an activity of the ferredoxin-NAD(P)$^+$ reductase AlkT and of a ferredoxin which is increased in comparison with their wild type.

Auxiliary enzymes for E_{1b}

It is preferred according to the invention that, when the activity of an enzyme E_{1b}, an AlkB alkane hydroxylase of EC 1.14.15.3, is reduced, the microorganism according to the invention likewise has an activity of an AlkT rubredoxin-NAD(P)$^+$ reductase of EC 1.18.1.1 or of EC 1.18.1.4 and/or of a rubredoxin AlkG which is increased in comparison with its wild type. This has the technical effect that the activity of the AlkB alkane hydroxylase is enhanced and the product yields are increased.
AlkT rubredoxin-NAD(P)$^+$ reductases of EC 1.18.1.1 or EC 1.18.1.4 catalyse the following reaction:
oxidized rubredoxin + NAD(P)H + H^+ = reduced rubredoxin + NAD(P)$^+$ and are preferably encoded by a gene which is located in the immediate vicinity of a gene of an abovementioned AlkB alkane hydroxylase of EC 1.14.15.3 or of a rubredoxin AlkG described in the context of the present invention.
The expression "in the immediate vicinity" means that not more than three other structural genes are located between the genes in question.
Rubredoxins AlkG catalyse the following reactions:

alkane monoxygenase + reduced rubredoxin + alkanoic acid (ester) = alkane monoxygenase + oxidized rubredoxin + ω-hydroxyalkanoic acid (ester) + H_2O, alkane monoxygenase + 2 reduced rubredoxins + alkanoic acid (ester) = alkane monoxygenase + 2 oxidized rubredoxins + ω-oxoalkanoic acid (ester) + 2 H_2O or

alkane monoxygenase + 3 reduced rubredoxins + alkanoic acid (ester) = alkane monoxygenase + 3 oxidized rubredoxins + ω-carboxyalkanoic acid (ester) + 3 H_2O and

are preferably encoded by a gene which is located in the immediate vicinity of a gene of an abovementioned AlkB alkane hydroxylase of EC 1.14.15.3 or of an abovementioned AlkT rubredoxin-NAD(P)$^+$ reductase of EC 1.18.1.1 or EC 1.18.1.4. The expression "in the immediate vicinity" means that not more than three other structural genes are located between the genes in question.

Preferred microorganisms have an activity of the AlkT rubredoxin-NAD(P)$^+$ reductase and of rubredoxin AlkG which is reduced in comparison to their wild type.

Specific embodiments of preferred microorganisms and enzymes

According to the invention, microorganisms are especially preferably selected from among those which include

a first and a second genetic modification within the meaning of the invention,

a first, a second and a fifth genetic modification within the meaning of the invention,

a first, a second and a sixth genetic modification within the meaning of the invention,

a first, a second and a seventh genetic modification within the meaning of the invention,

a first, a second, a fifth and a sixth genetic modification within the meaning of the invention,

a first, a second, a fifth and a seventh genetic modification within the meaning of the invention,

a first, a second, a sixth and a seventh genetic modification within the meaning of the invention,

a first, a second, a fifth, a sixth and a seventh genetic modification within the meaning of the invention,

a first, a second and a third genetic modification within the meaning of the invention,

a first, a second, a third and a fifth genetic modification within the meaning of the invention,

a first, a second, a third and a sixth genetic modification within the meaning of the invention,

a first, a second, a third and a seventh genetic modification within the meaning of the invention,
a first, a second, a third, a fifth and a sixth genetic modification within the meaning of the invention,
a first, a second, a third, a fifth and a seventh genetic modification within the meaning of the invention,
a first, a second, a third, a sixth and a seventh genetic modification within the meaning of the invention,
a first, a second, a third, a fifth, a sixth and a seventh genetic modification within the meaning of the invention,
a first, a second and a fourth genetic modification within the meaning of the invention,
a first, a second, a fourth and a fifth genetic modification within the meaning of the invention,
a first, a second, a fourth and a sixth genetic modification within the meaning of the invention,
a first, a second, a fourth and a seventh genetic modification within the meaning of the invention,
a first, a second, a fourth, a fifth and a sixth genetic modification within the meaning of the invention,
a first, a second, a fourth, a fifth and a seventh genetic modification within the meaning of the invention,
a first, a second, a fourth, a sixth and a seventh genetic modification within the meaning of the invention or
a first, a second, a fourth, a fifth, a sixth and a seventh genetic modification within the meaning of the invention.

Microorganisms which are especially preferred according to the invention are those which include a first genetic modification so that they are capable of forming more carboxylic acids and carboxylic acid derivatives from at least one simple carbon source in comparison with their wild type, where the first genetic modification represents an activity of at least one of the enzymes E_i or one of the enzymes with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% amino acid residues are modified by deletion, insertion, substitution or a combination thereof over the

sequences specified by references in the table hereinbelow and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90% of the activity of the protein with the respective reference sequence, which activity is increased in comparison with the enzymatic activity of the wild type of the microorganism and where activity in this context and in the context of the determination of the activity of the enzyme E_i generally means in particular the hydrolysis of dodecanoyl-ACP thioester with the carbon chain length assigned to the individual enzymes E_i in the table hereinbelow
and the carboxylic acid and carboxylic acid derivatives have a carbon chain length of the carboxylic acid moiety as represented in the table hereinbelow:

Enzyme E_i selected from among	Carbon chain length
AAC49269.1, CAB60830.1, AAC49179.1, AAC49784.1, ABB71579.1, CAC19934.1 and SEQ ID No.: 26, 29, 33, 38, 40, 97 and 99 of WO2011008565	C8
AAC49269.1, CAB60830.1, AAC49179.1, AAC49784.1, ABB71579.1, CAC19934.1 and SEQ ID No.: 73, 75, 87 and 89 of WO2011008565.	C10
Q41635.1, Q39473.1, AAC49180.1, CAC19934.1, AAC72881.1, AAC49783.1, AAC49784.1 and SEQ ID No.: 49 and 51 of WO2011008565.	C12
Q41635.1, Q39473.1, AAC49180.1, CAC19934.1, AAC72881.1 AAC49783.1, AAC49784.1 and SEQ ID No.: 49, 51, 53, 55, 61, 63, 67, 69, 77, 79, 83 and 85 of WO2011008565.	C14

The abovementioned deletions of amino acid residues over the sequences specified by references in the table hereinabove refer in particular to deletions at the N- and/or C-terminus, in particular the N-terminus. The abovementioned N-terminus is especially preferably that of a

plant plastid targeting sequence. Such plant plastid targeting sequences can be predicted for example with the aid of the algorithms employed by the prediction tool TargetP 1.1 (www.cbs.dtu.dk/services/TargetP/) and described in the following publications, preferably without using cutoffs:

Predicting subcellular localization of proteins based on their N-terminal amino acid sequence. Olof Emanuelsson, Henrik Nielsen, Søren Brunak and Gunnar von Heijne. J. Mol. Biol., 300: 1005-1016, 2000 and *Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites.*Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne. Protein Engineering, 10:1-6, 1997.

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of carboxylic acids and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the enzyme 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, Thl, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E	Reduced E
1	AlkL	
2	$AlkLE_i$	
3	$AlkLE_{ii}$	
4	$AlkLE_{ii}E_{iib}$	
5	$AlkLE_{iii}$	
6	$AlkLE_{iv}$	
7	AlkL	E_a
8	$AlkLE_i$	E_a
9	$AlkLE_{ii}$	E_a
10	$AlkLE_{ii}E_{iib}$	E_a
11	$AlkLE_{iii}$	E_a
12	$AlkLE_{iv}$	E_a
13	AlkL	E_b
14	$AlkLE_i$	E_b
15	$AlkLE_{ii}$	E_b
16	$AlkLE_{ii}E_{iib}$	E_b
17	$AlkLE_{iii}$	E_b
18	$AlkLE_{iv}$	E_b
19	AlkL	E_d
20	$AlkLE_i$	E_d
21	$AlkLE_{ii}$	E_d
22	$AlkLE_{ii}E_{iib}$	E_d
23	$AlkLE_{iii}$	E_d
24	$AlkLE_{iv}$	E_d
25	AlkL	E_e
26	$AlkLE_i$	E_e
27	$AlkLE_{ii}$	E_e
28	$AlkLE_{ii}E_{iib}$	E_e
29	$AlkLE_{iii}$	E_e
30	$AlkLE_{iv}$	E_e

31	AlkL	E_f	
32	$AlkLE_i$	E_f	
33	$AlkLE_{ii}$	E_f	
34	$AlkLE_{ii}E_{iib}$	E_f	
35	$AlkLE_{iii}$	E_f	
36	$AlkLE_{iv}$	E_f	
37	AlkL		E_1
38	$AlkLE_i$		E_1
39	$AlkLE_{ii}$		E_1
40	$AlkLE_{ii}E_{iib}$		E_1
41	$AlkLE_{iii}$		E_1
42	$AlkLE_{iv}$		E_1
43	AlkL	E_a	E_1
44	$AlkLE_i$	E_a	E_1
45	$AlkLE_{ii}$	E_a	E_1
46	$AlkLE_{ii}E_{iib}$	E_a	E_1
47	$AlkLE_{iii}$	E_a	E_1
48	$AlkLE_{iv}$	E_a	E_1
49	AlkL	E_b	E_1
50	$AlkLE_i$	E_b	E_1
51	$AlkLE_{ii}$	E_b	E_1
52	$AlkLE_{ii}E_{iib}$	E_b	E_1
53	$AlkLE_{iii}$	E_b	E_1
54	$AlkLE_{iv}$	E_b	E_1
55	AlkL	E_d	E_1
56	$AlkLE_i$	E_d	E_1
57	$AlkLE_{ii}$	E_d	E_1
58	$AlkLE_{ii}E_{iib}$	E_d	E_1
59	$AlkLE_{iii}$	E_d	E_1
60	$AlkLE_{iv}$	E_d	E_1
61	AlkL	E_e	E_1

62	$AlkLE_i$	E_e	E_1
63	$AlkLE_{ii}$	E_e	E_1
64	$AlkLE_{ii}E_{iib}$	E_e	E_1
65	$AlkLE_{iii}$	E_e	E_1
66	$AlkLE_{iv}$	E_e	E_1
67	AlkL	E_f	E_1
68	$AlkLE_i$	E_f	E_1
69	$AlkLE_{ii}$	E_f	E_1
70	$AlkLE_{ii}E_{iib}$	E_f	E_1
71	$AlkLE_{iii}$	E_f	E_1
72	$AlkLE_{iv}$	E_f	E_1

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of carboxylic acid esters and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the enzyme 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, Thl, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E		Reduced E
1	AlkL	E_v	
2	$AlkLE_i$	E_v	
3	$AlkLE_{ii}$	E_v	
4	$AlkLE_{ii}E_{iib}$	E_v	
5	$AlkLE_{iii}$	E_v	
6	$AlkLE_{iv}$	E_v	
7	AlkL	E_v	E_a
8	$AlkLE_i$	E_v	E_a
9	$AlkLE_{ii}$	E_v	E_a
10	$AlkLE_{ii}E_{iib}$	E_v	E_a
11	$AlkLE_{iii}$	E_v	E_a
12	$AlkLE_{iv}$	E_v	E_a
13	AlkL	E_v	E_b
14	$AlkLE_i$	E_v	E_b
15	$AlkLE_{ii}$	E_v	E_b
16	$AlkLE_{ii}E_{iib}$	E_v	E_b
17	$AlkLE_{iii}$	E_v	E_b
18	$AlkLE_{iv}$	E_v	E_b
19	AlkL	E_v	E_d
20	$AlkLE_i$	E_v	E_d
21	$AlkLE_{ii}$	E_v	E_d
22	$AlkLE_{ii}E_{iib}$	E_v	E_d
23	$AlkLE_{iii}$	E_v	E_d
24	$AlkLE_{iv}$	E_v	E_d
25	AlkL	E_v	E_e
26	$AlkLE_i$	E_v	E_e
27	$AlkLE_{ii}$	E_v	E_e
28	$AlkLE_{ii}E_{iib}$	E_v	E_e
29	$AlkLE_{iii}$	E_v	E_e
30	$AlkLE_{iv}$	E_v	E_e
31	AlkL	E_v	E_f
32	$AlkLE_i$	E_v	E_f
33	$AlkLE_{ii}$	E_v	E_f
34	$AlkLE_{ii}E_{iib}$	E_v	E_f
35	$AlkLE_{iii}$	E_v	E_f
36	$AlkLE_{iv}$	E_v	E_f
37	AlkL	E_vE_{vi}	
38	$AlkLE_i$	E_vE_{vi}	
39	$AlkLE_{ii}$	E_vE_{vi}	
40	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	
41	$AlkLE_{iii}$	E_vE_{vi}	
42	$AlkLE_{iv}$	E_vE_{vi}	
43	AlkL	E_vE_{vi}	E_a
44	$AlkLE_i$	E_vE_{vi}	E_a
45	$AlkLE_{ii}$	E_vE_{vi}	E_a
46	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_a
47	$AlkLE_{iii}$	E_vE_{vi}	E_a
48	$AlkLE_{iv}$	E_vE_{vi}	E_a
49	AlkL	E_vE_{vi}	E_b
50	$AlkLE_i$	E_vE_{vi}	E_b
51	$AlkLE_{ii}$	E_vE_{vi}	E_b
52	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_b
53	$AlkLE_{iii}$	E_vE_{vi}	E_b
54	$AlkLE_{iv}$	E_vE_{vi}	E_b
55	AlkL	E_vE_{vi}	E_d
56	$AlkLE_i$	E_vE_{vi}	E_d
57	$AlkLE_{ii}$	E_vE_{vi}	E_d
58	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_d
59	$AlkLE_{iii}$	E_vE_{vi}	E_d
60	$AlkLE_{iv}$	E_vE_{vi}	E_d

61	AlkL	E_vE_{vi}	E_e
62	AlkLE_i	E_vE_{vi}	E_e
63	AlkLE_{ii}	E_vE_{vi}	E_e
64	AlkL$E_{ii}E_{iib}$	E_vE_{vi}	E_e
65	AlkLE_{iii}	E_vE_{vi}	E_e
66	AlkLE_{iv}	E_vE_{vi}	E_e
67	AlkL	E_vE_{vi}	E_f
68	AlkLE_i	E_vE_{vi}	E_f
69	AlkLE_{ii}	E_vE_{vi}	E_f
70	AlkL$E_{ii}E_{iib}$	E_vE_{vi}	E_f
71	AlkLE_{iii}	E_vE_{vi}	E_f
72	AlkLE_{iv}	E_vE_{vi}	E_f
73	AlkL	E_{vii}	
74	AlkLE_i	E_{vii}	
75	AlkLE_{ii}	E_{vii}	
76	AlkL$E_{ii}E_{iib}$	E_{vii}	
77	AlkLE_{iii}	E_{vii}	
78	AlkLE_{iv}	E_{vii}	
79	AlkL	E_{vii}	E_a
80	AlkLE_i	E_{vii}	E_a
81	AlkLE_{ii}	E_{vii}	E_a
82	AlkL$E_{ii}E_{iib}$	E_{vii}	E_a
83	AlkLE_{iii}	E_{vii}	E_a
84	AlkLE_{iv}	E_{vii}	E_a
85	AlkL	E_{vii}	E_b
86	AlkLE_i	E_{vii}	E_b
87	AlkLE_{ii}	E_{vii}	E_b
88	AlkL$E_{ii}E_{iib}$	E_{vii}	E_b
89	AlkLE_{iii}	E_{vii}	E_b
90	AlkLE_{iv}	E_{vii}	E_b
91	AlkL	E_{vii}	E_d
92	AlkLE_i	E_{vii}	E_d
93	AlkLE_{ii}	E_{vii}	E_d
94	AlkL$E_{ii}E_{iib}$	E_{vii}	E_d
95	AlkLE_{iii}	E_{vii}	E_d
96	AlkLE_{iv}	E_{vii}	E_d
97	AlkL	E_{vii}	E_e
98	AlkLE_i	E_{vii}	E_e
99	AlkLE_{ii}	E_{vii}	E_e
100	AlkL$E_{ii}E_{iib}$	E_{vii}	E_e
101	AlkLE_{iii}	E_{vii}	E_e
102	AlkLE_{iv}	E_{vii}	E_e
103	AlkL	E_{vii}	E_f
104	AlkLE_i	E_{vii}	E_f
105	AlkLE_{ii}	E_{vii}	E_f
106	AlkL$E_{ii}E_{iib}$	E_{vii}	E_f
107	AlkLE_{iii}	E_{vii}	E_f
108	AlkLE_{iv}	E_{vii}	E_f
109	AlkL	$E_{vi}E_{vii}$	
110	AlkLE_i	$E_{vi}E_{vii}$	
111	AlkLE_{ii}	$E_{vi}E_{vii}$	
112	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{vii}$	
113	AlkLE_{iii}	$E_{vi}E_{vii}$	
114	AlkLE_{iv}	$E_{vi}E_{vii}$	
115	AlkL	$E_{vi}E_{vii}$	E_a
116	AlkLE_i	$E_{vi}E_{vii}$	E_a
117	AlkLE_{ii}	$E_{vi}E_{vii}$	E_a
118	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_a
119	AlkLE_{iii}	$E_{vi}E_{vii}$	E_a
120	AlkLE_{iv}	$E_{vi}E_{vii}$	E_a
121	AlkL	$E_{vi}E_{vii}$	E_b
122	AlkLE_i	$E_{vi}E_{vii}$	E_b

123	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_b
124	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_b
125	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_b
126	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_b
127	AlkL	$E_{vi}E_{vii}$	E_d
128	$AlkLE_i$	$E_{vi}E_{vii}$	E_d
129	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_d
130	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_d
131	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_d
132	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_d
133	AlkL	$E_{vi}E_{vii}$	E_e
134	$AlkLE_i$	$E_{vi}E_{vii}$	E_e
135	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_e
136	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_e
137	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_e
138	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_e
139	AlkL	$E_{vi}E_{vii}$	E_f
140	$AlkLE_i$	$E_{vi}E_{vii}$	E_f
141	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_f
142	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_f
143	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_f
144	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_f
145	AlkL	$E_{iib}E_{vi}E_{vii}$	
146	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	
147	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	
148	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	
149	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	
150	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	
151	AlkL	$E_{iib}E_{vi}E_{vii}$	E_a
152	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_a
153	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_a

154	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_a
155	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_a
156	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_a
157	AlkL	$E_{iib}E_{vi}E_{vii}$	E_b
158	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_b
159	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_b
160	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_b
161	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_b
162	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_b
163	AlkL	$E_{iib}E_{vi}E_{vii}$	E_d
164	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_d
165	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_d
166	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_d
167	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_d
168	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_d
169	AlkL	$E_{iib}E_{vi}E_{vii}$	E_e
170	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_e
171	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_e
172	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_e
173	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_e
174	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_e
175	AlkL	$E_{iib}E_{vi}E_{vii}$	E_f
176	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_f
177	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_f
178	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_f
179	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_f
180	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_f
181	AlkL	E_v	E_1
182	$AlkLE_i$	E_v	E_1
183	$AlkLE_{ii}$	E_v	E_1
184	$AlkLE_{ii}E_{iib}$	E_v	E_1

185	$AlkLE_{iii}$	E_v		E_1
186	$AlkLE_{iv}$	E_v		E_1
187	AlkL	E_v	E_a	E_1
188	$AlkLE_i$	E_v	E_a	E_1
189	$AlkLE_{ii}$	E_v	E_a	E_1
190	$AlkLE_{ii}E_{iib}$	E_v	E_a	E_1
191	$AlkLE_{iii}$	E_v	E_a	E_1
192	$AlkLE_{iv}$	E_v	E_a	E_1
193	AlkL	E_v	E_b	E_1
194	$AlkLE_i$	E_v	E_b	E_1
195	$AlkLE_{ii}$	E_v	E_b	E_1
196	$AlkLE_{ii}E_{iib}$	E_v	E_b	E_1
197	$AlkLE_{iii}$	E_v	E_b	E_1
198	$AlkLE_{iv}$	E_v	E_b	E_1
199	AlkL	E_v	E_d	E_1
200	$AlkLE_i$	E_v	E_d	E_1
201	$AlkLE_{ii}$	E_v	E_d	E_1
202	$AlkLE_{ii}E_{iib}$	E_v	E_d	E_1
203	$AlkLE_{iii}$	E_v	E_d	E_1
204	$AlkLE_{iv}$	E_v	E_d	E_1
205	AlkL	E_v	E_e	E_1
206	$AlkLE_i$	E_v	E_e	E_1
207	$AlkLE_{ii}$	E_v	E_e	E_1
208	$AlkLE_{ii}E_{iib}$	E_v	E_e	E_1
209	$AlkLE_{iii}$	E_v	E_e	E_1
210	$AlkLE_{iv}$	E_v	E_e	E_1
211	AlkL	E_v	E_f	E_1
212	$AlkLE_i$	E_v	E_f	E_1
213	$AlkLE_{ii}$	E_v	E_f	E_1
214	$AlkLE_{ii}E_{iib}$	E_v	E_f	E_1
215	$AlkLE_{iii}$	E_v	E_f	E_1

216	$AlkLE_{iv}$	E_v	E_f	E_1
217	AlkL	E_vE_{vi}		E_1
218	$AlkLE_i$	E_vE_{vi}		E_1
219	$AlkLE_{ii}$	E_vE_{vi}		E_1
220	$AlkLE_{ii}E_{iib}$	E_vE_{vi}		E_1
221	$AlkLE_{iii}$	E_vE_{vi}		E_1
222	$AlkLE_{iv}$	E_vE_{vi}		E_1
223	AlkL	E_vE_{vi}	E_a	E_1
224	$AlkLE_i$	E_vE_{vi}	E_a	E_1
225	$AlkLE_{ii}$	E_vE_{vi}	E_a	E_1
226	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_a	E_1
227	$AlkLE_{iii}$	E_vE_{vi}	E_a	E_1
228	$AlkLE_{iv}$	E_vE_{vi}	E_a	E_1
229	AlkL	E_vE_{vi}	E_b	E_1
230	$AlkLE_i$	E_vE_{vi}	E_b	E_1
231	$AlkLE_{ii}$	E_vE_{vi}	E_b	E_1
232	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_b	E_1
233	$AlkLE_{iii}$	E_vE_{vi}	E_b	E_1
234	$AlkLE_{iv}$	E_vE_{vi}	E_b	E_1
235	AlkL	E_vE_{vi}	E_d	E_1
236	$AlkLE_i$	E_vE_{vi}	E_d	E_1
237	$AlkLE_{ii}$	E_vE_{vi}	E_d	E_1
238	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_d	E_1
239	$AlkLE_{iii}$	E_vE_{vi}	E_d	E_1
240	$AlkLE_{iv}$	E_vE_{vi}	E_d	E_1
241	AlkL	E_vE_{vi}	E_e	E_1
242	$AlkLE_i$	E_vE_{vi}	E_e	E_1
243	$AlkLE_{ii}$	E_vE_{vi}	E_e	E_1
244	$AlkLE_{ii}E_{iib}$	E_vE_{vi}	E_e	E_1
245	$AlkLE_{iii}$	E_vE_{vi}	E_e	E_1
246	$AlkLE_{iv}$	E_vE_{vi}	E_e	E_1

247	AlkL	E_vE_{vi}	E_f	E_1
248	AlkLE_i	E_vE_{vi}	E_f	E_1
249	AlkLE_{ii}	E_vE_{vi}	E_f	E_1
250	AlkL$E_{ii}E_{iib}$	E_vE_{vi}	E_f	E_1
251	AlkLE_{iii}	E_vE_{vi}	E_f	E_1
252	AlkLE_{iv}	E_vE_{vi}	E_f	E_1
253	AlkL	E_{vii}		E_1
254	AlkLE_i	E_{vii}		E_1
255	AlkLE_{ii}	E_{vii}		E_1
256	AlkL$E_{ii}E_{iib}$	E_{vii}		E_1
257	AlkLE_{iii}	E_{vii}		E_1
258	AlkLE_{iv}	E_{vii}		E_1
259	AlkL	E_{vii}	E_a	E_1
260	AlkLE_i	E_{vii}	E_a	E_1
261	AlkLE_{ii}	E_{vii}	E_a	E_1
262	AlkL$E_{ii}E_{iib}$	E_{vii}	E_a	E_1
263	AlkLE_{iii}	E_{vii}	E_a	E_1
264	AlkLE_{iv}	E_{vii}	E_a	E_1
265	AlkL	E_{vii}	E_b	E_1
266	AlkLE_i	E_{vii}	E_b	E_1
267	AlkLE_{ii}	E_{vii}	E_b	E_1
268	AlkL$E_{ii}E_{iib}$	E_{vii}	E_b	E_1
269	AlkLE_{iii}	E_{vii}	E_b	E_1
270	AlkLE_{iv}	E_{vii}	E_b	E_1
271	AlkL	E_{vii}	E_d	E_1
272	AlkLE_i	E_{vii}	E_d	E_1
273	AlkLE_{ii}	E_{vii}	E_d	E_1
274	AlkL$E_{ii}E_{iib}$	E_{vii}	E_d	E_1
275	AlkLE_{iii}	E_{vii}	E_d	E_1
276	AlkLE_{iv}	E_{vii}	E_d	E_1
277	AlkL	E_{vii}	E_e	E_1
278	AlkLE_i	E_{vii}	E_e	E_1
279	AlkLE_{ii}	E_{vii}	E_e	E_1
280	AlkL$E_{ii}E_{iib}$	E_{vii}	E_e	E_1
281	AlkLE_{iii}	E_{vii}	E_e	E_1
282	AlkLE_{iv}	E_{vii}	E_e	E_1
283	AlkL	E_{vii}	E_f	E_1
284	AlkLE_i	E_{vii}	E_f	E_1
285	AlkLE_{ii}	E_{vii}	E_f	E_1
286	AlkL$E_{ii}E_{iib}$	E_{vii}	E_f	E_1
287	AlkLE_{iii}	E_{vii}	E_f	E_1
288	AlkLE_{iv}	E_{vii}	E_f	E_1
289	AlkL	$E_{vi}E_{vii}$		E_1
290	AlkLE_i	$E_{vi}E_{vii}$		E_1
291	AlkLE_{ii}	$E_{vi}E_{vii}$		E_1
292	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{vii}$		E_1
293	AlkLE_{iii}	$E_{vi}E_{vii}$		E_1
294	AlkLE_{iv}	$E_{vi}E_{vii}$		E_1
295	AlkL	$E_{vi}E_{vii}$	E_a	E_1
296	AlkLE_i	$E_{vi}E_{vii}$	E_a	E_1
297	AlkLE_{ii}	$E_{vi}E_{vii}$	E_a	E_1
298	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_a	E_1
299	AlkLE_{iii}	$E_{vi}E_{vii}$	E_a	E_1
300	AlkLE_{iv}	$E_{vi}E_{vii}$	E_a	E_1
301	AlkL	$E_{vi}E_{vii}$	E_b	E_1
302	AlkLE_i	$E_{vi}E_{vii}$	E_b	E_1
303	AlkLE_{ii}	$E_{vi}E_{vii}$	E_b	E_1
304	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_b	E_1
305	AlkLE_{iii}	$E_{vi}E_{vii}$	E_b	E_1
306	AlkLE_{iv}	$E_{vi}E_{vii}$	E_b	E_1
307	AlkL	$E_{vi}E_{vii}$	E_d	E_1
308	AlkLE_i	$E_{vi}E_{vii}$	E_d	E_1

309	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_d	E_1
310	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_d	E_1
311	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_d	E_1
312	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_d	E_1
313	AlkL	$E_{vi}E_{vii}$	E_e	E_1
314	$AlkLE_i$	$E_{vi}E_{vii}$	E_e	E_1
315	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_e	E_1
316	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_e	E_1
317	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_e	E_1
318	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_e	E_1
319	AlkL	$E_{vi}E_{vii}$	E_f	E_1
320	$AlkLE_i$	$E_{vi}E_{vii}$	E_f	E_1
321	$AlkLE_{ii}$	$E_{vi}E_{vii}$	E_f	E_1
322	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{vii}$	E_f	E_1
323	$AlkLE_{iii}$	$E_{vi}E_{vii}$	E_f	E_1
324	$AlkLE_{iv}$	$E_{vi}E_{vii}$	E_f	E_1
325	AlkL	$E_{iib}E_{vi}E_{vii}$		E_1
326	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$		E_1
327	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$		E_1
328	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$		E_1
329	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$		E_1
330	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$		E_1
331	AlkL	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
332	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
333	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
334	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
335	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
336	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_a	E_1
337	AlkL	$E_{iib}E_{vi}E_{vii}$	E_b	E_1
338	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_b	E_1
339	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_b	E_1

340	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_b	E_1
341	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_b	E_1
342	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_b	E_1
343	AlkL	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
344	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
345	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
346	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
347	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
348	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_d	E_1
349	AlkL	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
350	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
351	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
352	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
353	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
354	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_e	E_1
355	AlkL	$E_{iib}E_{vi}E_{vii}$	E_f	E_1
356	$AlkLE_i$	$E_{iib}E_{vi}E_{vii}$	E_f	E_1
357	$AlkLE_{ii}$	$E_{iib}E_{vi}E_{vii}$	E_f	E_1
358	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_{vii}$	E_f	E_1
359	$AlkLE_{iii}$	$E_{iib}E_{vi}E_{vii}$	E_f	E_1
360	$AlkLE_{iv}$	$E_{iib}E_{vi}E_{vii}$	E_f	E_1

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of alkan-1-ols and alkan-1-als and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, Thl, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E		Reduced E
1	AlkL	E_{viii}	
2	AlkLE_{i}	E_{viii}	
3	AlkLE_{ii}	E_{viii}	
4	AlkL$E_{ii}E_{iib}$	E_{viii}	
5	AlkLE_{iii}	E_{viii}	
6	AlkLE_{iv}	E_{viii}	
7	AlkL	E_{viii}	E_a
8	AlkLE_{i}	E_{viii}	E_a
9	AlkLE_{ii}	E_{viii}	E_a
10	AlkL$E_{ii}E_{iib}$	E_{viii}	E_a
11	AlkLE_{iii}	E_{viii}	E_a
12	AlkLE_{iv}	E_{viii}	E_a
13	AlkL	E_{viii}	E_b
14	AlkLE_{i}	E_{viii}	E_b
15	AlkLE_{ii}	E_{viii}	E_b
16	AlkL$E_{ii}E_{iib}$	E_{viii}	E_b
17	AlkLE_{iii}	E_{viii}	E_b
18	AlkLE_{iv}	E_{viii}	E_b
19	AlkL	E_{viii}	E_d
20	AlkLE_{i}	E_{viii}	E_d
21	AlkLE_{ii}	E_{viii}	E_d
22	AlkL$E_{ii}E_{iib}$	E_{viii}	E_d
23	AlkLE_{iii}	E_{viii}	E_d
24	AlkLE_{iv}	E_{viii}	E_d
25	AlkL	E_{viii}	E_e
26	AlkLE_{i}	E_{viii}	E_e
27	AlkLE_{ii}	E_{viii}	E_e
28	AlkL$E_{ii}E_{iib}$	E_{viii}	E_e
29	AlkLE_{iii}	E_{viii}	E_e
30	AlkLE_{iv}	E_{viii}	E_e
31	AlkL	E_{viii}	E_f
32	AlkLE_{i}	E_{viii}	E_f
33	AlkLE_{ii}	E_{viii}	E_f
34	AlkL$E_{ii}E_{iib}$	E_{viii}	E_f
35	AlkLE_{iii}	E_{viii}	E_f
36	AlkLE_{iv}	E_{viii}	E_f
37	AlkL	E_{ix}	
38	AlkLE_{i}	E_{ix}	
39	AlkLE_{ii}	E_{ix}	
40	AlkL$E_{ii}E_{iib}$	E_{ix}	
41	AlkLE_{iii}	E_{ix}	
42	AlkLE_{iv}	E_{ix}	
43	AlkL	E_{ix}	E_a
44	AlkLE_{i}	E_{ix}	E_a
45	AlkLE_{ii}	E_{ix}	E_a
46	AlkL$E_{ii}E_{iib}$	E_{ix}	E_a
47	AlkLE_{iii}	E_{ix}	E_a
48	AlkLE_{iv}	E_{ix}	E_a
49	AlkL	E_{ix}	E_b
50	AlkLE_{i}	E_{ix}	E_b
51	AlkLE_{ii}	E_{ix}	E_b
52	AlkL$E_{ii}E_{iib}$	E_{ix}	E_b
53	AlkLE_{iii}	E_{ix}	E_b
54	AlkLE_{iv}	E_{ix}	E_b
55	AlkL	E_{ix}	E_d
56	AlkLE_{i}	E_{ix}	E_d
57	AlkLE_{ii}	E_{ix}	E_d
58	AlkL$E_{ii}E_{iib}$	E_{ix}	E_d
59	AlkLE_{iii}	E_{ix}	E_d
60	AlkLE_{iv}	E_{ix}	E_d

61	AlkL	E_{ix}	E_e
62	$AlkLE_i$	E_{ix}	E_e
63	$AlkLE_{ii}$	E_{ix}	E_e
64	$AlkLE_{ii}E_{iib}$	E_{ix}	E_e
65	$AlkLE_{iii}$	E_{ix}	E_e
66	$AlkLE_{iv}$	E_{ix}	E_e
67	AlkL	E_{ix}	E_f
68	$AlkLE_i$	E_{ix}	E_f
69	$AlkLE_{ii}$	E_{ix}	E_f
70	$AlkLE_{ii}E_{iib}$	E_{ix}	E_f
71	$AlkLE_{iii}$	E_{ix}	E_f
72	$AlkLE_{iv}$	E_{ix}	E_f
73	AlkL	E_x	
74	$AlkLE_i$	E_x	
75	$AlkLE_{ii}$	E_x	
76	$AlkLE_{ii}E_{iib}$	E_x	
77	$AlkLE_{iii}$	E_x	
78	$AlkLE_{iv}$	E_x	
79	AlkL	E_x	E_a
80	$AlkLE_i$	E_x	E_a
81	$AlkLE_{ii}$	E_x	E_a
82	$AlkLE_{ii}E_{iib}$	E_x	E_a
83	$AlkLE_{iii}$	E_x	E_a
84	$AlkLE_{iv}$	E_x	E_a
85	AlkL	E_x	E_b
86	$AlkLE_i$	E_x	E_b
87	$AlkLE_{ii}$	E_x	E_b
88	$AlkLE_{ii}E_{iib}$	E_x	E_b
89	$AlkLE_{iii}$	E_x	E_b
90	$AlkLE_{iv}$	E_x	E_b
91	AlkL	E_x	E_d

92	$AlkLE_i$	E_x	E_d
93	$AlkLE_{ii}$	E_x	E_d
94	$AlkLE_{ii}E_{iib}$	E_x	E_d
95	$AlkLE_{iii}$	E_x	E_d
96	$AlkLE_{iv}$	E_x	E_d
97	AlkL	E_x	E_e
98	$AlkLE_i$	E_x	E_e
99	$AlkLE_{ii}$	E_x	E_e
100	$AlkLE_{ii}E_{iib}$	E_x	E_e
101	$AlkLE_{iii}$	E_x	E_e
102	$AlkLE_{iv}$	E_x	E_e
103	AlkL	E_x	E_f
104	$AlkLE_i$	E_x	E_f
105	$AlkLE_{ii}$	E_x	E_f
106	$AlkLE_{ii}E_{iib}$	E_x	E_f
107	$AlkLE_{iii}$	E_x	E_f
108	$AlkLE_{iv}$	E_x	E_f
109	AlkL	$E_{vi}E_{viii}$	
110	$AlkLE_i$	$E_{vi}E_{viii}$	
111	$AlkLE_{ii}$	$E_{vi}E_{viii}$	
112	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	
113	$AlkLE_{iii}$	$E_{vi}E_{viii}$	
114	$AlkLE_{iv}$	$E_{vi}E_{viii}$	
115	AlkL	$E_{vi}E_{viii}$	E_a
116	$AlkLE_i$	$E_{vi}E_{viii}$	E_a
117	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_a
118	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a
119	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_a
120	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_a
121	AlkL	$E_{vi}E_{viii}$	E_b
122	$AlkLE_i$	$E_{vi}E_{viii}$	E_b

123	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_b
124	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b
125	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_b
126	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_b
127	AlkL	$E_{vi}E_{viii}$	E_d
128	$AlkLE_{i}$	$E_{vi}E_{viii}$	E_d
129	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_d
130	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d
131	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_d
132	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_d
133	AlkL	$E_{vi}E_{viii}$	E_e
134	$AlkLE_{i}$	$E_{vi}E_{viii}$	E_e
135	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_e
136	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e
137	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_e
138	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_e
139	AlkL	$E_{vi}E_{viii}$	E_f
140	$AlkLE_{i}$	$E_{vi}E_{viii}$	E_f
141	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_f
142	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f
143	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_f
144	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_f
145	AlkL	$E_{iib}E_{vi}E_x$	
146	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	
147	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	
148	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	
149	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	
150	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	
151	AlkL	$E_{iib}E_{vi}E_x$	E_a
152	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	E_a
153	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_a
154	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a
155	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_a
156	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_a
157	AlkL	$E_{iib}E_{vi}E_x$	E_b
158	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	E_b
159	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_b
160	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b
161	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_b
162	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_b
163	AlkL	$E_{iib}E_{vi}E_x$	E_d
164	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	E_d
165	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_d
166	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d
167	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_d
168	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_d
169	AlkL	$E_{iib}E_{vi}E_x$	E_e
170	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	E_e
171	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_e
172	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e
173	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_e
174	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_e
175	AlkL	$E_{iib}E_{vi}E_x$	E_f
176	$AlkLE_{i}$	$E_{iib}E_{vi}E_x$	E_f
177	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_f
178	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f
179	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_f
180	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_f
181	AlkL	E_{viii}	E_1
182	$AlkLE_{i}$	E_{viii}	E_1
183	$AlkLE_{ii}$	E_{viii}	E_1
184	$AlkLE_{ii}E_{iib}$	E_{viii}	E_1

185	$AlkLE_{iii}$	E_{viii}		E_1
186	$AlkLE_{iv}$	E_{viii}		E_1
187	AlkL	E_{viii}	E_a	E_1
188	$AlkLE_i$	E_{viii}	E_a	E_1
189	$AlkLE_{ii}$	E_{viii}	E_a	E_1
190	$AlkLE_{ii}E_{iib}$	E_{viii}	E_a	E_1
191	$AlkLE_{iii}$	E_{viii}	E_a	E_1
192	$AlkLE_{iv}$	E_{viii}	E_a	E_1
193	AlkL	E_{viii}	E_b	E_1
194	$AlkLE_i$	E_{viii}	E_b	E_1
195	$AlkLE_{ii}$	E_{viii}	E_b	E_1
196	$AlkLE_{ii}E_{iib}$	E_{viii}	E_b	E_1
197	$AlkLE_{iii}$	E_{viii}	E_b	E_1
198	$AlkLE_{iv}$	E_{viii}	E_b	E_1
199	AlkL	E_{viii}	E_d	E_1
200	$AlkLE_i$	E_{viii}	E_d	E_1
201	$AlkLE_{ii}$	E_{viii}	E_d	E_1
202	$AlkLE_{ii}E_{iib}$	E_{viii}	E_d	E_1
203	$AlkLE_{iii}$	E_{viii}	E_d	E_1
204	$AlkLE_{iv}$	E_{viii}	E_d	E_1
205	AlkL	E_{viii}	E_e	E_1
206	$AlkLE_i$	E_{viii}	E_e	E_1
207	$AlkLE_{ii}$	E_{viii}	E_e	E_1
208	$AlkLE_{ii}E_{iib}$	E_{viii}	E_e	E_1
209	$AlkLE_{iii}$	E_{viii}	E_e	E_1
210	$AlkLE_{iv}$	E_{viii}	E_e	E_1
211	AlkL	E_{viii}	E_f	E_1
212	$AlkLE_i$	E_{viii}	E_f	E_1
213	$AlkLE_{ii}$	E_{viii}	E_f	E_1
214	$AlkLE_{ii}E_{iib}$	E_{viii}	E_f	E_1
215	$AlkLE_{iii}$	E_{viii}	E_f	E_1

216	$AlkLE_{iv}$	E_{viii}	E_f	E_1
217	AlkL	E_{ix}		E_1
218	$AlkLE_i$	E_{ix}		E_1
219	$AlkLE_{ii}$	E_{ix}		E_1
220	$AlkLE_{ii}E_{iib}$	E_{ix}		E_1
221	$AlkLE_{iii}$	E_{ix}		E_1
222	$AlkLE_{iv}$	E_{ix}		E_1
223	AlkL	E_{ix}	E_a	E_1
224	$AlkLE_i$	E_{ix}	E_a	E_1
225	$AlkLE_{ii}$	E_{ix}	E_a	E_1
226	$AlkLE_{ii}E_{iib}$	E_{ix}	E_a	E_1
227	$AlkLE_{iii}$	E_{ix}	E_a	E_1
228	$AlkLE_{iv}$	E_{ix}	E_a	E_1
229	AlkL	E_{ix}	E_b	E_1
230	$AlkLE_i$	E_{ix}	E_b	E_1
231	$AlkLE_{ii}$	E_{ix}	E_b	E_1
232	$AlkLE_{ii}E_{iib}$	E_{ix}	E_b	E_1
233	$AlkLE_{iii}$	E_{ix}	E_b	E_1
234	$AlkLE_{iv}$	E_{ix}	E_b	E_1
235	AlkL	E_{ix}	E_d	E_1
236	$AlkLE_i$	E_{ix}	E_d	E_1
237	$AlkLE_{ii}$	E_{ix}	E_d	E_1
238	$AlkLE_{ii}E_{iib}$	E_{ix}	E_d	E_1
239	$AlkLE_{iii}$	E_{ix}	E_d	E_1
240	$AlkLE_{iv}$	E_{ix}	E_d	E_1
241	AlkL	E_{ix}	E_e	E_1
242	$AlkLE_i$	E_{ix}	E_e	E_1
243	$AlkLE_{ii}$	E_{ix}	E_e	E_1
244	$AlkLE_{ii}E_{iib}$	E_{ix}	E_e	E_1
245	$AlkLE_{iii}$	E_{ix}	E_e	E_1
246	$AlkLE_{iv}$	E_{ix}	E_e	E_1

247	AlkL	E_{ix}	E_f	E_1
248	AlkLE_i	E_{ix}	E_f	E_1
249	AlkLE_{ii}	E_{ix}	E_f	E_1
250	AlkL$E_{ii}E_{iib}$	E_{ix}	E_f	E_1
251	AlkLE_{iii}	E_{ix}	E_f	E_1
252	AlkLE_{iv}	E_{ix}	E_f	E_1
253	AlkL	E_x		E_1
254	AlkLE_i	E_x		E_1
255	AlkLE_{ii}	E_x		E_1
256	AlkL$E_{ii}E_{iib}$	E_x		E_1
257	AlkLE_{iii}	E_x		E_1
258	AlkLE_{iv}	E_x		E_1
259	AlkL	E_x	E_a	E_1
260	AlkLE_i	E_x	E_a	E_1
261	AlkLE_{ii}	E_x	E_a	E_1
262	AlkL$E_{ii}E_{iib}$	E_x	E_a	E_1
263	AlkLE_{iii}	E_x	E_a	E_1
264	AlkLE_{iv}	E_x	E_a	E_1
265	AlkL	E_x	E_b	E_1
266	AlkLE_i	E_x	E_b	E_1
267	AlkLE_{ii}	E_x	E_b	E_1
268	AlkL$E_{ii}E_{iib}$	E_x	E_b	E_1
269	AlkLE_{iii}	E_x	E_b	E_1
270	AlkLE_{iv}	E_x	E_b	E_1
271	AlkL	E_x	E_d	E_1
272	AlkLE_i	E_x	E_d	E_1
273	AlkLE_{ii}	E_x	E_d	E_1
274	AlkL$E_{ii}E_{iib}$	E_x	E_d	E_1
275	AlkLE_{iii}	E_x	E_d	E_1
276	AlkLE_{iv}	E_x	E_d	E_1
277	AlkL	E_x	E_e	E_1
278	AlkLE_i	E_x	E_e	E_1
279	AlkLE_{ii}	E_x	E_e	E_1
280	AlkL$E_{ii}E_{iib}$	E_x	E_e	E_1
281	AlkLE_{iii}	E_x	E_e	E_1
282	AlkLE_{iv}	E_x	E_e	E_1
283	AlkL	E_x	E_f	E_1
284	AlkLE_i	E_x	E_f	E_1
285	AlkLE_{ii}	E_x	E_f	E_1
286	AlkL$E_{ii}E_{iib}$	E_x	E_f	E_1
287	AlkLE_{iii}	E_x	E_f	E_1
288	AlkLE_{iv}	E_x	E_f	E_1
289	AlkL	$E_{vi}E_{viii}$		E_1
290	AlkLE_i	$E_{vi}E_{viii}$		E_1
291	AlkLE_{ii}	$E_{vi}E_{viii}$		E_1
292	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{viii}$		E_1
293	AlkLE_{iii}	$E_{vi}E_{viii}$		E_1
294	AlkLE_{iv}	$E_{vi}E_{viii}$		E_1
295	AlkL	$E_{vi}E_{viii}$	E_a	E_1
296	AlkLE_i	$E_{vi}E_{viii}$	E_a	E_1
297	AlkLE_{ii}	$E_{vi}E_{viii}$	E_a	E_1
298	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a	E_1
299	AlkLE_{iii}	$E_{vi}E_{viii}$	E_a	E_1
300	AlkLE_{iv}	$E_{vi}E_{viii}$	E_a	E_1
301	AlkL	$E_{vi}E_{viii}$	E_b	E_1
302	AlkLE_i	$E_{vi}E_{viii}$	E_b	E_1
303	AlkLE_{ii}	$E_{vi}E_{viii}$	E_b	E_1
304	AlkL$E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b	E_1
305	AlkLE_{iii}	$E_{vi}E_{viii}$	E_b	E_1
306	AlkLE_{iv}	$E_{vi}E_{viii}$	E_b	E_1
307	AlkL	$E_{vi}E_{viii}$	E_d	E_1
308	AlkLE_i	$E_{vi}E_{viii}$	E_d	E_1

309	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_d	E_1
310	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d	E_1
311	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_d	E_1
312	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_d	E_1
313	AlkL	$E_{vi}E_{viii}$	E_e	E_1
314	$AlkLE_i$	$E_{vi}E_{viii}$	E_e	E_1
315	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_e	E_1
316	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e	E_1
317	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_e	E_1
318	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_e	E_1
319	AlkL	$E_{vi}E_{viii}$	E_f	E_1
320	$AlkLE_i$	$E_{vi}E_{viii}$	E_f	E_1
321	$AlkLE_{ii}$	$E_{vi}E_{viii}$	E_f	E_1
322	$AlkLE_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f	E_1
323	$AlkLE_{iii}$	$E_{vi}E_{viii}$	E_f	E_1
324	$AlkLE_{iv}$	$E_{vi}E_{viii}$	E_f	E_1
325	AlkL	$E_{iib}E_{vi}E_x$		E_1
326	$AlkLE_i$	$E_{iib}E_{vi}E_x$		E_1
327	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$		E_1
328	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$		E_1
329	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$		E_1
330	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$		E_1
331	AlkL	$E_{iib}E_{vi}E_x$	E_a	E_1
332	$AlkLE_i$	$E_{iib}E_{vi}E_x$	E_a	E_1
333	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
334	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a	E_1
335	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
336	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_a	E_1
337	AlkL	$E_{iib}E_{vi}E_x$	E_b	E_1
338	$AlkLE_i$	$E_{iib}E_{vi}E_x$	E_b	E_1
339	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
340	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b	E_1
341	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
342	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_b	E_1
343	AlkL	$E_{iib}E_{vi}E_x$	E_d	E_1
344	$AlkLE_i$	$E_{iib}E_{vi}E_x$	E_d	E_1
345	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
346	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d	E_1
347	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
348	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_d	E_1
349	AlkL	$E_{iib}E_{vi}E_x$	E_e	E_1
350	$AlkLE_i$	$E_{iib}E_{vi}E_x$	E_e	E_1
351	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
352	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e	E_1
353	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
354	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_e	E_1
355	AlkL	$E_{iib}E_{vi}E_x$	E_f	E_1
356	$AlkLE_i$	$E_{iib}E_{vi}E_x$	E_f	E_1
357	$AlkLE_{ii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
358	$AlkLE_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f	E_1
359	$AlkLE_{iii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
360	$AlkLE_{iv}$	$E_{iib}E_{vi}E_x$	E_f	E_1

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of alkanes and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the enzyme 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, Thl, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E	Reduced E
1	$AlkLE_{xii}$ E_{viii}	
2	$AlkLE_{xii}E_{i}$ E_{viii}	
3	$AlkLE_{xii}E_{ii}$ E_{viii}	
4	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	
5	$AlkLE_{xii}E_{iii}$ E_{viii}	
6	$AlkLE_{xii}E_{iv}$ E_{viii}	
7	$AlkLE_{xii}$ E_{viii}	E_a
8	$AlkLE_{xii}E_{i}$ E_{viii}	E_a
9	$AlkLE_{xii}E_{ii}$ E_{viii}	E_a
10	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	E_a
11	$AlkLE_{xii}E_{iii}$ E_{viii}	E_a
12	$AlkLE_{xii}E_{iv}$ E_{viii}	E_a
13	$AlkLE_{xii}$ E_{viii}	E_b
14	$AlkLE_{xii}E_{i}$ E_{viii}	E_b
15	$AlkLE_{xii}E_{ii}$ E_{viii}	E_b
16	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	E_b
17	$AlkLE_{xii}E_{iii}$ E_{viii}	E_b
18	$AlkLE_{xii}E_{iv}$ E_{viii}	E_b
19	$AlkLE_{xii}$ E_{viii}	E_d
20	$AlkLE_{xii}E_{i}$ E_{viii}	E_d
21	$AlkLE_{xii}E_{ii}$ E_{viii}	E_d
22	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	E_d
23	$AlkLE_{xii}E_{iii}$ E_{viii}	E_d
24	$AlkLE_{xii}E_{iv}$ E_{viii}	E_d
25	$AlkLE_{xii}$ E_{viii}	E_e
26	$AlkLE_{xii}E_{i}$ E_{viii}	E_e
27	$AlkLE_{xii}E_{ii}$ E_{viii}	E_e
28	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	E_e
29	$AlkLE_{xii}E_{iii}$ E_{viii}	E_e
30	$AlkLE_{xii}E_{iv}$ E_{viii}	E_e
31	$AlkLE_{xii}$ E_{viii}	E_f
32	$AlkLE_{xii}E_{i}$ E_{viii}	E_f
33	$AlkLE_{xii}E_{ii}$ E_{viii}	E_f
34	$AlkLE_{xii}E_{ii}E_{iib}$ E_{viii}	E_f
35	$AlkLE_{xii}E_{iii}$ E_{viii}	E_f
36	$AlkLE_{xii}E_{iv}$ E_{viii}	E_f
37	$AlkLE_{xii}$ E_{ix}	
38	$AlkLE_{xii}E_{i}$ E_{ix}	
39	$AlkLE_{xii}E_{ii}$ E_{ix}	
40	$AlkLE_{xii}E_{ii}E_{iib}$ E_{ix}	
41	$AlkLE_{xii}E_{iii}$ E_{ix}	
42	$AlkLE_{xii}E_{iv}$ E_{ix}	
43	$AlkLE_{xii}$ E_{ix}	E_a
44	$AlkLE_{xii}E_{i}$ E_{ix}	E_a
45	$AlkLE_{xii}E_{ii}$ E_{ix}	E_a
46	$AlkLE_{xii}E_{ii}E_{iib}$ E_{ix}	E_a
47	$AlkLE_{xii}E_{iii}$ E_{ix}	E_a
48	$AlkLE_{xii}E_{iv}$ E_{ix}	E_a
49	$AlkLE_{xii}$ E_{ix}	E_b
50	$AlkLE_{xii}E_{i}$ E_{ix}	E_b
51	$AlkLE_{xii}E_{ii}$ E_{ix}	E_b
52	$AlkLE_{xii}E_{ii}E_{iib}$ E_{ix}	E_b
53	$AlkLE_{xii}E_{iii}$ E_{ix}	E_b
54	$AlkLE_{xii}E_{iv}$ E_{ix}	E_b
55	$AlkLE_{xii}$ E_{ix}	E_d
56	$AlkLE_{xii}E_{i}$ E_{ix}	E_d
57	$AlkLE_{xii}E_{ii}$ E_{ix}	E_d
58	$AlkLE_{xii}E_{ii}E_{iib}$ E_{ix}	E_d
59	$AlkLE_{xii}E_{iii}$ E_{ix}	E_d
60	$AlkLE_{xii}E_{iv}$ E_{ix}	E_d

61	$AlkLE_{xii}$	E_{ix}	E_e
62	$AlkLE_{xii}E_i$	E_{ix}	E_e
63	$AlkLE_{xii}E_{ii}$	E_{ix}	E_e
64	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_e
65	$AlkLE_{xii}E_{iii}$	E_{ix}	E_e
66	$AlkLE_{xii}E_{iv}$	E_{ix}	E_e
67	$AlkLE_{xii}$	E_{ix}	E_f
68	$AlkLE_{xii}E_i$	E_{ix}	E_f
69	$AlkLE_{xii}E_{ii}$	E_{ix}	E_f
70	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_f
71	$AlkLE_{xii}E_{iii}$	E_{ix}	E_f
72	$AlkLE_{xii}E_{iv}$	E_{ix}	E_f
73	$AlkLE_{xii}$	E_x	
74	$AlkLE_{xii}E_i$	E_x	
75	$AlkLE_{xii}E_{ii}$	E_x	
76	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	
77	$AlkLE_{xii}E_{iii}$	E_x	
78	$AlkLE_{xii}E_{iv}$	E_x	
79	$AlkLE_{xii}$	E_x	E_a
80	$AlkLE_{xii}E_i$	E_x	E_a
81	$AlkLE_{xii}E_{ii}$	E_x	E_a
82	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_a
83	$AlkLE_{xii}E_{iii}$	E_x	E_a
84	$AlkLE_{xii}E_{iv}$	E_x	E_a
85	$AlkLE_{xii}$	E_x	E_b
86	$AlkLE_{xii}E_i$	E_x	E_b
87	$AlkLE_{xii}E_{ii}$	E_x	E_b
88	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_b
89	$AlkLE_{xii}E_{iii}$	E_x	E_b
90	$AlkLE_{xii}E_{iv}$	E_x	E_b
91	$AlkLE_{xii}$	E_x	E_d
92	$AlkLE_{xii}E_i$	E_x	E_d
93	$AlkLE_{xii}E_{ii}$	E_x	E_d
94	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_d
95	$AlkLE_{xii}E_{iii}$	E_x	E_d
96	$AlkLE_{xii}E_{iv}$	E_x	E_d
97	$AlkLE_{xii}$	E_x	E_e
98	$AlkLE_{xii}E_i$	E_x	E_e
99	$AlkLE_{xii}E_{ii}$	E_x	E_e
100	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_e
101	$AlkLE_{xii}E_{iii}$	E_x	E_e
102	$AlkLE_{xii}E_{iv}$	E_x	E_e
103	$AlkLE_{xii}$	E_x	E_f
104	$AlkLE_{xii}E_i$	E_x	E_f
105	$AlkLE_{xii}E_{ii}$	E_x	E_f
106	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_f
107	$AlkLE_{xii}E_{iii}$	E_x	E_f
108	$AlkLE_{xii}E_{iv}$	E_x	E_f
109	$AlkLE_{xii}$	$E_{vi}E_{viii}$	
110	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	
111	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	
112	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	
113	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	
114	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	
115	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_a
116	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	E_a
117	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_a
118	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a
119	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_a
120	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_a
121	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_b
122	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	E_b

123	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_b
124	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b
125	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_b
126	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_b
127	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_d
128	$AlkLE_{xii}E_{i}$	$E_{vi}E_{viii}$	E_d
129	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_d
130	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d
131	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_d
132	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_d
133	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_e
134	$AlkLE_{xii}E_{i}$	$E_{vi}E_{viii}$	E_e
135	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_e
136	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e
137	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_e
138	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_e
139	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_f
140	$AlkLE_{xii}E_{i}$	$E_{vi}E_{viii}$	E_f
141	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_f
142	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f
143	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_f
144	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_f
145	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	
146	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	
147	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	
148	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	
149	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	
150	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	
151	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_a
152	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_a
153	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_a
154	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a
155	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_a
156	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_a
157	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_b
158	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_b
159	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_b
160	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b
161	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_b
162	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_b
163	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_d
164	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_d
165	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_d
166	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d
167	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_d
168	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_d
169	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_e
170	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_e
171	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_e
172	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e
173	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_e
174	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_e
175	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_f
176	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_f
177	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_f
178	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f
179	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_f
180	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_f
181	$AlkLE_{xii}$	E_{viii}	E_1
182	$AlkLE_{xii}E_{i}$	E_{viii}	E_1
183	$AlkLE_{xii}E_{ii}$	E_{viii}	E_1
184	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_1

185	$AlkLE_{xii}E_{iii}$	E_{viii}		E_1
186	$AlkLE_{xii}E_{iv}$	E_{viii}		E_1
187	$AlkLE_{xii}$	E_{viii}	E_a	E_1
188	$AlkLE_{xii}E_i$	E_{viii}	E_a	E_1
189	$AlkLE_{xii}E_{ii}$	E_{viii}	E_a	E_1
190	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_a	E_1
191	$AlkLE_{xii}E_{iii}$	E_{viii}	E_a	E_1
192	$AlkLE_{xii}E_{iv}$	E_{viii}	E_a	E_1
193	$AlkLE_{xii}$	E_{viii}	E_b	E_1
194	$AlkLE_{xii}E_i$	E_{viii}	E_b	E_1
195	$AlkLE_{xii}E_{ii}$	E_{viii}	E_b	E_1
196	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_b	E_1
197	$AlkLE_{xii}E_{iii}$	E_{viii}	E_b	E_1
198	$AlkLE_{xii}E_{iv}$	E_{viii}	E_b	E_1
199	$AlkLE_{xii}$	E_{viii}	E_d	E_1
200	$AlkLE_{xii}E_i$	E_{viii}	E_d	E_1
201	$AlkLE_{xii}E_{ii}$	E_{viii}	E_d	E_1
202	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_d	E_1
203	$AlkLE_{xii}E_{iii}$	E_{viii}	E_d	E_1
204	$AlkLE_{xii}E_{iv}$	E_{viii}	E_d	E_1
205	$AlkLE_{xii}$	E_{viii}	E_e	E_1
206	$AlkLE_{xii}E_i$	E_{viii}	E_e	E_1
207	$AlkLE_{xii}E_{ii}$	E_{viii}	E_e	E_1
208	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_e	E_1
209	$AlkLE_{xii}E_{iii}$	E_{viii}	E_e	E_1
210	$AlkLE_{xii}E_{iv}$	E_{viii}	E_e	E_1
211	$AlkLE_{xii}$	E_{viii}	E_f	E_1
212	$AlkLE_{xii}E_i$	E_{viii}	E_f	E_1
213	$AlkLE_{xii}E_{ii}$	E_{viii}	E_f	E_1
214	$AlkLE_{xii}E_{ii}E_{iib}$	E_{viii}	E_f	E_1
215	$AlkLE_{xii}E_{iii}$	E_{viii}	E_f	E_1
216	$AlkLE_{xii}E_{iv}$	E_{viii}	E_f	E_1
217	$AlkLE_{xii}$	E_{ix}		E_1
218	$AlkLE_{xii}E_i$	E_{ix}		E_1
219	$AlkLE_{xii}E_{ii}$	E_{ix}		E_1
220	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}		E_1
221	$AlkLE_{xii}E_{iii}$	E_{ix}		E_1
222	$AlkLE_{xii}E_{iv}$	E_{ix}		E_1
223	$AlkLE_{xii}$	E_{ix}	E_a	E_1
224	$AlkLE_{xii}E_i$	E_{ix}	E_a	E_1
225	$AlkLE_{xii}E_{ii}$	E_{ix}	E_a	E_1
226	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_a	E_1
227	$AlkLE_{xii}E_{iii}$	E_{ix}	E_a	E_1
228	$AlkLE_{xii}E_{iv}$	E_{ix}	E_a	E_1
229	$AlkLE_{xii}$	E_{ix}	E_b	E_1
230	$AlkLE_{xii}E_i$	E_{ix}	E_b	E_1
231	$AlkLE_{xii}E_{ii}$	E_{ix}	E_b	E_1
232	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_b	E_1
233	$AlkLE_{xii}E_{iii}$	E_{ix}	E_b	E_1
234	$AlkLE_{xii}E_{iv}$	E_{ix}	E_b	E_1
235	$AlkLE_{xii}$	E_{ix}	E_d	E_1
236	$AlkLE_{xii}E_i$	E_{ix}	E_d	E_1
237	$AlkLE_{xii}E_{ii}$	E_{ix}	E_d	E_1
238	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_d	E_1
239	$AlkLE_{xii}E_{iii}$	E_{ix}	E_d	E_1
240	$AlkLE_{xii}E_{iv}$	E_{ix}	E_d	E_1
241	$AlkLE_{xii}$	E_{ix}	E_e	E_1
242	$AlkLE_{xii}E_i$	E_{ix}	E_e	E_1
243	$AlkLE_{xii}E_{ii}$	E_{ix}	E_e	E_1
244	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_e	E_1
245	$AlkLE_{xii}E_{iii}$	E_{ix}	E_e	E_1
246	$AlkLE_{xii}E_{iv}$	E_{ix}	E_e	E_1

247	$AlkLE_{xii}$	E_{ix}	E_f	E_1
248	$AlkLE_{xii}E_i$	E_{ix}	E_f	E_1
249	$AlkLE_{xii}E_{ii}$	E_{ix}	E_f	E_1
250	$AlkLE_{xii}E_{ii}E_{iib}$	E_{ix}	E_f	E_1
251	$AlkLE_{xii}E_{iii}$	E_{ix}	E_f	E_1
252	$AlkLE_{xii}E_{iv}$	E_{ix}	E_f	E_1
253	$AlkLE_{xii}$	E_x		E_1
254	$AlkLE_{xii}E_i$	E_x		E_1
255	$AlkLE_{xii}E_{ii}$	E_x		E_1
256	$AlkLE_{xii}E_{ii}E_{iib}$	E_x		E_1
257	$AlkLE_{xii}E_{iii}$	E_x		E_1
258	$AlkLE_{xii}E_{iv}$	E_x		E_1
259	$AlkLE_{xii}$	E_x	E_a	E_1
260	$AlkLE_{xii}E_i$	E_x	E_a	E_1
261	$AlkLE_{xii}E_{ii}$	E_x	E_a	E_1
262	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_a	E_1
263	$AlkLE_{xii}E_{iii}$	E_x	E_a	E_1
264	$AlkLE_{xii}E_{iv}$	E_x	E_a	E_1
265	$AlkLE_{xii}$	E_x	E_b	E_1
266	$AlkLE_{xii}E_i$	E_x	E_b	E_1
267	$AlkLE_{xii}E_{ii}$	E_x	E_b	E_1
268	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_b	E_1
269	$AlkLE_{xii}E_{iii}$	E_x	E_b	E_1
270	$AlkLE_{xii}E_{iv}$	E_x	E_b	E_1
271	$AlkLE_{xii}$	E_x	E_d	E_1
272	$AlkLE_{xii}E_i$	E_x	E_d	E_1
273	$AlkLE_{xii}E_{ii}$	E_x	E_d	E_1
274	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_d	E_1
275	$AlkLE_{xii}E_{iii}$	E_x	E_d	E_1
276	$AlkLE_{xii}E_{iv}$	E_x	E_d	E_1
277	$AlkLE_{xii}$	E_x	E_e	E_1

278	$AlkLE_{xii}E_i$	E_x	E_e	E_1
279	$AlkLE_{xii}E_{ii}$	E_x	E_e	E_1
280	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_e	E_1
281	$AlkLE_{xii}E_{iii}$	E_x	E_e	E_1
282	$AlkLE_{xii}E_{iv}$	E_x	E_e	E_1
283	$AlkLE_{xii}$	E_x	E_f	E_1
284	$AlkLE_{xii}E_i$	E_x	E_f	E_1
285	$AlkLE_{xii}E_{ii}$	E_x	E_f	E_1
286	$AlkLE_{xii}E_{ii}E_{iib}$	E_x	E_f	E_1
287	$AlkLE_{xii}E_{iii}$	E_x	E_f	E_1
288	$AlkLE_{xii}E_{iv}$	E_x	E_f	E_1
289	$AlkLE_{xii}$	$E_{vi}E_{viii}$		E_1
290	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$		E_1
291	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$		E_1
292	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$		E_1
293	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$		E_1
294	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$		E_1
295	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_a	E_1
296	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	E_a	E_1
297	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_a	E_1
298	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a	E_1
299	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_a	E_1
300	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_a	E_1
301	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_b	E_1
302	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	E_b	E_1
303	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_b	E_1
304	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b	E_1
305	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_b	E_1
306	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_b	E_1
307	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_d	E_1
308	$AlkLE_{xii}E_i$	$E_{vi}E_{viii}$	E_d	E_1

309	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_d	E_1
310	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d	E_1
311	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_d	E_1
312	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_d	E_1
313	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_e	E_1
314	$AlkLE_{xii}E_{i}$	$E_{vi}E_{viii}$	E_e	E_1
315	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_e	E_1
316	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e	E_1
317	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_e	E_1
318	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_e	E_1
319	$AlkLE_{xii}$	$E_{vi}E_{viii}$	E_f	E_1
320	$AlkLE_{xii}E_{i}$	$E_{vi}E_{viii}$	E_f	E_1
321	$AlkLE_{xii}E_{ii}$	$E_{vi}E_{viii}$	E_f	E_1
322	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f	E_1
323	$AlkLE_{xii}E_{iii}$	$E_{vi}E_{viii}$	E_f	E_1
324	$AlkLE_{xii}E_{iv}$	$E_{vi}E_{viii}$	E_f	E_1
325	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$		E_1
326	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$		E_1
327	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$		E_1
328	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$		E_1
329	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$		E_1
330	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$		E_1
331	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
332	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_a	E_1
333	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
334	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a	E_1
335	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
336	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_a	E_1
337	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
338	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_b	E_1
339	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
340	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b	E_1
341	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
342	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_b	E_1
343	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
344	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_d	E_1
345	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
346	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d	E_1
347	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
348	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_d	E_1
349	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
350	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_e	E_1
351	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
352	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e	E_1
353	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
354	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_e	E_1
355	$AlkLE_{xii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
356	$AlkLE_{xii}E_{i}$	$E_{iib}E_{vi}E_x$	E_f	E_1
357	$AlkLE_{xii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
358	$AlkLE_{xii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f	E_1
359	$AlkLE_{xii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
360	$AlkLE_{xii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_f	E_1

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of terminal olefins and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the enzyme 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, Thl, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E		Reduced E
1	AlkL	E_{xi}	
2	AlkLE$_i$	E_{xi}	
3	AlkLE$_{ii}$	E_{xi}	
4	AlkLE$_{ii}$E$_{iib}$	E_{xi}	
5	AlkLE$_{iii}$	E_{xi}	
6	AlkLE$_{iv}$	E_{xi}	
7	AlkL	E_{xi}	E_a
8	AlkLE$_i$	E_{xi}	E_a
9	AlkLE$_{ii}$	E_{xi}	E_a
10	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_a
11	AlkLE$_{iii}$	E_{xi}	E_a
12	AlkLE$_{iv}$	E_{xi}	E_a
13	AlkL	E_{xi}	E_b
14	AlkLE$_i$	E_{xi}	E_b
15	AlkLE$_{ii}$	E_{xi}	E_b
16	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_b
17	AlkLE$_{iii}$	E_{xi}	E_b
18	AlkLE$_{iv}$	E_{xi}	E_b
19	AlkL	E_{xi}	E_d
20	AlkLE$_i$	E_{xi}	E_d
21	AlkLE$_{ii}$	E_{xi}	E_d
22	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_d
23	AlkLE$_{iii}$	E_{xi}	E_d
24	AlkLE$_{iv}$	E_{xi}	E_d
25	AlkL	E_{xi}	E_e
26	AlkLE$_i$	E_{xi}	E_e
27	AlkLE$_{ii}$	E_{xi}	E_e
28	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_e
29	AlkLE$_{iii}$	E_{xi}	E_e
30	AlkLE$_{iv}$	E_{xi}	E_e

31	AlkL	E_{xi}	E_f	
32	AlkLE$_i$	E_{xi}	E_f	
33	AlkLE$_{ii}$	E_{xi}	E_f	
34	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_f	
35	AlkLE$_{iii}$	E_{xi}	E_f	
36	AlkLE$_{iv}$	E_{xi}	E_f	
37	AlkL	E_{xi}		E_1
38	AlkLE$_i$	E_{xi}		E_1
39	AlkLE$_{ii}$	E_{xi}		E_1
40	AlkLE$_{ii}$E$_{iib}$	E_{xi}		E_1
41	AlkLE$_{iii}$	E_{xi}		E_1
42	AlkLE$_{iv}$	E_{xi}		E_1
43	AlkL	E_{xi}	E_a	E_1
44	AlkLE$_i$	E_{xi}	E_a	E_1
45	AlkLE$_{ii}$	E_{xi}	E_a	E_1
46	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_a	E_1
47	AlkLE$_{iii}$	E_{xi}	E_a	E_1
48	AlkLE$_{iv}$	E_{xi}	E_a	E_1
49	AlkL	E_{xi}	E_b	E_1
50	AlkLE$_i$	E_{xi}	E_b	E_1
51	AlkLE$_{ii}$	E_{xi}	E_b	E_1
52	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_b	E_1
53	AlkLE$_{iii}$	E_{xi}	E_b	E_1
54	AlkLE$_{iv}$	E_{xi}	E_b	E_1
55	AlkL	E_{xi}	E_d	E_1
56	AlkLE$_i$	E_{xi}	E_d	E_1
57	AlkLE$_{ii}$	E_{xi}	E_d	E_1
58	AlkLE$_{ii}$E$_{iib}$	E_{xi}	E_d	E_1
59	AlkLE$_{iii}$	E_{xi}	E_d	E_1
60	AlkLE$_{iv}$	E_{xi}	E_d	E_1
61	AlkL	E_{xi}	E_e	E_1

62	$AlkLE_i$	E_{xi}	E_e	E_1
63	$AlkLE_{ii}$	E_{xi}	E_e	E_1
64	$AlkLE_{ii}E_{iib}$	E_{xi}	E_e	E_1
65	$AlkLE_{iii}$	E_{xi}	E_e	E_1
66	$AlkLE_{iv}$	E_{xi}	E_e	E_1
67	AlkL	E_{xi}	E_f	E_1
68	$AlkLE_i$	E_{xi}	E_f	E_1
69	$AlkLE_{ii}$	E_{xi}	E_f	E_1
70	$AlkLE_{ii}E_{iib}$	E_{xi}	E_f	E_1
71	$AlkLE_{iii}$	E_{xi}	E_f	E_1
72	$AlkLE_{iv}$	E_{xi}	E_f	E_1

Microorganisms (abbreviated to MO) which are very especially preferred according to the invention are outstandingly suitable for the production of alkan-1-amines and have increased or reduced enzymatic activities (abbreviated to E) which are described in the table hereinbelow, it being possible for these enzymatic activities additionally to be advantageously combined with an enzymatic activity described for the enzyme 3-ketoacyl-ACP (acyl carrier protein) synthase III (EC 2.3.1.41), which enzymatic activity is increased in comparison with the wild type of the microorganism, in particular the enzymatic activity of plants, preferably the enzymatic activity of plants whose seeds contain fatty acids with alkyl residues shorter than 14 C atoms and especially preferably the enzymatic activity of plants of the genera *Cuphea*, *Elaeis*, *Cocos*, *Umbellularia* and *Cinnamomum* and gene products selected from among AccA, AccB, AccC, AccD, AceE, AceF, Lpd, AcpP, FabA, FabB, FabD, FabF, FabG, FabH, FabI, FabZ, PanD, PanK, UdhA, PntA or PntB.

Any desired combinations of at least two of these enzymatic activities may advantageously be increased.

It may be additionally advantageous that the microorganism is equipped with an enzymatic activity which is described for the gene products selected from among TdcE, PflA, PflB, PflC, PflD, PoxB, YgfG, AckA, AckB, TdcD, Pta, LdhA, AdhE, MgsA, FdnG, FdnH, FdnI, FdhF, FdoG, FdoH, FdoI, PrpC, PrpD, PrpF , PrpB , TdcD, Pdc, PorA, PorB, PorC, PorD, AlsS, IlvB, IlvM, IlvN, IlvG, IlvI, IlvH, AlsD, ButB, ThI, ThlA, ThlB, PhaA, PhaB, Crt, BdhA, BdhB, Adc, Adh, CtfB, AtoA, AtoD, LdhL, GltA, FabR, FhuA, Dld, LldA or LldP, individually or in any desired combination, and which is reduced in comparison with the wild type of the microorganism.

MO	Increased E		Reduced E
1	$AlkLE_{vii}$	E_{viii}	
2	$AlkLE_{vii}E_{i}$	E_{viii}	
3	$AlkLE_{vii}E_{ii}$	E_{viii}	
4	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	
5	$AlkLE_{vii}E_{iii}$	E_{viii}	
6	$AlkLE_{vii}E_{iv}$	E_{viii}	
7	$AlkLE_{vii}$	E_{viii}	E_a
8	$AlkLE_{vii}E_{i}$	E_{viii}	E_a
9	$AlkLE_{vii}E_{ii}$	E_{viii}	E_a
10	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_a
11	$AlkLE_{vii}E_{iii}$	E_{viii}	E_a
12	$AlkLE_{vii}E_{iv}$	E_{viii}	E_a
13	$AlkLE_{vii}$	E_{viii}	E_b
14	$AlkLE_{vii}E_{i}$	E_{viii}	E_b
15	$AlkLE_{vii}E_{ii}$	E_{viii}	E_b
16	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_b
17	$AlkLE_{vii}E_{iii}$	E_{viii}	E_b
18	$AlkLE_{vii}E_{iv}$	E_{viii}	E_b
19	$AlkLE_{vii}$	E_{viii}	E_d
20	$AlkLE_{vii}E_{i}$	E_{viii}	E_d
21	$AlkLE_{vii}E_{ii}$	E_{viii}	E_d
22	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_d
23	$AlkLE_{vii}E_{iii}$	E_{viii}	E_d
24	$AlkLE_{vii}E_{iv}$	E_{viii}	E_d
25	$AlkLE_{vii}$	E_{viii}	E_e
26	$AlkLE_{vii}E_{i}$	E_{viii}	E_e
27	$AlkLE_{vii}E_{ii}$	E_{viii}	E_e
28	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_e
29	$AlkLE_{vii}E_{iii}$	E_{viii}	E_e
30	$AlkLE_{vii}E_{iv}$	E_{viii}	E_e
31	$AlkLE_{vii}$	E_{viii}	E_f
32	$AlkLE_{vii}E_{i}$	E_{viii}	E_f
33	$AlkLE_{vii}E_{ii}$	E_{viii}	E_f
34	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_f
35	$AlkLE_{vii}E_{iii}$	E_{viii}	E_f
36	$AlkLE_{vii}E_{iv}$	E_{viii}	E_f
37	$AlkLE_{vii}$	E_{ix}	
38	$AlkLE_{vii}E_{i}$	E_{ix}	
39	$AlkLE_{vii}E_{ii}$	E_{ix}	
40	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	
41	$AlkLE_{vii}E_{iii}$	E_{ix}	
42	$AlkLE_{vii}E_{iv}$	E_{ix}	
43	$AlkLE_{vii}$	E_{ix}	E_a
44	$AlkLE_{vii}E_{i}$	E_{ix}	E_a
45	$AlkLE_{vii}E_{ii}$	E_{ix}	E_a
46	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_a
47	$AlkLE_{vii}E_{iii}$	E_{ix}	E_a
48	$AlkLE_{vii}E_{iv}$	E_{ix}	E_a
49	$AlkLE_{vii}$	E_{ix}	E_b
50	$AlkLE_{vii}E_{i}$	E_{ix}	E_b
51	$AlkLE_{vii}E_{ii}$	E_{ix}	E_b
52	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_b
53	$AlkLE_{vii}E_{iii}$	E_{ix}	E_b
54	$AlkLE_{vii}E_{iv}$	E_{ix}	E_b
55	$AlkLE_{vii}$	E_{ix}	E_d
56	$AlkLE_{vii}E_{i}$	E_{ix}	E_d
57	$AlkLE_{vii}E_{ii}$	E_{ix}	E_d
58	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_d
59	$AlkLE_{vii}E_{iii}$	E_{ix}	E_d
60	$AlkLE_{vii}E_{iv}$	E_{ix}	E_d

61	$AlkLE_{vii}$	E_{ix}	E_e
62	$AlkLE_{vii}E_i$	E_{ix}	E_e
63	$AlkLE_{vii}E_{ii}$	E_{ix}	E_e
64	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_e
65	$AlkLE_{vii}E_{iii}$	E_{ix}	E_e
66	$AlkLE_{vii}E_{iv}$	E_{ix}	E_e
67	$AlkLE_{vii}$	E_{ix}	E_f
68	$AlkLE_{vii}E_i$	E_{ix}	E_f
69	$AlkLE_{vii}E_{ii}$	E_{ix}	E_f
70	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_f
71	$AlkLE_{vii}E_{iii}$	E_{ix}	E_f
72	$AlkLE_{vii}E_{iv}$	E_{ix}	E_f
73	$AlkLE_{vii}$	E_x	
74	$AlkLE_{vii}E_i$	E_x	
75	$AlkLE_{vii}E_{ii}$	E_x	
76	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	
77	$AlkLE_{vii}E_{iii}$	E_x	
78	$AlkLE_{vii}E_{iv}$	E_x	
79	$AlkLE_{vii}$	E_x	E_a
80	$AlkLE_{vii}E_i$	E_x	E_a
81	$AlkLE_{vii}E_{ii}$	E_x	E_a
82	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_a
83	$AlkLE_{vii}E_{iii}$	E_x	E_a
84	$AlkLE_{vii}E_{iv}$	E_x	E_a
85	$AlkLE_{vii}$	E_x	E_b
86	$AlkLE_{vii}E_i$	E_x	E_b
87	$AlkLE_{vii}E_{ii}$	E_x	E_b
88	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_b
89	$AlkLE_{vii}E_{iii}$	E_x	E_b
90	$AlkLE_{vii}E_{iv}$	E_x	E_b
91	$AlkLE_{vii}$	E_x	E_d
92	$AlkLE_{vii}E_i$	E_x	E_d
93	$AlkLE_{vii}E_{ii}$	E_x	E_d
94	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_d
95	$AlkLE_{vii}E_{iii}$	E_x	E_d
96	$AlkLE_{vii}E_{iv}$	E_x	E_d
97	$AlkLE_{vii}$	E_x	E_e
98	$AlkLE_{vii}E_i$	E_x	E_e
99	$AlkLE_{vii}E_{ii}$	E_x	E_e
100	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_e
101	$AlkLE_{vii}E_{iii}$	E_x	E_e
102	$AlkLE_{vii}E_{iv}$	E_x	E_e
103	$AlkLE_{vii}$	E_x	E_f
104	$AlkLE_{vii}E_i$	E_x	E_f
105	$AlkLE_{vii}E_{ii}$	E_x	E_f
106	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_f
107	$AlkLE_{vii}E_{iii}$	E_x	E_f
108	$AlkLE_{vii}E_{iv}$	E_x	E_f
109	$AlkLE_{vii}$	$E_{vi}E_{viii}$	
110	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	
111	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	
112	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	
113	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	
114	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	
115	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_a
116	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_a
117	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_a
118	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a
119	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_a
120	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_a
121	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_b
122	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_b

123	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_b
124	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b
125	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_b
126	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_b
127	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_d
128	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_d
129	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_d
130	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d
131	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_d
132	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_d
133	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_e
134	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_e
135	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_e
136	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e
137	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_e
138	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_e
139	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_f
140	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_f
141	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_f
142	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f
143	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_f
144	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_f
145	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	
146	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	
147	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	
148	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	
149	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	
150	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	
151	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	
152	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	
153	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	
154	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	
155	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	
156	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	
157	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_a
158	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_a
159	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_a
160	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a
161	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_a
162	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_a
163	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_b
164	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_b
165	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_b
166	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b
167	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_b
168	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_b
169	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_d
170	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_d
171	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_d
172	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d
173	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_d
174	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_d
175	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_e
176	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_e
177	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_e
178	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e
179	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_e
180	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_e
181	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_f
182	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_f
183	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_f
184	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f

185	AlkLE$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_{x}$	E$_{f}$
186	AlkLE$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_{x}$	E$_{f}$
187	AlkLE$_{vii}$	E$_{iib}$E$_{vi}$E$_{x}$	
188	AlkLE$_{vii}$E$_{i}$	E$_{iib}$E$_{vi}$E$_{x}$	
189	AlkLE$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_{x}$	
190	AlkLE$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_{x}$	
191	AlkLE$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_{x}$	
192	AlkLE$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_{x}$	
193	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	
194	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	
195	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	
196	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	
197	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	
198	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	
199	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{a}$
200	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{a}$
201	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{a}$
202	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{a}$
203	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{a}$
204	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{a}$
205	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{b}$
206	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{b}$
207	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{b}$
208	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{b}$
209	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{b}$
210	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{b}$
211	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{d}$
212	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{d}$
213	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{d}$
214	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{d}$
215	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{d}$

216	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{d}$
217	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{e}$
218	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{e}$
219	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{e}$
220	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{e}$
221	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{e}$
222	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{e}$
223	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{f}$
224	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{f}$
225	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{f}$
226	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{f}$
227	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{f}$
228	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{f}$
229	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$	
230	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$	
231	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$	
232	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$	
233	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$	
234	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$	
235	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$	E$_{a}$
236	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$	E$_{a}$
237	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$	E$_{a}$
238	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$	E$_{a}$
239	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$	E$_{a}$
240	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$	E$_{a}$
241	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$	E$_{b}$
242	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$	E$_{b}$
243	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$	E$_{b}$
244	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$	E$_{b}$
245	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$	E$_{b}$
246	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$	E$_{b}$

247	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_d
248	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_d
249	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_d
250	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_d
251	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_d
252	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_d
253	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_e
254	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_e
255	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_e
256	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_e
257	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_e
258	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_e
259	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_f
260	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_f
261	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_f
262	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_f
263	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_f
264	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_f
265	$AlkLE_{xiii}E_{vii}$	E_x	
266	$AlkLE_{xiii}E_{vii}E_i$	E_x	
267	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	
268	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	
269	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	
270	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	
271	$AlkLE_{xiii}E_{vii}$	E_x	E_a
272	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_a
273	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_a
274	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_a
275	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_a
276	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_a
277	$AlkLE_{xiii}E_{vii}$	E_x	E_b
278	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_b
279	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_b
280	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_b
281	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_b
282	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_b
283	$AlkLE_{xiii}E_{vii}$	E_x	E_d
284	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_d
285	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_d
286	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_d
287	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_d
288	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_d
289	$AlkLE_{xiii}E_{vii}$	E_x	E_e
290	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_e
291	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_e
292	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_e
293	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_e
294	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_e
295	$AlkLE_{xiii}E_{vii}$	E_x	E_f
296	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_f
297	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_f
298	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_f
299	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_f
300	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_f
301	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	
302	$AlkLE_{xiii}E_{vii}E_i$	$E_{vi}E_{viii}$	
303	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	
304	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	
305	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	
306	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	
307	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_a
308	$AlkLE_{xiii}E_{vii}E_i$	$E_{vi}E_{viii}$	E_a

309	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{vi}$E$_{viii}$	E$_a$
310	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{vi}$E$_{viii}$	E$_a$
311	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{vi}$E$_{viii}$	E$_a$
312	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{vi}$E$_{viii}$	E$_a$
313	AlkLE$_{xiii}$E$_{vii}$	E$_{vi}$E$_{viii}$	E$_b$
314	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{vi}$E$_{viii}$	E$_b$
315	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{vi}$E$_{viii}$	E$_b$
316	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{vi}$E$_{viii}$	E$_b$
317	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{vi}$E$_{viii}$	E$_b$
318	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{vi}$E$_{viii}$	E$_b$
319	AlkLE$_{xiii}$E$_{vii}$	E$_{vi}$E$_{viii}$	E$_d$
320	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{vi}$E$_{viii}$	E$_d$
321	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{vi}$E$_{viii}$	E$_d$
322	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{vi}$E$_{viii}$	E$_d$
323	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{vi}$E$_{viii}$	E$_d$
324	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{vi}$E$_{viii}$	E$_d$
325	AlkLE$_{xiii}$E$_{vii}$	E$_{vi}$E$_{viii}$	E$_e$
326	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{vi}$E$_{viii}$	E$_e$
327	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{vi}$E$_{viii}$	E$_e$
328	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{vi}$E$_{viii}$	E$_e$
329	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{vi}$E$_{viii}$	E$_e$
330	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{vi}$E$_{viii}$	E$_e$
331	AlkLE$_{xiii}$E$_{vii}$	E$_{vi}$E$_{viii}$	E$_f$
332	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{vi}$E$_{viii}$	E$_f$
333	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{vi}$E$_{viii}$	E$_f$
334	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{vi}$E$_{viii}$	E$_f$
335	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{vi}$E$_{viii}$	E$_f$
336	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{vi}$E$_{viii}$	E$_f$
337	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	
338	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	
339	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	

340	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	
341	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_x$	
342	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_x$	
343	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
344	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
345	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
346	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
347	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
348	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_x$	E$_a$
349	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
350	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
351	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
352	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
353	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
354	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_x$	E$_b$
355	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
356	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
357	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
358	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
359	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
360	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_x$	E$_d$
361	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
362	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
363	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
364	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
365	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
366	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_x$	E$_e$
367	AlkLE$_{xiii}$E$_{vii}$	E$_{iib}$E$_{vi}$E$_x$	E$_f$
368	AlkLE$_{xiii}$E$_{vii}$E$_i$	E$_{iib}$E$_{vi}$E$_x$	E$_f$
369	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_x$	E$_f$
370	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_x$	E$_f$

371	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_{x}$	E_f	
372	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_{x}$	E_f	
373	$AlkLE_{vii}$	E_{viii}		E_1
374	$AlkLE_{vii}E_{i}$	E_{viii}		E_1
375	$AlkLE_{vii}E_{ii}$	E_{viii}		E_1
376	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}		E_1
377	$AlkLE_{vii}E_{iii}$	E_{viii}		E_1
378	$AlkLE_{vii}E_{iv}$	E_{viii}		E_1
379	$AlkLE_{vii}$	E_{viii}	E_a	E_1
380	$AlkLE_{vii}E_{i}$	E_{viii}	E_a	E_1
381	$AlkLE_{vii}E_{ii}$	E_{viii}	E_a	E_1
382	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_a	E_1
383	$AlkLE_{vii}E_{iii}$	E_{viii}	E_a	E_1
384	$AlkLE_{vii}E_{iv}$	E_{viii}	E_a	E_1
385	$AlkLE_{vii}$	E_{viii}	E_b	E_1
386	$AlkLE_{vii}E_{i}$	E_{viii}	E_b	E_1
387	$AlkLE_{vii}E_{ii}$	E_{viii}	E_b	E_1
388	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_b	E_1
389	$AlkLE_{vii}E_{iii}$	E_{viii}	E_b	E_1
390	$AlkLE_{vii}E_{iv}$	E_{viii}	E_b	E_1
391	$AlkLE_{vii}$	E_{viii}	E_d	E_1
392	$AlkLE_{vii}E_{i}$	E_{viii}	E_d	E_1
393	$AlkLE_{vii}E_{ii}$	E_{viii}	E_d	E_1
394	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_d	E_1
395	$AlkLE_{vii}E_{iii}$	E_{viii}	E_d	E_1
396	$AlkLE_{vii}E_{iv}$	E_{viii}	E_d	E_1
397	$AlkLE_{vii}$	E_{viii}	E_e	E_1
398	$AlkLE_{vii}E_{i}$	E_{viii}	E_e	E_1
399	$AlkLE_{vii}E_{ii}$	E_{viii}	E_e	E_1
400	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_e	E_1
401	$AlkLE_{vii}E_{iii}$	E_{viii}	E_e	E_1

402	$AlkLE_{vii}E_{iv}$	E_{viii}	E_e	E_1
403	$AlkLE_{vii}$	E_{viii}	E_f	E_1
404	$AlkLE_{vii}E_{i}$	E_{viii}	E_f	E_1
405	$AlkLE_{vii}E_{ii}$	E_{viii}	E_f	E_1
406	$AlkLE_{vii}E_{ii}E_{iib}$	E_{viii}	E_f	E_1
407	$AlkLE_{vii}E_{iii}$	E_{viii}	E_f	E_1
408	$AlkLE_{vii}E_{iv}$	E_{viii}	E_f	E_1
409	$AlkLE_{vii}$	E_{ix}		E_1
410	$AlkLE_{vii}E_{i}$	E_{ix}		E_1
411	$AlkLE_{vii}E_{ii}$	E_{ix}		E_1
412	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}		E_1
413	$AlkLE_{vii}E_{iii}$	E_{ix}		E_1
414	$AlkLE_{vii}E_{iv}$	E_{ix}		E_1
415	$AlkLE_{vii}$	E_{ix}	E_a	E_1
416	$AlkLE_{vii}E_{i}$	E_{ix}	E_a	E_1
417	$AlkLE_{vii}E_{ii}$	E_{ix}	E_a	E_1
418	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_a	E_1
419	$AlkLE_{vii}E_{iii}$	E_{ix}	E_a	E_1
420	$AlkLE_{vii}E_{iv}$	E_{ix}	E_a	E_1
421	$AlkLE_{vii}$	E_{ix}	E_b	E_1
422	$AlkLE_{vii}E_{i}$	E_{ix}	E_b	E_1
423	$AlkLE_{vii}E_{ii}$	E_{ix}	E_b	E_1
424	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_b	E_1
425	$AlkLE_{vii}E_{iii}$	E_{ix}	E_b	E_1
426	$AlkLE_{vii}E_{iv}$	E_{ix}	E_b	E_1
427	$AlkLE_{vii}$	E_{ix}	E_d	E_1
428	$AlkLE_{vii}E_{i}$	E_{ix}	E_d	E_1
429	$AlkLE_{vii}E_{ii}$	E_{ix}	E_d	E_1
430	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_d	E_1
431	$AlkLE_{vii}E_{iii}$	E_{ix}	E_d	E_1
432	$AlkLE_{vii}E_{iv}$	E_{ix}	E_d	E_1

433	$AlkLE_{vii}$	E_{ix}	E_e	E_1
434	$AlkLE_{vii}E_i$	E_{ix}	E_e	E_1
435	$AlkLE_{vii}E_{ii}$	E_{ix}	E_e	E_1
436	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_e	E_1
437	$AlkLE_{vii}E_{iii}$	E_{ix}	E_e	E_1
438	$AlkLE_{vii}E_{iv}$	E_{ix}	E_e	E_1
439	$AlkLE_{vii}$	E_{ix}	E_f	E_1
440	$AlkLE_{vii}E_i$	E_{ix}	E_f	E_1
441	$AlkLE_{vii}E_{ii}$	E_{ix}	E_f	E_1
442	$AlkLE_{vii}E_{ii}E_{iib}$	E_{ix}	E_f	E_1
443	$AlkLE_{vii}E_{iii}$	E_{ix}	E_f	E_1
444	$AlkLE_{vii}E_{iv}$	E_{ix}	E_f	E_1
445	$AlkLE_{vii}$	E_x		E_1
446	$AlkLE_{vii}E_i$	E_x		E_1
447	$AlkLE_{vii}E_{ii}$	E_x		E_1
448	$AlkLE_{vii}E_{ii}E_{iib}$	E_x		E_1
449	$AlkLE_{vii}E_{iii}$	E_x		E_1
450	$AlkLE_{vii}E_{iv}$	E_x		E_1
451	$AlkLE_{vii}$	E_x	E_a	E_1
452	$AlkLE_{vii}E_i$	E_x	E_a	E_1
453	$AlkLE_{vii}E_{ii}$	E_x	E_a	E_1
454	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_a	E_1
455	$AlkLE_{vii}E_{iii}$	E_x	E_a	E_1
456	$AlkLE_{vii}E_{iv}$	E_x	E_a	E_1
457	$AlkLE_{vii}$	E_x	E_b	E_1
458	$AlkLE_{vii}E_i$	E_x	E_b	E_1
459	$AlkLE_{vii}E_{ii}$	E_x	E_b	E_1
460	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_b	E_1
461	$AlkLE_{vii}E_{iii}$	E_x	E_b	E_1
462	$AlkLE_{vii}E_{iv}$	E_x	E_b	E_1
463	$AlkLE_{vii}$	E_x	E_d	E_1
464	$AlkLE_{vii}E_i$	E_x	E_d	E_1
465	$AlkLE_{vii}E_{ii}$	E_x	E_d	E_1
466	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_d	E_1
467	$AlkLE_{vii}E_{iii}$	E_x	E_d	E_1
468	$AlkLE_{vii}E_{iv}$	E_x	E_d	E_1
469	$AlkLE_{vii}$	E_x	E_e	E_1
470	$AlkLE_{vii}E_i$	E_x	E_e	E_1
471	$AlkLE_{vii}E_{ii}$	E_x	E_e	E_1
472	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_e	E_1
473	$AlkLE_{vii}E_{iii}$	E_x	E_e	E_1
474	$AlkLE_{vii}E_{iv}$	E_x	E_e	E_1
475	$AlkLE_{vii}$	E_x	E_f	E_1
476	$AlkLE_{vii}E_i$	E_x	E_f	E_1
477	$AlkLE_{vii}E_{ii}$	E_x	E_f	E_1
478	$AlkLE_{vii}E_{ii}E_{iib}$	E_x	E_f	E_1
479	$AlkLE_{vii}E_{iii}$	E_x	E_f	E_1
480	$AlkLE_{vii}E_{iv}$	E_x	E_f	E_1
481	$AlkLE_{vii}$	$E_{vi}E_{viii}$		E_1
482	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$		E_1
483	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$		E_1
484	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$		E_1
485	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$		E_1
486	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$		E_1
487	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_a	E_1
488	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_a	E_1
489	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_a	E_1
490	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a	E_1
491	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_a	E_1
492	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_a	E_1
493	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_b	E_1
494	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_b	E_1

495	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_b	E_1
496	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b	E_1
497	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_b	E_1
498	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_b	E_1
499	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_d	E_1
500	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_d	E_1
501	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_d	E_1
502	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d	E_1
503	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_d	E_1
504	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_d	E_1
505	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_e	E_1
506	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_e	E_1
507	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_e	E_1
508	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e	E_1
509	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_e	E_1
510	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_e	E_1
511	$AlkLE_{vii}$	$E_{vi}E_{viii}$	E_f	E_1
512	$AlkLE_{vii}E_i$	$E_{vi}E_{viii}$	E_f	E_1
513	$AlkLE_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_f	E_1
514	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f	E_1
515	$AlkLE_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_f	E_1
516	$AlkLE_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_f	E_1
517	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$		E_1
518	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$		E_1
519	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$		E_1
520	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$		E_1
521	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$		E_1
522	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$		E_1
523	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$		E_1
524	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$		E_1
525	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$		E_1

526	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$		E_1
527	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$		E_1
528	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$		E_1
529	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
530	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_a	E_1
531	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
532	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a	E_1
533	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
534	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_a	E_1
535	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
536	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_b	E_1
537	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
538	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b	E_1
539	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
540	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_b	E_1
541	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
542	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_d	E_1
543	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
544	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d	E_1
545	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
546	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_d	E_1
547	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
548	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_e	E_1
549	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
550	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e	E_1
551	$AlkLE_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
552	$AlkLE_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_e	E_1
553	$AlkLE_{vii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
554	$AlkLE_{vii}E_i$	$E_{iib}E_{vi}E_x$	E_f	E_1
555	$AlkLE_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
556	$AlkLE_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f	E_1

557	AlkLE$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_{x}$	E$_{f}$	E$_{1}$
558	AlkLE$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_{x}$	E$_{f}$	E$_{1}$
559	AlkLE$_{vii}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
560	AlkLE$_{vii}$E$_{i}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
561	AlkLE$_{vii}$E$_{ii}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
562	AlkLE$_{vii}$E$_{ii}$E$_{iib}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
563	AlkLE$_{vii}$E$_{iii}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
564	AlkLE$_{vii}$E$_{iv}$	E$_{iib}$E$_{vi}$E$_{x}$		E$_{1}$
565	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$		E$_{1}$
566	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$		E$_{1}$
567	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$		E$_{1}$
568	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$		E$_{1}$
569	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$		E$_{1}$
570	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$		E$_{1}$
571	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{a}$	E$_{1}$
572	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{a}$	E$_{1}$
573	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{a}$	E$_{1}$
574	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{a}$	E$_{1}$
575	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{a}$	E$_{1}$
576	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{a}$	E$_{1}$
577	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{b}$	E$_{1}$
578	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{b}$	E$_{1}$
579	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{b}$	E$_{1}$
580	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{b}$	E$_{1}$
581	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{b}$	E$_{1}$
582	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{b}$	E$_{1}$
583	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{d}$	E$_{1}$
584	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{d}$	E$_{1}$
585	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{d}$	E$_{1}$
586	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{d}$	E$_{1}$
587	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{d}$	E$_{1}$

588	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{d}$	E$_{1}$
589	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{e}$	E$_{1}$
590	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{e}$	E$_{1}$
591	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{e}$	E$_{1}$
592	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{e}$	E$_{1}$
593	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{e}$	E$_{1}$
594	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{e}$	E$_{1}$
595	AlkLE$_{xiii}$E$_{vii}$	E$_{viii}$	E$_{f}$	E$_{1}$
596	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{viii}$	E$_{f}$	E$_{1}$
597	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{viii}$	E$_{f}$	E$_{1}$
598	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{viii}$	E$_{f}$	E$_{1}$
599	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{viii}$	E$_{f}$	E$_{1}$
600	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{viii}$	E$_{f}$	E$_{1}$
601	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$		E$_{1}$
602	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$		E$_{1}$
603	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$		E$_{1}$
604	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$		E$_{1}$
605	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$		E$_{1}$
606	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$		E$_{1}$
607	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$	E$_{a}$	E$_{1}$
608	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$	E$_{a}$	E$_{1}$
609	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$	E$_{a}$	E$_{1}$
610	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$	E$_{a}$	E$_{1}$
611	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$	E$_{a}$	E$_{1}$
612	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$	E$_{a}$	E$_{1}$
613	AlkLE$_{xiii}$E$_{vii}$	E$_{ix}$	E$_{b}$	E$_{1}$
614	AlkLE$_{xiii}$E$_{vii}$E$_{i}$	E$_{ix}$	E$_{b}$	E$_{1}$
615	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$	E$_{ix}$	E$_{b}$	E$_{1}$
616	AlkLE$_{xiii}$E$_{vii}$E$_{ii}$E$_{iib}$	E$_{ix}$	E$_{b}$	E$_{1}$
617	AlkLE$_{xiii}$E$_{vii}$E$_{iii}$	E$_{ix}$	E$_{b}$	E$_{1}$
618	AlkLE$_{xiii}$E$_{vii}$E$_{iv}$	E$_{ix}$	E$_{b}$	E$_{1}$

619	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_d	E_1
620	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_d	E_1
621	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_d	E_1
622	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_d	E_1
623	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_d	E_1
624	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_d	E_1
625	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_e	E_1
626	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_e	E_1
627	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_e	E_1
628	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_e	E_1
629	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_e	E_1
630	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_e	E_1
631	$AlkLE_{xiii}E_{vii}$	E_{ix}	E_f	E_1
632	$AlkLE_{xiii}E_{vii}E_i$	E_{ix}	E_f	E_1
633	$AlkLE_{xiii}E_{vii}E_{ii}$	E_{ix}	E_f	E_1
634	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_{ix}	E_f	E_1
635	$AlkLE_{xiii}E_{vii}E_{iii}$	E_{ix}	E_f	E_1
636	$AlkLE_{xiii}E_{vii}E_{iv}$	E_{ix}	E_f	E_1
637	$AlkLE_{xiii}E_{vii}$	E_x		E_1
638	$AlkLE_{xiii}E_{vii}E_i$	E_x		E_1
639	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x		E_1
640	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x		E_1
641	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x		E_1
642	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x		E_1
643	$AlkLE_{xiii}E_{vii}$	E_x	E_a	E_1
644	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_a	E_1
645	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_a	E_1
646	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_a	E_1
647	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_a	E_1
648	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_a	E_1
649	$AlkLE_{xiii}E_{vii}$	E_x	E_b	E_1
650	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_b	E_1
651	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_b	E_1
652	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_b	E_1
653	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_b	E_1
654	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_b	E_1
655	$AlkLE_{xiii}E_{vii}$	E_x	E_d	E_1
656	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_d	E_1
657	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_d	E_1
658	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_d	E_1
659	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_d	E_1
660	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_d	E_1
661	$AlkLE_{xiii}E_{vii}$	E_x	E_e	E_1
662	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_e	E_1
663	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_e	E_1
664	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_e	E_1
665	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_e	E_1
666	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_e	E_1
667	$AlkLE_{xiii}E_{vii}$	E_x	E_f	E_1
668	$AlkLE_{xiii}E_{vii}E_i$	E_x	E_f	E_1
669	$AlkLE_{xiii}E_{vii}E_{ii}$	E_x	E_f	E_1
670	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	E_x	E_f	E_1
671	$AlkLE_{xiii}E_{vii}E_{iii}$	E_x	E_f	E_1
672	$AlkLE_{xiii}E_{vii}E_{iv}$	E_x	E_f	E_1
673	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$		E_1
674	$AlkLE_{xiii}E_{vii}E_i$	$E_{vi}E_{viii}$		E_1
675	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$		E_1
676	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$		E_1
677	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$		E_1
678	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$		E_1
679	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_a	E_1
680	$AlkLE_{xiii}E_{vii}E_i$	$E_{vi}E_{viii}$	E_a	E_1

681	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_a	E_1
682	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_a	E_1
683	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_a	E_1
684	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_a	E_1
685	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_b	E_1
686	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{vi}E_{viii}$	E_b	E_1
687	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_b	E_1
688	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_b	E_1
689	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_b	E_1
690	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_b	E_1
691	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_d	E_1
692	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{vi}E_{viii}$	E_d	E_1
693	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_d	E_1
694	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_d	E_1
695	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_d	E_1
696	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_d	E_1
697	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_e	E_1
698	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{vi}E_{viii}$	E_e	E_1
699	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_e	E_1
700	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_e	E_1
701	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_e	E_1
702	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_e	E_1
703	$AlkLE_{xiii}E_{vii}$	$E_{vi}E_{viii}$	E_f	E_1
704	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{vi}E_{viii}$	E_f	E_1
705	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{vi}E_{viii}$	E_f	E_1
706	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{vi}E_{viii}$	E_f	E_1
707	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{vi}E_{viii}$	E_f	E_1
708	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{vi}E_{viii}$	E_f	E_1
709	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$		E_1
710	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$		E_1
711	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$		E_1
712	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$		E_1
713	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$		E_1
714	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$		E_1
715	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
716	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$	E_a	E_1
717	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
718	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_a	E_1
719	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_a	E_1
720	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_a	E_1
721	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
722	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$	E_b	E_1
723	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
724	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_b	E_1
725	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_b	E_1
726	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_b	E_1
727	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
728	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$	E_d	E_1
729	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
730	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_d	E_1
731	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_d	E_1
732	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_d	E_1
733	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
734	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$	E_e	E_1
735	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
736	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_e	E_1
737	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_x$	E_e	E_1
738	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_x$	E_e	E_1
739	$AlkLE_{xiii}E_{vii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
740	$AlkLE_{xiii}E_{vii}E_{i}$	$E_{iib}E_{vi}E_x$	E_f	E_1
741	$AlkLE_{xiii}E_{vii}E_{ii}$	$E_{iib}E_{vi}E_x$	E_f	E_1
742	$AlkLE_{xiii}E_{vii}E_{ii}E_{iib}$	$E_{iib}E_{vi}E_x$	E_f	E_1

743	$AlkLE_{xiii}E_{vii}E_{iii}$	$E_{iib}E_{vi}E_{x}$	E_f	E_1
744	$AlkLE_{xiii}E_{vii}E_{iv}$	$E_{iib}E_{vi}E_{x}$	E_f	E_1

Especially preferred alternative embodiments of microorganisms according to the invention are explained hereinafter:

For preparing carboxylic acids with 6 to 18 carbon atoms, in particular fatty acids, microorganisms according to the invention which are particularly preferably suitable are characterized in that the first genetic modification is an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i which comprises sequences selected from among: AAC49180.1 (encoded by SEQ ID No.: 10), AAC49269.1 (encoded by SEQ ID No.: 8), Q39513.1 (encoded by SEQ ID No.: 9), AAC49001.1 (encoded by SEQ ID No.: 37), AEM72521.1 (encoded by SEQ ID No.: 35)
and
proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,
and the alkL gene product is selected from among those that are encoded by the alkL gene of *Pseudomonas putida* GPo1, which is rendered by SEQ ID No. 1, and proteins with polypeptide sequence SEQ ID No. 2, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33 or with a polypeptide sequence in which up to 60%, preferably up to 25%, particularly preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, particularly preferably 80%, in particular more than 90%, of the activity of the protein with the respective reference sequence SEQ ID No. 2, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID

No. 33, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, more particularly in a system as is described in the exemplary embodiments, in which glucose is reacted to form palmitoleic acid in an *E. coli* cell.

In this context it can be advantageous when the microorganism contains a fifth genetic modification which has an activity which is reduced compared with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from among enzymes which comprise sequences selected from YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1) and

proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% of the activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to 2-dodecenoyl-CoA thioester.

For producing esters of carboxylic acids having 6 to 18 carbon atoms in the carboxylic acid portion in which the alcohol component is derived from methanol or ethanol, especially preferably, microorganisms according to the invention are suitable which are characterized in that the first genetic modification is an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i, which comprises sequences selected from among: AAC49180.1 (encoded by SEQ ID No.: 10), AAC49269.1 (encoded by SEQ ID No.: 8), Q39513.1 (encoded by SEQ ID No.: 9), AAC49001.1 (encoded by SEQ ID No.: 37), AEM72521.1 (encoded by SEQ ID No.: 35)

and

proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90 %, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from those which are encoded by the alkL gene of *Pseudomonas putida* GPo1, which is rendered by SEQ ID No. 1, and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1 % of the amino acid residues are modified in comparison with SEQ ID No. 2 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90% of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, namely in a system as described in the exemplary embodiments in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

in that it has a third genetic modification which has an activity of the enzymes E_v and E_{vi}, which is increased in comparison with the enzymatic activity of the wild type of the microorganism,

where E_v is selected from among YP_694462.1 (encoded by SEQ ID No. 67) and YP_045555.1 (encoded by SEQ ID No. 19), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_v is generally understood in particular as meaning the conversion of dodecanoyl-CoA thioester with methanol to form dodecanoyl methyl ester,

and E_{vi} is selected from among YP_001724804.1 (encoded by SEQ ID No.: 18), and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{vi} is generally understood in particular as meaning the synthesis of dodecanoyl-CoA thioester.

In this context, it can also be advantageous if the microorganism contains a fifth genetic modification which has an activity which is reduced compared with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from

enzymes which comprises sequences that are selected from among YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to form 2-dodecenoyl-CoA thioester.

In an alternative embodiment for producing esters of carboxylic acid with 6 to 18 carbon atoms in the carboxylic acid portion, in which the alcohol component is derived from methanol or ethanol, microorganisms according to the invention suitable which are particularly preferably are characterized in that the first genetic modification is an activity which is increased in comparison with the enzymatic activity of the wild type of at least one of the enzymes E_i which comprises sequences that are selected from among: AAC49269.1 (encoded by SEQ ID No.: 8), Q39513.1 (encoded by SEQ ID No.: 9), AAC49001.1 (encoded by SEQ ID No.: 37), AEM72521.1 (encoded by SEQ ID No.: 35)

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used

(units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from those which are encoded by the alkL gene of *Pseudomonas putida* GPo1, which is shown by SEQ ID No. 1, and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1 % of the amino acid residues are modified in comparison with SEQ ID No. 2 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, more precisely in a system as described in the exemplary embodiments in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

in that it has a third genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of the enzyme E_{va}, where E_{va} is selected from among YP_888622.1 (encoded by SEQ ID No. 114) and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the

activity of the enzyme E_{va} is generally understood in particular as meaning the conversion of lauric acid and S-adenosylmethionine to form lauric acid methyl ester and S-adenosylhomocysteine.

In this context it can also be advantageous if the microorganism contains a fifth genetic modification which has an activity which is reduced compared with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from enzymes which have sequences that are selected from among YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to give 2-dodecenoyl-CoA thioester.

For production of monohydric alcohols with 6 to 18 carbon atoms, microorganisms according to the invention which are especially preferably suitable are characterized in that the first genetic modification is an activity that is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i which comprises sequences selected from among: AAC49269.1 (encoded by SEQ ID No: 8), AEM72521.1 (encoded by SEQ ID No: 35)

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably

65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from among those encoded by the alkL gene of *Pseudomonas putida* GPo1, which is shown by SEQ ID No. 1, and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, namely in a system as described in the exemplary embodiments in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

in that it has a third genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of the enzyme E_{vi},

where E_{vi} is selected from among YP_001724804.1 (encoded by SEQ ID No: 18)

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference

protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{vi} is generally understood in particular as meaning the synthesis of dodecanoyl-CoA thioester, and

in that it has a fourth genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of the enzyme E_x, where E_x is selected from among BAB85476.1 (encoded by SEQ ID No. 77), YP_047869.1 (encoded by SEQ ID No. 79 or 81), YP_959486.1 (encoded by SEQ ID No. 83), YP_959769.1 (encoded by SEQ ID No. 139), B9TSP7.1 (encoded by SEQ ID No. 141), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), in comparison with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_x is generally understood in particular as meaning the synthesis of lauryl alcohol and $NAD(P)^+$ from lauryl-ACP, NAD(P)H and H^+.

In this context it can also be advantageous if the microorganism contains a fifth genetic modification which has an activity which is reduced compared with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, wherein E_b is selected from enzymes that have sequences which are selected from among YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution, or a combination thereof and which still have at least 50%, preferably

65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to form 2-dodecenoyl-CoA thioester.

For producing monohydric alcohols and aldehydes with 6 to 18 carbon atoms, microorganisms according to the invention which are especially preferably suitable are characterized in that the first genetic modification is an activity that is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i, which comprises sequences selected from among: AAC49269.1 (encoded by SEQ ID No: 8), Q39513.1 (encoded by SEQ ID No: 9), AAC49001.1 (encoded by SEQ ID No: 37), AEM72521.1 (encoded by SEQ ID No: 35)

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from those encoded by the alkL gene of *Pseudomonas putida* GPo1, which is shown by SEQ ID No. 1, and proteins with a polypeptide sequence in which up

to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, namely in a system as described in the exemplary embodiments, in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

in that it has a fourth genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of the enzyme E_{ix}, where E_{ix} is selected from among YP_887275.1 (encoded by SEQ ID No. 117), ABI83656.1 (encoded by SEQ ID No. 122), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{ix} is generally understood in particular as meaning the synthesis of lauryl aldehyde, NADP, AMP and 2 P_i from lauric acid, ATP, NADPH and H^+.

In this context it can also be advantageous if the microorganism contains a fifth genetic modification which has an activity which is reduced in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from

enzymes which comprise sequences selected from among YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to form 2-dodecenoyl-CoA thioester.

For production of alkylamines with 8 to 16 carbon atoms, microorganisms according to the invention which are especially preferably suitable are characterized in that the first genetic modification is an activity that is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i, which comprises sequences that are selected from among: AAC49269.1 (encoded by SEQ ID No: 8), Q39513.1 (encoded by SEQ ID No: 9), AAC49001.1 (encoded by SEQ ID No: 37),

and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), in comparison with the activity of the biocatalyst

without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from those encoded by the alkL gene of *Pseudomonas putida* GPo1, which is shown by SEQ ID No. 1, and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2 by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, more precisely in a system as described in the exemplary embodiments in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

it has a fourth genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one enzyme E_{xiii}, where this is selected from among NP_901695.1 (encoded by SEQ ID No. 132) and proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{xiii} is generally understood in particular as

meaning the reaction of ω-oxolauric acid and/or ω-oxolauric acid methyl ester to form ω-aminolauric acid and/or ω-aminolauric acid methyl ester.

It can also be advantageous in this context if the microorganism contains a fifth genetic modification which has an activity which is reduced in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from enzymes which have sequences selected from among YP_488518.1 (encoded by SEQ ID No. 14, formerly AP_000876.1), and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to form 2-dodecenoyl-CoA thioester.

For production of alkenes with 6 to 18 carbon atoms, microorganisms according to the invention which are particularly preferably suitable are characterized in that the first genetic modification is an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_i, which comprises sequences selected from among: AAC49269.1 (encoded by SEQ ID No: 8), Q39513.1 (encoded by SEQ ID No: 9), AAC49001.1 (encoded by SEQ ID No: 37), AEM72521.1 (encoded by SEQ ID No: 35) and

proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably

65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_i is generally understood in particular as meaning the hydrolysis of dodecanoyl-ACP thioester,

and

the alkL gene product is selected from among those encoded by the alkL gene of *Pseudomonas putida* GPo1, which is shown by SEQ ID No. 1, and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with SEQ ID No. 2, by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the reference sequence SEQ ID No. 2, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, namely in a system as is described in the exemplary embodiments, in which glucose is reacted to form palmitoleic acid in an *E. coli* cell,

and

it has a fourth genetic modification which has an activity which is increased in comparison with the enzymatic activity of the wild type of the microorganism of at least one enzyme E_{xi}, where this is selected from among ADW41779.1 (encoded by SEQ ID No. 168) and proteins with a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequence by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst,

that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_{xiii} is generally understood in particular as meaning the reaction of sodium palmitate with hydrogen peroxide to form pentadecene, CO_2 and water.

In this context it can also be advantageous if the microorganism contains a fifth genetic modification which has an activity which is reduced in comparison with the enzymatic activity of the wild type of the microorganism of at least one of the enzymes E_b, where E_b is selected from among enzymes which comprise sequences selected from among YP_488518.1 (encoded by SEQ ID No. 14),

and

proteins having a polypeptide sequence in which up to 60%, preferably up to 25%, especially preferably up to 15%, in particular up to 10, 9, 8, 7, 6, 5, 4, 3, 2, 1% of the amino acid residues are modified in comparison with the abovementioned reference sequences by deletion, insertion, substitution or a combination thereof and which still have at least 50%, preferably 65%, especially preferably 80%, in particular more than 90%, of the activity of the protein with the corresponding abovementioned reference sequence, where 100% activity of the reference protein is understood as meaning the increase of the activity of the cells used as biocatalyst, that is to say the amount of substance reacted per unit time, based on the cell weight used (units per gram of cell dry weight [U/g CDW]), compared with the activity of the biocatalyst without the presence of the reference protein, where activity in this context and in the context of the determination of the activity of the enzyme E_b is generally understood in particular as meaning the oxidation of dodecanoyl-CoA thioester to 2-dodecenoyl-CoA thioester.

Use of the microorganisms according to the invention

A further subject matter of the present invention relates to the use of the abovementioned microorganisms for the production of organic substances, in particular of fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alken-1-als, alken-1-ols, alken-1-amines, alkanes and alkenes, in particular 1-alkenes, which may optionally include a further double bond.

Organic substances and microorganisms which have been emphasized as being preferred in the context of the microorganisms according to the invention are also preferred in the context of the use according to the invention.

The organisms according to the invention which are preferably used for specific organic substances have already been emphasized in the context of the microorganisms according to the invention.

Process for the production of an organic substance from a simple carbon source

A further subject matter of the present invention relates to a process for the production of an organic substance, in particular of fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alken-1-als, alken-1-ols, alken-1-amines, alkanes and alkenes, in particular 1-alkenes, which may optionally include a further double bond, from a simple carbon source comprising the process steps

I) bringing a microorganism according to the invention into contact with a medium comprising the simple carbon source,

II) culturing the microorganism under conditions which make it possible for the microorganism to form the organic substance from the simple carbon source, and

III) if appropriate, isolation of the organic substance formed.

In the process according to the invention, the microorganisms according to the invention may, for the purpose of producing the organic substance, be brought into contact with the nutrient medium and thus cultured continuously or discontinuously in the batch method or in the fed-batch method or in the repeated fed-batch method. Also feasible is a semicontinuous process as described in GB-A-1009370. A summary of known culture methods is described in the textbook by Chmiel ("Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik", Gustav Fischer Verlag, Stuttgart, 1991) or in the textbook by Storhas ("Bioreaktoren und periphere Einrichtungen", Vieweg Verlag, Braunschweig/Wiesbaden, 1994).

The culture medium to be used must suitably satisfy the requirements of the respective strains. Descriptions of culture media of various microorganisms are contained in the handbook "Manual

of Methods for General Bacteriology" of the American Society for Bacteriology (Washington D. C., USA, 1981).

In the process according to the invention, it is preferred to employ preferred microorganisms according to the invention.

The simple carbon source which is employed in the process according to the invention are those mentioned above as being preferred.

Nitrogen sources which can be employed are organic nitrogenous compounds such as peptones, yeast extract, meat extract, malt extract, cornsteep liquor, soyabean meal and urea or inorganic compounds such as ammonium sulphate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate, ammonia, ammonium hydroxide or ammonia water. The nitrogen sources may be employed individually or as a mixture.

Phosphorus sources which can be used are phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts. The culture medium must furthermore contain salts of metals such as, for example, magnesium sulphate or iron sulphate, which are necessary for growth. Finally, essential growth factors such as amino acids and vitamins may be employed in addition to the abovementioned substances. Moreover, suitable precursors may be added to the culture medium. The feed substances mentioned may be added to the culture as a single batch or may be fed in a suitable manner during culturing.

The pH of the culture is controlled by employing basic compounds such as sodium hydroxide, potassium hydroxide, ammonia or ammonia water, or acidic compounds such as phosphoric acid or sulphuric acid in a suitable manner. Foaming may be controlled by using antifoams such as, for example, fatty acid polyglycol esters. To maintain stability of plasmids, suitable selective substances such as antibiotics, for example, may be added to the medium. Oxygen or oxygen-containing gas mixtures such as, for example, air are introduced into the culture so as to maintain aerobic conditions.

According to one embodiment of the process according to the invention, said process is carried out in a two-phase system comprising

A) an aqueous phase and

B) an organic phase,

where the organic substance is formed by the microorganism in process step II) in the aqueous phase and the organic substance formed accumulates in the organic phase. In this manner, it is possible for the organic substance formed to be extracted *in situ*.

Preferred organic substances which are produced by the process according to the invention are the substances mentioned hereinabove as being preferred, in particular the fatty acids and fatty acid derivatives.

In the examples mentioned hereinbelow, the present invention will be described with the aid of examples without it being intended to limit the invention, whose scope of use is revealed in the entire description and the claims, to the embodiments mentioned in the examples.

The organisms according to the invention which are preferably employed for specific organic substances in preferred processes according to the invention have already been emphasized in the context of the microorganisms according to the invention.

Examples:

Example 1: Preparation of an E. coli expression vector for the overexpression of the alkL gene from P. putida GPo1

To prepare an *E. coli* expression vector for the overexpression of the *Pseudomonas putida alkL* gene (SEQ ID No.: 01), this gene was prepared synthetically and then amplified like the P_{lacuv5} promoter (SEQ ID No.: 34) from a pJ294 derivative, with the introduction of homologous regions for recombination cloning. At the same time, a cleavage site was introduced upstream of the promoter and a cleavage site was introduced downstream of the *alkL* stop codon via the oligonucleotides used.

The following oligonucleotides were employed for the amplification of the *alkL* gene and the P_{lacuv5} promoter from the respective pJ294 derivatives as the template:

Promoter region:

fw-Prom+H1: 5'- ACC ACA GCC AGG ATC CTT CAA TAT TAT TGA AGC -3' (SEQ ID No.: 03)

rv-Prom: 5'- ATG CCA CTC TCC TTG -3' (SEQ ID No.: 04)

fw-alkL+H2: 5'- CAA GGA GAG TGG CAT GTG AGT TTT TCT AAT TAT -3' (SEQ ID No.: 05)

rv-alkL+H3: 5'- TTA CCA GAC TCG AGG GTA CCT TAG AAA ACA TAT GAC -3' (SEQ ID No.: 06)

The following parameters were employed for the PCR: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:30 min, annealing, 50.5°C, 0:45 min; elongation, 72°C, 0:15 min; 1 x: terminal elongation, 72°C, 5 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification, following the manufacturer's recommendations. Thereafter, in each case 100 µl of the PCR reactions were separated on a 2% agarose gel. The procedure of the PCR, the agarose gel electrophoresis, the ethidium bromide staining of the DNA and the determination of the PCR fragment sizes were carried out in a manner known to the skilled worker.

In both cases, PCR fragments of the expected size were successfully amplified. The size was 654 base pairs for the promoter region and 728 base pairs for the *alkL* construct.

To isolate the DNA from an agarose gel, the target DNA was excised from the gel using a surgical blade and purified using the "Quick Gel Extraction Kit" from Qiagen (Hilden). This was done following the manufacturer's instructions. In the next step, the PCR products together with the *Bam*HI-*Kpn*I-cut pCDFDuet-1 (71340-3, Merck, Darmstadt) underwent recombination by means of *in vitro* cloning using the "In-Fusion Advantage PCR Cloning Kit" from Clontech (Saint-Germain-en-Laye), giving rise to the resulting vector. The use corresponded to the manufacturer's instructions.

pCDFDuet-1 is an *E. coli* vector which confers spectinomycin/streptomycin resistance to the organism and which contains a ColDF13 replication origin. The transformation of chemically competent *E. coli* DH5α cells (New England Biolabs, Frankfurt) was performed in the manner known to the skilled worker.

The correctness of the plasmid was checked by restriction analysis with *Xba*I. The authenticity of the inserted fragments was verified by DNA sequencing. The finished *E. coli* expression vector was named pCDF[alkL] (SEQ ID No.:07).

Example 2: Preparation of expression vectors for the fatB2 and fatB1 genes from Cuphea hookeriana and fatB2 from Cuphea palustris

To prepare expression vectors for the *fatB2* and *fatB1* genes from *Cuphea hookeriana* (SEQ ID No. 08 and SEQ ID No. 09, respectively) and *fatB2* from *Cuphea palustris* (SEQ ID No. 10), these genes were codon-optimized for the expression in *Escherichia coli*. The genes were synthesized together with a *tac* promoter (SEQ ID No. 39) and, simultaneously, a cleavage site was introduced upstream of the promoter and a cleavage site was introduced downstream of the terminator. The synthesized DNA fragments P_{tac}-*ChFatB2*, P_{tac}-*ChFatB1* and P_{tac}-*CpFatB2* were digested with the restriction endonucleases *BamH*I and *Not*I and ligated into the correspondingly cut vector pJ294 (DNA 2.0 Inc.; Menlo Park, CA, USA). The finished *E.coli* expression vectors were named pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11), pJ294[Ptac-CpFATB2_optEc] (SEQ ID No. 13) and pJ294[Ptac-ChFATB1_optEc] (SEQ ID No. 12), respectively.

Example 3: Chromatographic quantification of products

Fatty acids were quantified following derivatization as fatty acid methyl esters, using gas chromatography. After the addition of 1 ml of acetone and 2 ml of water, 50 µl of heptadecanoic acid (10 g/l dissolved in ethanol) were added as internal reference substance to the samples, consisting of 2 ml of culture broth. The samples were acidified with 200 µl of acetic acid and treated with 10 ml of a 1:1 (v/v) chloroform/methanol mixture. The samples were mixed thoroughly for at least 1 min. Thereafter, the chloroform phase was removed and evaporated. The dry residue was taken up in 1 ml of 1.25 M methanolic hydrochloric acid and incubated at 50°C overnight to esterify the fatty acids present. The reaction was stopped by addition of 5 ml of saturated sodium carbonate solution (all substances from Sigma-Aldrich, Steinheim). The fatty acid methyl esters were extracted by addition of 1 ml of n-heptane and mixing vigorously

for 15 seconds. The heptane phase was measured by means of gas chromatography. To separate fatty acid methyl esters, the capillary column SP™-2560 of dimensions 100 m x 0.25 mm and a film thickness of 0.2 µm (Supelco, Sigma-Aldrich, Steinheim) was employed as the stationary phase. The carrier gas employed was helium. The separation was carried out within 45 min at an injector temperature of 260°C, a detector temperature of 260°C and a column temperature of 140°C at the beginning, held for 5 min, and increased to 240°C at a rate of 4°C/min and held for 15 min. The injection volume was 1 µl, the split rate was 1:20 and the flow rate of the carrier gas 1 ml/min. Detection was by means of a flame ionization detector (GC Perkin Elmer Clarus 500, Perkin Elmer, Rodgau). Heptadecanoic acid (Sigma-Aldrich, Steinheim) was used as the internal reference substance for quantifying the fatty acid methyl esters. The reference substances C8:0-Me caprylic acid methyl ester, C10:0-Me capric acid methyl ester, C12:0-Me lauric acid methyl ester, C14:0-Me myristic acid methyl ester, C16:0-Me palmitic acid methyl ester, C16:1-Me palmitoleic acid methyl ester, C18:0-Me stearic acid methyl ester, C18:1-Me oleic acid methyl ester (GLC Standard Mix GLC-20 1892-1AMP, GLC-30 1893-1AMP, GLC-50 1894-1AMP, Sigma-Aldrich, Steinheim) were used for the calibration. The lower detection limits were a concentration of 10 mg/l for all fatty acid methyl esters.

Example 4: Production of fatty acids by E.coli strains with deletion in the fadE gene, which overexpress the alkL genes from Pseudomonas putida GPo1 in various modifications and fatB2 from Cuphea hookeriana.

The first step was to construct an *E.coli* strain with deletion in the *fadE* gene (SEQ ID No. 14). To make the gene deletion, a plasmid which carries the DNA sequence Δ*fadE* (SEQ ID No. 15) was constructed. This sequence was synthesized and is composed of homologous regions 500 base pairs upstream and downstream of the *fadE* gene and the recognition sequence for the restriction endonuclease *Not*I at the 5' and the 3' end. The sequence Δ*fadE* was digested with the restriction endonuclease *Not*I and ligated into the analogously cut vector pKO3. The strain *E.coli* W3110 Δ*fadE* was constructed using the pKO3-Δ*fadE* construct (SEQ ID No. 16) using methods known to the skilled worker (see Link AJ, Phillips D, Church GM. J.Bacteriol. 1997. 179(20).). The DNA sequence after the deletion is shown in SEQ ID No. 17.
To generate *E.coli* strains with the expression vector for the *alkL* gene from *Pseudomonas putida* GPo1 in combination with the expression vector for the *fatB2* gene from *Cuphea*

hookeriana, electrocompetent cells of *E. coli* W3110 Δ*fadE* were prepared. This was done in a manner known to the skilled worker. The cells were transformed with the plasmids pCDFDuet-1 or pCDF[alkL] in combination with pJ294[Ptac-ChFATB2_optEc] and plated onto LB plates supplemented with spectinomycin (100 µg/ml) and ampicillin (100 µg/ml). Transformants were checked for the presence of the correct plasmids by plasmid preparation and analytical restriction analysis.

The following *E. coli* strains were generated in this manner:

- E.coli W3110 ΔfadE pCDFDuet-1/pJ294[Ptac-ChFATB2_optEc]
- E.coli W3110 ΔfadE pCDF[alkL]/pJ294[Ptac-ChFATB2_optEc]

These strains were used to study their ability to produce fatty acids. The following procedure was employed:

The strains were subjected to a multi-stage aerobic culturing process. The strains to be studied were first grown from in each case one single colony in Luria-Bertani broth as described by Miller (Merck, Darmstadt) as a 5 ml preculture. The next culturing step was performed in M9 medium. The medium, composed of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all chemicals from Merck, Darmstadt) and 0.1% (v/v) trace element solution, was brought to pH 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution, composed of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate, dissolved in 37% hydrochloric acid solution (all chemicals from Merck, Darmstadt), was filter-sterilized before being added to the M9 medium. 10 ml of M9 medium together with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin were introduced into 100 ml baffled Erlenmeyer flasks and inoculated with 0.5 ml of the preculture. Culturing was done at 37°C and 200 rpm in a shaker-incubator. After a culturing time of 8 hours, 50 ml of M9 medium supplemented with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin were introduced into a 250 ml baffled Erlenmeyer flask and inoculated with the 10 ml culture so that an optical density (600 nm) of 0.2 was obtained. Culturing was done at 30°C and 200 rpm in a shaker-incubator. When an optical density (600 nm) of from 0.4 to 0.5 had been reached, the gene expression was induced by

adding 1 mM of IPTG (time t_0). The strains were cultured for at least another 24 hours under identical conditions. During the culture period, 2 ml samples were taken, and the concentration of fatty acids with different carbon chain length was quantified analogously to Example 3. The results are shown in the table which follows.

Table 1: Production of fatty acids using *E.coli* W3110 Δ*fadE*, which overexpresses *fatB2* from *C.hookeriana* and *alkL* from *P.putida* GPo1. The data shown are the concentrations of fatty acids with different carbon chain lengths after incubation for 29 hours.

Strain	$c_{Caprylic\ acid}$ [mg/l*OD]	$c_{Capric\ acid}$ [mg/l*OD]	$c_{Myristic\ acid}$ [mg/l*OD]	$c_{Palmitic\ acid}$ [mg/l*OD]	$c_{Palmitoleic\ acid}$ [mg/l*OD]	$c_{Stearic\ acid}$ [mg/l*OD]	$c_{Oleic\ acid}$ [mg/l*OD]
E.coli W3110 Δ*fadE* pCDFDuet-1/pJ294[Ptac-ChFATB2_optEc]	30.1	2.4	1.9	13.6	17.3	3.6	1.9
E.coli W3110 Δ*fadE* pCDF[alkL]/pJ294[Ptac-ChFATB2_optEc]	82.6	10.6	4.1	23.7	74.0	9.1	4.1

This demonstrated that the strains with *alkL* form considerably more caprylic acid, capric acid, myristic acid, palmitic acid, palmitoleic acid, stearic acid and oleic acid than the strains without *alkL*. This demonstrates that enhancing *alkL* promotes the production of fatty acids of different chain lengths and degrees of saturation from nonrelated carbon sources.

Example 5: Preparation of an E. coli expression vector for the genes fadD from Escherichia coli and atfA from Acinetobacter sp. ADP1

To prepare the *E. coli* expression vector for the genes *fadD* (SEQ ID No.: 18) from *Escherichia coli* and *atfA* with terminator (SEQ ID No.: 19) from *Acinetobacter sp.* ADP1 under the control of a *tac* promoter, these genes were amplified by PCR from chromosomal DNA of *E. coli* W3110 and *Acinetobacter calcoaceticus* ADP1, respectively, with the introduction of homologous regions for recombination cloning. The synthetic *tac* promoter (SEQ ID No.: 20) was amplified with ribosome binding site from a pJ294 derivative, with introduction of homologous regions.

Chromosomal DNA was prepared from *E. coli* W3110 and *Acinetobacter calcoaceticus* ADP1, respectively, by means of the DNeasy Blood & Tissue Kit (Qiagen, Hilden) following the manufacturer's instructions. The following oligonucleotides were employed in the amplification of the genes *fadD* from *E. coli* and *atfA* from *Acinetobacter sp.* ADP1 with chromosomal DNA of *E. coli* W3110 and *Acinetobacter calcoaceticus* ADP1, respectively, as the template and in the amplification of the synthetic P_{tac} promoter from a pJ294 derivative:

P_{tac}:

11-001_fw: 5'-TTATGCGACTCCTGCGTTTAGGGAAAGAGCATTTG-3'
(SEQ ID No.: 21)

Ptac-rv: 5'- GTTAACATATGTTTTACCTCCTGTTAAACAAA-3'
(SEQ ID No.: 22)

fadD [*E.coli*]:

fadD-fw: 5'-TAAAACATATGTTAACGGCATGTATATCATTT-3'
(SEQ ID No.: 23)

fadD-rv: 5'-TCTCCTCAGACTTAACGCTCAGGCTTTATTGT-3'
(SEQ ID No.: 24)

atfA [*Acinetobacter* sp. ADP1]:

atfA-fw: 5'-GTTAAGTCTGAGGAGATCCACGCTATGCGCCC-3'
(SEQ ID No.: 25)

11-002_rv: 5'-CAATTGAGATCTGCCACGACTGCAATGGTTCATC-3'
(SEQ ID No.: 26)

The following parameters were employed for the PCR: 1 x: initial denaturation, 103°C, 3:00 min; 35 x: denaturation, 98°C, 0:10 min, annealing, 65°C, 0:15 min; elongation, 72°C, 0:45 min; 1 x: terminal elongation, 72°C, 10 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification, following the manufacturer's recommendations. Thereafter, in each case 50 µl of the PCR reactions were separated on a 1% TAE agarose gel. The procedure of the PCR, the agarose gel electrophoresis, the ethidium

bromide staining of the DNA and the determination of the PCR fragment sizes were carried out in a manner known to the skilled worker.

In all cases, PCR fragments of the expected size were successfully amplified. The size was 607 bp for the P_{tac} promoter region, 1778 bp for *fadD* and 1540 bp for *atfA*.

To isolate the DNA from an agarose gel, the target DNA was isolated from the gel using a surgical blade and purified using the "Quick Gel Extraction Kit" from Qiagen (Hilden) following the manufacturer's instructions. The purified PCR products underwent recombination with the *EcoNI*/*Nde*I-cut vector pCDFDuet™-1 (71340-3, Merck, Darmstadt) by means of *in-vitro* cloning using the Geneart Seamless Cloning and Assembly Kit from Invitrogen (Darmstadt). The use corresponded to the manufacturer's instructions. pCDFDuet-1 is an *E. coli* vector which confers spectinomycin/streptomycin resistance to the organism and which contains a ColDF13 replication origin. The transformation of chemically competent *E. coli* DH5α cells (New England Biolabs, Frankfurt) was performed in the manner known to the skilled worker.

The correctness of the plasmid was checked by restriction analysis with *Xba*I. The authenticity of the inserted fragments was verified by DNA sequencing. The finished *E. coli* expression vector was named pCDF[fadD-atfA] (SEQ ID No.:27).

Example 6: Preparation of an E. coli expression vector for the genes fadD from Escherichia coli, atfA from Acinetobacter sp. ADP1 and alkL from Pseudomonas putida GPo1

To prepare an *E. coli* expression vector for the genes *fadD* from *Escherichia coli*, *atfA* from *Acinetobacter sp.* ADP1 and *alkL* from *Pseudomonas putida* GPo1, the plasmid pCDF[alkL] (SEQ ID No.: 07) is digested with *Fse*I and *Xho*I, and the fragment which carries the *alkL* gene from *Pseudomonas putida* GPo1 under the control of the P_{lacuv5} promoter (see Example 1) is subsequently isolated.

To this end, the digested plasmid is separated on a 1% TAE agarose gel. The procedure of the restriction digestion, the agarose gel electrophoresis, the ethidium bromide staining of the DNA and the determination of the restriction fragment sizes are performed in a manner known to the skilled worker. To isolate the DNA from an agarose gel, the target DNA is isolated from the gel using a surgical blade and purified using the Quick Gel Extraktion Kit from Qiagen (Hilden) following the manufacturer's instructions.

Thereafter, the purified restriction fragment is ligated with the likewise *Fse*I- and *Xho*I-cut vector fragment (7290 bp) of pCDF[fadD-atfA] (SEQ ID No.: 27). Ligation of the DNA fragment and transformation of chemically competent *E. coli* DH5α cells (New England Biolabs, Frankfurt) are performed in the manner known to the skilled worker.

The correctness of the plasmids produced is checked by restriction analysis with *Fse*I and *Xho*I. The authenticity of the inserted fragments is verified by DNA sequencing. The finished *E. coli* expression vector is named pCDF[fadD-atfA]-[alkL] (SEQ ID No.:28).

Example 7: Chromatographic quantification of products

The quantification of fatty acid esters is performed using gas chromatography. 100 µl of methyl heptadecanoate solution (5 g/l dissolved in acetone) are added to the samples, consisting of 1 ml of culture broth, and then 1.1 ml of n-heptane are added and the samples are vortexed vigorously for 15 seconds. The heptane phase is measured by means of gas chromatography. To separate fatty acid esters, the capillary column SP™-2560 of dimensions 100 m x 0.25 mm and a film thickness of 0.2 µm (Supelco, Sigma-Aldrich, Steinheim) is employed as the stationary phase. The carrier gas employed is helium. The separation is carried out within 45 min at an injector temperature of 260°C, a detector temperature of 260°C and a column temperature of 140°C at the beginning, held for 5 min, and increased to 240°C at a rate of 4°C/min and held for 15 min. The injection volume is 1 µl, the split rate is 1:20 and the flow rate of the carrier gas 1 ml/min. Detection is by means of a flame ionization detector (GC Perkin Elmer Clarus 500, Perkin Elmer, Rodgau). Methyl heptanoate (Sigma-Aldrich, Steinheim) is used as the internal reference substance for quantifying the fatty acid esters. The reference substances C8:0-Me caprylic acid methyl ester, C10:0-Me capric acid methyl ester, C12:0-Me lauric acid methyl ester, C14:0-Me myristic acid methyl ester, C16:0-Me palmitic acid methyl ester, C16:1-Me palmitoleic acid methyl ester, C18:0-Me stearic acid methyl ester, C18:1-Me oleic acid methyl ester (GLC Standard Mix GLC-20 1892-1AMP, GLC-30 1893-1AMP, GLC-50 1894-1AMP, Sigma-Aldrich, Steinheim), C8:0-Et caprylic acid ethyl ester, C10:0-Et capric acid ethyl ester, C12:0-Et lauric acid ethyl ester, C14:0-Et myristic acid ethyl ester, C16:0-Et palmitic acid ethyl ester, C18:0-Et stearic acid ethyl ester, C18:1-Et oleic acid ethyl ester (all from Sigma-Aldrich, Steinheim) and C16:1-Et palmitoleic acid ethyl ester (Biomol, Hamburg) are used for the calibration. The lower detection limits are a concentration of 10 mg/l for all fatty acid esters.

Example 8: Production of fatty acid esters by E. coli strains which have a deletion in the fadE gene and which overexpress the alkL genes from Pseudomonas putida GPo1, ChfatB1 and ChfatB2 from Cuphea hookeriana, and Cpfat2" from Cuphea palustris, fadD *from* E. coli *and* atfA *from* Acinetobacter sp. *ADP1.*

To generate *E.coli* strains with the expression vector for the *alkL* genes from *Pseudomonas putida* GPo1, *fadD* from *Escherichia coli* and *atfA* from *Acinetobacter sp.* ADP1 from *Pseudomonas putida* GPo1 in combination with the expression vector for the *fatB2* gene from *Cuphea hookeriana*, electrocompetent cells of *E. coli* W3110 Δ*fadE* (see Example 4) are prepared. This was done in a manner known to the skilled worker. They are transformed with the plasmids pCDF[fadD-atfA] (SEQ ID No.: 27) and pCDF[fadD-atfA]-[alkL] (SEQ ID No.: 28), respectively, in combination with pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11), pJ294[Ptac-CpFATB2_optEc] (SEQ ID No.: 13) and pJ294[Ptac-ChFATB1_optEc] (SEQ ID No.: 12), respectively, in and plated onto LB plates supplemented with spectinomycin (100 µg/ml) and ampicillin (100 µg/ml). Transformants are checked for the presence of the correct plasmids by plasmid preparation and analytical restriction analysis.

The following *E. coli* strains are generated in this manner:

- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-/pJ294[Ptac-ChFATB2_optEc]
- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB2_optEc]
- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]/pJ294[Ptac-CpFATB2_optEc]
- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-CpFATB2_optEc]
- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]/pJ294[Ptac-ChFATB1_optEc]
- *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB1_optEc]

These strains are used to study their ability to produce fatty acid esters. The following procedure is employed:

The strains are subjected to a multi-stage aerobic culturing process. The strains to be studied are first grown from in each case one single colony in Luria-Bertani broth as described by Miller

(Merck, Darmstadt) as a 5 ml preculture. The next culturing step is performed in M9 medium. The medium, composed of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all chemicals from Merck, Darmstadt) and 0.1% (v/v) trace element solution, is brought to pH 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution, composed of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate, dissolved in 37% hydrochloric acid solution (all chemicals from Merck, Darmstadt), is filter-sterilized before being added to the M9 medium. 10 ml of M9 medium together with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are introduced into 100 ml baffled Erlenmeyer flasks and inoculated with 0.5 ml of the preculture. Culturing is done at 37°C and 200 rpm in a shaker-incubator. After a culturing time of 8 hours, 50 ml of M9 medium supplemented with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are introduced into a 250 ml baffled Erlenmeyer flask and inoculated with the 10 ml culture so that an optical density (600 nm) of 0.2 is obtained. Culturing is done at 30°C and 200 rpm in a shaker-incubator. When an optical density (600 nm) of from 0.4 to 0.5 has been reached, the gene expression is induced by adding 1 mM of IPTG (time t_0). The strains are cultured for at least another 24 hours under identical conditions. During the culture period, 2 ml samples are taken, and the concentration of fatty acid methyl esters or fatty acid ethyl esters with different carbon chain lengths is quantified analogously to Example 7.

This demonstrates that the strains *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-/pJ294[Ptac-ChFATB2_optEc] and *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB2_optEc] are predominantly capable of forming C8:0-Me caprylic acid methyl ester, C10:0-Me capric acid methyl ester, C16:0-Me palmitic acid methyl ester, C16:1-Me palmitoleic acid methyl ester and C18:1-Me oleic acid methyl ester (when methanol is added) and C8:0-Et caprylic acid ethyl ester, C10:0-Et capric acid ethyl ester, C16:0-Et palmitic acid ethyl ester, C16:1-Et palmitoleic acid ethyl ester and C18:1-Et oleic acid ethyl ester (when ethanol is added), respectively.

Furthermore, it is demonstrated that the strains *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-/pJ294[Ptac-CpFATB2_optEc] and *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-CpFATB2_optEc] are capable of predominantly forming C12:0-Me lauric acid methy ester,

C14:0-Me myristic acid methyl ester, C16:0-Me palmitic acid methyl ester, C16:1-Me palmitoleic acid methyl ester, C18:0-Me stearic acid methyl ester and C18:1-Me oleic acid methyl ester (when methanol is added) and C12:0-Et lauric acid ethyl ester, C14:0-Et myristic acid ethyl ester, C16:0-Et palmitic acid ethyl ester, C16:1-Et palmitoleic acid ethyl ester and C18:1-Et oleic acid ethyl ester (when ethanol is added), respectively.

Furthermore, it is demonstrated that the strains *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-/pJ294[Ptac-ChFATB1_optEc] and *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB1_optEc] are capable of predominantly forming C14:0-Me methyl myristate, C16:0-Me methyl palmitate, C16:1-Me methyl palmitoleate, C18:0-Me methyl stearate and C18:1-Me methyl oleate (when methanol is added) and C14:0-Et ethyl myristate, C16:0-Et ethyl palmitate, C16:1-Et ethyl palmitoleate and C18:1-Et ethyl oleate (when ethanol is added), respectively.

Finally, it is demonstrated that the strains *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB2_optEc], *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-CpFATB2_optEc] and *E.coli* W3110 ΔfadE pCDF[fadD-atfA]-[alkL]/pJ294[Ptac-ChFATB1_optEc]t, which are named in this example, form substantially more of the respective fatty acid methyl esters (when methanol is added) and fatty acid ethyl esters (when ethanol is added), respectively, than the strains *E.coli* W3110 ΔfadE pCDF[fadD-atfA]/pJ294[Ptac-ChFATB2_optEc], *E.coli* W3110 ΔfadE pCDF[fadD-atfA]/pJ294[Ptac-CpFATB2_optEc] and *E.coli* W3110 ΔfadE pCDF[fadD-atfA]/pJ294[Ptac-ChFATB1_optEc]. This demonstrates that the enhancement of the *alkL* gene product promotes the production of fatty acid esters with various chain lengths of the alkyl chain both of the fatty acid residue and the alcohol residue of the fatty acid esters and with a different degree of saturation of the alkyl chain of the fatty acid, respectively, from unrelated carbon sources.

Example 9: Preparation of expression vectors for the genes CnfatB3 from Cocos nucifera and synUcTE from Umbellularia californica

To prepare expression vectors for the genes *fatB3* (SEQ ID No. 35) from *Cocos nucifera* and *synUcTE* (SEQ ID No. 37) from *Umbellularia californica* (each encoding one enzyme E_i), these genes were codon-optimized for expression in *Escherichia coli*. The genes were synthesized in each case together with a *tac* promoter (SEQ ID No. 39) and at the same time a cleavage site was introduced upstream of the promoter and a cleavage site was introduced downstream of

the terminator. The synthesized DNA fragments P_{tac}-*CnFATB3* and P_{tac} synUcTE were digested with the restriction endonucleases *BamH*I and *Not*I and ligated into the correspondingly cut vector pJ294 (DNA2.0 Inc., Menlo Park, CA, USA). The completed *E.coli* expression vectors were termed pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40), pJ294[Ptac-synUcTE] (SEQ ID No. 41). The vector pJ294 is an *E.coli* vector which imparts ampicillin resistance and also carries a p15A replication origin and therefore has a low copy number (10-15 copies per cell).

Example 10: Preparation of expression vectors for the genes alkL_Oa from Oceanocaulis alexandrii, alkL_Ma from Marinobacter aquaeolei, alkL_CspK31 from Caulobacter sp. K31

To prepare expression vectors for the genes alkL_Oa (SEQ ID No. 42) from *Oceanocaulis alexandrii* HTCC2633, alkL_Ma (SEQ ID No. 44) from *Marinobacter aquaeolei* VT8, alkL_CspK31 (SEQ ID No. 46) from *Caulobacter sp. K31* (in each case encoding one AlkL gene product), these genes were synthesized together with a *lacuv5* promoter (SEQ ID No. 34). The synthesized DNA fragments P_{lacuv5} *alkL*_Oa, P_{lacuv5} *alkL*_Ma and P_{lacuv5} *alkL*_CspK31 were amplified with introduction of homologous regions for recombination cloning.
The following oligonucleotides were used for amplification of the target genes.
alkL_H1_fw: 5'-GCTTACTGAATTTGCCTGAACCATGGGGCAGTGAG-3' (SEQ ID No. 48)
alkL_H2_rv: 5'-TTCTGAAGTGGGGGCGGCCGCCCTTTTGACGGGTACC-3' (SEQ ID No. 49)

The following parameters were used for the PCR: 1 x: initial denaturation, 98°C, 1 min; 35 x: denaturation, 98°C, 0:15 min, annealing, 60°C, 0:45 min; elongation, 72°C, 1:30 min; 1 x: terminal elongation, 72°C, 10 min. For the amplification, the Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used in accordance with the manufacturer's recommendations. In each case 50 µl of the PCR reactions were then separated on a 1% strength TAE agarose gel. The PCR, agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in a manner known to those skilled in the art. In all cases PCR fragments of the expected size were able to be amplified. These were 906 base pairs for P_{lacuv5} *alkL*_Oa, 960 base pairs for P_{lacuv5} *alkL*_Ma and 903 base pairs for P_{lacuv5} *alkL*_CspK31. To isolate the DNA from the TAE agarose gel, the target DNA was cut out of the gel with a scalpel and purified using the QiaQuick Gel extraction kit

according to the manufacturer's instructions (Qiagen, Hilden). The purified PCR products were cloned together with the *NotI*-cut vector pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11) by recombination, using the Geneart® Seamless Cloning and Assembly Kit according to the manufacturer's instructions (Life Technologies, Carlsbad, CA, USA). From the resultant pJ294 derivatives pJ294{Ptac}[ChFATB2(co_Ec){Placuv5}[alkL_Oa] (SEQ ID No. 50), pJ294{Ptac}[ChFATB2(co_Ec){Placuv5}[alkL_Ma] (SEQ ID No. 51) and pJ294{Ptac}[ChFATB2(co_Ec){Placuv5}[alkL_CspK31] (SEQ ID No. 52) the fragments P_{lacuv5} alkL_Oa, P_{lacuv5} alkL_Ma and P_{lacuv5} alkL_CspK31 were cut out using a restriction digest with the restriction endonucleases *Nco*I and *NotI* and ligated into the corresponding cut vector pCDFDuet-1 (71340-3, Merck, Darmstadt; SEQ ID No. 53). Chemically competent *E.coli* DH5α (New England Biolabs, Frankfurt) was transformed in a manner known to those skilled in the art. Correct insertion of the target genes was examined by restriction analysis, and authenticity of the introduced genes was validated by DNA sequencing. The resultant expression vectors were named pCDF[alkL_Oa] (SEQ ID No. 54) , pCDF[alkL_Ma] (SEQ ID No. 55) and pCDF[alkL_CspK31] (SEQ ID No. 56).

Example 11: HPLC/ESI-based quantification of fatty acids

Octanoic acid, 3-hydroxydecanoic acid, decanoic acid, lauric acid, 3-hydroxymyristic acid, myristic acid, palmitoleic acid, palmitic acid, oleic acid and stearic acid in fermentation samples were quantified by means of HPLC-ESI/MS on the basis of internal calibration for all analytes and using the internal standards D3-lauric acid (methyl-D3, 99%) for octanoic acid, 3-hydroxydecanoic acid, decanoic acid, lauric acid, 3-hydroxymyristic acid, myristic acid, palmitoleic acid and D3-stearic acid (methyl-D3, 98%) for palmitic acid, oleic acid, stearic acid.

The following apparatuses were used:

- HPLC system: Surveyor (Thermo Fisher Scientific, Waltham, Massachusetts, USA), consisting of Surveyor MS Pump, Surveyor Autosampler plus and Surveyor PDA Surveyor
- Mass spectrometer: TSQ Vantage with HESI II - source (Thermo Fisher Scientific, Waltham, Massachusetts, USA)

- HPLC columns: XBridge BEH C8, 100 x 2.1 mm, particle size: 2.5 µm, pore size 130 Å (Waters, Milford Massachusetts, USA)

The samples were prepared in that 1200 µl of acetone and 300 µl of sample were mixed for approximately 10 seconds and then centrifuged at approximately 13 000 rpm for 5 min. The clear supernatant was taken off and analysed after appropriate dilution with acetone. To each 900 µl of the diluted sample were added 100 µl of ISTD by pipette.
HPLC separation proceeded using the abovementioned HPLC column. The injection volume was 2 µl, the column temperature was 25°C, and the flow rate was 0.3 ml/min. The mobile phase consisted of eluent A (water + 10 mmol of ammonium acetate adjusted with ammonia to pH = 9) and eluent B (acetonitrile/eluent A 95/5). The following gradient profile was used

Time [min]	Eluent A [%]	Eluent B [%]
0	95	5
1	95	5
1.1	70	30
7	5	95
8	5	95

The ESI-MS analysis proceeded with negative ionization using the following parameters of the ESI source:

- Spray voltage: 3000 V
- Vaporizer temperature: 380 °C
- Sheath gas pressure: 40
- Aux gas pressure: 15
- Capillary temperature: 380°C

The individual compounds were detected and quantified using "single ion monitoring" (SIM) using the following parameters:

Analyte	Ion $[M-H]^-$ [m/z]	Scan width [m/z]	Scan time [ms]	Peak width Q_3
Octanoic acid	143.13	0.002	100	0.7
3-Hydroxydecanoic acid	187.13	0.002	50	0.7
Decanoic acid	171.13	0.002	100	0.7
Lauric acid	199.16	0.002	50	0.7

3-Hydroxymyristic acid	243.18	0.002	50	0.7
Myristic acid	227.19	0.002	50	0.7
Palmitoleic acid	253.18	0.002	50	0.7
Palmitic acid	255.22	0.002	30	0.7
Oleic acid	281.23	0.002	30	0.7
Stearic acid	283.25	0.002	30	0.7
D3-lauric acid	202.16	0.002	50	0.7
D3-stearic acid	286.25	0.002	30	0.7

Example 12: Production of fatty acids by E.coli strains with a deletion in the fadE gene, which overexpresses the genes alkL from Pseudomonas putida GPo1, alkL from Oceanocaulis alexandrii HTCC2633 or alkL from Caulobacter sp. K31 and fatB1 from Cuphea hookeriana, fatB2 from Cuphea hookeriana, synUcTE from Umbellularia californica or fatB3 from Cocos nucifera.

To generate *E.coli* strains having the expression vector for the gene *alkL* from *Pseudomonas putida* GPo1, *alkL* from *Oceanocaulis alexandrii* HTCC2633 or *alkL* from *Caulobacter sp. K31* in combination with the expression vector for the *fatB1* gene from *Cuphea hookeriana*, *fatB2* from *Cuphea hookeriana, synUcTE* from *Umbellularia californica* or *fatB3* from *Cocos nucifera* electrocompetent cells of *E.coli* W3110 ΔfadE and *E.coli* JW5020-1 Kan^S were prepared. This was carried out in a manner known to those skilled in the art. *E.coli* JW5020-1 Kan^S is a derivative of *E.coli* JW5020-1 (CGSC, The coli genetic stock center, Yale University, New Haven, USA), and this in turn is an *E.coli* BW25113 derivative, which carries a deletion of the *fadE* gene. The *fadE* gene was replaced by a kanamycin cassette. This was removed before equipping the strain with the expression vectors using a helper plasmid which encodes flp recombinase, in a manner known to those skilled in the art (see Datsenko K.A. and Wanner B.L. (2000) PNAS 97(12):6640-6645) resulting in strain *E.coli* JW5020-1 Kan^S. *E.coli* JW5020-1 Kan^S was transformed with the plasmids pJ294[Ptac-ChFATB1_optEc] (SEQ ID No. 12), pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11) or pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40) in combination with pCDFDuet-1, pCDF[alkL] (SEQ ID No. 7) or pCDF[alkL_Oa] (SEQ ID No. 54) or pCDF[alkL_CspK31] (SEQ ID No. 56), and *E.coli* W3110 ΔfadE was transformed with the plasmids pJ294[Ptac-synUcTE] (SEQ ID No. 41) in combination with pCDFDuet-1 (SEQ ID No. 53) or pCDF[alkL] (SEQ ID No. 7) and plated onto LB-agar plates with spectinomycin (100

µg/ml) and ampicillin (100 µg/ml). Transformants were checked for presence of the correct plasmids by plasmid preparation and analytical restriction analysis.
The following *E. coli* strains were generated in this manner:

- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc]/pCDFDuet-1
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc]/pCDF[alkL]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc]/pCDFDuet-1
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc]/pCDF[alkL_Oa]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc]/pCDF[alkL_CspK31]
- *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)]/pCDFDuet-1
- *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)]/pCDF[alkL]
- *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE]/pCDFDuet-1
- *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE]/pCDF[alkL]

These strains were employed to investigate their ability to produce fatty acids. The following procedure was used:
The strains were subjected to a multistage aerobic culturing process. The strains under investigation were first initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) with 100 µg/ml ampicillin and 100 µg/ml spectinomycin as 5 ml preliminary culture from one single colony each. The next culturing step proceeded in M9 medium. The medium, consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution, was adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in

1 M hydrochloric acid (all substances from Merck, Darmstadt) was sterile-filtered before addition to the M9 medium. 10 ml of M9 medium were charged with 100 µg/ml spectinomycin and 100 µg/ml ampicillin into 100 ml conical flasks with chicane and inoculated with 0.5 ml from the preliminary culture. The culturing proceeded at 37°C and 200 rpm in an incubating shaker. After a cultivating time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are charged into a 250 ml conical flask with chicane and inoculated with the 10 ml culture, in such a manner that an optical density (600 nm) of 0.2 is achieved. The cuturing proceeded at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, gene expression is induced by adding 1 mM IPTG. The strains were cultured for a further 24 hours at 30°C and 200 rpm. During the culturing, samples of 300 µl are taken off and the concentration of fatty acids of differing carbon chain lengths is quantified as described in Example 10. The results are shown in the tables hereinafter.

Production of fatty acids using *E.coli* JW5020-1 Kan^S, which overexpresses *fatB2* from *C.hookeriana* and *alkL* from *Oceanocaulis alexandrii* HTCC2633 and *alkL* from *Caulobacter sp.* K31. The concentrations of fatty acids of differing carbon chain length are reported after culturing for 24 hours (n.d. = not detectable):

Strain	$c_{Caprylic\ acid}$ [mg/l/OD]	$c_{Capric\ acid}$ [mg/l/OD]	$c_{Palmitoleic\ acid}$ [mg/l/OD]	$c_{Vaccenic\ acid}$ [mg/l/OD]
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDFDuet-1	21.0	1.8	0.1	1.3
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[alkL_Oa]	27.5	6.3	5.9	2.3
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[alkL_CspK31]	38.6	4.7		

Production of fatty acids with *E.coli* JW5020-1 Kan^S, which overexpresses *fatB3* from *C.nucifera* and *alkL* from *Pseudomonas putida* GPo1. The concentrations of fatty acids of differing carbon chain length are reported after 48 hours of culturing (n.d. = not detectable):

Strain	$c_{Caprylic\ acid}$ [mg/l/OD]	$c_{Lauric\ acid}$ [mg/l/OD]	$c_{Myristic\ acid}$ [mg/l/OD]	$c_{Palmitoleic\ acid}$ [mg/l/OD]	$c_{Palmitic\ acid}$ [mg/l/OD]	$c_{Vaccenic\ acid}$ [mg/l/OD]
E.coli JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDFDuet-1	0.1	3.2	4.5	13.4	1.7	4.0
E.coli JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL]	0.5	6.8	9.9	21.2	3.1	5.6

Production of fatty acids with *E.coli* JW5020-1 Kan^S, which overexpresses *fatB1* from *C.hookeriana* and *alkL* from *Pseudomonas putida* GPo1. The concentrations of fatty acids of differing carbon chain lengths are reported after 24 hours of culturing (n.d. = not detectable):

Strain	$c_{Myristic\ acid}$ [mg/l/OD]	$c_{Palmitoleic\ acid}$ [mg/l/OD]
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDFDuet-1	38.2	0.1
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDF[alkL]	42.8	62.0

Production of fatty acids using *E.coli* JW5020-1 Kan^S, which overexpresses *synUcTE* from *U. californica* and *alkL* from *Pseudomonas putida* GPo1. The concentrations of fatty acids of differing carbon chain lengths are reported after 24 hours of culturing (n.d. = not detectable):

Strain	$c_{Lauric\ acid}$ [mg/l/OD]	$c_{Myristic\ acid}$ [mg/l/OD]
E.coli W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDFDuet-1	0.1	0.1
E.coli W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[alkL]	20.1	1.9

Therefore it was found that strains which overexpress *alkL* from *P.putida*, *O.alexandrii* or *Caulobacter sp.* are able to form more caprylic acid, capric acid, lauric acid, myristic acid, palmitic acid, palmitoleic acid or vaccenic acid, depending on the specificity of the overexpressed acyl-ACP thioesterase. This shows that reinforcement of *alkL* is required for the preparation of fatty acids of differing chain lengths and degrees of saturation from unrelated carbon sources.

Example 13: Preparation of vectors for the coexpression of the genes fatB2 from Cuphea hookeriana, fatB3 from Cocos nucifera, synUcTE from Umbellularia californica with alkL from Pseudomonas putida

For preparation of vectors for the coexpression of the gene *fatB2* (SEQ ID No. 8) from *Cuphea hookeriana*, *fatB3* (SEQ ID No. 35) from *Cocos nucifera*, *synUcTE* (SEQ ID No. 37) from *Umbellularia californica* with an *alkL* gene from *Pseudomonas putida*, the gene *alkL* (SEQ ID No. 1) was amplified together with the *lacuv5* promotor and terminator from the vector pCDF[alkL] (SEQ ID No. 7).

For amplification of the fragment P-*alkL*-T (SEQ ID No. 58) for coexpression with *fatB2* and *synUcTE*, the following oligonucleotides were used.
NP-FA-P19: 5'-ATCCGCTCACAATTGCAAATGCCTGAGGTTTCAGC-3' (SEQ ID No. 59)
NP-FA-P20: 5'-CTTCCCTTCATTTTGGTCTCGGTCGATCATTCAGC-3' (SEQ ID No. 60)

For amplification of the fragment P-*alkL*-T (SEQ ID No. 58) for coexpression with *fatB3*, the following oligonucleotides were used.
NP-FA-P19: 5'-ATCCGCTCACAATTGCAAATGCCTGAGGTTTCAGC-3' (SEQ ID No. 59)
NP-FA-P21:5'-ACTTAGTCGCTGAAGGTCTCGGTCGATCATTCAGC-3' (SEQ ID No. 61)

The following parameters were used for the PCR: 1 x: initial denaturation, 98°C, 1 min; 35 x: denaturation, 98°C, 0:15 min, annealing, 65°C, 0:45 min; elongation, 72°C, 1:30 min; 1 x: terminal elongation, 72°C, 10 min. For the amplification, the Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used in accordance with the recommendations of the

manufacturer. In each case 50 µl of the PCR reactions were then separated on a 1% strength TAE agarose gel. The PCR, agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in a manner known to those skilled in the art. The PCR fragments with an expected size of 1095 base pairs were able to be amplified. To isolate the DNA from the TAE agarose gel, the target DNA was cut out from the gel with a scalpel and purified by the *QiaQuick Gel extraction Kit* according to the manufacturer's instructions (Qiagen, Hilden). The purified PCR products were cloned together with the above-described vectors pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11), pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40), pJ294[Ptac-synUcTE] (SEQ ID No. 41), which were linearized with *BamHI*, by means of recombination, using the Geneart® Seamless Cloning and Assembly Kit according to the manufacturer's instructions (Life Technologies, Carlsbad, CA, USA). The resultant expression vectors were named pJ294{Placuv5}[alkL]{Ptac}[ChFATB2(co_Ec)] (SEQ ID No. 62), pJ294{Placuv5}[alkL]{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 63) and pJ294[Placuv5}[alkL]{Ptac}[synUcTE(co_Ec)] (SEQ ID No. 64). The transformation of chemically competent *E.coli* DH5α proceeded in a manner known to those skilled in the art. Correct insertion of the target genes was checked by restriction analysis and the authenticity of the insert was verified by DNA sequencing.

Example 14: Preparation of expression vectors for the genes fadD from Escherichia coli and wax-dgaT (atfA) from Acinetobacter sp. ADP1 and atfA1 from Alcanivorax borkumensis

To produce expression vectors for the genes *fadD* (SEQ ID No. 57) from *Escherichia coli* (encoding an enzyme E_{vi}) and *wax-dgaT* (*atfA* in Example 5) (SEQ ID No. 65) from *Acinetobacter sp.* ADP1 and *atfA1* (SEQ ID No. 67) from *Alcanivorax borkumensis* SK2 (in each case encoding an enzyme E_v), the genes *wax-dgaT* and *atfA1* were codon-optimized for expression in *Escherichia coli* and synthesized in combination with the gene *fadD* from E.coli. The synthesized DNA fragments *wax-dgaT_AsADP1-fadD_Ec* (SEQ ID No. 69) and *atfA1_Ab-fadD_Ec* (SEQ ID No. 70) were amplified with introduction of homologous regions for recombination cloning.

To amplify the fragment *wax-dgaT_AsADP1-fadD_Ec*, the following oligonucleotides were used:
wax-dgaT_H1_fw: 5'- ACAGGAGGTAAAACATATGCGTCCTCTGCACCCG-3' (SEQ ID No. 71)
fadD_H2_rv: 5'- GTTTCTTTACCAGACTCGAGATTGTTTTCTCTTTAGTGGGCGTC-3' (SEQ ID No. 72)

To amplify the fragment *atfA1_Ab-fadD_Ec*, the following oligonucleotides were used:
atfA_Ab_fw_kurz: 5'- ACAGGAGGTAAAACATATGAAAGCGCTGTCCC-3' (SEQ ID No. 73)
fadD_H2_rv_N: 5'-GTTTCTTTACCAGACTCGAGATTGTTTTCTCTTTAGTGGGC-3' (SEQ ID No. 74)

The following parameters were used for the PCR: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:10 min, annealing, 70°C, 0:20 min; elongation, 72°C, 1 min; 1 x: terminal elongation, 72°C, 10 min. For the amplification, the Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used in accordance with the manufacturer's recommendations. Each 50 µl of the PCR reactions was then separated on a 1% strength TAE agarose gel. The PCR, agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes was carried out in a manner known to those skilled in the art. In both cases, PCR fragments of the expected size were able to be amplified. These were for *wax-dgaT_AsADP1-fadD_Ec* 3192 base pairs and *atfA1_Ab-fadD_Ec* 3189 base pairs. To isolate the DNA from the agarose gel, the target DNA was cut out of the gel using a scalpel and purified with the *QiaQuick Gel extraction kit* according to the manufacturer's instructions (Qiagen, Hilden). The purified PCR products were cloned into a *NdeI*- and *XhoI*-cut pCDF derivative which already contains a synthetic *tac* promotor (SEQ ID No. 39), by recombination, using the Geneart® Seamless Cloning and Assembly Kit according to the manufacturer's instructions (Life Technologies, Carlsbad, CA, USA). Chemically competent *E.coli* DH5α (New England Biolabs, Frankfurt) was transformed in a manner known to those skilled in the art. Correct insertion of the target genes was checked by restriction analysis and the authenticity of the introduced genes was verified by DNA sequencing. The resultant expression vectors were named pCDF[wax-dgaT_AsAPD1(co_Ec)-fadD_Ec] (SEQ ID No. 75) and pCDF[atfA1_Ab(co_Ec)-fadD_Ec] (SEQ ID No. 76).

Example 15: Gas-chromatographic quantification of fatty acid methyl esters

Fatty acid methyl esters were quantified in the culture broth by means of gas chromatography. 500 mg/l of heptadecanoic acid methyl ester were added to the culture broth as internal reference substance. The culture broth was shaken in an equivalent volume of n-heptane for 15 min at 12 Hz to extract the fatty acid methyl esters. For phase separation, the sample was centrifuged for 10 min at 16 000 x g and the organic phase was measured by gas chromatography. To separate fatty acid methyl esters, the capillary column SP™-2560 with the dimensions 100 m x 0.25 mm and a film thickness of 0.2 µm (Supelco, Sigma-Aldrich, Steinheim) was used as stationary phase. The carrier gas used was helium. The separation proceeded in the course of 45 min with an injector temperature of 260°C, detector temperature of 260°C and column temperature of 140°C at the start, held for 5 min and increased to 240°C at a rate of 4°C/min and held for 15 min. The injection volume was 1 µl, the split rate 1:20 and the flow rate of the carrier gas 1 ml/min. The detection was carried out by means of a flame-ionization detector (GC Perkin Elmer Clarus 500, Perkin Elmer, Rodgau). Heptadecanoic acid methyl ester (Sigma-Aldrich, Steinheim) was used as internal reference substance for quantifying the fatty acid methyl esters. The reference substances C8:0-Me caprylic acid methyl ester, C10:0-Me capric acid methyl ester, C12:0-Me lauric acid methyl ester, C14:0-Me myristic acid methyl ester, C16:0-Me palmitic acid methyl ester, C16:1-Me palmitoleic acid methyl ester, C18:0-Me stearic acid methyl ester, C18:1-Me oleic acid methyl ester (GLC Standard Mix GLC-20 1892-1AMP, GLC-30 1893-1AMP, GLC-50 1894-1AMP, Sigma-Aldrich, Steinheim) were used for calibration. The determination limits for all fatty acid methyl esters were at a concentration of 10 mg/l.

Example 16: Production of fatty acid methyl esters by E.coli strains with deletion in the fadE gene which overexpresses the genes alkL from Pseudomonas putida GPo1 and a plant acyl-ACP thioesterase and an acyl-CoA synthetase and a wax-ester synthase.

To generate *E.coli* strains having the expression vector for the genes *alkL* from *Pseudomonas putida* GPo1 and *fatB2* from *Cuphea hookeriana, fatB3* from *Cocos nucifera* and *synUcTE* from *Umbellularia californica* in combination with the expression vector for the genes *fadD* from

Escherichia coli and *wax-dgaT* from *Acinetobacter sp. ADP1* and *atfA1* from *Alcanivorax borkumensis* SK2, electrocompetent cells of *E.coli* W3110 Δ*fadE* and *E.coli* JW5020-1 Kan^S were produced. This took place in *a* manner known to those skilled in the art. *E.coli* JW5020-1 Kan^S was transformed with the vectors pJ294{Placuv5}[alkL]{Ptac}[ChFATB2(co_Ec)] (SEQ ID No. 62) or pJ294[Placuv5}[alkL]{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 63) and pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11) or pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40) in combination with pCDF[atfA1_Ab(co_Ec)-fadD_Ec] (SEQ ID No. 76) and *E.coli* W3110 ΔfadE with the vectors pJ294{Placuv5}[alkL]{Ptac}[synUcTE] (SEQ ID No. 62) and pJ294[Ptac-synUcTE] (SEQ ID No. 41) in combination with pCDF[wax-dgaT_AsAPD1(co_Ec)-fadD_Ec] (SEQ ID No. 75) and were plated onto LB-agar plates containing spectinomycin (100 µg/ml) and ampicillin (100 µg/ml). Transformants were checked for the presence of the correct plasmids by plasmid preparation and analytical restriction analysis.

In this manner the *E. coli* strains hereinafter were generated:

- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]
- *E.coli* JW5020-1 Kan^S pJ294{Placuv5}[alkL][Ptac}[ChFATB2(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]
- *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]
- *E.coli* JW5020-1 Kan^S pJ294{Placuv5}[alkL]{Ptac}[CnFATB3(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]
- *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[wax-dgaT_AsAPD1(co_Ec)-fadD_Ec]
- *E.coli* W3110 ΔfadE pJ294{Placuv5}[alkL]{Ptac}[synUcTE] / pCDF[wax-dgaT_AsAPD1(co_Ec)-fadD_Ec]

These strains were employed to investigate their ability to produce fatty acid methyl esters. In this process the following procedure was used:

The strains are subjected to a multistage aerobic culturing process. The strains under test were initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) containing 100 µg/ml of ampicillin and 100 µg/ml of spectinomycin as 5 ml preliminary culture from a single

colony each time. The next culture step proceeded in M9 medium. The medium, consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution was adjusted to pH 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) was sterile-filtered before addition to the M9 medium. 10 ml of M9 medium were charged with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin into 100 ml conical flasks with chicane and inoculated with 0.5 ml from the preliminary culture. The culturing proceeded at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin were charged in a 250 ml conical flask with chicane and inoculated with the 10 ml culture, in such a manner that an optical density (600 nm) of 0.2 was achieved. The culturing proceeded at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, the gene expression is induced by adding 1 mM IPTG. The strains were cultured for a further 24 hours at 30°C and 200 rpm. One hour after induction of gene expression, 1% (v/v) methanol is added to the culture broth. During the culturing, samples are withdrawn and the concentration of fatty acid methyl ester of different carbon chain lengths are quantified as described in Example 15. The results are shown in the tables hereinafter.

Production of fatty acid methyl esters with *E.coli* JW5020-1 Kan^S and *E.coli* W3110 ΔfadE, which overexpress *one* acyl-ACP thioesterase, *fadD* from *E.coli* and a wax-ester synthase. Strains with and without overexpression of *alkL* from *P.putida* GPo1 are shown. The concentrations of fatty acid methyl ester of differing carbon chain length are reported after 24 hours of culturing (n.d. = not detectable):

Strain	$C_{Caprylic\ acid\ methyl\ ester}$ [mg/L/OD]	$C_{Capric\ acid\ methyl\ ester}$ [mg/L/OD]	$C_{Lauric\ acid\ methyl\ ester}$ [mg/L/OD]	$C_{Myristic\ acid\ methyl\ ester}$ [mg/L/OD]
E.coli W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[wax-dgaT_AsADP1(co_Ec)-fadD_Ec]	n.d.	n.d.	0.1	1.5
E.coli W3110 ΔfadE pJ294[alkL][Ptac-synUcTE] / pCDF[wax-dgaT_AsADP1(co_Ec)-fadD_Ec]	n.d.	n.d.	11.1	3.7
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]	8.0	4.0		
E.coli JW5020-1 Kan^S pJ294{Placuv5}[alkL]{Ptac}[ChFATB2(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]	9.5	4.8		
E.coli JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]	n.d.	n.d.	3.1	6.3
E.coli JW5020-1 Kan^S pJ294{Placuv5}[alkL]{Ptac}[CnFATB3(co_Ec)] / pCDF[atfA1_Ab(co_Ec)-fadD_Ec]	n.d.	n.d.	4.3	8.5

It was thus shown that strains which overexpress *alkL* from *P.putida* are able to form more caprylic acid methyl ester, capric acid methyl ester, lauric acid methyl ester and myristic acid methyl ester, depending on the specificity of the overexpressed acyl-ACP thioesterase. This shows that a reinforcement of alkL is necessary for the preparation of fatty acid methyl esters of differing carbon chain length from unrelated carbon sources.

Example 17: Preparation of expression vectors for the coexpression of acyl-ACP reductase genes with the acyl-CoA synthetase gene fadD from Escherichia coli and alkL from Pseudomonas putida

To produce expression vectors for the coexpression of *fadD* (SEQ ID No. 57) from *Escherichia coli* (encoding an enzyme E_{vi}) and *acrM* (SEQ ID No. 77) from *Acinetobacter sp. M-1*, *acr1b* (SEQ ID No 79) from *Acinetobacter sp.* ADP1, *acr1a* (SEQ ID No. 81) from *Acinetobacter sp. ADP1* and *Maqu_2220* (SEQ ID No. 83) from *Marinobacter aquaeolei* VT8 (encoding an enzyme E_x) and *alkL* from *Pseudomonas putida* (SEQ ID No. 1, encoding an AlkL gene product), the genes *acr1a* from *Acinetobacter sp. ADP1* and *Maqu_2220* were codon-optimized for expression in *Escherichia coli* and these genes and the gene *acrM* from Acinetobacter sp. M-1 were synthesized (DNA2.0 Inc., Menlo Park, CA, USA). These genes were amplified by PCR proceeding from the synthetic DNA and also the gene *acr1b* from *Acinetobacter sp. ADP1* proceeding from chromosomal DNA as a matrix. Via the oligonucleotides used, the amplified DNA fragments were provided with homologous regions to the respective neighbouring fragment and to the *PspXI*-linearized target vector pCDF[alkL] (SEQ ID No. 7) for recombination cloning. At the same time, the gene *fadD* from *Escherichia coli* was amplified by PCR together with a synthetic *tac* promotor (SEQ ID No. 39) proceeding from a pCDF derivative as a matrix and likewise provided with homologous regions via the oligonucleotides used.
To produce the expression vector for the genes *luxC, luxD* and *luxE* from the lux operon of *Photorhabdus luminescens* and *alkL* from *Pseudomonas putida* GPo1, the *luxCDE* operon (SEQ ID No. 85) was codon-optimized for expression in *Escherichia coli* and synthesized (DNA2.0 Inc., Menlo Park, CA, USA). The operon was amplified by PCR proceeding from the synthesized DNA as matrix, and the *tac* promotor, proceeding from a pCDF derivative which contains this promotor (SEQ ID No. 39). Both DNA fragments were provided via the oligonucleotides used with homologous regions for the target vector to the respective neighbouring fragment and to the linearized target vector for the recombination cloning.

The following oligonucleotides were employed in amplification of the *tac* promotor, the acyl-CoA synthetase gene and the acyl-ACP reductase genes for the coexpression with *alkL*:

P_{tac} and *fadD* for the coexpression with *acr1a* [*Acinetobacter sp. ADP1*]:
NP-FA-P1: 5'-TTTTCTAAGGTACCCGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 86)
NP-FA-P2: 5'-CTCCTTCAGCTCAGGCTTTATTGTCCAC-3' (SEQ ID No. 87)

P_{tac} and *fadD* for the coexpression with *acrM* [*Acinetobacter sp. M-1*]:

NP-FA-P1: 5'-TTTTCTAAGGTACCCGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 86)
NP-FA-P5: 5'-CTCCTTCAGCTCAGGCTTTATTGTC-3' (SEQ ID No. 88)

P_{tac} and *fadD* for the coexpression with Maqu_2220 [*Marinobacterium aquaeolei* VT8]:
NP-FA-P1: 5'-TTTTCTAAGGTACCCGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 86)
NP-FA-P8: 5'-TCCTTCTCGCTCAGGCTTTATTGTCC-3' (SEQ ID No. 89)

P_{tac} and *fadD* for the coexpression with *acr1b* [*Acinetobacter sp. ADP1*]:
NP-FA-P1: 5'-TTTTCTAAGGTACCCGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 86)
NP-FA-P14: 5'-CCTGATTGGCTCAGGCTTTATTGTC-3' (SEQ ID No. 90)

P_{tac} for the expression of *luxCDE* [*Photorhabdus luminescens*]:
NP-FA-P1: 5'-TTTTCTAAGGTACCCGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 86)
NP-FA-P11: 5'-ACCTCCTAGTTTTACCTCCTGTTAAACAA-3' (SEQ ID No. 91)

acr1a [*Acinetobacter sp.* ADP1]:
NP-FA-P3: 5'- CCTGAGCTGAAGGAGTTACAGTTTGATC-3' (SEQ ID No. 92)
NP-FA-P4: 5'- GTTTCTTTACCAGACTTATCACCAGTGCTCACC-3' (SEQ ID No. 93)

acrM [*Acinetobacter sp. M1*]:
NP-FA-P6: 5'-CCTGAGCTGAAGGAGTTACAGTATGAATG-3' (SEQ ID No. 94)
NP-FA-P7: 5'-GTTTCTTTACCAGACTTATTACCAGTGTTCG-3' (SEQ ID No. 95)

Maqu_2220 [*Marinobacterium aquaeolei* VT8]:
NP-FA-P9: 5'-CCTGAGCGAGAAGGAGTTCTATCATGG-3' (SEQ ID No. 96)
NP-FA-P10: 5'-GTTTCTTTACCAGACTCATTACGCGGCCTTTTTGC-3' (SEQ ID No. 97)

acr1b [*Acinetobacter sp.* ADP1]:
NP-FA-P15: 5'-CCTGAGCCAATCAGGGAAAAACGCGTG-3' (SEQ ID No. 98)
NP-FA-P16: 5'-GTTTCTTTACCAGACCTCTCGGTATGAGAGGCTTC-3' (SEQ ID No. 99)

luxCDE [*Photorhabdus luminescens*]:

NP-FA-P12: 5'-GTAAAACTAGGAGGTAAAAAAAATGACG-3' (SEQ ID No. 100)
NP-FA-P13: 5'-GTTTCTTTACCAGACTTAGCTATCGAACGAACGCCTCG-3' (SEQ ID No. 101)

The following parameters were used for the PCR: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:10 min, annealing, 60°C, 0:45 min; elongation, 72°C, 1:30 min; 1 x: terminal elongation, 72°C, 10 min. For the amplification, the Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used in accordance with the manufacturer's recommendations. In each case 50 µl of the PCR reactions were then separated on a 1% strength TAE-agarose gel. The PCR, the agarose-gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in a manner known to those skilled in the art.

In all cases, PCR fragments of the expected size were able to be amplified. These were, for the *tac* promotor 171 base pairs, for the *tac* promotor and *fadD* for coexpression with *acr1a* [*A.sp.* ADP1] and Maqu2220 1927 base pairs, for coexpression with *acrM* 1919 base pairs and for coexpression with *acr1b* [*A.sp.* ADP1] 1933 base pairs. The PCR fragments for *acr1a* [*A.sp.* ADP1] were 952 base pairs, for *acrM* 906 base pairs, for Maqu2220 1561 base pairs, for *acr1b* [*A.sp.*ADP1] 903 base pairs, and for *luxCDE* 3621 base pairs.

For isolation of the DNA from the agarose gel, the target DNA was cut out from the gel using a scalpel and purified using the *QiaQuick Gel extraction kit* according to the manufacturer's instructions (Qiagen, Hilden). The purified PCR products were cloned by recombination, using the Geneart® Seamless Cloning and Assembly Kit according to the manufacturer's instructions (Life Technologies, Carlsbad, CA, USA) into the *PspXI*-linearized vector pCDF[alkL] (SEQ ID No. 7). Chemically competent *E.coli* DH5α (New England Biolabs, Frankfurt) was transformed in a manner known to those skilled in the art. The correct insertion of the target genes was checked by restriction analysis and the authenticity of the introduced genes was validated by DNA sequencing.

In this manner the following expression vectors resulted:

- pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1b_AsADP1] (SEQ ID No. 102)
- pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)] (SEQ ID No. 103)
- pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acrM_AsM1] (SEQ ID No. 104)
- pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-Maqu2220(co_Ec)] (SEQ ID No. 105)
- pCDF{Placuv5}[alkL]{Ptac}[luxCDE_Pl(co_Ec)] (SEQ ID No. 106)

For preparation of vectors for the coexpression of *fadD* from *Escherichia coli* and *acrM* from *Acinetobacter sp. M-1*, *acr1b* from *Acinetobacter sp. ADP1*, *acr1a* from *Acinetobacter sp.* ADP1 (codon-optimized) and *Maqu_2220* from *Marinobacter aquaeolei* VT8 (codon-optimized) and the expression of *luxC, luxD* and *luxE* from *Photorhabdus luminescens* (codon-optimized) without the coexpression of *alkL*, these genes were amplified by PCR starting from the previously generated expression vectors pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1b_AsADP1], pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)], pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acrM_AsM1], pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-Maqu2220(co_Ec)] und pCDF{Placuv5}[alkL]{Ptac}[luxCDE_Pl(co_Ec)] with introduction of homologous regions to *PspXI / NcoI*-cut target vector pCDF[alkL] (SEQ ID No. 7).

The following oligonucleotides were employed here:
NP-FA-P17: 5'-AATAAGGAGATATACGATAACAATTACGAGCTTCATG-3' (SEQ ID No. 107)
NP-FA-P18: 5'-GTTTCTTTACCAGACGCGTTCAAATTTCGCAGCAG-3' (SEQ ID No. 108)

The following parameters were employed for the PCR: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:15 min, annealing, 60°C, 0:45 min; elongation, 72°C, 1:30 min; 1 x: terminal elongation, 72°C, 10 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification, following the manufacturer's recommendations. 50 µl of the PCR reactions in each case were then separated on a 1% strength TAE-agarose gel. The PCR, the agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in a manner known to those skilled in the art.
In all cases, PCR fragments of the expected size were able to be amplified. These were 2901 base pairs for P_{tac}-*fadD_Ec-acr1a_AsADP1*, 2877 base pairs for P_{tac}-*fadD_Ec-acrM_AsM1*, 3532 base pairs for P_{tac}-*fadD_Ec-Maqu_2220*, 2907 base pairs for P_{tac}-*fadD_Ec-acr1b_AsADP1*, and 3810 base pairs for P_{tac}-*luxCDE*.
To isolate the DNA from the agarose gel, the target gel was cut out of the gel using a scalpel and purified using the *QiaQuick Gel extraction kit* according to the manufacturer's instructions (Qiagen, Hilden). The purified PCR products were cloned into the vector pCDF[alkL] (SEQ ID No. 7) digested with *PspXI* and *NcoI* by means of recombination, using the Geneart® Seamless

Cloning and Assembly Kit according to the manufacturer's instructions (Life Technologies, Carlsbad, CA, USA). Owing to the restriction of the vector, the *alkL* gene is removed therefrom. The transformation of chemically competent *E.coli* DH5α (New England Biolabs, Frankfurt) was performed in a manner known to those skilled in the art. The correct insertion of the target genes was checked by restriction analysis and the authenticity of the introduced genes was verified by DNA sequencing.

The expression vectors hereinafter resulted in this manner:

- pCDF{Ptac}[fadD_Ec-acr1b_AsADP1] (SEQ ID No. 109)
- pCDF{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)] (SEQ ID No. 110)
- pCDF{Ptac}[fadD_Ec-acrM_AsM1] (SEQ ID No. 111)
- pCDF{Ptac}[fadD_Ec-Maqu2220(co_Ec)] (SEQ ID No. 112)
- pCDF{Ptac}[luxCDE_Pl(co_Ec)] (SEQ ID No. 113)

Example 18: Chromatographic quantification of fatty alcohols and fatty aldehydes

Fatty alcohols and fatty aldehydes are quantified by gas chromatography with mass-spectrometric coupling (GC/MS).

To extract the samples consisting of 1 ml of culture broth they are admixed with 500 µl of ethyl acetate (Chromasolv®Plus 99.9%, Sigma No. 650528-1L), shaken for 10 min at 12 Hz and sedimented for 5 min at 13 200 rpm in a bench centrifuge (Eppendorf, Hamburg). The organic phase (ethyl acetate) is transferred to HPLC vials with an insert and analysed for fatty alcohols and fatty aldehydes of differing chain length (C8-C18) by GC/MS coupling.

To separate fatty alcohols and fatty aldehydes, the ZB-50 capillary column having the dimensions 30 m x 320 µm and a film thickness of 0.5 µm (Phenomenex, Aschaffenburg) is used as stationary phase. The carrier gas used is helium at a constant flow rate of 1.5 ml/min. The separation proceeds in the course of 45 min at an injection temperature of 250°C and a detector temperature of 250°C. The column temperature at the start is 40°C and is held for 2 min. Thereafter the column temperature is increased at 7°C/min to 150°C, then at 15°C/min to 320°C and held for 10 min. The injection volume is 1 µl splitless. Detection is performed by means of MS (DSQ II) detector (Thermo Fisher Scientific) with a mass range of 12-800 m/z. The reference substance employed is a standard mixture consisting of in each case 10 µg/ml

1-octanal (99%, Sigma-Aldrich), 1-octanol (Sigma-Aldrich), 1-decanal (>98%, Sigma-Aldrich), 1-decanol (>99%, Sigma-Aldrich), 1-dodecanal (>92%, Sigma-Aldrich), 1-dodecanol (>98%, Sigma-Aldrich), 1-tetradecanal, 1-tetradecanol (>99%, Fluka), 1-hexadecanal and 1-hexadecanol (99%, Sigma-Aldrich) for calibration. Relative quantification of the samples is performed via the peak areas.

Example 19: Production of fatty alcohols by E.coli strains having a deletion in the fadE gene which overexpresses the alkL genes from Pseudomonas putida GPo1 and fatB2 from Cuphea hookeriana or fatB3 from Cocos nucifera and the fadD gene from Escherichia coli and an acyl-ACP reductase gene.

To generate *E.coli* strains having the expression vector for the *alkL* gene from *Pseudomonas putida* GPo1 and the *fadD* gene from *E.coli*, and the genes *acr1a* from *Acinetobacter sp.* ADP1 or *acr1b* from *Acinetobacter sp. ADP1* or *acrM* from *Acinetobacter sp.* M-1 or *Maqu2220* from *Marinobacterium aquaeolei* VT8 or *luxCDE* from *Photorhabdus luminescens* in combination with the expression vector for the *fatB2* gene from *Cuphea hookeriana* and/or *fatB3* from *Cocos nucifera*, electrocompetent cells of *E.coli* W3110 ΔfadE and *E.coli* JW5020-1 Kan^S were prepared. This took place in a manner known to those skilled in the art. *E.coli* JW5020-1 Kan^S is a derivative of *E.coli* JW5020-1 (CGSC, The coli genetic stock center, Yale University, New Haven, USA), this in turn is a *E.coli* BW25113 derivative which bears a deletion of the *fadE* gene. The *fadE* gene was replaced by a kanamycin cassette. This was removed in a manner known to those skilled in the art before the strain was equipped with the expression vectors using a helper plasmid which encodes flp recombinase (see Datsenko K.A. and Wanner B.L. (2000) PNAS 97(12):6640-6645) resulting in strain *E.coli* JW5020-1 Kan^S. *E.coli* JW5020-1 Kan^S was transformed with the plasmids pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 10) in combination with pCDF{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)] (SEQ ID No. 110), pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)] (SEQ ID No. 103), pCDF{Ptac}[fadD_Ec-Maqu2220(co_Ec)] (SEQ ID No. 112) or pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-Maqu2220(co_Ec)] (SEQ ID No. 105) and *E.coli* W3110 ΔfadE with the plasmids pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40) in combination with pCDF{Ptac}[fadD_Ec-acr1b_AsADP1] (SEQ ID No. 109), pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-

acr1b_AsADP1] (SEQ ID No. 102), pCDF{Ptac}[fadD_Ec-acrM_AsM1] (SEQ ID No. 111), pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acrM_AsM1] (SEQ ID No. 104), pCDF{Ptac}[luxCDE_Pl(co_Ec)] (SEQ ID No. 113) or pCDF{Placuv5}[alkL]{Ptac}[luxCDE_Pl(co_Ec)] (SEQ ID No. 106) and plated out on LB-agar plates containing spectinomycin (100 µg/ml) and ampicillin (100 µg/ml). Transformants were checked for the presence of the correct plasmids by plasmid preparation and analytical restriction analysis.

In this manner the *E. coli* strains hereinafter were generated:

- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Ptac}[fadD_Ec-Maqu2220(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-Maqu2220(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[fadD_Ec-acrM_AsM1]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[alkL][fadD_Ec-acrM_AsM1]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[fadD_Ec-acr1b_AsADP1]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1b_AsADP1]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[luxCDE_Pl(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Placuv5}[alkL]{Ptac}[luxCDE_Pl(co_Ec)]

These strains were used to study their ability to produce fatty alcohols. The following procedure was adopted here:

The strains are subjected to a multistage aerobic culturing process. The strains under investigation were first initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) containing 100 µg/ml of ampicillin and 100 µg/ml of spectinomycin as a 5 ml preliminary culture in each case from a single colony. The next culturing step proceeded in M9 medium. The medium consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution were adjusted to a pH of 7.4 with 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) was sterile-filtered before addition to the M9 medium. 10 ml of M9 medium were charged into a 100 ml conical flask with chicane with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin and inoculated with 0.5 ml from the preliminary culture. The culturing proceeded at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin were charged into a 250 ml conical flask with chicane and inoculated with the 10 ml culture, in such a manner that an optical density (600 nm) of 0.2 is achieved. Culturing proceeded at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, the gene expression is induced by adding 1 mM IPTG. The strains were cultured for a further 24 hours at 30°C and 200 rpm. During culturing, samples are withdrawn and the concentration of fatty alcohols of differing carbon chain lengths is quantified as described in Example 18. The results are shown in the table hereinafter.

Production of fatty alcohols using *E.coli* JW5020-1 Kan^S and *E.coli* W3110 ΔfadE which overexpress a plant acyl-ACP thioesterase, *fadD* from *E.coli* and also a fatty acyl-CoA reductase. Strains with and without overexpression of *alkL* from *P.putida* GPo1 are shown. The

concentrations of fatty alcohols of differing carbon chain length are reported after culturing for 24 hours (n.d. = not detectable):

	Decanol [Peak area/OD]	Dodecanol [Peak area/OD]	Tetradecanol [Peak area/OD]	Hexadecanol [Peak area/OD]
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[fadD_Ec-acrM_AsM1(co_Ec)]	n.d.	2.53E+06	9.74E+06	1.39E+07
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acrM_AsM1(co_Ec)]	n.d.	1.15E+07	2.90E+07	3.01E+07
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[luxCDE_Pl(co_Ec)]	n.d.	1.42E+06	6.91E+06	n.d.
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Placuv5}[alkL]{Ptac}[luxCDE_Pl(co_Ec)]	n.d.	3.78E+06	1.77E+07	n.d.
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Ptac}[fadD_Ec-acr1b_AsADP1)]	n.d.	2.43E+04	1.59E+06	n.d.
E.coli W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1b_AsADP1)]	n.d.	8.65E+05	2.44E+06	n.d.
E.coli JW5020-1 Kan^S pJ294{Ptac}[Ptac-ChFATB2_optEc] / pCDF{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)]	4.65E+06	n.d.	3.49E+06	5.63E+06
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-acr1a_AsADP1(co_Ec)]	1.61E+07	n.d.	4.23E+07	3.45E+07
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Ptac}[fadD_Ec-Maqu2220_Ma(co_Ec)]	n.d.	n.d.	5.66E+04.	7.12E+04.
E.coli JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF{Placuv5}[alkL]{Ptac}[fadD_Ec-Maqu2220_Ma(co_Ec)]	n.d.	n.d.	6.74E+07	2.48E+08

It was thus shown that strains which overexpress *alkL* from *P.putida* are able to form more decanol, dodecanol, tetradecanol and hexadecanol than strains without *alkL*. This shows that reinforcement of *alkL* is necessary for producing fatty alcohols of various chain lengths from unrelated carbon sources.

Example 20: Preparation of an expression vector for the Mmar_3356 gene from Mycobacterium marinum

To produce an expression vector for the *Mmar_3356* gene (SEQ ID No. 114) from *Mycobacterium marinum*, the gene was codon-optimized for expression in *E.coli*. The synthesized gene for the SAM-dependent methyltransferase (E_{va}) was amplified with introduction of an *NdeI* cleavage site upstream and an *XbaI* cleavage site downstream. The restriction cleavage sites were introduced via the oligonucleotides used.

mt_fw_NdeI: 5'- TATATACATATGCCAAGAGAGATTAGATTACC-3' (SEQ ID No.119)
mt_rv_XbaI: 5'- TATATATCTAGACTGAGTTAGGCACGTTTCG-3' (SEQ ID No. 120)

The following parameters were used for the PCR: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:10 min, annealing, 62°C, 0:20 min; elongation, 72°C, 0:30 min; 1 x: terminal elongation, 72°C, 10 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification in accordance with the manufacturer's recommendations. 50 µl of the PCR reactions were then separated in each case on a 1.5% strength TAE-agarose gel. The PCR, the agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in a manner known to those skilled in the art.
The PCR fragment having the expected size of 1133 base pairs was able to be amplified. To isolate the DNA from the agarose gel, the target DNA was cut out of the gel using a scalpel and purified using the *QiaQuick Gel extraction kit* in accordance with the manufacturer's instructions (Qiagen, Hilden). The purified PCR product was digested using the restriction endonucleases *NdeI* and *XbaI* and was ligated into an appropriately cut pJ281 derivative (SEQ ID No. 121) which contains a *lacuv5* promotor. The transformation of chemically competent *E.coli* DH5α (New England Biolabs, Frankfurt) proceeded according to a manner known to those skilled in the art. Correct insertion of the target genes was checked by restriction analysis and the authenticity of the introduced genes was validated by DNA sequencing. The completed *E.coli* expression vector was termed pJ281{Placuv5}[Mmar_3356(co_Ec)] (SEQ ID No. 116).

Example 21: Production of fatty acid esters by E.col strains with a deletion in the fadE gene which overexpress a plant acyl-ACP thioesterase gene, the alkL genes from Pseudomonas putida GPo1 and Mmar_3356 from Mycobacterium marinum.

To generate an *E.coli* strain having expression vectors for the genes *fatB1* from *Cuphea hookeriana*, *fatB2* from *Cuphea hookeriana*, *fatB3* from *Cocos nucifera* or *synUcTE* from *Umbellularia californica* in combination with an expression vector for the *Mmar_3356* gene from *Mycobacterium marinum* and an expression vector for the *alkL* gene from *Pseudomonas putida GPo1*, electrocompetent cells of *E. coli* JW5020-1 Kan^S and *E.coli* W3110 ΔfadE are produced. This proceeded in a manner are known to those skilled in the art. The strains are transformed sequentially with the vectors pJ294[Ptac-ChFATB1_optEc] (SEQ ID No. 12), pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 10), pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40) and/or pJ294[Ptac-synUcTE] (SEQ ID No. 41) and pJ281{Placuv5}[Mmar_3356(co_Ec)] (SEQ ID No. 116) and pCDF[alkL] (SEQ ID No. 7) and/or pCDFDuet-1 (71340-3, Merck, Darmstadt) and plated onto LB-agar plates containing ampicillin (100 µg/ml), kanamycin (50 µg/ml) and spectinomycin (100 µg/ml). Transformants are checked by plasmid preparation and analytical restriction analysis with respect to the presence of the correct plasmids. In this manner the strains hereinafter were constructed:

- *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL]
- *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDFDuet-1
- *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL]
- *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDFDuet-1
- *E. coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL]

- *E. coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDFDuet-1
- *E. coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL]
- *E. coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDFDuet-1

These strains are used to study their ability to produce fatty acid methyl esters from glucose. The following procedure is adopted here:

The strains are subjected to a multistage aerobic culturing process. The strains under investigation are first initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) containing 50 µg/ml of kanamycin, 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin as 5 ml preliminary culture from a single colony in each case. The next culture step proceeds in M9 medium. The medium, consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution, is adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) is sterile-filtered before addition to the M9 medium. 10 ml of M9 medium are charged together with 50 µg/ml kanamycin, 100 µg/ml spectinomycin and 100 µg/ml ampicillin into a 100 ml conical flask with chicane and inoculated with 0.5 ml of the preliminary culture. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 50 µg/ml of kanamycin, 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are charged in a 250 ml conical flask with chicane and inoculated with the 10 ml culture in such a manner that an optical density (600 nm) of 0.2 is achieved. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is reached, the gene expression is induced by adding 1 mM IPTG. The strains are cultured for at least a further

24 hours at 30°C and 200 rpm. During the culturing, samples are withdrawn and the concentration of fatty acid methyl esters of differing carbon chain lengths is quantified as described in Example 15. It is shown that the strains *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL], *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL], *E. coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] and *E. coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] are able, depending on the specificity of the overexpressed acyl-CoA thioesterase gene, to form fatty acid methyl esters of different carbon chain length and degree of saturation compared with the corresponding strains which do not overexpress the *alkL* gene. In particular, *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] can produce more fatty acid methyl esters of chain length C14:0, C16:0 and C16:1, *E. coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] can produce more fatty acid methyl esters of chain length C8:0 and C10:0, *E. coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] can produce more fatty acid methyl esters of chain length C12:0, C14:0 and C16:1 and *E. coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pJ281{Placuv5}[Mmar_3356(co_Ec)] / pCDF[alkL] can produce more fatty acid methyl esters of chain length C12:0 and C14:0 from glucose than the corresponding strains which lack the *alkL* gene from *Pseudomonas putida* GPo1.

Example 22: Preparation of an expression vector for the coexpression of the genes MSMEG_2956 from Mycobacterium smegmatis, npt from Nocardia sp. with alkL from Pseudomonas putida

To prepare a *E. coli* expression vector for the genes *MSMEG_2956* (SEQ ID No. 117) from *Mycobacterium smegmatis, npt* (SEQ ID No: 122) from *Nocardia sp.* and *alkL* (SEQ ID No. 1) from *Pseudomonas putida* GPo1, the genes *MSMEG_2956* and *npt* are codon-optimized for expression in *Escherichia coli* and synthesized. The synthesized genes are cloned as an operon following a *lacuv5* promoter using recombination cloning. *MSMEG_2956* and *npt* are amplified starting from the synthetic DNA as a matrix and the promoter P_{lacuv5} from a pJ294

derivative with introduction of homologous regions for recombination cloning. The oligonucleotides hereinafter are used here:

Promoter region P_{lacuv5}:
NP-FA-P22: 5'-CCGGTAGTCAATAAAATCGCACCTGGTGTTTAAACG-3' (SEQ ID No. 126)
NP-FA-P23: 5'-TGTCATATGCCACTCTCCTTGGTTCC-3' (SEQ ID No. 127)

MSMEG_2956(co_Ec) and npt_Noc(co_Ec):
NP-FA-P24: 5'-GAGTGGCATATGACAATTGAAACGCGCGAAG-3' (SEQ ID No. 128)
NP-FA-P25: 5'-TCTATTGCTGGTTTACCTAGGTTATCATTATCATGC-3' (SEQ ID No. 129)

The following parameters are used for the PCR: 1x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:15 min, annealing, 60°C, 0:30 min; elongation, 72°C, 0:20 min; 1 x: terminal elongation, 72°C, 10 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) is used for the amplification in accordance with the manufacturer's recommendations. 50 µl of the PCR reactions in each case are then separated on a 1% strength TAE agarose gel and cut out from the agarose gel and purified. The PCR, agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes and purification of the DNA fragments are carried out in a manner known to those skilled in the art. PCR fragments of 210 base pairs for the *lacuv5* promoter region and 4241 base pairs for the DNA fragment *MSMEG_2956(co_Ec)-npt_Noc(co_Ec)* are expected. The purified PCR fragments are cloned into the restriction endonuclease-*AgeI*-digested vector pCDF[alkL] (SEQ ID No. 7) and pCDFDuet-1 (71340-3, Merck, Darmstadt) by means of recombination and using the Geneart ® Seamless Cloning and Assembly Kit in accordance with the manufacturer's instructions (life Technologies, Carlsbad, CA, USA). This generates the vectors pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 124) and pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 125). Chemically competent *E.coli* DH10β is transformed in a manner known to those skilled in the art. Correct insertion of the target genes is checked by restriction analysis and the authenticity of the insert is validated by DNA sequencing.

Example 23: Production of fatty aldehydes and fatty alcohols by E.coli strains with a deletion in the fadE gene which overexpress a plant acyl-ACP thioesterase gene, the genes alkL from Pseudomonas putida GPo1 and MSMEG_2956 from Mycobacterium smegmatis and npt from Nocardia sp.

To generate *E.coli* strains having expression vectors for the genes *fatB1* from *Cuphea hookeriana*, *fatB2* from *Cuphea hookeriana*, *fatB3* from *Cocos nucifera* or *synUcTE* from *Umbellularia californica* in combination with an expression vector for the genes MSMEG_2956 from *Mycobacterium smegmatis*, *npt* from *Nocardia sp.* and *alkL* from *Pseudomonas putida GPo1* electrocompetent cells of *E. coli* JW5020-1 Kan^S and *E.coli* W3110 ΔfadE are prepared. This is performed in a manner known to those skilled in the art. The strains are transformed with the vectors pJ294[Ptac-ChFATB1_optEc] (SEQ ID No. 12), pJ294[Ptac-ChFATB2_optEc] (SEQ ID No. 11), pJ294{Ptac}[CnFATB3(co_Ec)] (SEQ ID No. 40) and/or pJ294[Ptac-synUcTE] (SEQ ID No. 41) and pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 124) and/or pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 128) and plated onto LB-agar plates containing ampicillin (100 µg/ml) and spectinomycin (100 µg/ml). Transformants are checked with respect to the presence of the correct plasmids by plasmid preparation and analytical restriction analysis. The strains hereinafter are constructed in this manner:

- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]

- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]

These strains are employed to study their ability to produce fatty alcohols and fatty aldehydes from glucose. The following procedure is adopted here:
The strains are subjected to a multistage aerobic culturing process. The strains under investigation are initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) containing 100 µg/ml of ampicillin and 100 µg/ml of spectinomycin as a 5 ml preliminary culture from a single colony in each case. The next culturing step proceeds in M9 medium. The medium, consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution, is adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) is sterile-filtered before addition to the M9 medium. 10 ml of M9 medium are charged with 100 µg/ml spectinomycin and 100 µg/ml ampicillin into 100 ml conical flasks with chicane and inoculated with 0.5 ml of the preliminary culture. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium are charged with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin in a 250 ml conical flask with chicane and inoculated with the 10 ml culture in such a manner that an optical density (600 nm) of 0.2 is achieved. The culturing proceeds at 37°C and

200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, the gene expression is induced by adding 1 mM IPTG. The strains are cultured for at least a further 24 hours at 30°C and 200 rpm. During the culturing, samples are withdrawn and the concentration of fatty alcohols and fatty aldehydes of different carbon chain lengths is quantified as described in Example 18. It is shown that the strains *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] , *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)], *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)], *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] and *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] are able, depending on the specificity of the overexpressed acyl-CoA thioesterase gene, to form fatty alcohols and fatty aldehydes of differing carbon chain length and differing degree of saturation compared to the corresponding strains which do not overexpress the gene *alkL*. In particular, *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more fatty alcohols and fatty aldehydes of chain length C14:0, C16:0 and C16:1, *E.coli* JW5020-1 Kan^S pJ294[Ptac-ChFATB2_optEc] /pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more fatty alcohols and fatty aldehydes of chain length C8:0 and C10:0, *E.coli* JW5020-1 Kan^S pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more fatty alcohols and fatty aldehydes of chain length C12:0, C14:0 and C16:1, *E.coli* W3110 ΔfadE pJ294{Ptac}[CnFATB3(co_Ec)] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more fatty alcohols and fatty aldehydes of chain length C12:0, C14:0 and C16:1 and *E.coli* W3110 ΔfadE pJ294[Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more fatty alcohols and fatty aldehydes of chain length C12:0 and C14:0, than the corresponding strains which lack the gene *alkL* from *Pseudomonas putida* GPo1.

Example 24: Preparation of expression vectors for the coexpression of an acyl-ACP thioesterase gene, ald from Bacillus subtilis and Cv_2025 from Chromobacterium violaceum.

To produce *E. coli* expression vectors for the genes *fatB1* (SEQ ID No. 9) from *Cuphea hookeriana*, *fatB2* (SEQ ID No. 8) from *Cuphea hookeriana* and *synUcTE* (SEQ ID No. 37) from *Umbellularia californica* (in each case encoding an enzyme E_i) and *ald* (SEQ ID No. 130) from *Bacillus subtilis* (encoding an enzyme E_{xiv}) and *Cv_2025* (SEQ ID No. 132) from *Chromobacterium violaceum* (encoding an enzyme E_{xiii}), the genes *fatB1, fatB2* and *synUcTE* are codon-optimized for expression in *Escherichia coli* and synthesized together with a *tac* promotor (SEQ ID No. 39). During the synthesis, a cleavage site is introduced upstream of the promoter and a cleavage site is introduced downstream of the terminator. The synthesized DNA fragments are digested with the restriction endonucleases *BamH*I and *Not*I and ligated into the correspondingly cut vector pJ294_alaDH_B.s._TA_C.v.(Ct) (SEQ ID No. 121). The expression vector used here has already been described in German patent application DE102011110946 and recorded there under SEQ ID No. 17. The completed vectors are named pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] (SEQ ID No. 134), pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] (SEQ ID No. 135) and pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] (SEQ ID No. 136).

Example 25: Production of alkylamines by E.coli strains having a deletion in the fadE gene which overexpress an acyl-CoA thioesterase gene, the genes Cv_2025 from Chromobacterium violaceum and ald from Bacillus subtilis, alkL from Pseudomonas putida GPo1, carA from Mycobacterium smegmatis and npt from Nocardia sp.

To generate *E.coli* strains having expression vectors for the genes *ald* from *Bacillus subtilis*, *Cv_2025* from *Chromobacterium violaceum* and *fatB1* from *Cuphea hookeriana*, *fatB2* from *Cuphea hookeriana*, *synUcTE* from *Umbellularia californica* in combination with an expression vector for the genes MSMEG_2956 from *Mycobacterium smegmatis*, *npt* from *Nocardia sp.* and *alkL* from *Pseudomonas putida GPo1*, electrocompetent cells of *E. coli* JW5020-1 Kan^S and *E.coli* W3110 ΔfadE are prepared. This takes place in a manner known to those skilled in the art. The strains are transformed with the vectors pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] (SEQ ID No. 134), pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] (SEQ ID No. 135) and/or pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] (SEQ ID No. 136) in combination with pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 124) and/or

pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] (SEQ ID No. 125) and plated onto LB-agar plates containing ampicillin (100 µg/ml) and spectinomycin (100 µg/ml). Transformants are checked with regard to the presence of the correct plasmids via plasmid preparation and analytical restriction analysis. The strains hereinafter are constructed in this manner:

- *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]
- *E.coli* W3110 ΔfadE pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] / pCDF[MSMEG_2956(co_Ec)-npt_Noc(co_Ec)]

These strains are employed to study their ability to produce alkylamines and glucose. The following procedure is adopted here:

The strains are subjected to a multistage aerobic culturing process. The strains under investigation are initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) containing 100 µg/ml of ampicillin and 100 µg/ml of spectinomycin as 5 ml preliminary culture each from an individual colony. The next culturing step proceeds in M9 medium. The medium consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution is adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III),

4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) is sterile-filtered before addition to the M9 medium. 10 ml of M9 medium are charged with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin in 100 ml conical flask with chicane and inoculated with 0.5 ml of the preliminary culture. Culturing proceeds at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are charged in a 250 ml conical flask with chicane and inoculated with the 10 ml culture, in such a manner that an optical density (600 nm) of 0.2 is achieved. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, the gene expression is induced by addition of 1 mM IPTG. The strains are cultured for at least a further 24 hours at 30°C and 200 rpm. During the culturing, samples are withdrawn and the concentration of fatty aldehydes of differing carbon chain lengths is quantified. It is shown that the strains *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)], *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] and *E.coli* W3110 ΔfadE pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] are able, depending on the specificity of the overexpressed alkyl-CoA thioesterase gene, to form alkylamines of differing carbon chain length and differing degree of saturation in comparison with the corresponding strains which do not overexpress the *alkL* gene. In particular, *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB1_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more alkylamines of chain length C14:0, C16:0 and C16:1, *E.coli* JW5020-1 Kan^S pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-ChFATB2_optEc] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more alkylamines of chain length C8:0 and C10:0 and *E.coli* W3110 ΔfadE pJ294[alaDH_B.s._TA_C.v.(Ct)_Ptac-synUcTE] / pCDF[alkL][MSMEG_2956(co_Ec)-npt_Noc(co_Ec)] can produce from glucose more alkylamines of chain length C12:0 and C14:0 than the corresponding strains which lack the gene *alkL* from *Pseudomonas putida* GPo1.

Example 26: Preparation of E. coli expression vectors for the expression of various acyl-CoA reductases for preparation of fatty alcohols and fatty aldehydes

The gene *Maqu_2220* (SEQ ID No. 137) from *Marinobacter aquaeolei* VT8 or *Maqu_2507* (SEQ ID No. 139) from *Marinobacter aquaeolei* VT8 or *AtFAR6* (SEQ ID No. 141) from *Arabidopsis thaliana* or *AcrM* (SEQ ID No. 143) from *Acinetobacter sp.* M-1 or *Acr1a* (SEQ ID No. 145) from *Acinetobacter sp.* ADP1 or *Acr1b* (SEQ ID No. 147) from *Acinetobacter sp.* ADP1 (in each case encoding an enzyme E_x) was cloned into a pJ294 derivative (DNA2.0 Inc., Menlo Park, CA, USA) following the P_{lac} promotor (SEQ ID No. 149) via the cleavage sites *Nde*I and *Not*I.

The genes *Maqu_2220*, *Maqu_2507*, *AtFAR6*, *AcrM* and *Acr1a* are codon-optimized sequences for *E-coli*. The *Acr1b* gene is the wild type sequence. All codon-optimizations were carried out by DNA2.0 (DNA2.0 Inc., Menlo Park, Ca, USA). The DNA sequences were held in a vector specific to DNA2.0.

The genes *Maqu_2220*, *Maqu_2507*, *AtFAR6* and *AcrM* were amplified using the polymerase chain reaction (PCR), while introducing the restriction cleavage sites *Nde*I (at the 5' end of the respective gene) and *Not*I (at the 3' end of the respective gene) as described hereinafter. The matrices used were the vectors from DNA2.0 (DNA2.0 Inc., Menlo Park, CA, USA) pJ221[Maqu_2220(co_ec)], pJ207[Maqu_2507(co_Ec)], pJ201[AtFAR6(co_Ec)] and pJ221[AcrM(AsM1)].

The oligonucleotides hereinafter were used in the PCR solutions:

Gene	**Primer**	**Sequence (5' => 3')**	**Seq ID NO.**
Maqu_2220	Pr-DesFA-1-FW	TATATACATATGGCAATTCAGCAGGTACATCACG	*150*
	Pr-DesFA-1-RV	TATATAGCGGCCGCTCATTACGCGGCCTTTTTGC	*151*
Maqu_2507	Pr-DesFA-2-FW	TATATACATATGAACTATTTTCTTACAGGCGGTACAGG	*152*
	Pr-DesFA-2-RV	TATATAGCGGCCGCTTATTACCAGTAAATACCACGCATAATTGC	*153*
AtFAR6	Pr-DesFA-3-FW	TATATACATATGGCGACGACGAATGTACTGGC	*154*
	Pr-DesFA-3-RV	TATATAGCGGCCGCTTATTACTCGGTTTTCTTCTTGCTCAGG	*155*
AcrM	Pr-DesFA-5-FW	TATATACATATGAATGCAAAACTCAAAAAACTTTTTCAGC	*156*
	Pr-DesFA-5-RV	TATATAGCGGCCGCTTATTACCAGTGTTCGCCTGGG	*157*

The following parameters were used for the PCRs: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:30 min, annealing, 50°C (*Maqu_2220*) / 60°C (*Maqu_2507, AcrM, AtFAR6*), 0:20 min; elongation, 72°C, 0:35 min; 1 x: terminal elongation, 72°C, 5 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification in accordance with the manufacturer's recommendations. 50 µl of the PCR reactions in each case were then separated on a 1% strength agarose gel. The PCR, the agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes was carried out in the manner known to those skilled in the art.

The genes *Acr1a and Acr1b* from *Acinetobacter sp.* ADP1 were cloned via in-vitro cloning using the "GeneArt® Seamless Cloning and Assembly Kit" (Cat.No. A13288, Life Technologies GmbH, Darmstadt) in accordance with the manufacturer's instructions. For this purpose, both genes were amplified by PCR, while introducing homologous regions for recombination cloning. The matrices used were the DNA2.0 vector pJ221[Acr1a_AsADP1(co_Ec)] and the vector pCDF{Ptac}[fadD_Ec-acr1b_AsADP1] (SEQ ID No. 109).

The oligonucleotides hereinafter were used in the PCR solutions:

Gene	Primer	Sequence (5' => 3')	Seq ID NO.
Acr1a	Pr-FA_4.1-FW	AACAGGAGGTAAAACATTGATCTCGATCCGTGAAAAACGT	158
	Pr-FA_4.1-RV	TGAAGTGGGGGCGGCCTTATCACCAGTGCTCACCCGGGAA	159
Acr1b	Pr-DesFA_4.2-FW	AACAGGAGGTAAAACAGTGAACAAAAAACTTGAAGCTCTC	160
	Pr-DesFA_4.2-RV	TGAAGTGGGGGCGGCCTTATTACCAGTGTTCGCCTGGGAA	161

The following parameters were used for the PCRs: 1 x: initial denaturation, 98°C, 0:30 min; 35 x: denaturation, 98°C, 0:30 min, annealing, 64°C, 0:20 min; elongation, 72°C, 0:15 min; 1 x: terminal elongation, 72°C, 5 min. The Phusion™ High-Fidelity Master Mix from New England Biolabs (Frankfurt) was used for the amplification in accordance with the manufacturer's

recommendations. 50 µl of the PCR reactions in each case were then separated on a 1% strength agarose gel. The PCR, the agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the PCR fragment sizes were carried out in the manner known to those skilled in the art.

In all cases, PCR fragments of the expected size were able to be amplified. These were 1568 base pairs (bp) for *Maqu_2220*, 2012 bp for *Maqu_2507*, 1673 bp for *AtFAR6*, 914 bp for *AcrM*, 947 bp for *Acr1a* and 923 base pairs for *Acr1b* 923.

To isolate the DNA from an agarose gel, the target DNA was cut out of the gel using a scalpel and purified using the "Quick Gel Extraction Kit" from Qiagen (Hilden). The procedure was carried out according to the manufacturer's instructions.

In the next step, the PCR products of *Maqu_2220*, *Maqu_2507*, *AtFAR6* and *AcrM*, just like the pJ294 derivate (DNA2.0 Inc., Menlo Park, CA, USA), were cut using the restriction enzymes *Nde*I and *Not*I (New England Biolabs, Frankfurt) in accordance with the manufacturer's instructions. The cut vector was then applied to a 1% strength agarose gel. The agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the fragment sizes were carried out in the manner known to those skilled in the art. To isolate the DNA from an agarose gel, the target DNA was cut out from the gel using a scalpel and purified with the "Quick Gel Extraction Kit" from Qiagen (Hilden). The procedure was carried out according to the manufacturer's instructions. The *Nde*I-*Not*I-cut PCR amplificates *Maqu_2220*, *Maqu_2507*, *AtFAR6* and *AcrM* were then ligated in each case with the *Nde*I-*Not*I-cut vector via the T4 DNA ligase (New England Biolabs, Frankfurt) in accordance with the manufacturer's instructions, obtaining the resultant vectors.

The PCR products of *Acr1a* and *Acr1b* from *Acinetobacter sp.* ADP1 were recombined together with the *NdeI*-*Not*I-cut pJ294 derivative using *in-vitro* cloning, using the "GeneArt® Seamless Cloning and Assembly Kit" (Cat.No. A13288, Life Technologies GmbH, Darmstadt), obtaining the resulting vectors. The use corresponded to the manufacturer's recommendations.

The vector pJ294 is a *E. coli* expression vector which imparts an ampicillin resistance to the organism, and bears a p15A replication origin. Upstream of the cleavage site *Nde*I there is a P_{lac} promotor. The transformation of chemically competent *E. coli* DH5α cells (New England Biolabs, Frankfurt) proceeded in the manner known to those skilled in the art.

The correctness of the respective plasmid was controlled by restriction analysis using *Nru*I. The authenticity of the inserted fragments was checked by DNA sequencing.

The completed *E. coli* expression vectors were named as follows:

Vector name	Vector	Gene	SEQ ID No.
pHg-12-58	pJ294	*Maqu_2220*	162
pHg-12-59	pJ294	*Maqu_2507*	163
pHg-12-60	pJ294	*AtFAR6*	164
pHg-12-61	pJ294	*AcrM*	165
pHg-12-62	pJ294	*Acr1a*	166
pHg-12-63	pJ294	*Acr1b*	167

Example 27: Production of fatty alcohols and fatty aldehydes by E.coli strains having a deletion in the fadE gene and expression vectors for the genes Maqu_2220 from Marinobacter aquaeolei VT8, Maqu_2507 from Marinobacter aquaeolei VT8, AtFAR6 from Arabidopsis thaliana, AcrM from Acinetobacter sp. M-1, Acr1 from Acinetobacter sp. ADP1 or Acr1 from Acinetobacter calcoaceticus in combination with an expression vector for the alkL gene from Pseudomonas putida.

First, a *E.coli* W3110 strain having a deletion in the *fadE* gene is produced as described in Example 4.

To generate *E.coli* strains having the expression vector for the *alkL* gene from *Pseudomonas putida* GPo1 in combination with the expression vector for the *Maqu_2220* gene from *Marinobacter aquaeolei* VT8 or *Maqu_2507 from Marinobacter aquaeolei* VT8 or *AtFAR6 from Arabidopsis thaliana* or *AcrM* from *Acinetobacter sp.* M-1 or *Acr1* from *Acinetobacter sp.* ADP1 or *Acr1* from *Acinetobacter calcoaceticus*, electrocompetent cells of *E. coli* W3110 Δ*fadE* and *E. coli* JW5020-1 Kan^{s} were prepared. This proceeds in a manner known to those skilled in the art. The host strain *E. coli* JW5020-1 Kan^{S} is a descendant of the *E. coli* JW5020-1 (CSGC, The coli genetic stock center, Yale University, New Haven, USA) and is a *E. coli* BW25113 derivative which carries a deletion of the *fadE* gene. The *fadE* gene was replaced by a kanamycin cassette. It was removed in a manner known to those skilled in the art (see Datsenko K.A. and Wanner B.L. (2000) PNAS 97(12):6640-6645) before the strain is equipped with the expression vectors using a helper plasmid which encodes the Flp recombinase, resulting in strain *E. coli* JW5020-1 Kan^{S}.

The competent cells were transformed with the plasmids pCDFDuet-1 or pCDF[alkL] in combination with pHg-12-58 or pHg-12-59 or pHg-12-60 or pHg-12-61 or pHg-12-62 or pHg-12-63 and plated out on LB plates containing spectinomycin (100 µg/ml) and ampicillin (100 µg/ml). Transformants were examined with respect to the presence of the correct plasmids via plasmid preparation and analytical restriction analysis.

In this manner the *E. coli* strains hereinafter were generated:

- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-58
- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-59
- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-60
- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-61
- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-62
- *E.coli* W3110 *ΔfadE* pCDF[alkL] / pHg-12-63

- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-58
- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-59
- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-60
- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-61
- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-62
- *E.coli* W3110 *ΔfadE* pCDFDuet-1 / pHg-12-63

- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-58
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-59
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-60
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-61
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-62
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDF[alkL] / pHg-12-63

- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDFDuet-1 / pHg-12-58
- *E. coli* JW5020-1 Kan^{s} *ΔfadE* pCDFDuet-1 / pHg-12-59

- *E. coli* JW5020-1 Kan^s *ΔfadE* pCDFDuet-1 / pHg-12-60
- *E. coli* JW5020-1 Kan^s *ΔfadE* pCDFDuet-1 / pHg-12-61
- *E. coli* JW5020-1 Kan^s *ΔfadE* pCDFDuet-1 / pHg-12-62
- *E. coli* JW5020-1 Kan^s *ΔfadE* pCDFDuet-1 / pHg-12-63

These strains are employed to investigate their ability to produce fatty alcohols and fatty aldehydes from glucose. The following procedure is followed here:
The strains are subjected to a multistage aerobic culturing process. The strains under examination are initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) as a 5 ml preliminary culture from an individual colony in each case. The next culturing step proceeds in M9 medium. The medium consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution is adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1 M hydrochloric acid (all substances from Merck, Darmstadt) is sterile-filtered before addition to the M9 medium. 10 ml of M9 medium are charged with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin into 100 ml conical flasks with chicane and inoculated with 0.5 ml of the preliminary culture. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are charged in a 250 ml conical flask with chicane and inoculated with the 10 ml culture in such a manner that an optical density (600 nm) of 0.2 is achieved. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. When an optical density (600 nm) of 0.6 to 0.8 is achieved, the gene expression is induced by adding 1 mM of IPTG. The strains are cultured for a further 48 hours at 30°C and 200 rpm in an incubating shaker. During the culturing, samples of 1 ml are withdrawn and the concentration of fatty alcohols and fatty aldehydes of differing carbon chain lengths is quantified using the method described in Example 18. It is shown that the strains *E.coli* W3110 *ΔfadE*

pCDF[alkL]/pHg-12-58, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-59, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-60, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-61, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-62, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-63 and the strains *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-58, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-59, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-60, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-61, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-62 and *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-63 can produce a higher titre of fatty alcohols and fatty aldehydes of differing chain length from glucose than the strains which lack the gene *alkL* from *Pseudomonas putida* GPo1. In particular, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-58 can produce more fatty alcohols and fatty aldehydes of chain length C14:0, C16:0 and C16:1, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-59 can produce more fatty alcohols and fatty aldehydes of chain length C14:0, C16:0 and C16:1, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-60 can produce more fatty alcohols and fatty aldehydes of chain length C16:0 and C16:1, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-61 can produce more fatty alcohols and fatty aldehydes of chain length C8:0 and C10:0, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-62 can produce more fatty alcohols and fatty aldehydes of chain length C12:0 and C14:0, *E.coli* W3110 *ΔfadE* pCDF[alkL]/pHg-12-63 can produce more fatty alcohols and fatty aldehydes of chain length C12:0 and C14:0, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-58 can produce more fatty alcohols and fatty aldehydes of chain length C14:0, C16:0 and C16:1, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-59 can produce more fatty alcohols and fatty aldehydes of chain length C14:0, C16:0 and C16:1, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-60 can produce more fatty alcohols and fatty aldehydes of chain length C16:0 and C16:1, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-61 can produce more fatty alcohols and fatty aldehydes of chain length C8:0 and C10:0, *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-62 can produce more fatty alcohols and fatty aldehydes of chain length C12:0 and C14:0 and *E. coli* JW5020-1 Kan^s *ΔfadE* pCDF[alkL]/pHg-12-63 can produce more fatty alcohols and fatty aldehydes of chain length C12:0 and C14:0 from glucose than the corresponding strains which lack the gene *alkL* from *Pseudomonas putida* GPo1.

Example 28: Preparation of E. coli *expression vectors for the gene oleT$_{JE}$ from Jeotgalicoccus sp. ATCC 8456 for preparation of alkenes*

For the preparation of expression vectors, the sequence of the gene *oleT*$_{JE}$ (SEQ ID No. 168) from *Jeotgalicoccus sp.* ATCC 8456 (encoding an enzyme E_{xi}) was codon-optimized for expression in *E.coli* with DNA2.0 (DNA2.0 Inc., Menlo Park, CA, USA) and synthesized in combination with the P_{lac} promotor (SEQ ID No. 149) or the P_{lac} promotor and the *alkL* gene (SEQ ID No. 1). The cloning of the constructs P_{lac}-*oleT*$_{JE}$ (SEQ ID No. 170) and P_{lac}-*oleT*$_{JE}$-*alkL* (SEQ ID No. 171) proceeded in vectors specific to DNA2.0. Both constructs are terminated by a terminator sequence (SEQ ID No. 172). In addition, a cleavage site (*Eco*NI or *Not*I) was introduced upstream of the P_{lac} promotor and downstream of the terminator in each case.

The synthesized DNA fragments P_{lac}-*oleT*$_{JE}$ and P_{lac}-*oleT*$_{JE}$–*alkL* and the vector pCDFDuet-1 (Merck, Darmstadt) (SEQ ID No 53) were cut with the restriction endonucleases *Eco*NI and *Not*I (New England Biolabs, Frankfurt) in accordance with the manufacturer's instructions. The *Nde*I-*Not*I-cut constructs and the cut vector were then applied to a 1% strength agarose gel. The agarose gel electrophoresis, ethidium bromide staining of the DNA and determination of the fragment sizes was carried out in the manner known to those skilled in the art. For isolation of the DNA from an agarose gel, the target DNA was cut out from the gel with a scalpel and purified using the "Quick Gel Extraction Kit" from Qiagen (Hilden). The procedure was in accordance with the manufacturer's instructions.

Subsequently, the fragment P_{lac}-*oleT*$_{JE}$ or P_{lac}-*oleT*$_{JE}$–*alkL* carried out was ligated into the vector pCDFDuet-1 vector via the T4 DNA ligase (New England Biolabs, Frankfurt) in accordance with the manufacturer's instructions, obtaining the resultant vectors.

The vector pCDFDuet-1 is an *E. coli* vector which imparts a spectinomycin/streptomycin resistance to the organism, and also carries a ColDF13 replication origin. The transformations of chemically competent *E. coli* DH5α cells (New England Biolabs, Frankfurt) proceeded in the manner known to those skilled in the art.

The correctness of the respective plasmid was controlled by restriction analysis with *Eco*RV. The authenticity of the inserted fragments was checked by DNA sequencing.

The completed *E.coli* expression vectors were named pHg-12-66 (pCDF[P_{lac}-*oleT*$_{JE}$]; SEQ ID No 173) and pHg-12-67 (pCDF[P_{lac}-*oleT*$_{JE}$–*alkL*]; SEQ ID No 174).

Example 29: Production of alkenes by E.coli strains having a deletion in the fadE gene and expression vectors for the genes fatB1 from Cuphea hookeriana, fatB2 from Cuphea hookeriana, fatB3 from Cocos nucifera, synUcTE from Umbellularia californica in combination with expression vectors for the gene oleT$_{JE}$ from Jeotgalicoccus sp. ATCC 8456 and alkL from Pseudomonas putida.

First, an *E.coli* W3110 strain having a deletion in the *fadE* gene is prepared as described in Example 4.

To generate *E.coli* strains having the expression vectors for the genes *fatB1* from *Cuphea palustris* or *fatB2* from *Cuphea palustris* or *fatB3* from *Cocos nucifera* or *synUcTE* from *Umbellularia californica* in combination with the expression vectors for the gene *oleT*$_{JE}$ from *Jeotgalicoccus* sp. ATCC 8456 or the genes *oleT*$_{JE}$ from *Jeotgalicoccus* sp. ATCC 8456 and *alkL* from *Pseudomonas putida*, electrocompetent cells of *E. coli* W3110 Δ*fadE* and *E. coli* JW5020-1 Kan^S are prepared. This proceeds in a manner known to those skilled in the art. The host strain *E. coli* JW5020-1 Kan^S is a descendant of *E. coli* JW5020-1 (CSGC, The coli genetic stock center, Yale University, New Haven, USA) and is an *E. coli* BW25113 derivative which carries a deletion of the *fadE* gene. The *fadE* gene was replaced by a kanamycin cassette. This was removed in a manner known to those skilled in the art (see Datsenko K.A. and Wanner B.L. (2000) PNAS 97(12):6640-6645) before equipping the strain with the expression vectors using a helper plasmid which encodes the Flp recombinase, resulting in strain *E. coli* JW5020-1 Kan^S.

The competent cells were transformed using the plasmids pJ294[Ptac-ChFATB1_optEc] or pJ294[Ptac-ChFATB2_optEc] or pJ294{Ptac}[CnFATB3(co_Ec)] or pJ294[Ptac-synUcTE] in combination with pHg-12-66 or pHg-12-67 and plated onto LB plates containing ampicillin (100 µg/ml) and spectinomycin (100 µg/ml). Transformants were checked with respect to the presence of the correct plasmids by plasmid preparation and analytical restriction analysis.

In this manner the *E. coli* strains hereinafter were generated:

- *E.coli* W3110 Δ*fadE* pJ294[Ptac-ChFATB1_optEc] / pHg-12-66
- *E.coli* W3110 Δ*fadE* pJ294[Ptac-ChFATB1_optEc] / pHg-12-67
- *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB1_optEc] / pHg-12-66
- *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB1_optEc] / pHg-12-67

- *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB2_optEc] / pHg-12-66
- *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB2_optEc] / pHg-12-67
- *E. coli* JW5020-1 Kan^s pJ294[Ptac-CnFATB3_optEc] / pHg-12-66
- *E. coli* JW5020-1 Kan^s pJ294[Ptac-CnFATB3_optEc] / pHg-12-67
- *E.coli* W3110 *ΔfadE* pJ294[Ptac-synUcTE] / pHg-12-66
- *E.coli* W3110 *ΔfadE* pJ294[Ptac-synUcTE] / pHg-12-67

These strains are employed in order to investigate their ability to produce alkenes via the production of fatty acids from glucose. The following procedure is used:

The strains are subjected to a multistage aerobic culturing process. The strains under examination are initially grown in Luria-Bertani Bouillon according to Miller (Merck, Darmstadt) as a 5 ml preliminary culture each from a single colony. The next culturing step proceeds in M9 medium. The medium consisting of 38 mM disodium hydrogenphosphate dihydrate, 22 mM potassium dihydrogenphosphate, 8.6 mM sodium chloride, 37 mM ammonium chloride, 2% (w/v) glucose, 2 mM magnesium sulphate heptahydrate (all substances from Merck, Darmstadt) and 0.1% (v/v) trace element solution is adjusted to a pH of 7.4 using 25% strength ammonium hydroxide solution. The added trace element solution consisting of 9.7 mM manganese(II) chloride tetrahydrate, 6.5 mM zinc sulphate heptahydrate, 2.5 mM sodium EDTA (Titriplex III), 4.9 mM boric acid, 1 mM sodium molybdate dihydrate, 32 mM calcium chloride dihydrate, 64 mM iron(II) sulphate heptahydrate and 0.9 mM copper(II) chloride dihydrate dissolved in 1M hydrochloric acid (all substances from Merck, Darmstadt) is sterile-filtered before addition to the M9 medium. 10 ml of M9 medium are charged with 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin into 100 ml conical flasks having chicane and inoculated with 0.5 ml from the preliminary culture. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. After a culturing time of 8 hours, 50 ml of M9 medium containing 100 µg/ml of spectinomycin and 100 µg/ml of ampicillin are charged in a 250 ml conical flask with chicane and inoculated with the 10 ml culture in such a manner that an optical density (600 nm) of 0.2 is achieved. The culturing proceeds at 37°C and 200 rpm in an incubating shaker. On reaching an optical density (600 nm) of 0.6 to 0.8, the gene expression is induced by addition of 1 mM IPTG. The strains are cultured for a further 48 hours at 30°C and 200 rpm in an incubating shaker. During the culturing, samples of 1 ml are withdrawn and the concentration of free fatty acids and alkenes of

differing carbon chain lengths are quantified using the method described in Example 30. It is shown that the strains *E.coli* W3110 *ΔfadE* pJ294[Ptac-ChFATB1_optEc]/pHg-12-67, *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB1_optEc]/pHg-12-67, *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB2_optEc]/pHg-12-67, *E. coli* JW5020-1 Kan^s pJ294[Ptac-CnFATB3_optEc]/pHg-12-67 and *E.coli* W3110 *ΔfadE* pJ294[Ptac-synUcTE]/pHg-12-67 can produce higher titres of alkenes of different chain length from glucose than the strains which lack the gene *alkL* from *Pseudomonas putida* GPo1. In particular *E.coli* W3110 *ΔfadE* pJ294[Ptac-ChFATB1_optEc]/pHg-12-67 can produce more 1-alkenes of chain length C13 and C15 and also 1,8-dienes of chain length C15, *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB1_optEc]/pHg-12-67 can produce more 1-alkenes of chain length C13 and C15 and also 1,8-dienes of chain length C15, *E. coli* JW5020-1 Kan^s pJ294[Ptac-ChFATB2_optEc]/pHg-12-67 can produce more 1-alkenes of chain length C7 and C9, *E. coli* JW5020-1 Kan^s pJ294[Ptac-CnFATB3_optEc]/pHg-12-67 can produce more 1-alkenes of chain length C11 and C13 and also 1,8-dienes of chain length C15 and *E.coli* W3110 *ΔfadE* pJ294[Ptac-synUcTE]/pHg-12-67 can produce more 1-alkenes of chain length C11 and C13 from glucose than the corresponding strains which lack the gene *alkL* from *Pseudomonas putida* GPo1.

Example 30: Chromatographic quantification of alkenes

Alkenes are quantified by means of gas chromatography with coupled mass spectrometry (GC/MS).

To extract the samples, consisting of 1 ml of culture broth, they are admixed with 500 µl of ethyl acetate (Chromasolv®Plus 99.9%, Sigma No. 650528-1L), shaken for 10 min at 12 Hz and sedimented for 5 min at 13 200 rpm in a bench centrifuge (Eppendorf, Hamburg). The organic phase (ethyl acetate) is transferred to HPLC vials with an insert and analysed by means of coupled GC/MS for alkenes of differing chain length (C8-C18).

For separation of alkenes, the capillary column ZB-50 having the dimensions 30 m x 320 µm and a film thickness of 0.5 µm (Phenomenex, Aschaffenburg) is used as stationary phase. The carrier gas used is helium at a constant flow rate of 1.5 ml/min. The separation proceeds in the course of 45 min at an injector temperature of 250°C and a detector temperature of 250°C. The column temperature at the start is 40°C and is held for 2 min. Subsequently, the column

temperature is raised at 7°C/min to 150°C, then raised at 15°C/min to 320°C and held for 10 min. The injection volume is 1 µl splitless. The detection proceeds by means of an MS (DSQ II) detector (Thermo Fisher Scientific) with a mass range of 12-800 m/z (0-8 min SIM at m/z 55.97). The reference substance employed for the alkenes is a standard mixture consisting of in each case 10 µg/ml 1-octene (Sigma-Aldrich), 1-decene (94%, Sigma-Aldrich), 1-dodecene (>99%, Sigma-Aldrich), 1-tetradecene (>97%, Sigma-Aldrich), 1-hexadecene (99.9%, Sigma-Aldrich), 1-octadecene (Sigma-Aldrich), for calibration. Relative quantification of the samples is performed via the peak areas.

Patent Claims

1. Microorganism which includes a first genetic modification so that it is capable of forming more organic substance from at least one simple carbon source in comparison with its wild type,
characterized in that
the microorganism includes a second genetic modification so that it forms more alkL gene product in comparison with its wild type.

2. Microorganism according to Claim 1, characterized in that the organic substance is selected from the group comprising
carboxylic acids, in particular having 3 to 34 carbon atoms,
carboxylic acid esters, in particular having 3 to 34 carbon atoms in the carboxylic acid moiety, in which the alcohol component is derived from methanol, ethanol or other primary alcohols having 3-18 carbon atoms
alkanes having 3 to 34 carbon atoms,
alkenes having 3 to 34 carbon atoms,
monohydric alcohols having 3 to 34 carbon atoms,
aldehydes having 3 to 34 carbon atoms,
monovalent amines having 3 to 34 carbon atoms,
and substituted compounds of the above group members, in particular those which carry, as further substituents, one or more hydroxyl, amine, keto, carboxyl, methyl, ethyl, cyclopropyl or epoxy functions.

3. Microorganism according to Claim 1 or 2, characterized in that the organic substance is selected from the group of the fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alkanes and alkenes, in particular 1-alkenes.

4. Microorganism according to at least one of the preceding claims, characterized in that the alkL gene product is encoded by alkL genes from Gram-negative bacteria, in particular from the group comprising, preferably consisting of, *Pseudomonas* sp., *Azotobacter* sp., *Desulfitobacterium* sp., *Burkholderia* sp., preferably *Burkholderia cepacia*, *Xanthomonas*

sp., *Rhodobacter* sp., *Ralstonia* sp., *Delftia* sp. and *Rickettsia* sp., *Oceanicaulis* sp., *Caulobacter* sp., *Marinobacter* sp. and *Rhodopseudomonas* sp., preferably *Pseudomonas putida*, *Oceanicaulis alexandrii*, *Marinobacter aquaeolei*, in particular *Pseudomonas putida* GPo1 and P1, *Oceanicaulis alexandrii* HTCC2633, *Caulobacter* sp. K31 and *Marinobacter aquaeolei* VT8.

5. Microorganism according to at least one of the preceding claims, characterized in that the alkL gene product is selected from the group consisting of
proteins encoded by SEQ ID No. 1 and SEQ ID No. 3 and
proteins with the polypeptide sequence SEQ ID No. 2, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32 and SEQ ID No. 33 and
proteins with a polypeptide sequence in which up to 60% of the amino acid residues are modified over SEQ ID No. 2, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33 by deletion, insertion, substitution or a combination thereof and which still have at least 50% of the activity of the protein with the respective reference sequence SEQ ID No. 2, No. 30, SEQ ID No. 31, SEQ ID No. 32 or SEQ ID No. 33.

6. Microorganism according to at least one of the preceding claims, characterized in that it is selected from the group of the Gram-negative bacteria.

7. Microorganism according to at least one of the preceding claims, characterized in that the first genetic modification is an activity of at least one of the enzymes selected from the group
E_i acyl-ACP thioesterase, preferably of EC 3.1.2.14 or EC 3.1.2.22,
E_{ii} acyl-CoA thioesterase, preferably of EC 3.1.2.2, EC 3.1.2.18, EC 3.1.2.19, EC 3.1.2.20 or EC 3.1.2.22,
E_{iib} acyl-CoA:ACP transacylase,
E_{iii} polyketide synthase, which catalyses a reaction which is involved in the synthesis of carboxylic acids and carboxylic acid esters, and
E_{iv} hexanoic acid synthase,
which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

8. Microorganism according to at least one of the preceding claims, characterized in that it includes a third genetic modification which comprises an activity of at least one of the enzymes E_{iib}, E_v, E_{vi} or E_{vii} selected from the group

E_{iib} acyl-CoA:ACP transacylase,

E_v wax ester synthase or alcohol O-acyl transferase, preferably of EC 2.3.1.75 or EC 2.3.1.84,

E_{va} fatty acid-O-methyltransferase, preferably of the EC 2.1.1.15, which catalyses the synthesis of a fatty acid methyl ester from a fatty acid and S-adenosylmethionine,

E_{vi} acyl-CoA synthetase, preferably of EC 6.2.1.3, and

E_{vii} acyl thioesterase, preferably of EC 3.1.2.2, EC 3.1.2.4, EC 3.1.2.18, EC 3.1.2.19, EC 3.1.2.20 or EC 3.1.2.22,

which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

9. Microorganism according to at least one of the preceding claims, characterized in that it includes a fourth genetic modification which comprises an activity of at least one of the enzymes E_{iib}, E_v, E_{vi} or E_{vii} selected from the group

E_{iib} acyl-CoA:ACP transacylase,

E_{vi} acyl-CoA synthetase, preferably of EC 6.2.1.3,

E_{viii} acyl-CoA reductase, preferably of EC 1.2.1.42 or EC 1.2.1.50,

E_{ix} fatty acid reductase, preferably of EC 1.2.1.3, EC 1.2.1.20 or EC 1.2.1.48,

E_x acyl-ACP reductase, preferably of EC 1.2.1.80,

E_{xi} cytochrome P450 fatty acid decarboxylase, which catalyses the conversion of an alkanoic acid with n carbon atoms into a corresponding terminal olefin with n-1 carbon atoms, in particular of dodecanoic acid to undec-10-enoic acid,

E_{xii} alkan-1-al decarbonylase, which catalyses the conversion of an alkan-1-al (n carbon atoms) into a corresponding alkane (n-1 carbon atoms) or terminal olefin (n-1 carbon atoms, and

E_{xiii} alkan-1-al transaminase, which catalyses the conversion of an alkan-1-al into a corresponding alkan-1-amine,

which is increased in comparison with the enzymatic activity of the wild type of the microorganism.

10. Microorganism according to at least one of the preceding claims, characterized in that it includes, besides the first and second genetic modification, a fifth genetic modification which includes an activity of at least one of the enzymes selected from the group

E_a acyl-CoA synthetase (EC 6.2.1.3), which catalyses the synthesis of an acyl-coenzyme A thioester,

E_b acyl-CoA dehydrogenase (EC 1.3.99.-, EC 1.3.99.3 or EC 1.3.99.13), which catalyses the oxidation of an acyl-coenzyme A thioester to give the corresponding enoyl-coenzyme A thioester,

E_c acyl-CoA oxidase (EC 1.3.3.6), which catalyses the oxidation of an acyl-coenzyme A thioester to give the corresponding enoyl-coenzyme A thioester,

E_d enoyl-CoA hydratase (EC 4.2.1.17 or EC 4.2.1.74), which catalyses the hydratization of an enoyl-coenzyme A thioester to give the corresponding 3-hydroxyacyl-coenzyme A thioester,

E_f 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35 or EC 1.1.1.211), which catalyses the oxidation of a 3-hydroxyacyl-coenzyme A thioester to give the corresponding 3-oxoacyl-coenzyme A thioester, and

E_g acetyl-CoA acyltransferase (EC 2.3.1.16), which catalyses the transfer of an acetyl residue from a 3-oxoacyl-coenzyme A thioester to coenzymes A and thus generates an acyl-coenzyme A thioester which is shortened by two carbon atoms,

which is reduced in comparison with the enzymatic activity of the wild type of the microorganism.

11. Microorganism according to at least one of the preceding claims, characterized in that it includes a seventh genetic modification comprising an activity of at least one enzyme E_1 selected from the group

E_1 P450 alkane hydroxylases,

E_{1b} AlkB alkane hydroxylases of EC 1.14.15.3,

E_{1c} fatty alcohol oxidases of EC 1.1.3.20,

E_{1d} AlkJ alcohol dehydrogenases of EC 1.1.99.-,

E_{1e} alcohol dehydrogenase of EC 1.1.1.1 or EC 1.1.1.2 and

E_{1f} aldehyde dehydrogenases of EC 1.2.1.3, EC 1.2.1.4 or EC 1.2.1.5

which is reduced in comparison with its wild type.

12. Use of a microorganism according to at least one of the preceding claims for the production of organic substances, in particular of fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alken-1-als, alken-1-ols, alken-1-amines, alkanes and alkenes, in particular 1-alkenes, which may optionally include a further double bond.

13. Process for the production of an organic substance, preferably fatty acids, fatty acid esters, alkan-1-als, alkan-1-ols and alkan-1-amines, alken-1-als, alken-1-ols, alken-1-amines, alkanes and alkenes, in particular 1-alkenes, which may optionally include a further double bond, from a simple carbon source comprising the process steps

I) bringing a microorganism according to at least one of Claims 1 to 8 into contact with a medium comprising the simple carbon source,

II) culturing the microorganism under conditions which make it possible for the microorganism to form the organic substance from the simple carbon source, and

III) if appropriate, isolation of the organic substance formed.

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Ile Ser Ala Leu Gly Arg Val Ser Glu Val Asp Tyr Gly Pro Ala Ile
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Leu Ser Leu Gln Tyr His Phe Asp Asn Phe Glu Arg Leu Tyr Pro Tyr
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Val Gly Leu Gly Val Gly Arg Val Phe Phe Phe Asp Lys Thr Asp Gly
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Ala Leu Thr Ser Phe Asp Ile Lys Asp Lys Trp Ala Pro Ala Val Gln
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Ala Asp Phe Asp Leu Lys Asp Ala Trp Ala Pro Ala Val Gln Val Gly
165 170 175

Met Arg Tyr Gln Met Ser Asp Asn Trp Phe Ala Asn Ala Asp Ile Arg
180 185 190

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

Val Arg Gly Lys Ile Ser Val Asp Pro Thr Ile Leu Asn Ile Gly Ile
210 215 220

Ala Tyr Arg Phe
225

<210> 33
<211> 227
<212> PRT
<213> Caulobacter sp. K31

<400> 33

Met Arg Lys Asn Gly Ala Tyr Met Tyr Ala Arg Leu Ala Gln Tyr Ala
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Thr Ala Leu Ala Val Leu Ser Val Phe Pro Gln Ala Ala Leu Ala Gln
20 25 30

Asn Ser Glu Gly Phe Lys Leu Trp Ala Val Ser Leu Asn Ala Thr Arg
35 40 45

Val Phe Val Asp Glu Asp Ala Pro Asp Ile Thr Leu Ala Gly Gly Pro
50 55 60

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

Asp Ile Gly Tyr Phe Phe Thr Pro Asn Val Ala Gly Asn Leu Phe Leu
85 90 95

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

Leu Gly Thr Leu Ala Lys Val Asn Tyr Gly Pro Ile Ile Leu Ser Ala
115 120 125

Gln Tyr His Phe Asn Asn Leu Gly Lys Val His Pro Tyr Leu Gly Val
130 135 140

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

Asn Phe Ser Ile Asp Asp Ser Trp Ala Pro Ala Ala Gln Val Gly Val
165 170 175

Arg Tyr Glu Leu Gly Ala Glu Trp Met Leu Asn Ala Asp Val Arg Tyr
180 185 190

Val Pro Phe Ser Thr His Ala Thr Gly Ser Leu Gly Gly Ala Pro Val
195 200 205

Arg Thr Arg Leu Asp Ile Asp Pro Ile Leu Thr Ser Ala Gly Val Thr
210 215 220

Tyr Arg Phe
225

<210> 34
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter

<400> 34
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cactttatgc ttccggctcg tataatgtgt ggaattgtga gcggataaca at 112

<210> 35
<211> 984
<212> DNA
<213> Cocos nucifera

<220>
<221> CDS
<222> (1)..(984)

<400> 35

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Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile Arg Thr Ile Phe Ser
1               5                  10                  15

gca gcc gaa aaa cag tgg acc ctg ctg gat agc aag aaa cgc ggt gcg          96
Ala Ala Glu Lys Gln Trp Thr Leu Leu Asp Ser Lys Lys Arg Gly Ala
            20                  25                  30

gat gca gtt gcg gac gcg tct ggc gtg ggc aag atg gtg aaa aac ggt         144
Asp Ala Val Ala Asp Ala Ser Gly Val Gly Lys Met Val Lys Asn Gly
        35                  40                  45

ctg gtc tac cgt cag aat ttc agc atc cgt agc tat gag att ggt gtg         192
Leu Val Tyr Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Val
    50                  55                  60

gac aag cgt gcg agc gtt gag gct ctg atg aat cat ttt caa gaa acg         240
Asp Lys Arg Ala Ser Val Glu Ala Leu Met Asn His Phe Gln Glu Thr
65                  70                  75                  80

agc ttg aat cac tgc aaa tgc atc ggt ctg atg cat ggc ggt ttt ggt         288
Ser Leu Asn His Cys Lys Cys Ile Gly Leu Met His Gly Gly Phe Gly
                85                  90                  95

tgc acc ccg gaa atg acg cgt cgt aat ctg atc tgg gtc gtt gcc aag         336
Cys Thr Pro Glu Met Thr Arg Arg Asn Leu Ile Trp Val Val Ala Lys
            100                 105                 110

atg ctg gtt cac gtg gag cgt tat ccg tgg tgg ggt gac gta gtg cag         384
Met Leu Val His Val Glu Arg Tyr Pro Trp Trp Gly Asp Val Val Gln
        115                 120                 125

att aac acc tgg att agc agc agc ggt aag aac ggc atg ggt cgc gac         432
Ile Asn Thr Trp Ile Ser Ser Ser Gly Lys Asn Gly Met Gly Arg Asp
    130                 135                 140

tgg cac gtg cac gac tgt cag acg ggc ctg ccg att atg cgt ggc acc         480
Trp His Val His Asp Cys Gln Thr Gly Leu Pro Ile Met Arg Gly Thr
145                 150                 155                 160

tct gtg tgg gtc atg atg gat aaa cac act cgc cgt ctg agc aag ctg         528
Ser Val Trp Val Met Met Asp Lys His Thr Arg Arg Leu Ser Lys Leu
                165                 170                 175

ccg gaa gag gtt cgc gca gaa atc acc ccg ttc ttc agc gaa cgc gac         576
Pro Glu Glu Val Arg Ala Glu Ile Thr Pro Phe Phe Ser Glu Arg Asp
            180                 185                 190

gcg gtc ctg gat gat aac ggc cgt aaa ctg ccg aaa ttt gac gat gat         624
Ala Val Leu Asp Asp Asn Gly Arg Lys Leu Pro Lys Phe Asp Asp Asp
        195                 200                 205

agc gcg gca cac gtc cgc cgt ggt ttg acc cct cgt tgg cat gat ttc         672
Ser Ala Ala His Val Arg Arg Gly Leu Thr Pro Arg Trp His Asp Phe
    210                 215                 220

gac gtc aat cag cat gtc aac aac gtg aaa tac gtc ggt tgg att ctg         720
Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Val Gly Trp Ile Leu
225                 230                 235                 240

gag agc gtt ccg gtt tgg atg ctg gac ggt tac gag gtt gcc act atg         768
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Glu Ser Val Pro Val Trp Met Leu Asp Gly Tyr Glu Val Ala Thr Met
                245                 250                 255

tct ctg gaa tat cgt cgc gag tgt cgt atg gat agc gtg gtt cag tcc        816
Ser Leu Glu Tyr Arg Arg Glu Cys Arg Met Asp Ser Val Val Gln Ser
            260                 265                 270

ctg acc gcg gtt agc tcg gat cac gcg gac ggc agc ccg atc gtt tgt        864
Leu Thr Ala Val Ser Ser Asp His Ala Asp Gly Ser Pro Ile Val Cys
        275                 280                 285

caa cac ctg ctg cgc ctg gaa gat ggt acg gag atc gtg cgt ggt caa        912
Gln His Leu Leu Arg Leu Glu Asp Gly Thr Glu Ile Val Arg Gly Gln
    290                 295                 300

acc gag tgg cgt ccg aag caa caa gca cgc gac ctg ggc aat atg ggt        960
Thr Glu Trp Arg Pro Lys Gln Gln Ala Arg Asp Leu Gly Asn Met Gly
305                 310                 315                 320

ttg cat ccg acc gag tcc aag taa                                      984
Leu His Pro Thr Glu Ser Lys
                325
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<210> 36
<211> 327
<212> PRT
<213> Cocos nucifera

<400> 36

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Leu Pro Asp Trp Ser Met Leu Leu Ala Ala Ile Arg Thr Ile Phe Ser
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Ala Ala Glu Lys Gln Trp Thr Leu Leu Asp Ser Lys Lys Arg Gly Ala
            20                  25                  30

Asp Ala Val Ala Asp Ala Ser Gly Val Gly Lys Met Val Lys Asn Gly
        35                  40                  45

Leu Val Tyr Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Val
    50                  55                  60

Asp Lys Arg Ala Ser Val Glu Ala Leu Met Asn His Phe Gln Glu Thr
65                  70                  75                  80

Ser Leu Asn His Cys Lys Cys Ile Gly Leu Met His Gly Gly Phe Gly
                85                  90                  95

Cys Thr Pro Glu Met Thr Arg Arg Asn Leu Ile Trp Val Val Ala Lys
            100                 105                 110

Met Leu Val His Val Glu Arg Tyr Pro Trp Trp Gly Asp Val Val Gln
        115                 120                 125

Ile Asn Thr Trp Ile Ser Ser Ser Gly Lys Asn Gly Met Gly Arg Asp
    130                 135                 140

Trp His Val His Asp Cys Gln Thr Gly Leu Pro Ile Met Arg Gly Thr
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145 150 155 160

Ser Val Trp Val Met Met Asp Lys His Thr Arg Arg Leu Ser Lys Leu
165 170 175

Pro Glu Glu Val Arg Ala Glu Ile Thr Pro Phe Phe Ser Glu Arg Asp
180 185 190

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

Ser Ala Ala His Val Arg Arg Gly Leu Thr Pro Arg Trp His Asp Phe
210 215 220

Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Val Gly Trp Ile Leu
225 230 235 240

Glu Ser Val Pro Val Trp Met Leu Asp Gly Tyr Glu Val Ala Thr Met
245 250 255

Ser Leu Glu Tyr Arg Arg Glu Cys Arg Met Asp Ser Val Val Gln Ser
260 265 270

Leu Thr Ala Val Ser Ser Asp His Ala Asp Gly Ser Pro Ile Val Cys
275 280 285

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

Thr Glu Trp Arg Pro Lys Gln Gln Ala Arg Asp Leu Gly Asn Met Gly
305 310 315 320

Leu His Pro Thr Glu Ser Lys
325

<210> 37
<211> 906
<212> DNA
<213> Umbellularia californica

<220>
<221> CDS
<222> (1)..(906)

<400> 37
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Met Thr Leu Glu Trp Lys Pro Lys Pro Lys Leu Pro Gln Leu Leu Asp
1 5 10 15

gat cac ttc ggt ctg cac ggt ctg gtg ttt cgt cgt act ttc gca att 96
Asp His Phe Gly Leu His Gly Leu Val Phe Arg Arg Thr Phe Ala Ile
20 25 30

cgt tct tat gaa gtg ggt cca gat cgt tct acc tcc atc ctg gcc gtc 144
Arg Ser Tyr Glu Val Gly Pro Asp Arg Ser Thr Ser Ile Leu Ala Val

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        35                  40                  45

atg aac cac atg cag gaa gcc acc ctg aat cac gcg aaa tct gtt ggt        192
Met Asn His Met Gln Glu Ala Thr Leu Asn His Ala Lys Ser Val Gly
    50                  55                  60

atc ctg ggt gat ggt ttc ggc act act ctg gaa atg tct aaa cgt gac        240
Ile Leu Gly Asp Gly Phe Gly Thr Thr Leu Glu Met Ser Lys Arg Asp
65                  70                  75                  80

ctg atg tgg gta gtg cgt cgc acc cac gta gca gta gag cgc tac cct        288
Leu Met Trp Val Val Arg Arg Thr His Val Ala Val Glu Arg Tyr Pro
                85                  90                  95

act tgg ggt gac act gtg gaa gtc gag tgt tgg att ggc gcg tcc ggt        336
Thr Trp Gly Asp Thr Val Glu Val Glu Cys Trp Ile Gly Ala Ser Gly
            100                 105                 110

aac aat ggt atg cgt cgc gat ttt ctg gtc cgt gac tgt aaa acg ggc        384
Asn Asn Gly Met Arg Arg Asp Phe Leu Val Arg Asp Cys Lys Thr Gly
        115                 120                 125

gaa atc ctg acg cgt tgc acc tcc ctg agc gtt ctg atg aac acc cgc        432
Glu Ile Leu Thr Arg Cys Thr Ser Leu Ser Val Leu Met Asn Thr Arg
    130                 135                 140

act cgt cgc ctg tct acc atc ccg gac gaa gtg cgc ggt gag atc ggt        480
Thr Arg Arg Leu Ser Thr Ile Pro Asp Glu Val Arg Gly Glu Ile Gly
145                 150                 155                 160

cct gct ttc atc gat aac gtg gca gtt aaa gac gac gaa atc aag aaa        528
Pro Ala Phe Ile Asp Asn Val Ala Val Lys Asp Asp Glu Ile Lys Lys
                165                 170                 175

ctg caa aaa ctg aac gac tcc acc gcg gac tac atc cag ggc ggt ctg        576
Leu Gln Lys Leu Asn Asp Ser Thr Ala Asp Tyr Ile Gln Gly Gly Leu
            180                 185                 190

act ccg cgc tgg aac gac ctg gat gtt aat cag cat gtg aac aac ctg        624
Thr Pro Arg Trp Asn Asp Leu Asp Val Asn Gln His Val Asn Asn Leu
        195                 200                 205

aaa tac gtt gct tgg gtc ttc gag act gtg ccg gac agc att ttc gaa        672
Lys Tyr Val Ala Trp Val Phe Glu Thr Val Pro Asp Ser Ile Phe Glu
    210                 215                 220

agc cat cac att tcc tct ttt act ctg gag tac cgt cgc gaa tgt act        720
Ser His His Ile Ser Ser Phe Thr Leu Glu Tyr Arg Arg Glu Cys Thr
225                 230                 235                 240

cgc gac tcc gtt ctg cgc agc ctg acc acc gta agc ggc ggt tct agc        768
Arg Asp Ser Val Leu Arg Ser Leu Thr Thr Val Ser Gly Gly Ser Ser
                245                 250                 255

gag gca ggt ctg gtc tgc gac cat ctg ctg caa ctg gaa ggc ggc tcc        816
Glu Ala Gly Leu Val Cys Asp His Leu Leu Gln Leu Glu Gly Gly Ser
            260                 265                 270

gaa gtc ctg cgt gcg cgt acg gag tgg cgt cca aag ctg acg gat tct        864
Glu Val Leu Arg Ala Arg Thr Glu Trp Arg Pro Lys Leu Thr Asp Ser
        275                 280                 285

ttc cgc ggc atc tcc gta att ccg gcg gaa cct cgt gtt taa                906
Phe Arg Gly Ile Ser Val Ile Pro Ala Glu Pro Arg Val
    290                 295                 300
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<210> 38

<211> 301
<212> PRT
<213> Umbellularia californica

<400> 38

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Met Thr Leu Glu Trp Lys Pro Lys Pro Lys Leu Pro Gln Leu Leu Asp
1               5                  10                  15

Asp His Phe Gly Leu His Gly Leu Val Phe Arg Arg Thr Phe Ala Ile
            20                  25                  30

Arg Ser Tyr Glu Val Gly Pro Asp Arg Ser Thr Ser Ile Leu Ala Val
        35                  40                  45

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

Ile Leu Gly Asp Gly Phe Gly Thr Thr Leu Glu Met Ser Lys Arg Asp
65                  70                  75                  80

Leu Met Trp Val Val Arg Arg Thr His Val Ala Val Glu Arg Tyr Pro
                85                  90                  95

Thr Trp Gly Asp Thr Val Glu Val Glu Cys Trp Ile Gly Ala Ser Gly
            100                 105                 110

Asn Asn Gly Met Arg Arg Asp Phe Leu Val Arg Asp Cys Lys Thr Gly
        115                 120                 125

Glu Ile Leu Thr Arg Cys Thr Ser Leu Ser Val Leu Met Asn Thr Arg
    130                 135                 140

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

Pro Ala Phe Ile Asp Asn Val Ala Val Lys Asp Asp Glu Ile Lys Lys
                165                 170                 175

Leu Gln Lys Leu Asn Asp Ser Thr Ala Asp Tyr Ile Gln Gly Gly Leu
            180                 185                 190

Thr Pro Arg Trp Asn Asp Leu Asp Val Asn Gln His Val Asn Asn Leu
        195                 200                 205

Lys Tyr Val Ala Trp Val Phe Glu Thr Val Pro Asp Ser Ile Phe Glu
    210                 215                 220

Ser His His Ile Ser Ser Phe Thr Leu Glu Tyr Arg Arg Glu Cys Thr
225                 230                 235                 240

Arg Asp Ser Val Leu Arg Ser Leu Thr Thr Val Ser Gly Gly Ser Ser
                245                 250                 255
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Glu Ala Gly Leu Val Cys Asp His Leu Leu Gln Leu Glu Gly Gly Ser
260 265 270

Glu Val Leu Arg Ala Arg Thr Glu Trp Arg Pro Lys Leu Thr Asp Ser
275 280 285

Phe Arg Gly Ile Ser Val Ile Pro Ala Glu Pro Arg Val
290 295 300

<210> 39
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> promoter

<400> 39
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caattaatca tcggctcgta taatgtgtgg atgtggaatt gtgagcgctc acaattccac 120

aacggtttcc ctctagaaat aattttgttt aacaggagg 159

<210> 40
<211> 4961
<212> DNA
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<220>
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gcgctgcgat gataccgcga gaaccacgct caccggctcc ggatttatca gcaataaacc 180

agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 240

ctattaattg ttgccgggaa gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg 300

ttgttgccat cgctacaggc atcgtggtgt cacgctcgtc gtttggtatg gcttcattca 360

gctccggttc ccaacgatca aggcgagtta catgatcccc catgttgtgc aaaaaagcgg 420

ttagctcctt cggtcctccg atcgttgtca gaagtaagtt ggccgcagtg ttatcactca 480

tggttatggc agcactgcat aattctctta ctgtcatgcc atccgtaaga tgcttttctg 540

tgactggtga gtactcaacc aagtcattct gagaatagtg tatgcggcga ccgagttgct 600

cttgcccggc gtcaatacgg gataataccg cgccacatag cagaacttta aaagtgctca 660

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gttcgatgta acccactcgt gcacccaact gatcttcagc atcttttact ttcaccagcg 780

tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa aaagggaata agggcgacac 840

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attgtctcat gagcggatac atatttgaat gtatttagaa aaataaacaa ataggggtca 960

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gttcagtccg accgctgcgc cttatccggt aactatcgtc ttgagtccaa cccggaaaga 3540

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tcatcttatt aatcactgcc cgctttccag tcgggaaacc tgtcgtgcca gctgcattaa 3840

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tttcaccagt gagactggca acagctgatt gcccttcacc gcctggccct gagagagttg 3960

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cagctccgcc atcgccgctt ccacttttтc ccgcgttttc gcagaaacgt ggctggcctg 4800

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<211> 4977
<212> DNA
<213> Artificial Sequence

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<223> vector

<400> 41
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gcgctgcgat gataccgcga gaaccacgct caccggctcc ggatttatca gcaataaacc 180

agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 240

ctattaattg ttgccgggaa gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg 300

ttgttgccat cgctacaggc atcgtggtgt cacgctcgtc gtttggtatg gcttcattca 360

gctccggttc ccaacgatca aggcgagtta catgatcccc catgttgtgc aaaaaagcgg 420

ttagctcctt cggtcctccg atcgttgtca gaagtaagtt ggccgcagtg ttatcactca 480

tggttatggc agcactgcat aattctctta ctgtcatgcc atccgtaaga tgcttttctg 540

tgactggtga gtactcaacc aagtcattct gagaatagtg tatgcggcga ccgagttgct 600

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<210> 42
<211> 690
<212> DNA
<213> Oceanocaulis alexandrii

<220>
<221> CDS
<222> (1)..(690)

<400> 42

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atg aaa caa tct aat gta aaa tcc aag ggg cct ttt gcc tcg aag ttt        48
Met Lys Gln Ser Asn Val Lys Ser Lys Gly Pro Phe Ala Ser Lys Phe
1               5                  10                  15

gtg tta atc acg atg atc ggt ggc ttt tcg tcg ttc agc gtc gca aat        96
Val Leu Ile Thr Met Ile Gly Gly Phe Ser Ser Phe Ser Val Ala Asn
            20                  25                  30

gcg gaa ccg ctt tac tcc aag ggc gac tgg ctt ttt ggc ctg aat gcg       144
Ala Glu Pro Leu Tyr Ser Lys Gly Asp Trp Leu Phe Gly Leu Asn Ala
        35                  40                  45

gcg aaa gta ttc acg aac gaa acg ttg gat tca atc agc gcg ggc ggt       192
Ala Lys Val Phe Thr Asn Glu Thr Leu Asp Ser Ile Ser Ala Gly Gly
    50                  55                  60
```

```
gcg cca ata ccc ggg gct ggt gtc aat atc acc gat gac acc acg ctg        240
Ala Pro Ile Pro Gly Ala Gly Val Asn Ile Thr Asp Asp Thr Thr Leu
65                  70                  75                  80

agt ttc gac gtt tcc tat ttt ttg aat tca tct gta gcg ttg aac ttc        288
Ser Phe Asp Val Ser Tyr Phe Leu Asn Ser Ser Val Ala Leu Asn Phe
                85                  90                  95

ttt ggt ggt ttg cct gcc agc gct aat ctt gca ggg agc ggc agt ttg        336
Phe Gly Gly Leu Pro Ala Ser Ala Asn Leu Ala Gly Ser Gly Ser Leu
            100                 105                 110

gca gga ctg cct gtt gga gag acg gaa tat ggc cct gct gtt ttg tcg        384
Ala Gly Leu Pro Val Gly Glu Thr Glu Tyr Gly Pro Ala Val Leu Ser
        115                 120                 125

ctt caa tat cac ttt tcg act aat tca tcc gtt agc cct tat gtt ggt        432
Leu Gln Tyr His Phe Ser Thr Asn Ser Ser Val Ser Pro Tyr Val Gly
    130                 135                 140

gcc ggt atc gct cga atc ttg ttt ctg gaa gaa caa ggg gat gca ctc        480
Ala Gly Ile Ala Arg Ile Leu Phe Leu Glu Glu Gln Gly Asp Ala Leu
145                 150                 155                 160

gcg gac ttc gac ttg aaa gac gcc tgg gcg ccc gct gtc caa gtt gga        528
Ala Asp Phe Asp Leu Lys Asp Ala Trp Ala Pro Ala Val Gln Val Gly
                165                 170                 175

atg cgc tat caa atg agc gat aat tgg ttt gcc aat gcc gat ata cgt        576
Met Arg Tyr Gln Met Ser Asp Asn Trp Phe Ala Asn Ala Asp Ile Arg
            180                 185                 190

tac acg cca ttc gaa aca gat atc tct ggg aca ctc ggc ggg gcg cca        624
Tyr Thr Pro Phe Glu Thr Asp Ile Ser Gly Thr Leu Gly Gly Ala Pro
        195                 200                 205

gtc aga ggc aag att tcg gtg gac cca aca att ctc aat atc ggt att        672
Val Arg Gly Lys Ile Ser Val Asp Pro Thr Ile Leu Asn Ile Gly Ile
    210                 215                 220

gcc tac cgg ttt taa taa                                              690
Ala Tyr Arg Phe
225
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<210> 43
<211> 228
<212> PRT
<213> Oceanocaulis alexandrii

<400> 43

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Met Lys Gln Ser Asn Val Lys Ser Lys Gly Pro Phe Ala Ser Lys Phe
1               5                   10                  15

Val Leu Ile Thr Met Ile Gly Gly Phe Ser Ser Phe Ser Val Ala Asn
            20                  25                  30

Ala Glu Pro Leu Tyr Ser Lys Gly Asp Trp Leu Phe Gly Leu Asn Ala
        35                  40                  45

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

```
Ala Pro Ile Pro Gly Ala Gly Val Asn Ile Thr Asp Asp Thr Thr Leu
65                  70                  75                  80

Ser Phe Asp Val Ser Tyr Phe Leu Asn Ser Ser Val Ala Leu Asn Phe
                85                  90                  95

Phe Gly Gly Leu Pro Ala Ser Ala Asn Leu Ala Gly Ser Gly Ser Leu
            100                 105                 110

Ala Gly Leu Pro Val Gly Glu Thr Glu Tyr Gly Pro Ala Val Leu Ser
        115                 120                 125

Leu Gln Tyr His Phe Ser Thr Asn Ser Ser Val Ser Pro Tyr Val Gly
    130                 135                 140

Ala Gly Ile Ala Arg Ile Leu Phe Leu Glu Glu Gln Gly Asp Ala Leu
145                 150                 155                 160

Ala Asp Phe Asp Leu Lys Asp Ala Trp Ala Pro Ala Val Gln Val Gly
                165                 170                 175

Met Arg Tyr Gln Met Ser Asp Asn Trp Phe Ala Asn Ala Asp Ile Arg
            180                 185                 190

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

Val Arg Gly Lys Ile Ser Val Asp Pro Thr Ile Leu Asn Ile Gly Ile
    210                 215                 220

Ala Tyr Arg Phe
225


<210>  44
<211>  744
<212>  DNA
<213>  Marinobacter aquaeolei


<220>
<221>  CDS
<222>  (1)..(744)

<400>  44
ttg tgt tac gaa aaa ttg cag ttt tac cta aag cca att tgt ttt aat        48
Leu Cys Tyr Glu Lys Leu Gln Phe Tyr Leu Lys Pro Ile Cys Phe Asn
1               5                   10                  15

acc aaa aag gat aat aaa aaa atg aaa cct aaa ata att agt aaa gtc        96
Thr Lys Lys Asp Asn Lys Lys Met Lys Pro Lys Ile Ile Ser Lys Val
            20                  25                  30

tcg tta gtg gcg ttc ctt tta ctt tca ctt gct gcg agc ctg gcc aac       144
Ser Leu Val Ala Phe Leu Leu Leu Ser Leu Ala Ala Ser Leu Ala Asn
        35                  40                  45
```

```
gct caa tct gag ccg gtt tac agt aga ggc gac tgg gtg gtt gga ctg        192
Ala Gln Ser Glu Pro Val Tyr Ser Arg Gly Asp Trp Val Val Gly Leu
    50                  55                  60

aat gcc act aga gtt tta acc gat gaa gat ttg cga tca gcc tct gcg        240
Asn Ala Thr Arg Val Leu Thr Asp Glu Asp Leu Arg Ser Ala Ser Ala
65                  70                  75                  80

ggg ggt gcc ccc gtt cca aat tcc aac ctg tct att aac aac gat acg        288
Gly Gly Ala Pro Val Pro Asn Ser Asn Leu Ser Ile Asn Asn Asp Thr
                85                  90                  95

acc gtt tca ttc gac gtg tcg tat ttt ctg agt aat cag ctg gca ttt        336
Thr Val Ser Phe Asp Val Ser Tyr Phe Leu Ser Asn Gln Leu Ala Phe
            100                 105                 110

aac att ttt ggc ggc att ccc gct agt gcg gac ctc cag ggc gaa gag        384
Asn Ile Phe Gly Gly Ile Pro Ala Ser Ala Asp Leu Gln Gly Glu Glu
        115                 120                 125

tct ctc tcc ggt ctt ttt ctt ggt caa aca gat tat ggt ccg gta att        432
Ser Leu Ser Gly Leu Phe Leu Gly Gln Thr Asp Tyr Gly Pro Val Ile
    130                 135                 140

ctt tcg ctt cag tat cat gtc tta acg ggt agc aac ttc tct ccg tac        480
Leu Ser Leu Gln Tyr His Val Leu Thr Gly Ser Asn Phe Ser Pro Tyr
145                 150                 155                 160

ttt gga gcg ggt gta gga cgg att ctc ttt tta gat gag aag gat cgc        528
Phe Gly Ala Gly Val Gly Arg Ile Leu Phe Leu Asp Glu Lys Asp Arg
                165                 170                 175

gca cta acc gac ttc gac gtc gaa gat aca tgg gcc cct gcg att cag        576
Ala Leu Thr Asp Phe Asp Val Glu Asp Thr Trp Ala Pro Ala Ile Gln
            180                 185                 190

gct ggt ttt cgc tgg agg ata cac aat aac tgg tcg gca aat ttt gac        624
Ala Gly Phe Arg Trp Arg Ile His Asn Asn Trp Ser Ala Asn Phe Asp
        195                 200                 205

gtt aga tat gca ccc ttc aaa gcg gat atc acc ggt aac cta ggc ccg        672
Val Arg Tyr Ala Pro Phe Lys Ala Asp Ile Thr Gly Asn Leu Gly Pro
    210                 215                 220

gcc cct gtt cag gca gaa gtg gaa gtg gac ccc act atc gtg agc atc        720
Ala Pro Val Gln Ala Glu Val Glu Val Asp Pro Thr Ile Val Ser Ile
225                 230                 235                 240

ggt gtc gca tat cgc ttt taa taa                                      744
Gly Val Ala Tyr Arg Phe
                245
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<210> 45
<211> 246
<212> PRT
<213> Marinobacter aquaeolei

<400> 45

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

Thr Lys Lys Asp Asn Lys Lys Met Lys Pro Lys Ile Ile Ser Lys Val
            20                  25                  30
```

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Ser Leu Val Ala Phe Leu Leu Leu Ser Leu Ala Ala Ser Leu Ala Asn
        35                  40                  45

Ala Gln Ser Glu Pro Val Tyr Ser Arg Gly Asp Trp Val Val Gly Leu
    50                  55                  60

Asn Ala Thr Arg Val Leu Thr Asp Glu Asp Leu Arg Ser Ala Ser Ala
65                  70                  75                  80

Gly Gly Ala Pro Val Pro Asn Ser Asn Leu Ser Ile Asn Asn Asp Thr
                85                  90                  95

Thr Val Ser Phe Asp Val Ser Tyr Phe Leu Ser Asn Gln Leu Ala Phe
            100                 105                 110

Asn Ile Phe Gly Gly Ile Pro Ala Ser Ala Asp Leu Gln Gly Glu Glu
        115                 120                 125

Ser Leu Ser Gly Leu Phe Leu Gly Gln Thr Asp Tyr Gly Pro Val Ile
    130                 135                 140

Leu Ser Leu Gln Tyr His Val Leu Thr Gly Ser Asn Phe Ser Pro Tyr
145                 150                 155                 160

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

Ala Leu Thr Asp Phe Asp Val Glu Asp Thr Trp Ala Pro Ala Ile Gln
            180                 185                 190

Ala Gly Phe Arg Trp Arg Ile His Asn Asn Trp Ser Ala Asn Phe Asp
        195                 200                 205

Val Arg Tyr Ala Pro Phe Lys Ala Asp Ile Thr Gly Asn Leu Gly Pro
    210                 215                 220

Ala Pro Val Gln Ala Glu Val Glu Val Asp Pro Thr Ile Val Ser Ile
225                 230                 235                 240

Gly Val Ala Tyr Arg Phe
                245
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<210> 46
<211> 687
<212> DNA
<213> Caulobacter sp. K31

<220>
<221> CDS
<222> (1)..(687)

<400> 46
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Met Arg Lys Asn Gly Ala Tyr Met Tyr Ala Arg Leu Ala Gln Tyr Ala
1               5                  10                  15

acc gcg ctc gcc gtc ttg agc gtc ttc ccc cag gct gca ttg gcc cag          96
Thr Ala Leu Ala Val Leu Ser Val Phe Pro Gln Ala Ala Leu Ala Gln
            20                  25                  30

aat tcg gaa gga ttc aag ctg tgg gcc gta agt ctg aat gca act agg         144
Asn Ser Glu Gly Phe Lys Leu Trp Ala Val Ser Leu Asn Ala Thr Arg
        35                  40                  45

gtc ttc gtg gat gag gat gcg ccc gac atc acc ttg gct gga ggg cct         192
Val Phe Val Asp Glu Asp Ala Pro Asp Ile Thr Leu Ala Gly Gly Pro
    50                  55                  60

gtt ccg ggc tcg aat gtg agg atc ggg gat gcc acg tcg gcg acc att         240
Val Pro Gly Ser Asn Val Arg Ile Gly Asp Ala Thr Ser Ala Thr Ile
65                  70                  75                  80

gat atc gga tat ttc ttc acg ccc aat gtt gct ggt aat ttg ttt ctc         288
Asp Ile Gly Tyr Phe Phe Thr Pro Asn Val Ala Gly Asn Leu Phe Leu
                85                  90                  95

ggc gtg ccg gcg acc gcg caa att gac ggc gct ggg tca ctt gag ccg         336
Gly Val Pro Ala Thr Ala Gln Ile Asp Gly Ala Gly Ser Leu Glu Pro
            100                 105                 110

ctc gga act cta gcc aag gtc aac tat gga ccc atc atc ttg tcg gcc         384
Leu Gly Thr Leu Ala Lys Val Asn Tyr Gly Pro Ile Ile Leu Ser Ala
        115                 120                 125

cag tac cat ttc aac aat ctt ggc aag gtt cat ccc tat ctg gga gtg         432
Gln Tyr His Phe Asn Asn Leu Gly Lys Val His Pro Tyr Leu Gly Val
    130                 135                 140

ggc gtc ggg cgg atc gtc ttt ctg aat gag cgt gac aga gct ttg ctt         480
Gly Val Gly Arg Ile Val Phe Leu Asn Glu Arg Asp Arg Ala Leu Leu
145                 150                 155                 160

aat ttc agt atc gac gac agt tgg gcg cct gcg gct cag gtg ggt gtt         528
Asn Phe Ser Ile Asp Asp Ser Trp Ala Pro Ala Ala Gln Val Gly Val
                165                 170                 175

cgg tac gag ctt ggc gca gaa tgg atg ctg aac gct gac gtt cga tac         576
Arg Tyr Glu Leu Gly Ala Glu Trp Met Leu Asn Ala Asp Val Arg Tyr
            180                 185                 190

gtt ccc ttc tcc acg cac gct acc ggt tca ctg ggt gga gcg cct gtc         624
Val Pro Phe Ser Thr His Ala Thr Gly Ser Leu Gly Gly Ala Pro Val
        195                 200                 205

cgg aca cgt ttg gac atc gac ccg atc ctg acg agc gcc gga gtg act         672
Arg Thr Arg Leu Asp Ile Asp Pro Ile Leu Thr Ser Ala Gly Val Thr
    210                 215                 220

tac cgg ttt tag taa                                                    687
Tyr Arg Phe
225
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<210> 47
<211> 227
<212> PRT
<213> Caulobacter sp. K31

<400> 47

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Met Arg Lys Asn Gly Ala Tyr Met Tyr Ala Arg Leu Ala Gln Tyr Ala
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1 5 10 15

Thr Ala Leu Ala Val Leu Ser Val Phe Pro Gln Ala Ala Leu Ala Gln
20 25 30

Asn Ser Glu Gly Phe Lys Leu Trp Ala Val Ser Leu Asn Ala Thr Arg
35 40 45

Val Phe Val Asp Glu Asp Ala Pro Asp Ile Thr Leu Ala Gly Gly Pro
50 55 60

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

Asp Ile Gly Tyr Phe Phe Thr Pro Asn Val Ala Gly Asn Leu Phe Leu
85 90 95

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

Leu Gly Thr Leu Ala Lys Val Asn Tyr Gly Pro Ile Ile Leu Ser Ala
115 120 125

Gln Tyr His Phe Asn Asn Leu Gly Lys Val His Pro Tyr Leu Gly Val
130 135 140

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

Asn Phe Ser Ile Asp Asp Ser Trp Ala Pro Ala Ala Gln Val Gly Val
165 170 175

Arg Tyr Glu Leu Gly Ala Glu Trp Met Leu Asn Ala Asp Val Arg Tyr
180 185 190

Val Pro Phe Ser Thr His Ala Thr Gly Ser Leu Gly Gly Ala Pro Val
195 200 205

Arg Thr Arg Leu Asp Ile Asp Pro Ile Leu Thr Ser Ala Gly Val Thr
210 215 220

Tyr Arg Phe
225

<210> 48
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48

gcttactgaa tttgcctgaa ccatggggca gtgag 35

<210> 49
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
ttctgaagtg ggggcggccg ccctttttgac gggtacc 37

<210> 50
<211> 5857
<212> DNA
<213> Artificial Sequence

<220>
<223> vector

<400> 50
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ttgcctgact ccccgtcgtg tagataacta cgatacggga gggcttacca tctggcccca 120

gcgctgcgat gataccgcga gaaccacgct caccggctcc ggatttatca gcaataaacc 180

agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 240

ctattaattg ttgccgggaa gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg 300

ttgttgccat cgctacaggc atcgtggtgt cacgctcgtc gtttggtatg gcttcattca 360

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tgactggtga gtactcaacc aagtcattct gagaatagtg tatgcggcga ccgagttgct 600

cttgcccggc gtcaatacgg gataataccg cgccacatag cagaacttta aaagtgctca 660

tcattggaaa acgttcttcg gggcgaaaac tctcaaggat cttaccgctg ttgagatcca 720

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tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa aaagggaata agggcgacac 840

ggaaatgttg aatactcata ttcttccttt ttcaatatta ttgaagcatt tatcagggtt 900

attgtctcat gagcggatac atatttgaat gtatttagaa aaataaacaa ataggggtca 960

gtgttacaac caattaacca attctgaaca ttatcgcgag cccatttata cctgaatatg 1020

gctcataaca ccccttgttt gcctggcggc agtagcgcgg tggtcccacc tgaccccatg 1080

ccgaactcag aagtgaaacg ccgtagcgcc gatggtagtg tggggactcc ccatgcgaga 1140

gtagggaact gccaggcatc aaataaaacg aaaggctcag tcgaaagact gggcctttcg 1200

cccgggctaa ttatggggtg tcgcccttat tcgactctat agtgaagttc ctattctcta 1260

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tactggtttc atattcacca ccctgaattg actctcttcc gggcgctatc atgccatacc 6000

gcgaaaggtt ttgcgccatt cgatggcgcg ccgctttt 6038

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<212> DNA
<213> Acinetobacter sp. ADP1

<220>
<221> CDS
<222> (1)..(1377)

<400> 65

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

cgc cag cag cct atg cat gtc ggt ggc ctg ttc ttg ttt caa att ccg        96
Arg Gln Gln Pro Met His Val Gly Gly Leu Phe Leu Phe Gln Ile Pro
            20                  25                  30

gat aat gcg ccg gac acc ttt atc caa gac ctg gtg aat gat atc cgc       144
Asp Asn Ala Pro Asp Thr Phe Ile Gln Asp Leu Val Asn Asp Ile Arg
        35                  40                  45

att agc aaa tct att ccg gtc ccg cca ttc aac aac aaa ctg aac ggc       192
Ile Ser Lys Ser Ile Pro Val Pro Pro Phe Asn Asn Lys Leu Asn Gly
    50                  55                  60

ctg ttt tgg gac gag gac gag gaa ttt gat ctg gat cac cat ttt cgt       240
Leu Phe Trp Asp Glu Asp Glu Glu Phe Asp Leu Asp His His Phe Arg
65                  70                  75                  80

cac atc gca ttg ccg cac cca ggt cgt att cgt gaa ctg ctg atc tac       288
His Ile Ala Leu Pro His Pro Gly Arg Ile Arg Glu Leu Leu Ile Tyr
                85                  90                  95

att agc caa gag cac agc acc ttg ctg gat cgc gcc aag ccg ctg tgg       336
Ile Ser Gln Glu His Ser Thr Leu Leu Asp Arg Ala Lys Pro Leu Trp
            100                 105                 110

acg tgc aac att att gag ggc att gaa ggt aat cgt ttt gcg atg tat       384
Thr Cys Asn Ile Ile Glu Gly Ile Glu Gly Asn Arg Phe Ala Met Tyr
        115                 120                 125

ttc aag att cac cac gcg atg gtt gat ggt gtt gct ggt atg cgt ctg       432
Phe Lys Ile His His Ala Met Val Asp Gly Val Ala Gly Met Arg Leu
    130                 135                 140

atc gaa aag agc ctg tct cac gat gtg acc gag aaa agc atc gtg ccg       480
Ile Glu Lys Ser Leu Ser His Asp Val Thr Glu Lys Ser Ile Val Pro
145                 150                 155                 160

ccg tgg tgt gtg gag ggt aag cgt gct aaa cgc ctg cgt gaa ccg aaa       528
Pro Trp Cys Val Glu Gly Lys Arg Ala Lys Arg Leu Arg Glu Pro Lys
                165                 170                 175

acg ggt aag atc aaa aag att atg tcc ggt atc aaa tct cag ctg caa       576
Thr Gly Lys Ile Lys Lys Ile Met Ser Gly Ile Lys Ser Gln Leu Gln
            180                 185                 190

gca act ccg acc gtg atc cag gaa ctg tcc cag acc gtc ttt aag gac       624
Ala Thr Pro Thr Val Ile Gln Glu Leu Ser Gln Thr Val Phe Lys Asp
        195                 200                 205
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atc ggt cgc aac cct gat cac gtc agc agc ttc cag gca ccg tgc tcc        672
Ile Gly Arg Asn Pro Asp His Val Ser Ser Phe Gln Ala Pro Cys Ser
    210                 215                 220

att ctg aat cag cgt gtc agc agc agc cgt cgc ttt gcg gcg caa agc        720
Ile Leu Asn Gln Arg Val Ser Ser Ser Arg Arg Phe Ala Ala Gln Ser
225                 230                 235                 240

ttc gac ctg gat cgc ttc cgt aac atc gcc aaa agc ctg aat gtc acc        768
Phe Asp Leu Asp Arg Phe Arg Asn Ile Ala Lys Ser Leu Asn Val Thr
                245                 250                 255

att aac gac gtt gtt ctg gcg gtg tgt tcc ggc gct ctg cgt gcg tac        816
Ile Asn Asp Val Val Leu Ala Val Cys Ser Gly Ala Leu Arg Ala Tyr
            260                 265                 270

ctg atg agc cat aat agc ctg ccg agc aaa ccg ttg att gcg atg gtg        864
Leu Met Ser His Asn Ser Leu Pro Ser Lys Pro Leu Ile Ala Met Val
        275                 280                 285

ccg gca agc att cgt aat gac gac agc gac gtt agc aac cgt att acg        912
Pro Ala Ser Ile Arg Asn Asp Asp Ser Asp Val Ser Asn Arg Ile Thr
    290                 295                 300

atg atc ctg gcg aat ctg gca acc cat aaa gat gat cca ttg cag cgt        960
Met Ile Leu Ala Asn Leu Ala Thr His Lys Asp Asp Pro Leu Gln Arg
305                 310                 315                 320

ctg gaa atc att cgt cgc agc gtc caa aac agc aag cag cgt ttc aag       1008
Leu Glu Ile Ile Arg Arg Ser Val Gln Asn Ser Lys Gln Arg Phe Lys
                325                 330                 335

cgc atg acg agc gac cag atc ctg aac tat tcg gcc gtg gtt tac ggt       1056
Arg Met Thr Ser Asp Gln Ile Leu Asn Tyr Ser Ala Val Val Tyr Gly
            340                 345                 350

ccg gca ggc ctg aac atc atc agc ggt atg atg ccg aaa cgt caa gcg       1104
Pro Ala Gly Leu Asn Ile Ile Ser Gly Met Met Pro Lys Arg Gln Ala
        355                 360                 365

ttc aat ctg gtt att tct aac gtc ccg ggt ccg cgc gag ccg ttg tat       1152
Phe Asn Leu Val Ile Ser Asn Val Pro Gly Pro Arg Glu Pro Leu Tyr
    370                 375                 380

tgg aat ggc gcg aaa ctg gat gct ctg tac ccg gcc agc att gtt ctg       1200
Trp Asn Gly Ala Lys Leu Asp Ala Leu Tyr Pro Ala Ser Ile Val Leu
385                 390                 395                 400

gat ggt cag gcc ctg aat atc acc atg acg tcc tac ttg gac aag ttg       1248
Asp Gly Gln Ala Leu Asn Ile Thr Met Thr Ser Tyr Leu Asp Lys Leu
                405                 410                 415

gag gtt ggc ctg atc gcg tgc cgc aat gcc ctg ccg cgt atg cag aac       1296
Glu Val Gly Leu Ile Ala Cys Arg Asn Ala Leu Pro Arg Met Gln Asn
            420                 425                 430

ttg ctg acc cat ctg gag gaa gag atc caa ctg ttc gaa ggc gtg att       1344
Leu Leu Thr His Leu Glu Glu Glu Ile Gln Leu Phe Glu Gly Val Ile
        435                 440                 445

gca aag caa gag gac atc aaa acg gcg aac taa                           1377
Ala Lys Gln Glu Asp Ile Lys Thr Ala Asn
    450                 455
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<210> 66
<211> 458

<212> PRT
<213> Acinetobacter sp. ADP1

<400> 66

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Arg Gln Gln Pro Met His Val Gly Gly Leu Phe Leu Phe Gln Ile Pro
            20                  25                  30

Asp Asn Ala Pro Asp Thr Phe Ile Gln Asp Leu Val Asn Asp Ile Arg
        35                  40                  45

Ile Ser Lys Ser Ile Pro Val Pro Pro Phe Asn Asn Lys Leu Asn Gly
    50                  55                  60

Leu Phe Trp Asp Glu Asp Glu Glu Phe Asp Leu Asp His His Phe Arg
65                  70                  75                  80

His Ile Ala Leu Pro His Pro Gly Arg Ile Arg Glu Leu Leu Ile Tyr
                85                  90                  95

Ile Ser Gln Glu His Ser Thr Leu Leu Asp Arg Ala Lys Pro Leu Trp
            100                 105                 110

Thr Cys Asn Ile Ile Glu Gly Ile Glu Gly Asn Arg Phe Ala Met Tyr
        115                 120                 125

Phe Lys Ile His His Ala Met Val Asp Gly Val Ala Gly Met Arg Leu
    130                 135                 140

Ile Glu Lys Ser Leu Ser His Asp Val Thr Glu Lys Ser Ile Val Pro
145                 150                 155                 160

Pro Trp Cys Val Glu Gly Lys Arg Ala Lys Arg Leu Arg Glu Pro Lys
                165                 170                 175

Thr Gly Lys Ile Lys Lys Ile Met Ser Gly Ile Lys Ser Gln Leu Gln
            180                 185                 190

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

Ile Gly Arg Asn Pro Asp His Val Ser Ser Phe Gln Ala Pro Cys Ser
    210                 215                 220

Ile Leu Asn Gln Arg Val Ser Ser Ser Arg Arg Phe Ala Ala Gln Ser
225                 230                 235                 240

Phe Asp Leu Asp Arg Phe Arg Asn Ile Ala Lys Ser Leu Asn Val Thr
                245                 250                 255
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Ile Asn Asp Val Val Leu Ala Val Cys Ser Gly Ala Leu Arg Ala Tyr
260 265 270

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

Pro Ala Ser Ile Arg Asn Asp Asp Ser Asp Val Ser Asn Arg Ile Thr
290 295 300

Met Ile Leu Ala Asn Leu Ala Thr His Lys Asp Asp Pro Leu Gln Arg
305 310 315 320

Leu Glu Ile Ile Arg Arg Ser Val Gln Asn Ser Lys Gln Arg Phe Lys
325 330 335

Arg Met Thr Ser Asp Gln Ile Leu Asn Tyr Ser Ala Val Val Tyr Gly
340 345 350

Pro Ala Gly Leu Asn Ile Ile Ser Gly Met Met Pro Lys Arg Gln Ala
355 360 365

Phe Asn Leu Val Ile Ser Asn Val Pro Gly Pro Arg Glu Pro Leu Tyr
370 375 380

Trp Asn Gly Ala Lys Leu Asp Ala Leu Tyr Pro Ala Ser Ile Val Leu
385 390 395 400

Asp Gly Gln Ala Leu Asn Ile Thr Met Thr Ser Tyr Leu Asp Lys Leu
405 410 415

Glu Val Gly Leu Ile Ala Cys Arg Asn Ala Leu Pro Arg Met Gln Asn
420 425 430

Leu Leu Thr His Leu Glu Glu Glu Ile Gln Leu Phe Glu Gly Val Ile
435 440 445

Ala Lys Gln Glu Asp Ile Lys Thr Ala Asn
450 455

<210> 67
<211> 1374
<212> DNA
<213> Alkanivorax borkumensis SK2

<220>
<221> CDS
<222> (1)..(1374)

<400> 67
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Met Lys Ala Leu Ser Pro Val Asp Gln Leu Phe Leu Trp Leu Glu Lys
1 5 10 15

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cgt cag caa ccg atg cat gtt ggt ggt ctg cag ctg ttt agc ttc cca          96
Arg Gln Gln Pro Met His Val Gly Gly Leu Gln Leu Phe Ser Phe Pro
            20                  25                  30

gag ggt gcg ggt cct aag tac gtt agc gag ttg gct cag caa atg cgt         144
Glu Gly Ala Gly Pro Lys Tyr Val Ser Glu Leu Ala Gln Gln Met Arg
        35                  40                  45

gac tac tgt cac ccg gtg gcc ccg ttc aat cag cgc ctg acc cgt cgc         192
Asp Tyr Cys His Pro Val Ala Pro Phe Asn Gln Arg Leu Thr Arg Arg
    50                  55                  60

ctg ggt caa tac tat tgg acg cgc gac aaa caa ttt gac att gac cac         240
Leu Gly Gln Tyr Tyr Trp Thr Arg Asp Lys Gln Phe Asp Ile Asp His
65                  70                  75                  80

cat ttt cgc cat gaa gcg ctg ccg aag ccg ggt cgc att cgc gaa ctg         288
His Phe Arg His Glu Ala Leu Pro Lys Pro Gly Arg Ile Arg Glu Leu
                85                  90                  95

ctg tcc ttg gtt agc gcg gag cac agc aat ctg ttg gac cgc gag cgc         336
Leu Ser Leu Val Ser Ala Glu His Ser Asn Leu Leu Asp Arg Glu Arg
            100                 105                 110

cct atg tgg gaa gcg cac ctg att gag ggc atc cgt ggc cgc caa ttc         384
Pro Met Trp Glu Ala His Leu Ile Glu Gly Ile Arg Gly Arg Gln Phe
        115                 120                 125

gct ttg tac tat aag atc cac cat agc gtg atg gat ggc atc agc gct         432
Ala Leu Tyr Tyr Lys Ile His His Ser Val Met Asp Gly Ile Ser Ala
    130                 135                 140

atg cgc att gcg tct aaa acg ctg agc acc gac ccg tct gag cgc gaa         480
Met Arg Ile Ala Ser Lys Thr Leu Ser Thr Asp Pro Ser Glu Arg Glu
145                 150                 155                 160

atg gca cca gca tgg gcc ttc aat acc aag aaa cgt agc cgt agc ctg         528
Met Ala Pro Ala Trp Ala Phe Asn Thr Lys Lys Arg Ser Arg Ser Leu
                165                 170                 175

cct tcc aat cca gtt gat atg gcg agc agc atg gcc cgt ctg acg gct         576
Pro Ser Asn Pro Val Asp Met Ala Ser Ser Met Ala Arg Leu Thr Ala
            180                 185                 190

tct atc agc aaa cag gcg gcg acc gtt ccg ggt ctg gct cgt gaa gtg         624
Ser Ile Ser Lys Gln Ala Ala Thr Val Pro Gly Leu Ala Arg Glu Val
        195                 200                 205

tac aag gtc acc cag aaa gct aag aag gat gag aac tac gtg agc att         672
Tyr Lys Val Thr Gln Lys Ala Lys Lys Asp Glu Asn Tyr Val Ser Ile
    210                 215                 220

ttt caa gcg ccg gat acc atc ttg aac aac acc att acc ggt tcc cgt         720
Phe Gln Ala Pro Asp Thr Ile Leu Asn Asn Thr Ile Thr Gly Ser Arg
225                 230                 235                 240

cgt ttt gca gca cag agc ttt ccg ctg ccg cgt ctg aaa gtt atc gcg         768
Arg Phe Ala Ala Gln Ser Phe Pro Leu Pro Arg Leu Lys Val Ile Ala
                245                 250                 255

aag gcg tat aac tgc acc atc aac acc gtc gtc ctg tct atg tgt ggc         816
Lys Ala Tyr Asn Cys Thr Ile Asn Thr Val Val Leu Ser Met Cys Gly
            260                 265                 270

cac gcg ctg cgt gaa tat ctg att agc caa cac gca ctg ccg gat gag         864
His Ala Leu Arg Glu Tyr Leu Ile Ser Gln His Ala Leu Pro Asp Glu
        275                 280                 285
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ccg ctg atc gcg atg gtg ccg atg agc ctg cgt cag gac gac agc acg        912
Pro Leu Ile Ala Met Val Pro Met Ser Leu Arg Gln Asp Asp Ser Thr
    290                 295                 300

ggt ggt aat cag att ggc atg atc ctg gcc aac ctg ggc acc cat atc        960
Gly Gly Asn Gln Ile Gly Met Ile Leu Ala Asn Leu Gly Thr His Ile
305                 310                 315                 320

tgc gat ccg gcg aat cgt ttg cgt gtt att cac gac tcc gtc gag gaa       1008
Cys Asp Pro Ala Asn Arg Leu Arg Val Ile His Asp Ser Val Glu Glu
                325                 330                 335

gcg aaa tcg cgt ttc agc cag atg agc ccg gag gag atc ctg aac ttt       1056
Ala Lys Ser Arg Phe Ser Gln Met Ser Pro Glu Glu Ile Leu Asn Phe
            340                 345                 350

acc gca ctg act atg gcc ccg acg ggc ttg aat ctg ctg acc ggc ctg       1104
Thr Ala Leu Thr Met Ala Pro Thr Gly Leu Asn Leu Leu Thr Gly Leu
        355                 360                 365

gca ccg aaa tgg cgt gcg ttc aac gtc gtc att agc aac att ccg ggt       1152
Ala Pro Lys Trp Arg Ala Phe Asn Val Val Ile Ser Asn Ile Pro Gly
    370                 375                 380

ccg aag gaa ccg ctg tat tgg aat ggc gcc cag ctg caa ggt gtg tac       1200
Pro Lys Glu Pro Leu Tyr Trp Asn Gly Ala Gln Leu Gln Gly Val Tyr
385                 390                 395                 400

ccg gta agc att gcg ttg gac cgt att gca ctg aac atc acg ctg act       1248
Pro Val Ser Ile Ala Leu Asp Arg Ile Ala Leu Asn Ile Thr Leu Thr
                405                 410                 415

agc tac gtg gat cag atg gag ttc ggt ctg atc gca tgc cgt cgc acg       1296
Ser Tyr Val Asp Gln Met Glu Phe Gly Leu Ile Ala Cys Arg Arg Thr
            420                 425                 430

ctg ccg agc atg caa cgt ctg ctg gat tat ctg gaa caa agc att cgt       1344
Leu Pro Ser Met Gln Arg Leu Leu Asp Tyr Leu Glu Gln Ser Ile Arg
        435                 440                 445

gag ttg gaa atc ggt gcc ggc atc aag taa                              1374
Glu Leu Glu Ile Gly Ala Gly Ile Lys
    450                 455
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<210> 68
<211> 457
<212> PRT
<213> Alkanivorax borkumensis SK2

<400> 68

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Arg Gln Gln Pro Met His Val Gly Gly Leu Gln Leu Phe Ser Phe Pro
            20                  25                  30

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

Asp Tyr Cys His Pro Val Ala Pro Phe Asn Gln Arg Leu Thr Arg Arg
    50                  55                  60
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Leu Gly Gln Tyr Tyr Trp Thr Arg Asp Lys Gln Phe Asp Ile Asp His
65                  70                  75                  80

His Phe Arg His Glu Ala Leu Pro Lys Pro Gly Arg Ile Arg Glu Leu
                85                  90                  95

Leu Ser Leu Val Ser Ala Glu His Ser Asn Leu Leu Asp Arg Glu Arg
            100                 105                 110

Pro Met Trp Glu Ala His Leu Ile Glu Gly Ile Arg Gly Arg Gln Phe
        115                 120                 125

Ala Leu Tyr Tyr Lys Ile His His Ser Val Met Asp Gly Ile Ser Ala
    130                 135                 140

Met Arg Ile Ala Ser Lys Thr Leu Ser Thr Asp Pro Ser Glu Arg Glu
145                 150                 155                 160

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

Pro Ser Asn Pro Val Asp Met Ala Ser Ser Met Ala Arg Leu Thr Ala
            180                 185                 190

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

Tyr Lys Val Thr Gln Lys Ala Lys Lys Asp Glu Asn Tyr Val Ser Ile
    210                 215                 220

Phe Gln Ala Pro Asp Thr Ile Leu Asn Asn Thr Ile Thr Gly Ser Arg
225                 230                 235                 240

Arg Phe Ala Ala Gln Ser Phe Pro Leu Pro Arg Leu Lys Val Ile Ala
                245                 250                 255

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

His Ala Leu Arg Glu Tyr Leu Ile Ser Gln His Ala Leu Pro Asp Glu
        275                 280                 285

Pro Leu Ile Ala Met Val Pro Met Ser Leu Arg Gln Asp Asp Ser Thr
    290                 295                 300

Gly Gly Asn Gln Ile Gly Met Ile Leu Ala Asn Leu Gly Thr His Ile
305                 310                 315                 320

Cys Asp Pro Ala Asn Arg Leu Arg Val Ile His Asp Ser Val Glu Glu
                325                 330                 335
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Ala Lys Ser Arg Phe Ser Gln Met Ser Pro Glu Glu Ile Leu Asn Phe
340 345 350

Thr Ala Leu Thr Met Ala Pro Thr Gly Leu Asn Leu Leu Thr Gly Leu
355 360 365

Ala Pro Lys Trp Arg Ala Phe Asn Val Val Ile Ser Asn Ile Pro Gly
370 375 380

Pro Lys Glu Pro Leu Tyr Trp Asn Gly Ala Gln Leu Gln Gly Val Tyr
385 390 395 400

Pro Val Ser Ile Ala Leu Asp Arg Ile Ala Leu Asn Ile Thr Leu Thr
405 410 415

Ser Tyr Val Asp Gln Met Glu Phe Gly Leu Ile Ala Cys Arg Arg Thr
420 425 430

Leu Pro Ser Met Gln Arg Leu Leu Asp Tyr Leu Glu Gln Ser Ile Arg
435 440 445

Glu Leu Glu Ile Gly Ala Gly Ile Lys
450 455

<210> 69
<211> 3087
<212> DNA
<213> Artificial Sequence

<220>
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<400> 69
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caagacctgg tgaatgatat ccgcattagc aaatctattc cggtcccgcc attcaacaac 180

aaactgaacg gcctgttttg ggacgaggac gaggaatttg atctggatca ccattttcgt 240

cacatcgcat tgccgcaccc aggtcgtatt cgtgaactgc tgatctacat tagccaagag 300

cacagcacct tgctggatcg cgccaagccg ctgtggacgt gcaacattat tgagggcatt 360

gaaggtaatc gttttgcgat gtatttcaag attcaccacg cgatggttga tggtgttgct 420

ggtatgcgtc tgatcgaaaa gagcctgtct cacgatgtga ccgagaaaag catcgtgccg 480

ccgtggtgtg tggagggtaa gcgtgctaaa cgcctgcgtg aaccgaaaac gggtaagatc 540

aaaaagatta tgtccggtat caaatctcag ctgcaagcaa ctccgaccgt gatccaggaa 600

ctgtcccaga ccgtctttaa ggacatcggt cgcaaccctg atcacgtcag cagcttccag 660

gcaccgtgct ccattctgaa tcagcgtgtc agcagcagcc gtcgctttgc ggcgcaaagc 720

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aaccgtatta cgatgatcct ggcgaatctg gcaacccata aagatgatcc attgcagcgt 960

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gaccagatcc tgaactattc ggccgtggtt tacggtccgg caggcctgaa catcatcagc 1080

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ttggtgccga aataccatct gccagatgcc atttcatttc gtagcgcact gcataacggc 1980

taccggatgc agtacgtcaa acccgaactg gtgccggaag atttagcttt tctgcaatac 2040

accggcggca ccactggtgt ggcgaaaggc gcgatgctga ctcaccgcaa tatgctggcg 2100

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Met Asn Ala Lys Leu Lys Lys Leu Phe Gln Gln Lys Val Asp Gly Lys
1               5                  10                  15

aca atc att gtc aca gga gca tca agt ggt att ggt tta acg gtt tca          96
Thr Ile Ile Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Thr Val Ser
            20                  25                  30

aaa tac ctt gct caa gca ggt gct cat gtc tta ttg ctc gct cgt act         144
Lys Tyr Leu Ala Gln Ala Gly Ala His Val Leu Leu Leu Ala Arg Thr
        35                  40                  45

aaa gag aag tta gat gag gtc aaa gca gag atc gag gct gaa ggt gga         192
Lys Glu Lys Leu Asp Glu Val Lys Ala Glu Ile Glu Ala Glu Gly Gly
    50                  55                  60

aaa gcg acc gta ttt cca tgt gat ctc aat gat atg gaa tct att gat         240
Lys Ala Thr Val Phe Pro Cys Asp Leu Asn Asp Met Glu Ser Ile Asp
65                  70                  75                  80

gcc gtt tca aaa gaa atc tta gca gca gta gat cac att gat att ctt         288
Ala Val Ser Lys Glu Ile Leu Ala Ala Val Asp His Ile Asp Ile Leu
                85                  90                  95

gta aat aac gca gga cgt tca atc cgt cgt gcg gta cat gag tca gtt         336
Val Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Val
            100                 105                 110

gat cgt ttc cat gac ttc gaa cgt acc atg cag tta aat tac ttt ggt         384
Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

gca gta cgt tta gtc ttg aat gtt tta ccg cac atg atg cag cgt aaa         432
Ala Val Arg Leu Val Leu Asn Val Leu Pro His Met Met Gln Arg Lys
    130                 135                 140

gac ggt caa atc att aac atc agc tca att ggt gtt ctt gcc aac gca         480
Asp Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

act cgc ttt tct gct tac gtt gcg tct aaa gct gca ttg gat gca ttt         528
Thr Arg Phe Ser Ala Tyr Val Ala Ser Lys Ala Ala Leu Asp Ala Phe
                165                 170                 175

agt cgt tgt tta tct gcg gaa gtt cac tca cac aaa att gcg att acc         576
Ser Arg Cys Leu Ser Ala Glu Val His Ser His Lys Ile Ala Ile Thr
            180                 185                 190

tct att tat atg cct ttg gtc cgc aca cca atg att gca cca acc aaa         624
Ser Ile Tyr Met Pro Leu Val Arg Thr Pro Met Ile Ala Pro Thr Lys
        195                 200                 205

att tat aaa tat gta cca acg ctt tca cct gaa gaa gca gcc gat tta         672
Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

att gct tat gca atc gtg aag cgt ccg aaa aag atc gcg acg aac tta         720
Ile Ala Tyr Ala Ile Val Lys Arg Pro Lys Lys Ile Ala Thr Asn Leu
225                 230                 235                 240

ggt cgc ctt gct tcg att act tat gcg att gca cca gac att aac aac         768
Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

att tta atg tcg att ggt ttc aac tta ttc cca agt tct acc gcg tct         816
Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ser
            260                 265                 270
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gtt ggt gag caa gag aag ttg aat tta att caa cgt gcc tat gca cgt        864
Val Gly Glu Gln Glu Lys Leu Asn Leu Ile Gln Arg Ala Tyr Ala Arg
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ttg ttc cca ggc gaa cac tgg taa                                      888
Leu Phe Pro Gly Glu His Trp
    290                 295


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<213>  Acinetobacter sp. M-1

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

Lys Tyr Leu Ala Gln Ala Gly Ala His Val Leu Leu Leu Ala Arg Thr
        35                  40                  45

Lys Glu Lys Leu Asp Glu Val Lys Ala Glu Ile Glu Ala Glu Gly Gly
    50                  55                  60

Lys Ala Thr Val Phe Pro Cys Asp Leu Asn Asp Met Glu Ser Ile Asp
65                  70                  75                  80

Ala Val Ser Lys Glu Ile Leu Ala Ala Val Asp His Ile Asp Ile Leu
                85                  90                  95

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

Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

Ala Val Arg Leu Val Leu Asn Val Leu Pro His Met Met Gln Arg Lys
    130                 135                 140

Asp Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

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

Ser Arg Cys Leu Ser Ala Glu Val His Ser His Lys Ile Ala Ile Thr
            180                 185                 190

Ser Ile Tyr Met Pro Leu Val Arg Thr Pro Met Ile Ala Pro Thr Lys
        195                 200                 205
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Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

Ile Ala Tyr Ala Ile Val Lys Arg Pro Lys Lys Ile Ala Thr Asn Leu
225                 230                 235                 240

Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ser
            260                 265                 270

Val Gly Glu Gln Glu Lys Leu Asn Leu Ile Gln Arg Ala Tyr Ala Arg
        275                 280                 285

Leu Phe Pro Gly Glu His Trp
    290                 295


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Val Asn Lys Lys Leu Glu Ala Leu Phe Arg Glu Asn Val Lys Gly Lys
1               5                   10                  15

gtg gct ttg atc act ggt gca tct agt gga atc ggt ttg acg att gca          96
Val Ala Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Thr Ile Ala
            20                  25                  30

aaa aga att gct gcg gca ggt gct cat gta tta ttg gtt gcc cga acc         144
Lys Arg Ile Ala Ala Ala Gly Ala His Val Leu Leu Val Ala Arg Thr
        35                  40                  45

caa gaa aca ctg gaa gaa gtg aaa gct gca att gaa cag caa ggg gga         192
Gln Glu Thr Leu Glu Glu Val Lys Ala Ala Ile Glu Gln Gln Gly Gly
    50                  55                  60

cag gcc tct att ttt cct tgt gac ctg act gac atg aat gcg att gac         240
Gln Ala Ser Ile Phe Pro Cys Asp Leu Thr Asp Met Asn Ala Ile Asp
65                  70                  75                  80

cag tta tca caa caa att atg gcc agt gtc gat cat gtc gat ttc ctg         288
Gln Leu Ser Gln Gln Ile Met Ala Ser Val Asp His Val Asp Phe Leu
                85                  90                  95

atc aat aat gca ggg cgt tcg att cgc cgt gcc gta cac gag tcg ttt         336
Ile Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Phe
            100                 105                 110

gat cgc ttc cat gat ttt gaa cgc acc atg cag ctg aat tac ttt ggt         384
Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125
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gcg gta cgt tta gtg tta aat tta ctg cca cat atg att aag cgt aaa        432
Ala Val Arg Leu Val Leu Asn Leu Leu Pro His Met Ile Lys Arg Lys
    130                 135                 140

aat ggc cag atc atc aat atc agc tct att ggt gta ttg gcc aat gcg        480
Asn Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

acc cgt ttt tct gct tat gtc gcg tct aaa gct gcg ctg gat gcc ttc        528
Thr Arg Phe Ser Ala Tyr Val Ala Ser Lys Ala Ala Leu Asp Ala Phe
                165                 170                 175

agt cgc tgt ctt tca gcc gag gta ctc aag cat aaa atc tca att acc        576
Ser Arg Cys Leu Ser Ala Glu Val Leu Lys His Lys Ile Ser Ile Thr
            180                 185                 190

tcg att tat atg cca ttg gtg cgt acc cca atg atc gca ccc acc aaa        624
Ser Ile Tyr Met Pro Leu Val Arg Thr Pro Met Ile Ala Pro Thr Lys
        195                 200                 205

att tat aaa tac gtg ccc acg ctt tcc cca gaa gaa gcc gca gat ctc        672
Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

att gtc tac gcc att gtg aaa cgt cca aaa cgt att gcg acg cac ttg        720
Ile Val Tyr Ala Ile Val Lys Arg Pro Lys Arg Ile Ala Thr His Leu
225                 230                 235                 240

ggt cgt ctg gcg tca att acc tat gcc atc gca cca gac atc aat aat        768
Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

att ctg atg tcg att gga ttt aac cta ttc cca agc tca acg gct gca        816
Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ala
            260                 265                 270

ctg ggt gaa cag gaa aaa ttg aat ctg cta caa cgt gcc tat gcc cgc        864
Leu Gly Glu Gln Glu Lys Leu Asn Leu Leu Gln Arg Ala Tyr Ala Arg
        275                 280                 285

ttg ttc cca ggc gaa cac tgg taa                                      888
Leu Phe Pro Gly Glu His Trp
    290                 295


<210>  80
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<212>  PRT
<213>  Acinetobacter sp. ADP1

<400>  80

Val Asn Lys Lys Leu Glu Ala Leu Phe Arg Glu Asn Val Lys Gly Lys
1               5                   10                  15


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


Lys Arg Ile Ala Ala Ala Gly Ala His Val Leu Leu Val Ala Arg Thr
        35                  40                  45


Gln Glu Thr Leu Glu Glu Val Lys Ala Ala Ile Glu Gln Gln Gly Gly
    50                  55                  60
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Gln Ala Ser Ile Phe Pro Cys Asp Leu Thr Asp Met Asn Ala Ile Asp
65                  70                  75                  80

Gln Leu Ser Gln Gln Ile Met Ala Ser Val Asp His Val Asp Phe Leu
                85                  90                  95

Ile Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Phe
            100                 105                 110

Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

Ala Val Arg Leu Val Leu Asn Leu Leu Pro His Met Ile Lys Arg Lys
    130                 135                 140

Asn Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

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

Ser Arg Cys Leu Ser Ala Glu Val Leu Lys His Lys Ile Ser Ile Thr
            180                 185                 190

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

Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

Ile Val Tyr Ala Ile Val Lys Arg Pro Lys Arg Ile Ala Thr His Leu
225                 230                 235                 240

Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ala
            260                 265                 270

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

Leu Phe Pro Gly Glu His Trp
    290                 295

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<222> (1)..(912)

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1               5                  10                  15

ttt cgt gag aat gtc aaa ggc aag gtt gcc ctg atc acg ggt gct agc          96
Phe Arg Glu Asn Val Lys Gly Lys Val Ala Leu Ile Thr Gly Ala Ser
            20                  25                  30

agc ggc atc ggc ctg acg att gcc aaa cgc att gct gcg gca ggt gca         144
Ser Gly Ile Gly Leu Thr Ile Ala Lys Arg Ile Ala Ala Ala Gly Ala
        35                  40                  45

cat gtt ctg ttg gtc gcg cgc acc cag gaa acc ctg gaa gaa gtg aag         192
His Val Leu Leu Val Ala Arg Thr Gln Glu Thr Leu Glu Glu Val Lys
    50                  55                  60

gca gca atc gag caa cag ggt ggc cag gcc agc att ttc ccg tgt gac         240
Ala Ala Ile Glu Gln Gln Gly Gly Gln Ala Ser Ile Phe Pro Cys Asp
65                  70                  75                  80

ctg acc gat atg aat gcg att gat cag ctg agc caa cag att atg gca         288
Leu Thr Asp Met Asn Ala Ile Asp Gln Leu Ser Gln Gln Ile Met Ala
                85                  90                  95

tcc gtc gac cac gta gat ttt ctg atc aac aat gcc ggt cgc agc att         336
Ser Val Asp His Val Asp Phe Leu Ile Asn Asn Ala Gly Arg Ser Ile
            100                 105                 110

cgt cgc gca gtg cac gaa agc ttc gac cgt ttt cat gat ttc gag cgt         384
Arg Arg Ala Val His Glu Ser Phe Asp Arg Phe His Asp Phe Glu Arg
        115                 120                 125

acg atg caa ttg aac tac ttc ggt gcg gtg cgt ctg gtc ctg aac ctg         432
Thr Met Gln Leu Asn Tyr Phe Gly Ala Val Arg Leu Val Leu Asn Leu
    130                 135                 140

ctg ccg cac atg atc aaa cgt aag aac ggt caa atc atc aat atc agc         480
Leu Pro His Met Ile Lys Arg Lys Asn Gly Gln Ile Ile Asn Ile Ser
145                 150                 155                 160

agc atc ggc gtg ctg gcg aat gcg act cgc ttt agc gcg tac gtt gcg         528
Ser Ile Gly Val Leu Ala Asn Ala Thr Arg Phe Ser Ala Tyr Val Ala
                165                 170                 175

agc aaa gca gcg ctg gat gcg ttt tct cgt tgc ctg agc gca gaa gtt         576
Ser Lys Ala Ala Leu Asp Ala Phe Ser Arg Cys Leu Ser Ala Glu Val
            180                 185                 190

ttg aaa cat aag att agc atc acg agc att tac atg ccg ttg gtg cgt         624
Leu Lys His Lys Ile Ser Ile Thr Ser Ile Tyr Met Pro Leu Val Arg
        195                 200                 205

acc ccg atg atc gcc ccg acc aaa atc tat aag tat gtg ccg acg ctg         672
Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Lys Tyr Val Pro Thr Leu
    210                 215                 220

agc ccg gaa gag gca gct gac ctg att gtc tac gct att gtt aaa cgt         720
Ser Pro Glu Glu Ala Ala Asp Leu Ile Val Tyr Ala Ile Val Lys Arg
225                 230                 235                 240

cca aag cgt att gcg acc cac ctg ggt cgc ttg gcg tcc atc acc tac         768
Pro Lys Arg Ile Ala Thr His Leu Gly Arg Leu Ala Ser Ile Thr Tyr
                245                 250                 255

gcg att gcg ccg gac att aac aat att ctg atg tcc att ggt ttc aac         816
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Ala Ile Ala Pro Asp Ile Asn Asn Ile Leu Met Ser Ile Gly Phe Asn
260 265 270

ctg ttc cct agc tct acc gcg gct ctg ggc gag cag gag aag ctg aat 864
Leu Phe Pro Ser Ser Thr Ala Ala Leu Gly Glu Gln Glu Lys Leu Asn
275 280 285

ctg ctg caa cgt gcc tat gcg cgc ctg ttc ccg ggt gag cac tgg tga 912
Leu Leu Gln Arg Ala Tyr Ala Arg Leu Phe Pro Gly Glu His Trp
290 295 300

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<212> PRT
<213> Acinetobacter sp. ADP1

<400> 82

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Phe Arg Glu Asn Val Lys Gly Lys Val Ala Leu Ile Thr Gly Ala Ser
20 25 30

Ser Gly Ile Gly Leu Thr Ile Ala Lys Arg Ile Ala Ala Ala Gly Ala
35 40 45

His Val Leu Leu Val Ala Arg Thr Gln Glu Thr Leu Glu Glu Val Lys
50 55 60

Ala Ala Ile Glu Gln Gln Gly Gly Gln Ala Ser Ile Phe Pro Cys Asp
65 70 75 80

Leu Thr Asp Met Asn Ala Ile Asp Gln Leu Ser Gln Gln Ile Met Ala
85 90 95

Ser Val Asp His Val Asp Phe Leu Ile Asn Asn Ala Gly Arg Ser Ile
100 105 110

Arg Arg Ala Val His Glu Ser Phe Asp Arg Phe His Asp Phe Glu Arg
115 120 125

Thr Met Gln Leu Asn Tyr Phe Gly Ala Val Arg Leu Val Leu Asn Leu
130 135 140

Leu Pro His Met Ile Lys Arg Lys Asn Gly Gln Ile Ile Asn Ile Ser
145 150 155 160

Ser Ile Gly Val Leu Ala Asn Ala Thr Arg Phe Ser Ala Tyr Val Ala
165 170 175

Ser Lys Ala Ala Leu Asp Ala Phe Ser Arg Cys Leu Ser Ala Glu Val
180 185 190

Leu Lys His Lys Ile Ser Ile Thr Ser Ile Tyr Met Pro Leu Val Arg

195 200 205

Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Lys Tyr Val Pro Thr Leu
210 215 220

Ser Pro Glu Glu Ala Ala Asp Leu Ile Val Tyr Ala Ile Val Lys Arg
225 230 235 240

Pro Lys Arg Ile Ala Thr His Leu Gly Arg Leu Ala Ser Ile Thr Tyr
245 250 255

Ala Ile Ala Pro Asp Ile Asn Asn Ile Leu Met Ser Ile Gly Phe Asn
260 265 270

Leu Phe Pro Ser Ser Thr Ala Ala Leu Gly Glu Gln Glu Lys Leu Asn
275 280 285

Leu Leu Gln Arg Ala Tyr Ala Arg Leu Phe Pro Gly Glu His Trp
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ttg ggt caa ctg cgt ggc aag cgt gtc ctg att acg ggc acc acg ggt 96
Leu Gly Gln Leu Arg Gly Lys Arg Val Leu Ile Thr Gly Thr Thr Gly
20 25 30

ttc ctg ggt aag gtc gtg ctg gag cgc ttg att cgc gct gtg ccg gac 144
Phe Leu Gly Lys Val Val Leu Glu Arg Leu Ile Arg Ala Val Pro Asp
35 40 45

att ggt gcg atc tat ttg ttg atc cgt ggt aat aag cgt cac ccg gat 192
Ile Gly Ala Ile Tyr Leu Leu Ile Arg Gly Asn Lys Arg His Pro Asp
50 55 60

gca cgt tct cgc ttt ttg gaa gag atc gcg acc agc tcg gtg ttc gat 240
Ala Arg Ser Arg Phe Leu Glu Glu Ile Ala Thr Ser Ser Val Phe Asp
65 70 75 80

cgc ctg cgt gaa gca gac tcc gag ggt ttt gac gca ttc ctg gaa gag 288
Arg Leu Arg Glu Ala Asp Ser Glu Gly Phe Asp Ala Phe Leu Glu Glu
85 90 95

cgc att cac tgt gtg act ggc gag gtc acg gaa gca ggt ttt ggc atc 336
Arg Ile His Cys Val Thr Gly Glu Val Thr Glu Ala Gly Phe Gly Ile
100 105 110

ggc caa gag gac tac cgc aaa ctg gcg acc gaa ttg gac gcg gtg att 384
Gly Gln Glu Asp Tyr Arg Lys Leu Ala Thr Glu Leu Asp Ala Val Ile

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aac agc gca gcg agc gtg aac ttt cgt gaa gaa ctg gac aag gcg ctg        432
Asn Ser Ala Ala Ser Val Asn Phe Arg Glu Glu Leu Asp Lys Ala Leu
    130                 135                 140

gcg atc aac act ctg tgc ctg cgc aat atc gcg ggt atg gtg gat ctg        480
Ala Ile Asn Thr Leu Cys Leu Arg Asn Ile Ala Gly Met Val Asp Leu
145                 150                 155                 160

aat cca aaa ctg gcg gtc ctg caa gtt agc act tgc tat gtg aac ggt        528
Asn Pro Lys Leu Ala Val Leu Gln Val Ser Thr Cys Tyr Val Asn Gly
                165                 170                 175

atg aac agc ggt caa gtt acc gaa agc gtg atc aag ccg gca ggt gaa        576
Met Asn Ser Gly Gln Val Thr Glu Ser Val Ile Lys Pro Ala Gly Glu
            180                 185                 190

gcg gtt ccg cgt agc ccg gat ggt ttt tac gag att gaa gag ctg gtg        624
Ala Val Pro Arg Ser Pro Asp Gly Phe Tyr Glu Ile Glu Glu Leu Val
        195                 200                 205

cgc ctg ctg cag gac aaa atc gag gac gtt cag gct cgt tat agc ggc        672
Arg Leu Leu Gln Asp Lys Ile Glu Asp Val Gln Ala Arg Tyr Ser Gly
    210                 215                 220

aag gtc ctg gag cgt aag ctg gtt gat ctg ggc att cgt gaa gcg aat        720
Lys Val Leu Glu Arg Lys Leu Val Asp Leu Gly Ile Arg Glu Ala Asn
225                 230                 235                 240

cgt tat ggc tgg agc gac acg tac acg ttt acc aag tgg ctg ggt gag        768
Arg Tyr Gly Trp Ser Asp Thr Tyr Thr Phe Thr Lys Trp Leu Gly Glu
                245                 250                 255

cag ctg ttg atg aaa gcg ctg aat ggt cgc acc ttg acc atc ctg cgt        816
Gln Leu Leu Met Lys Ala Leu Asn Gly Arg Thr Leu Thr Ile Leu Arg
            260                 265                 270

ccg agc att att gag tct gcc ctg gaa gaa cct gcg cct ggc tgg atc        864
Pro Ser Ile Ile Glu Ser Ala Leu Glu Glu Pro Ala Pro Gly Trp Ile
        275                 280                 285

gag ggt gtg aag gtt gca gac gca atc att ctg gcc tat gcg cgt gag        912
Glu Gly Val Lys Val Ala Asp Ala Ile Ile Leu Ala Tyr Ala Arg Glu
    290                 295                 300

aag gtt acc ctg ttc ccg ggt aag cgt agc ggt att atc gat gtc atc        960
Lys Val Thr Leu Phe Pro Gly Lys Arg Ser Gly Ile Ile Asp Val Ile
305                 310                 315                 320

ccg gtt gac ctg gtc gcc aac agc att att ctg agc ctg gcg gaa gcg       1008
Pro Val Asp Leu Val Ala Asn Ser Ile Ile Leu Ser Leu Ala Glu Ala
                325                 330                 335

ctg ggc gag cca ggc cgt cgc cgc atc tat caa tgc tgt tct ggt ggt       1056
Leu Gly Glu Pro Gly Arg Arg Arg Ile Tyr Gln Cys Cys Ser Gly Gly
            340                 345                 350

ggt aac ccg atc agc ctg ggt gag ttc atc gac cat ctg atg gcc gag       1104
Gly Asn Pro Ile Ser Leu Gly Glu Phe Ile Asp His Leu Met Ala Glu
        355                 360                 365

agc aaa gca aat tac gcc gca tac gat cac ctg ttc tac cgt cag ccg       1152
Ser Lys Ala Asn Tyr Ala Ala Tyr Asp His Leu Phe Tyr Arg Gln Pro
    370                 375                 380

tcc aaa ccg ttt ttg gcg gtc aat cgc gcg ctg ttc gat ctg gtt att       1200
Ser Lys Pro Phe Leu Ala Val Asn Arg Ala Leu Phe Asp Leu Val Ile
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385 390 395 400

agc ggt gtt cgt ctg ccg ctg agc ctg acg gat cgc gtt ctg aag ctg 1248
Ser Gly Val Arg Leu Pro Leu Ser Leu Thr Asp Arg Val Leu Lys Leu
405 410 415

ttg ggt aac tcc cgt gat ctg aaa atg ctg cgc aat ctg gac acc acc 1296
Leu Gly Asn Ser Arg Asp Leu Lys Met Leu Arg Asn Leu Asp Thr Thr
420 425 430

caa tcc ctg gcc acc att ttc ggc ttc tat acc gct ccg gac tac atc 1344
Gln Ser Leu Ala Thr Ile Phe Gly Phe Tyr Thr Ala Pro Asp Tyr Ile
435 440 445

ttc cgt aat gat gaa ctg atg gcc ctg gcc aac cgt atg ggc gag gtc 1392
Phe Arg Asn Asp Glu Leu Met Ala Leu Ala Asn Arg Met Gly Glu Val
450 455 460

gat aaa ggc ctg ttt ccg gtt gat gcg cgt ctg att gac tgg gag ctg 1440
Asp Lys Gly Leu Phe Pro Val Asp Ala Arg Leu Ile Asp Trp Glu Leu
465 470 475 480

tac ctg cgt aaa atc cat ctg gct ggc ctg aac cgt tac gca ttg aaa 1488
Tyr Leu Arg Lys Ile His Leu Ala Gly Leu Asn Arg Tyr Ala Leu Lys
485 490 495

gaa cgt aaa gtc tac tcg ctg aaa acc gct cgt cag cgc aaa aag gcc 1536
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gcg taa 1542
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<212> PRT
<213> Marinobacter aquaeolei VT8

<400> 84

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20 25 30

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

Ile Gly Ala Ile Tyr Leu Leu Ile Arg Gly Asn Lys Arg His Pro Asp
50 55 60

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

Arg Leu Arg Glu Ala Asp Ser Glu Gly Phe Asp Ala Phe Leu Glu Glu
85 90 95

Arg Ile His Cys Val Thr Gly Glu Val Thr Glu Ala Gly Phe Gly Ile
100 105 110

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

Asn Ser Ala Ala Ser Val Asn Phe Arg Glu Glu Leu Asp Lys Ala Leu
130 135 140

Ala Ile Asn Thr Leu Cys Leu Arg Asn Ile Ala Gly Met Val Asp Leu
145 150 155 160

Asn Pro Lys Leu Ala Val Leu Gln Val Ser Thr Cys Tyr Val Asn Gly
165 170 175

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

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

Arg Leu Leu Gln Asp Lys Ile Glu Asp Val Gln Ala Arg Tyr Ser Gly
210 215 220

Lys Val Leu Glu Arg Lys Leu Val Asp Leu Gly Ile Arg Glu Ala Asn
225 230 235 240

Arg Tyr Gly Trp Ser Asp Thr Tyr Thr Phe Thr Lys Trp Leu Gly Glu
245 250 255

Gln Leu Leu Met Lys Ala Leu Asn Gly Arg Thr Leu Thr Ile Leu Arg
260 265 270

Pro Ser Ile Ile Glu Ser Ala Leu Glu Glu Pro Ala Pro Gly Trp Ile
275 280 285

Glu Gly Val Lys Val Ala Asp Ala Ile Ile Leu Ala Tyr Ala Arg Glu
290 295 300

Lys Val Thr Leu Phe Pro Gly Lys Arg Ser Gly Ile Ile Asp Val Ile
305 310 315 320

Pro Val Asp Leu Val Ala Asn Ser Ile Ile Leu Ser Leu Ala Glu Ala
325 330 335

Leu Gly Glu Pro Gly Arg Arg Arg Ile Tyr Gln Cys Cys Ser Gly Gly
340 345 350

Gly Asn Pro Ile Ser Leu Gly Glu Phe Ile Asp His Leu Met Ala Glu
355 360 365

Ser Lys Ala Asn Tyr Ala Ala Tyr Asp His Leu Phe Tyr Arg Gln Pro
370 375 380

Ser Lys Pro Phe Leu Ala Val Asn Arg Ala Leu Phe Asp Leu Val Ile
385 390 395 400

Ser Gly Val Arg Leu Pro Leu Ser Leu Thr Asp Arg Val Leu Lys Leu
405 410 415

Leu Gly Asn Ser Arg Asp Leu Lys Met Leu Arg Asn Leu Asp Thr Thr
420 425 430

Gln Ser Leu Ala Thr Ile Phe Gly Phe Tyr Thr Ala Pro Asp Tyr Ile
435 440 445

Phe Arg Asn Asp Glu Leu Met Ala Leu Ala Asn Arg Met Gly Glu Val
450 455 460

Asp Lys Gly Leu Phe Pro Val Asp Ala Arg Leu Ile Asp Trp Glu Leu
465 470 475 480

Tyr Leu Arg Lys Ile His Leu Ala Gly Leu Asn Arg Tyr Ala Leu Lys
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<212> DNA
<213> Photorhabdus luminescens

<400> 85
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tcccacgtca aaaacattat cgactgtaat ggcaataatg aattgcgtct gcacaacatc 180

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gccaactgga ttagcatgat tttgtgcagc aagggtggtc tgtacgacgt ggtggaaaat 360

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cggcaaatac ccgggtgttt tggtcgagat tctgcgtcgc gtgaacaccc gtacccaaaa 3540

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<210> 88
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attgaagcat ttatcagggt tattgtctca tgagcggata catatttgaa tgtatttaga 180

aaaataaaca aataggggtc agtgttacaa ccaattaacc aattctgaac attatcgcga 240

gcccatttat acctgaatat ggctcataac acccttgtt tgcctggcgg cagtagcgcg 300

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tagtgaagtt cctattctct agaaagtata ggaacttctg aagtggggat ccggccggcc 540

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Leu Val Val Leu Thr Met Ala Leu Asp Glu His Gly His Phe Gly Tyr
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Val Ala Arg Ala Glu Lys Asp Leu Arg Ala Pro Phe Ala Pro Arg Gly
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Trp Phe Glu Gly Leu Thr Ile Glu Gln Leu Asp Val Phe Asn Ala Glu
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gat cgc ttc tgg gcg gct ttt cag agc gat ggt gac gca gag agc ttc        912
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Gln Asp Phe Leu Ala Phe Arg Gly Arg Glu Leu Cys Pro Gly Gly Arg
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Val Ala Arg Ala Glu Lys Asp Leu Arg Ala Pro Phe Ala Pro Arg Gly
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Trp Phe Glu Gly Leu Thr Ile Glu Gln Leu Asp Val Phe Asn Ala Glu
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tttgtgtcgc ccttattcga ctcactatag aagttcctat tctctagtaa gtataggaac 3840

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tgagcggata acaataacaa tttcacacag gatctaggaa ccaaggagag tggcatatgc 4080

caagagagat tagattacca gaatcgtcag tagtagtaag accagcaccg atggagagcg 4140

cgacctatag ccaatccagc cgtctgcagg cagcgggtct gagcccggca attaccttgt 4200

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ctt ttt gaa aca gac ccg cag ttc gca gcg gca cgt ccg gac gaa gct          96
Leu Phe Glu Thr Asp Pro Gln Phe Ala Ala Ala Arg Pro Asp Glu Ala
            20                  25                  30

att agc gct gca gca gcc gat ccg gag ctg cgc ctg cca gcc gca gtc         144
Ile Ser Ala Ala Ala Ala Asp Pro Glu Leu Arg Leu Pro Ala Ala Val
        35                  40                  45

aag cag att ctg gcc ggt tat gcg gac cgt ccg gcc ctg ggt aag cgt         192
Lys Gln Ile Leu Ala Gly Tyr Ala Asp Arg Pro Ala Leu Gly Lys Arg
    50                  55                  60

gct gtg gag ttc gtt acg gac gaa gaa ggc cgt acc acc gca aag ttg         240
Ala Val Glu Phe Val Thr Asp Glu Glu Gly Arg Thr Thr Ala Lys Leu
65                  70                  75                  80

ctg ccg cgt ttc gat acg atc acc tac cgt caa ttg gca ggt cgt att         288
Leu Pro Arg Phe Asp Thr Ile Thr Tyr Arg Gln Leu Ala Gly Arg Ile
                85                  90                  95

cag gcg gtg act aac gcg tgg cac aat cac ccg gtg aat gcg ggt gac         336
Gln Ala Val Thr Asn Ala Trp His Asn His Pro Val Asn Ala Gly Asp
            100                 105                 110

cgt gtc gca att ttg ggc ttc acg agc gtt gac tat acg acc atc gat         384
Arg Val Ala Ile Leu Gly Phe Thr Ser Val Asp Tyr Thr Thr Ile Asp
        115                 120                 125

atc gca ctg ctg gaa ctg ggt gct gtt agc gtt ccg ttg caa acg tct         432
Ile Ala Leu Leu Glu Leu Gly Ala Val Ser Val Pro Leu Gln Thr Ser
    130                 135                 140

gct ccg gtt gcg cag ctg caa ccg att gtg gcc gaa acc gag ccg aag         480
Ala Pro Val Ala Gln Leu Gln Pro Ile Val Ala Glu Thr Glu Pro Lys
145                 150                 155                 160

gtc att gcg agc agc gtc gat ttc ctg gca gat gcg gtc gca ctg gtt         528
Val Ile Ala Ser Ser Val Asp Phe Leu Ala Asp Ala Val Ala Leu Val
                165                 170                 175

gag agc ggt cca gcc ccg agc cgt ctg gtc gtt ttt gat tat agc cac         576
Glu Ser Gly Pro Ala Pro Ser Arg Leu Val Val Phe Asp Tyr Ser His
            180                 185                 190

gag gtc gac gat cag cgt gag gcc ttc gaa gcg gcc aag ggt aaa ctg         624
Glu Val Asp Asp Gln Arg Glu Ala Phe Glu Ala Ala Lys Gly Lys Leu
        195                 200                 205

gcg ggt acc ggt gtt gtg gtg gaa acg att acg gat gtc ttg gat cgc         672
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Ala Gly Thr Gly Val Val Val Glu Thr Ile Thr Asp Val Leu Asp Arg
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ggt cgc agc ctg gct gat gcg ccg ctg tat gtc cca gac gaa acg gac        720
Gly Arg Ser Leu Ala Asp Ala Pro Leu Tyr Val Pro Asp Glu Thr Asp
225                 230                 235                 240

ccg ctg acc ctg ctg atc tat acc agc ggt agc acc ggt acg ccg aag        768
Pro Leu Thr Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly Thr Pro Lys
                245                 250                 255

ggt gct atg tat ccg gaa tcc aag acc gcg acg atg tgg caa gct ggt        816
Gly Ala Met Tyr Pro Glu Ser Lys Thr Ala Thr Met Trp Gln Ala Gly
            260                 265                 270

agc aag gcg cgt tgg gat gaa acc ctg ggc gtt atg ccg agc atc acc        864
Ser Lys Ala Arg Trp Asp Glu Thr Leu Gly Val Met Pro Ser Ile Thr
        275                 280                 285

ctg aac ttc atg cca atg tcc cac gtg atg ggt cgc ggc atc ctg tgt        912
Leu Asn Phe Met Pro Met Ser His Val Met Gly Arg Gly Ile Leu Cys
    290                 295                 300

agc acc ctg gcg agc ggc ggt act gcg tat ttt gcc gca cgt agc gac        960
Ser Thr Leu Ala Ser Gly Gly Thr Ala Tyr Phe Ala Ala Arg Ser Asp
305                 310                 315                 320

ttg tct acc ttt ctg gag gac ctg gcg ttg gtc cgc ccg acc caa ctg       1008
Leu Ser Thr Phe Leu Glu Asp Leu Ala Leu Val Arg Pro Thr Gln Leu
                325                 330                 335

aat ttc gtc cct cgc atc tgg gat atg ctg ttc caa gag tat cag agc       1056
Asn Phe Val Pro Arg Ile Trp Asp Met Leu Phe Gln Glu Tyr Gln Ser
            340                 345                 350

cgt ctg gac aat cgt cgt gcc gag ggt agc gag gat cgc gcg gaa gcg       1104
Arg Leu Asp Asn Arg Arg Ala Glu Gly Ser Glu Asp Arg Ala Glu Ala
        355                 360                 365

gcc gta ctg gaa gag gtt cgt acc caa ttg ctg ggc ggt cgt ttc gtt       1152
Ala Val Leu Glu Glu Val Arg Thr Gln Leu Leu Gly Gly Arg Phe Val
    370                 375                 380

tcc gct ctg acc ggt agc gct cca atc agc gcg gaa atg aaa agc tgg       1200
Ser Ala Leu Thr Gly Ser Ala Pro Ile Ser Ala Glu Met Lys Ser Trp
385                 390                 395                 400

gtc gag gac ctg ctg gac atg cat ttg ctg gaa ggt tac ggt tcc acc       1248
Val Glu Asp Leu Leu Asp Met His Leu Leu Glu Gly Tyr Gly Ser Thr
                405                 410                 415

gag gcg ggt gcc gtg ttc att gac ggt caa atc caa cgt cca cct gtt       1296
Glu Ala Gly Ala Val Phe Ile Asp Gly Gln Ile Gln Arg Pro Pro Val
            420                 425                 430

atc gat tac aaa ctg gtt gat gtt ccg gac ttg ggt tac ttt gcg acc       1344
Ile Asp Tyr Lys Leu Val Asp Val Pro Asp Leu Gly Tyr Phe Ala Thr
        435                 440                 445

gat cgt cca tac cct cgc ggc gag ctg ctg gtg aag agc gag cag atg       1392
Asp Arg Pro Tyr Pro Arg Gly Glu Leu Leu Val Lys Ser Glu Gln Met
    450                 455                 460

ttc ccg ggc tac tat aag cgt ccg gag att acg gcg gag atg ttt gac       1440
Phe Pro Gly Tyr Tyr Lys Arg Pro Glu Ile Thr Ala Glu Met Phe Asp
465                 470                 475                 480

gag gac ggt tat tac cgt acc ggc gac atc gtg gcc gaa ctg ggt ccg       1488
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Glu Asp Gly Tyr Tyr Arg Thr Gly Asp Ile Val Ala Glu Leu Gly Pro
                485                 490                 495

gat cat ctg gag tat ctg gac cgc cgt aac aac gtc ctg aag ctg agc      1536
Asp His Leu Glu Tyr Leu Asp Arg Arg Asn Asn Val Leu Lys Leu Ser
            500                 505                 510

cag ggt gag ttt gtt acc gtt tcc aaa ctg gaa gcg gtc ttt ggc gat      1584
Gln Gly Glu Phe Val Thr Val Ser Lys Leu Glu Ala Val Phe Gly Asp
        515                 520                 525

agc cca ctg gtg cgc cag att tat gtc tac ggt aac tct gca cgc agc      1632
Ser Pro Leu Val Arg Gln Ile Tyr Val Tyr Gly Asn Ser Ala Arg Ser
    530                 535                 540

tat ctg ctg gcg gtt gtc gtt ccg acc gaa gag gca ctg agc cgc tgg      1680
Tyr Leu Leu Ala Val Val Val Pro Thr Glu Glu Ala Leu Ser Arg Trp
545                 550                 555                 560

gac ggc gat gaa ctg aag agc cgc atc agc gac agc ttg caa gat gcg      1728
Asp Gly Asp Glu Leu Lys Ser Arg Ile Ser Asp Ser Leu Gln Asp Ala
                565                 570                 575

gca cgt gcc gca ggt ttg caa agc tat gag atc ccg cgt gac ttt ctg      1776
Ala Arg Ala Ala Gly Leu Gln Ser Tyr Glu Ile Pro Arg Asp Phe Leu
            580                 585                 590

gtt gaa acc acg ccg ttc acg ttg gag aac ggt ctg ctg acc ggc att      1824
Val Glu Thr Thr Pro Phe Thr Leu Glu Asn Gly Leu Leu Thr Gly Ile
        595                 600                 605

cgc aaa ctg gcg cgt ccg aag ctg aaa gcg cat tat ggc gaa cgt ctg      1872
Arg Lys Leu Ala Arg Pro Lys Leu Lys Ala His Tyr Gly Glu Arg Leu
    610                 615                 620

gaa caa ctg tac acg gat ctg gct gaa ggc caa gcc aat gag ctg cgt      1920
Glu Gln Leu Tyr Thr Asp Leu Ala Glu Gly Gln Ala Asn Glu Leu Arg
625                 630                 635                 640

gaa ctg cgc cgt aat ggt gcg gat cgt ccg gtt gtt gaa acg gtt tcg      1968
Glu Leu Arg Arg Asn Gly Ala Asp Arg Pro Val Val Glu Thr Val Ser
                645                 650                 655

cgt gcc gcg gtc gcc ttg ctg ggt gcg tct gtg acg gac ctg cgt tct      2016
Arg Ala Ala Val Ala Leu Leu Gly Ala Ser Val Thr Asp Leu Arg Ser
            660                 665                 670

gac gcc cac ttt acg gac ctg ggc ggt gat tcc ctg agc gcc ctg agc      2064
Asp Ala His Phe Thr Asp Leu Gly Gly Asp Ser Leu Ser Ala Leu Ser
        675                 680                 685

ttc agc aac ctg ctg cac gag att ttt gac gtc gat gtc ccg gtg ggc      2112
Phe Ser Asn Leu Leu His Glu Ile Phe Asp Val Asp Val Pro Val Gly
    690                 695                 700

gtg att gtc agc ccg gca acc gac ctg gcc ggt gtt gcc gcc tat att      2160
Val Ile Val Ser Pro Ala Thr Asp Leu Ala Gly Val Ala Ala Tyr Ile
705                 710                 715                 720

gag ggt gag ctg cgt ggt agc aaa cgt ccg acc tac gca agc gtc cac      2208
Glu Gly Glu Leu Arg Gly Ser Lys Arg Pro Thr Tyr Ala Ser Val His
                725                 730                 735

ggt cgt gac gca acc gag gtg cgt gct cgc gat ctg gcg ctg ggc aaa      2256
Gly Arg Asp Ala Thr Glu Val Arg Ala Arg Asp Leu Ala Leu Gly Lys
            740                 745                 750

ttc atc gac gca aaa acg ctg agc gca gca ccg ggt ctg ccg cgc tcc      2304
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Phe Ile Asp Ala Lys Thr Leu Ser Ala Ala Pro Gly Leu Pro Arg Ser
        755                 760                 765

ggt acg gag atc cgt acg gtg ctg ctg acg ggt gcg acc ggt ttt ctg       2352
Gly Thr Glu Ile Arg Thr Val Leu Leu Thr Gly Ala Thr Gly Phe Leu
    770                 775                 780

ggt cgc tac ttg gcc ttg gag tgg ctg gaa cgt atg gac ctg gtt gac       2400
Gly Arg Tyr Leu Ala Leu Glu Trp Leu Glu Arg Met Asp Leu Val Asp
785                 790                 795                 800

ggc aag gtg atc tgt ttg gtt cgt gcg cgt agc gac gac gaa gca cgt       2448
Gly Lys Val Ile Cys Leu Val Arg Ala Arg Ser Asp Asp Glu Ala Arg
                805                 810                 815

gcg cgt ctg gac gca acc ttc gat acc ggc gat gct acc ttg ctg gag       2496
Ala Arg Leu Asp Ala Thr Phe Asp Thr Gly Asp Ala Thr Leu Leu Glu
            820                 825                 830

cac tac cgt gcc ctg gcg gct gac cat ctg gaa gtt att gcg ggt gat       2544
His Tyr Arg Ala Leu Ala Ala Asp His Leu Glu Val Ile Ala Gly Asp
        835                 840                 845

aag ggt gaa gcc gac ttg ggc ctg gat cac gat acc tgg cag cgt ctg       2592
Lys Gly Glu Ala Asp Leu Gly Leu Asp His Asp Thr Trp Gln Arg Leu
    850                 855                 860

gca gat acg gtc gac ctg atc gtt gac ccg gct gcg ctg gtt aac cac       2640
Ala Asp Thr Val Asp Leu Ile Val Asp Pro Ala Ala Leu Val Asn His
865                 870                 875                 880

gtt ttg ccg tac agc cag atg ttc ggc cca aac gct ctg ggc act gca       2688
Val Leu Pro Tyr Ser Gln Met Phe Gly Pro Asn Ala Leu Gly Thr Ala
                885                 890                 895

gag ctg att cgc att gca ctg acc acc acc att aaa ccg tac gtc tac       2736
Glu Leu Ile Arg Ile Ala Leu Thr Thr Thr Ile Lys Pro Tyr Val Tyr
            900                 905                 910

gtg agc acc att ggt gtt ggt cag ggc atc agc cca gaa gcc ttt gtt       2784
Val Ser Thr Ile Gly Val Gly Gln Gly Ile Ser Pro Glu Ala Phe Val
        915                 920                 925

gaa gat gcg gac atc cgc gaa atc agc gcc acg cgt cgc gtt gac gac       2832
Glu Asp Ala Asp Ile Arg Glu Ile Ser Ala Thr Arg Arg Val Asp Asp
    930                 935                 940

agc tac gcg aat ggt tat ggt aac agc aaa tgg gca ggt gag gtt ctg       2880
Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys Trp Ala Gly Glu Val Leu
945                 950                 955                 960

ctg cgc gaa gcg cac gac tgg tgc ggc ctg ccg gtg agc gtg ttt cgt       2928
Leu Arg Glu Ala His Asp Trp Cys Gly Leu Pro Val Ser Val Phe Arg
                965                 970                 975

tgt gac atg atc ttg gcc gac acc acc tac tcc ggc cag ctg aat ctg       2976
Cys Asp Met Ile Leu Ala Asp Thr Thr Tyr Ser Gly Gln Leu Asn Leu
            980                 985                 990

ccg gat atg ttc acc cgt ctg atg  ttg agc ctg gtg gca  act ggc atc     3024
Pro Asp Met Phe Thr Arg Leu Met  Leu Ser Leu Val Ala  Thr Gly Ile
        995                 1000                1005

gca ccg  ggc agc ttt tat gag  ctg gac gcg gac ggt  aat cgt caa        3069
Ala Pro  Gly Ser Phe Tyr Glu  Leu Asp Ala Asp Gly  Asn Arg Gln
    1010                1015                1020

cgt gca  cat tat gat ggt ctg  ccg gtg gag ttt atc  gcg gaa gca        3114
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Arg Ala  His Tyr Asp Gly Leu  Pro Val Glu Phe Ile  Ala Glu Ala
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atc agc  acg atc ggc tct caa  gtg act gac ggt ttc  gaa acg ttc        3159
Ile Ser  Thr Ile Gly Ser Gln  Val Thr Asp Gly Phe  Glu Thr Phe
    1040                  1045                  1050

cat gtc  atg aat cct tat gat  gat ggt atc ggc ctg  gac gag tac        3204
His Val  Met Asn Pro Tyr Asp  Asp Gly Ile Gly Leu  Asp Glu Tyr
    1055                  1060                  1065

gtc gac  tgg ctg att gag gct  ggc tac ccg gtt cac  cgt gtt gat        3249
Val Asp  Trp Leu Ile Glu Ala  Gly Tyr Pro Val His  Arg Val Asp
    1070                  1075                  1080

gat tat  gcg acg tgg ttg agc  cgt ttt gaa acc gcc  ttg cgt gcg        3294
Asp Tyr  Ala Thr Trp Leu Ser  Arg Phe Glu Thr Ala  Leu Arg Ala
    1085                  1090                  1095

ctg ccg  gag cgt caa cgt cag  gca tcc ctg ctg ccg  ctg ttg cac        3339
Leu Pro  Glu Arg Gln Arg Gln  Ala Ser Leu Leu Pro  Leu Leu His
    1100                  1105                  1110

aac tac  cag cag cct tct ccg  ccg gtt tgc ggt gct  atg gct cct        3384
Asn Tyr  Gln Gln Pro Ser Pro  Pro Val Cys Gly Ala  Met Ala Pro
    1115                  1120                  1125

acc gac  cgt ttc cgt gca gct  gtc cag gac gcc aaa  att ggc cca        3429
Thr Asp  Arg Phe Arg Ala Ala  Val Gln Asp Ala Lys  Ile Gly Pro
    1130                  1135                  1140

gat aaa  gac atc cca cat gta  acg gcg gac gtg atc  gtg aaa tac        3474
Asp Lys  Asp Ile Pro His Val  Thr Ala Asp Val Ile  Val Lys Tyr
    1145                  1150                  1155

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Ile Ser Ala Ala Ala Ala Asp Pro Glu Leu Arg Leu Pro Ala Ala Val
        35                  40                  45

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

Ala Val Glu Phe Val Thr Asp Glu Glu Gly Arg Thr Thr Ala Lys Leu
65                  70                  75                  80

Leu Pro Arg Phe Asp Thr Ile Thr Tyr Arg Gln Leu Ala Gly Arg Ile
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85 90 95

Gln Ala Val Thr Asn Ala Trp His Asn His Pro Val Asn Ala Gly Asp
100 105 110

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

Ile Ala Leu Leu Glu Leu Gly Ala Val Ser Val Pro Leu Gln Thr Ser
130 135 140

Ala Pro Val Ala Gln Leu Gln Pro Ile Val Ala Glu Thr Glu Pro Lys
145 150 155 160

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

Glu Ser Gly Pro Ala Pro Ser Arg Leu Val Val Phe Asp Tyr Ser His
180 185 190

Glu Val Asp Asp Gln Arg Glu Ala Phe Glu Ala Ala Lys Gly Lys Leu
195 200 205

Ala Gly Thr Gly Val Val Val Glu Thr Ile Thr Asp Val Leu Asp Arg
210 215 220

Gly Arg Ser Leu Ala Asp Ala Pro Leu Tyr Val Pro Asp Glu Thr Asp
225 230 235 240

Pro Leu Thr Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly Thr Pro Lys
245 250 255

Gly Ala Met Tyr Pro Glu Ser Lys Thr Ala Thr Met Trp Gln Ala Gly
260 265 270

Ser Lys Ala Arg Trp Asp Glu Thr Leu Gly Val Met Pro Ser Ile Thr
275 280 285

Leu Asn Phe Met Pro Met Ser His Val Met Gly Arg Gly Ile Leu Cys
290 295 300

Ser Thr Leu Ala Ser Gly Gly Thr Ala Tyr Phe Ala Ala Arg Ser Asp
305 310 315 320

Leu Ser Thr Phe Leu Glu Asp Leu Ala Leu Val Arg Pro Thr Gln Leu
325 330 335

Asn Phe Val Pro Arg Ile Trp Asp Met Leu Phe Gln Glu Tyr Gln Ser
340 345 350

Arg Leu Asp Asn Arg Arg Ala Glu Gly Ser Glu Asp Arg Ala Glu Ala

355 360 365

Ala Val Leu Glu Glu Val Arg Thr Gln Leu Leu Gly Gly Arg Phe Val
370 375 380

Ser Ala Leu Thr Gly Ser Ala Pro Ile Ser Ala Glu Met Lys Ser Trp
385 390 395 400

Val Glu Asp Leu Leu Asp Met His Leu Leu Glu Gly Tyr Gly Ser Thr
405 410 415

Glu Ala Gly Ala Val Phe Ile Asp Gly Gln Ile Gln Arg Pro Pro Val
420 425 430

Ile Asp Tyr Lys Leu Val Asp Val Pro Asp Leu Gly Tyr Phe Ala Thr
435 440 445

Asp Arg Pro Tyr Pro Arg Gly Glu Leu Leu Val Lys Ser Glu Gln Met
450 455 460

Phe Pro Gly Tyr Tyr Lys Arg Pro Glu Ile Thr Ala Glu Met Phe Asp
465 470 475 480

Glu Asp Gly Tyr Tyr Arg Thr Gly Asp Ile Val Ala Glu Leu Gly Pro
485 490 495

Asp His Leu Glu Tyr Leu Asp Arg Arg Asn Asn Val Leu Lys Leu Ser
500 505 510

Gln Gly Glu Phe Val Thr Val Ser Lys Leu Glu Ala Val Phe Gly Asp
515 520 525

Ser Pro Leu Val Arg Gln Ile Tyr Val Tyr Gly Asn Ser Ala Arg Ser
530 535 540

Tyr Leu Leu Ala Val Val Val Pro Thr Glu Glu Ala Leu Ser Arg Trp
545 550 555 560

Asp Gly Asp Glu Leu Lys Ser Arg Ile Ser Asp Ser Leu Gln Asp Ala
565 570 575

Ala Arg Ala Ala Gly Leu Gln Ser Tyr Glu Ile Pro Arg Asp Phe Leu
580 585 590

Val Glu Thr Thr Pro Phe Thr Leu Glu Asn Gly Leu Leu Thr Gly Ile
595 600 605

Arg Lys Leu Ala Arg Pro Lys Leu Lys Ala His Tyr Gly Glu Arg Leu
610 615 620

Glu Gln Leu Tyr Thr Asp Leu Ala Glu Gly Gln Ala Asn Glu Leu Arg

625 630 635 640

Glu Leu Arg Arg Asn Gly Ala Asp Arg Pro Val Val Glu Thr Val Ser
645 650 655

Arg Ala Ala Val Ala Leu Leu Gly Ala Ser Val Thr Asp Leu Arg Ser
660 665 670

Asp Ala His Phe Thr Asp Leu Gly Gly Asp Ser Leu Ser Ala Leu Ser
675 680 685

Phe Ser Asn Leu Leu His Glu Ile Phe Asp Val Asp Val Pro Val Gly
690 695 700

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

Glu Gly Glu Leu Arg Gly Ser Lys Arg Pro Thr Tyr Ala Ser Val His
725 730 735

Gly Arg Asp Ala Thr Glu Val Arg Ala Arg Asp Leu Ala Leu Gly Lys
740 745 750

Phe Ile Asp Ala Lys Thr Leu Ser Ala Ala Pro Gly Leu Pro Arg Ser
755 760 765

Gly Thr Glu Ile Arg Thr Val Leu Leu Thr Gly Ala Thr Gly Phe Leu
770 775 780

Gly Arg Tyr Leu Ala Leu Glu Trp Leu Glu Arg Met Asp Leu Val Asp
785 790 795 800

Gly Lys Val Ile Cys Leu Val Arg Ala Arg Ser Asp Asp Glu Ala Arg
805 810 815

Ala Arg Leu Asp Ala Thr Phe Asp Thr Gly Asp Ala Thr Leu Leu Glu
820 825 830

His Tyr Arg Ala Leu Ala Ala Asp His Leu Glu Val Ile Ala Gly Asp
835 840 845

Lys Gly Glu Ala Asp Leu Gly Leu Asp His Asp Thr Trp Gln Arg Leu
850 855 860

Ala Asp Thr Val Asp Leu Ile Val Asp Pro Ala Ala Leu Val Asn His
865 870 875 880

Val Leu Pro Tyr Ser Gln Met Phe Gly Pro Asn Ala Leu Gly Thr Ala
885 890 895

Glu Leu Ile Arg Ile Ala Leu Thr Thr Thr Ile Lys Pro Tyr Val Tyr

900 905 910

Val Ser Thr Ile Gly Val Gly Gln Gly Ile Ser Pro Glu Ala Phe Val
915 920 925

Glu Asp Ala Asp Ile Arg Glu Ile Ser Ala Thr Arg Arg Val Asp Asp
930 935 940

Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys Trp Ala Gly Glu Val Leu
945 950 955 960

Leu Arg Glu Ala His Asp Trp Cys Gly Leu Pro Val Ser Val Phe Arg
965 970 975

Cys Asp Met Ile Leu Ala Asp Thr Thr Tyr Ser Gly Gln Leu Asn Leu
980 985 990

Pro Asp Met Phe Thr Arg Leu Met Leu Ser Leu Val Ala Thr Gly Ile
995 1000 1005

Ala Pro Gly Ser Phe Tyr Glu Leu Asp Ala Asp Gly Asn Arg Gln
1010 1015 1020

Arg Ala His Tyr Asp Gly Leu Pro Val Glu Phe Ile Ala Glu Ala
1025 1030 1035

Ile Ser Thr Ile Gly Ser Gln Val Thr Asp Gly Phe Glu Thr Phe
1040 1045 1050

His Val Met Asn Pro Tyr Asp Asp Gly Ile Gly Leu Asp Glu Tyr
1055 1060 1065

Val Asp Trp Leu Ile Glu Ala Gly Tyr Pro Val His Arg Val Asp
1070 1075 1080

Asp Tyr Ala Thr Trp Leu Ser Arg Phe Glu Thr Ala Leu Arg Ala
1085 1090 1095

Leu Pro Glu Arg Gln Arg Gln Ala Ser Leu Leu Pro Leu Leu His
1100 1105 1110

Asn Tyr Gln Gln Pro Ser Pro Pro Val Cys Gly Ala Met Ala Pro
1115 1120 1125

Thr Asp Arg Phe Arg Ala Ala Val Gln Asp Ala Lys Ile Gly Pro
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1160 1165

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<220>
<223> primer

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<210> 127
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<220>

<223> primer

<400> 127
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<210> 128
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<400> 128
gagtggcata tgacaattga aacgcgcgaa g 31

<210> 129
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<220>
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<400> 129
tctattgctg gtttacctag gttatcatta tcatgc 36

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<211> 1137
<212> DNA
<213> Bacillus subtilis

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<222> (1)..(1137)

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Met Ile Ile Gly Val Pro Lys Glu Ile Lys Asn Asn Glu Asn Arg Val
1 5 10 15

gca tta aca ccc ggg ggc gtt tct cag ctc att tca aac ggc cac cgg 96
Ala Leu Thr Pro Gly Gly Val Ser Gln Leu Ile Ser Asn Gly His Arg
20 25 30

gtg ctg gtt gaa aca ggc gcg ggc ctt gga agc gga ttt gaa aat gaa 144
Val Leu Val Glu Thr Gly Ala Gly Leu Gly Ser Gly Phe Glu Asn Glu
35 40 45

gcc tat gag tca gca gga gcg gaa atc att gct gat ccg aag cag gtc 192
Ala Tyr Glu Ser Ala Gly Ala Glu Ile Ile Ala Asp Pro Lys Gln Val
50 55 60

tgg gac gcc gaa atg gtc atg aaa gta aaa gaa ccg ctg ccg gaa gaa 240
Trp Asp Ala Glu Met Val Met Lys Val Lys Glu Pro Leu Pro Glu Glu
65 70 75 80

tat gtt tat ttt cgc aaa gga ctt gtg ctg ttt acg tac ctt cat tta 288
Tyr Val Tyr Phe Arg Lys Gly Leu Val Leu Phe Thr Tyr Leu His Leu
85 90 95

gca gct gag cct gag ctt gca cag gcc ttg aag gat aaa gga gta act 336
Ala Ala Glu Pro Glu Leu Ala Gln Ala Leu Lys Asp Lys Gly Val Thr
100 105 110

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gcc atc gca tat gaa acg gtc agt gaa ggc cgg aca ttg cct ctt ctg        384
Ala Ile Ala Tyr Glu Thr Val Ser Glu Gly Arg Thr Leu Pro Leu Leu
        115                 120                 125

acg cca atg tca gag gtt gcg ggc aga atg gca gcg caa atc ggc gct        432
Thr Pro Met Ser Glu Val Ala Gly Arg Met Ala Ala Gln Ile Gly Ala
    130                 135                 140

caa ttc tta gaa aag cct aaa ggc gga aaa ggc att ctg ctt gcc ggg        480
Gln Phe Leu Glu Lys Pro Lys Gly Gly Lys Gly Ile Leu Leu Ala Gly
145                 150                 155                 160

gtg cct ggc gtt tcc cgc gga aaa gta aca att atc gga gga ggc gtt        528
Val Pro Gly Val Ser Arg Gly Lys Val Thr Ile Ile Gly Gly Gly Val
                165                 170                 175

gtc ggg aca aac gcg gcg aaa atg gct gtc ggc ctc ggt gca gat gtg        576
Val Gly Thr Asn Ala Ala Lys Met Ala Val Gly Leu Gly Ala Asp Val
            180                 185                 190

acg atc att gac tta aac gca gac cgc ttg cgc cag ctt gat gac atc        624
Thr Ile Ile Asp Leu Asn Ala Asp Arg Leu Arg Gln Leu Asp Asp Ile
        195                 200                 205

ttc ggc cat cag att aaa acg tta att tct aat ccg gtc aat att gct        672
Phe Gly His Gln Ile Lys Thr Leu Ile Ser Asn Pro Val Asn Ile Ala
    210                 215                 220

gat gct gtg gcg gaa gcg gat ctc ctc att tgc gcg gta tta att ccg        720
Asp Ala Val Ala Glu Ala Asp Leu Leu Ile Cys Ala Val Leu Ile Pro
225                 230                 235                 240

ggt gct aaa gct ccg act ctt gtc act gag gaa atg gta aaa caa atg        768
Gly Ala Lys Ala Pro Thr Leu Val Thr Glu Glu Met Val Lys Gln Met
                245                 250                 255

aaa ccc ggt tca gtt att gtt gat gta gcg atc gac caa ggc ggc atc        816
Lys Pro Gly Ser Val Ile Val Asp Val Ala Ile Asp Gln Gly Gly Ile
            260                 265                 270

gtc gaa act gtc gac cat atc aca aca cat gat cag cca aca tat gaa        864
Val Glu Thr Val Asp His Ile Thr Thr His Asp Gln Pro Thr Tyr Glu
        275                 280                 285

aaa cac ggg gtt gtg cat tat gct gta gcg aac atg cca ggc gca gtc        912
Lys His Gly Val Val His Tyr Ala Val Ala Asn Met Pro Gly Ala Val
    290                 295                 300

cct cgt aca tca aca atc gcc ctg act aac gtt act gtt cca tac gcg        960
Pro Arg Thr Ser Thr Ile Ala Leu Thr Asn Val Thr Val Pro Tyr Ala
305                 310                 315                 320

ctg caa atc gcg aac aaa ggg gca gta aaa gcg ctc gca gac aat acg       1008
Leu Gln Ile Ala Asn Lys Gly Ala Val Lys Ala Leu Ala Asp Asn Thr
                325                 330                 335

gca ctg aga gcg ggt tta aac acc gca aac gga cac gtg acc tat gaa       1056
Ala Leu Arg Ala Gly Leu Asn Thr Ala Asn Gly His Val Thr Tyr Glu
            340                 345                 350

gct gta gca aga gat cta ggc tat gag tat gtt cct gcc gag aaa gct       1104
Ala Val Ala Arg Asp Leu Gly Tyr Glu Tyr Val Pro Ala Glu Lys Ala
        355                 360                 365

tta cag gat gaa tca tct gtg gcg ggt gct taa                          1137
Leu Gln Asp Glu Ser Ser Val Ala Gly Ala
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<212> PRT
<213> Bacillus subtilis

<400> 131

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            20                  25                  30

Val Leu Val Glu Thr Gly Ala Gly Leu Gly Ser Gly Phe Glu Asn Glu
        35                  40                  45

Ala Tyr Glu Ser Ala Gly Ala Glu Ile Ile Ala Asp Pro Lys Gln Val
    50                  55                  60

Trp Asp Ala Glu Met Val Met Lys Val Lys Glu Pro Leu Pro Glu Glu
65                  70                  75                  80

Tyr Val Tyr Phe Arg Lys Gly Leu Val Leu Phe Thr Tyr Leu His Leu
                85                  90                  95

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

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

Thr Pro Met Ser Glu Val Ala Gly Arg Met Ala Ala Gln Ile Gly Ala
    130                 135                 140

Gln Phe Leu Glu Lys Pro Lys Gly Gly Lys Gly Ile Leu Leu Ala Gly
145                 150                 155                 160

Val Pro Gly Val Ser Arg Gly Lys Val Thr Ile Ile Gly Gly Gly Val
                165                 170                 175

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

Thr Ile Ile Asp Leu Asn Ala Asp Arg Leu Arg Gln Leu Asp Asp Ile
        195                 200                 205

Phe Gly His Gln Ile Lys Thr Leu Ile Ser Asn Pro Val Asn Ile Ala
    210                 215                 220

Asp Ala Val Ala Glu Ala Asp Leu Leu Ile Cys Ala Val Leu Ile Pro
225                 230                 235                 240
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Gly Ala Lys Ala Pro Thr Leu Val Thr Glu Glu Met Val Lys Gln Met
                245                 250                 255

Lys Pro Gly Ser Val Ile Val Asp Val Ala Ile Asp Gln Gly Gly Ile
            260                 265                 270

Val Glu Thr Val Asp His Ile Thr Thr His Asp Gln Pro Thr Tyr Glu
        275                 280                 285

Lys His Gly Val Val His Tyr Ala Val Ala Asn Met Pro Gly Ala Val
    290                 295                 300

Pro Arg Thr Ser Thr Ile Ala Leu Thr Asn Val Thr Val Pro Tyr Ala
305                 310                 315                 320

Leu Gln Ile Ala Asn Lys Gly Ala Val Lys Ala Leu Ala Asp Asn Thr
                325                 330                 335

Ala Leu Arg Ala Gly Leu Asn Thr Ala Asn Gly His Val Thr Tyr Glu
            340                 345                 350

Ala Val Ala Arg Asp Leu Gly Tyr Glu Tyr Val Pro Ala Glu Lys Ala
        355                 360                 365

Leu Gln Asp Glu Ser Ser Val Ala Gly Ala
    370                 375


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<212>  DNA
<213>  Chromobacterium violaceum


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<222>  (1)..(1380)

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Met Gln Lys Gln Arg Thr Thr Ser Gln Trp Arg Glu Leu Asp Ala Ala
1               5                   10                  15

cat cat ctc cat ccg ttt acc gat acc gcg agc ctc aat cag gcg ggt          96
His His Leu His Pro Phe Thr Asp Thr Ala Ser Leu Asn Gln Ala Gly
            20                  25                  30

gcg cgt gtg atg acc cgt ggc gaa ggc gtg tat ctc tgg gat agc gaa         144
Ala Arg Val Met Thr Arg Gly Glu Gly Val Tyr Leu Trp Asp Ser Glu
        35                  40                  45

ggc aac aaa att att gat ggc atg gcg ggc ctc tgg tgc gtg aac gtg         192
Gly Asn Lys Ile Ile Asp Gly Met Ala Gly Leu Trp Cys Val Asn Val
    50                  55                  60

ggc tat ggc cgt aaa gat ttt gcg gaa gcg gcg cgt cgt cag atg gaa         240
Gly Tyr Gly Arg Lys Asp Phe Ala Glu Ala Ala Arg Arg Gln Met Glu
65                  70                  75                  80
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gaa ctc ccg ttt tat aac acc ttc ttt aaa acc acc cat ccg gcg gtg        288
Glu Leu Pro Phe Tyr Asn Thr Phe Phe Lys Thr Thr His Pro Ala Val
                85                  90                  95

gtg gaa ctc agc agc ctc ctc gcc gaa gtt acc ccg gca ggt ttt gat        336
Val Glu Leu Ser Ser Leu Leu Ala Glu Val Thr Pro Ala Gly Phe Asp
            100                 105                 110

cgt gtg ttt tat acc aac agc ggc agc gaa agc gtg gat acc atg att        384
Arg Val Phe Tyr Thr Asn Ser Gly Ser Glu Ser Val Asp Thr Met Ile
        115                 120                 125

cgt atg gtg cgt cgt tat tgg gat gtg cag ggc aaa ccg gaa aaa aaa        432
Arg Met Val Arg Arg Tyr Trp Asp Val Gln Gly Lys Pro Glu Lys Lys
    130                 135                 140

acc ctc att ggc cgt tgg aac ggc tat cac ggc agc acc att ggc ggt        480
Thr Leu Ile Gly Arg Trp Asn Gly Tyr His Gly Ser Thr Ile Gly Gly
145                 150                 155                 160

gcg agc ctc ggc ggc atg aaa tat atg cat gaa cag ggc gat ctc ccg        528
Ala Ser Leu Gly Gly Met Lys Tyr Met His Glu Gln Gly Asp Leu Pro
                165                 170                 175

att ccg ggc atg gcg cat att gaa cag ccg tgg tgg tat aaa cat ggc        576
Ile Pro Gly Met Ala His Ile Glu Gln Pro Trp Trp Tyr Lys His Gly
            180                 185                 190

aaa gat atg acc ccg gat gaa ttt ggc gtg gtt gcg gcg cgt tgg ctc        624
Lys Asp Met Thr Pro Asp Glu Phe Gly Val Val Ala Ala Arg Trp Leu
        195                 200                 205

gaa gaa aaa att ctc gaa atc ggc gcg gat aaa gtg gcg gcg ttt gtg        672
Glu Glu Lys Ile Leu Glu Ile Gly Ala Asp Lys Val Ala Ala Phe Val
    210                 215                 220

ggc gaa ccg att cag ggt gcg ggc ggt gtg att gtt ccg ccg gca acc        720
Gly Glu Pro Ile Gln Gly Ala Gly Gly Val Ile Val Pro Pro Ala Thr
225                 230                 235                 240

tat tgg ccg gaa att gaa cgt att tgc cgc aaa tat gat gtg ctc ctc        768
Tyr Trp Pro Glu Ile Glu Arg Ile Cys Arg Lys Tyr Asp Val Leu Leu
                245                 250                 255

gtt gcg gat gaa gtg att tgc ggc ttt ggc cgt acc ggc gaa tgg ttt        816
Val Ala Asp Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Glu Trp Phe
            260                 265                 270

ggc cat cag cat ttt ggc ttt cag ccg gac ctc ttt acc gcg gcg aaa        864
Gly His Gln His Phe Gly Phe Gln Pro Asp Leu Phe Thr Ala Ala Lys
        275                 280                 285

ggc ctc agc agc ggc tat ctc ccg att ggc gcg gtg ttt gtg ggc aaa        912
Gly Leu Ser Ser Gly Tyr Leu Pro Ile Gly Ala Val Phe Val Gly Lys
    290                 295                 300

cgt gtt gcg gaa ggt ctc att gcg ggc ggt gat ttt aac cat ggc ttt        960
Arg Val Ala Glu Gly Leu Ile Ala Gly Gly Asp Phe Asn His Gly Phe
305                 310                 315                 320

acc tat agc ggc cat ccg gtg tgt gcg gcg gtg gcg cat gcg aat gtt       1008
Thr Tyr Ser Gly His Pro Val Cys Ala Ala Val Ala His Ala Asn Val
                325                 330                 335

gcg gcg ctc cgt gat gaa ggc att gtg cag cgt gtg aaa gat gat att       1056
Ala Ala Leu Arg Asp Glu Gly Ile Val Gln Arg Val Lys Asp Asp Ile
            340                 345                 350
```

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ggc ccg tat atg cag aaa cgt tgg cgt gaa acc ttt agc cgt ttt gaa       1104
Gly Pro Tyr Met Gln Lys Arg Trp Arg Glu Thr Phe Ser Arg Phe Glu
        355                 360                 365

cat gtg gat gat gtg cgt ggc gtg ggc atg gtg cag gcg ttt acc ctc       1152
His Val Asp Asp Val Arg Gly Val Gly Met Val Gln Ala Phe Thr Leu
    370                 375                 380

gtg aaa aac aaa gcg aaa cgt gaa ctc ttt ccg gat ttt ggc gaa att       1200
Val Lys Asn Lys Ala Lys Arg Glu Leu Phe Pro Asp Phe Gly Glu Ile
385                 390                 395                 400

ggc acc ctc tgc cgc gat att ttt ttt cgc aac aac ctc att atg cgt       1248
Gly Thr Leu Cys Arg Asp Ile Phe Phe Arg Asn Asn Leu Ile Met Arg
                405                 410                 415

gcg tgc ggc gat cac att gtg tct gca ccg ccg ctc gtt atg acc cgt       1296
Ala Cys Gly Asp His Ile Val Ser Ala Pro Pro Leu Val Met Thr Arg
            420                 425                 430

gcg gaa gtg gat gaa atg ctc gcc gtg gcg gaa cgt tgc ctc gaa gaa       1344
Ala Glu Val Asp Glu Met Leu Ala Val Ala Glu Arg Cys Leu Glu Glu
        435                 440                 445

ttt gaa cag acc ctc aaa gcg cgt ggc ctc gcc taa                      1380
Phe Glu Gln Thr Leu Lys Ala Arg Gly Leu Ala
    450                 455
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<210> 133
<211> 459
<212> PRT
<213> Chromobacterium violaceum

<400> 133

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His His Leu His Pro Phe Thr Asp Thr Ala Ser Leu Asn Gln Ala Gly
            20                  25                  30

Ala Arg Val Met Thr Arg Gly Glu Gly Val Tyr Leu Trp Asp Ser Glu
        35                  40                  45

Gly Asn Lys Ile Ile Asp Gly Met Ala Gly Leu Trp Cys Val Asn Val
    50                  55                  60

Gly Tyr Gly Arg Lys Asp Phe Ala Glu Ala Ala Arg Arg Gln Met Glu
65                  70                  75                  80

Glu Leu Pro Phe Tyr Asn Thr Phe Phe Lys Thr Thr His Pro Ala Val
                85                  90                  95

Val Glu Leu Ser Ser Leu Leu Ala Glu Val Thr Pro Ala Gly Phe Asp
            100                 105                 110

Arg Val Phe Tyr Thr Asn Ser Gly Ser Glu Ser Val Asp Thr Met Ile
        115                 120                 125
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Arg Met Val Arg Arg Tyr Trp Asp Val Gln Gly Lys Pro Glu Lys Lys
    130                 135                 140

Thr Leu Ile Gly Arg Trp Asn Gly Tyr His Gly Ser Thr Ile Gly Gly
145                 150                 155                 160

Ala Ser Leu Gly Gly Met Lys Tyr Met His Glu Gln Gly Asp Leu Pro
                165                 170                 175

Ile Pro Gly Met Ala His Ile Glu Gln Pro Trp Trp Tyr Lys His Gly
            180                 185                 190

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

Glu Glu Lys Ile Leu Glu Ile Gly Ala Asp Lys Val Ala Ala Phe Val
    210                 215                 220

Gly Glu Pro Ile Gln Gly Ala Gly Gly Val Ile Val Pro Pro Ala Thr
225                 230                 235                 240

Tyr Trp Pro Glu Ile Glu Arg Ile Cys Arg Lys Tyr Asp Val Leu Leu
                245                 250                 255

Val Ala Asp Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Glu Trp Phe
            260                 265                 270

Gly His Gln His Phe Gly Phe Gln Pro Asp Leu Phe Thr Ala Ala Lys
        275                 280                 285

Gly Leu Ser Ser Gly Tyr Leu Pro Ile Gly Ala Val Phe Val Gly Lys
    290                 295                 300

Arg Val Ala Glu Gly Leu Ile Ala Gly Gly Asp Phe Asn His Gly Phe
305                 310                 315                 320

Thr Tyr Ser Gly His Pro Val Cys Ala Ala Val Ala His Ala Asn Val
                325                 330                 335

Ala Ala Leu Arg Asp Glu Gly Ile Val Gln Arg Val Lys Asp Asp Ile
            340                 345                 350

Gly Pro Tyr Met Gln Lys Arg Trp Arg Glu Thr Phe Ser Arg Phe Glu
        355                 360                 365

His Val Asp Asp Val Arg Gly Val Gly Met Val Gln Ala Phe Thr Leu
    370                 375                 380

Val Lys Asn Lys Ala Lys Arg Glu Leu Phe Pro Asp Phe Gly Glu Ile
385                 390                 395                 400
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Gly Thr Leu Cys Arg Asp Ile Phe Phe Arg Asn Asn Leu Ile Met Arg
405 410 415

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

Ala Glu Val Asp Glu Met Leu Ala Val Ala Glu Arg Cys Leu Glu Glu
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Phe Glu Gln Thr Leu Lys Ala Arg Gly Leu Ala
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ttg ggt caa ctg cgt ggc aag cgt gtc ctg att acg ggc acc acg ggt        96
Leu Gly Gln Leu Arg Gly Lys Arg Val Leu Ile Thr Gly Thr Thr Gly
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ttc ctg ggt aag gtc gtg ctg gag cgc ttg att cgc gct gtg ccg gac       144
Phe Leu Gly Lys Val Val Leu Glu Arg Leu Ile Arg Ala Val Pro Asp
        35                  40                  45

att ggt gcg atc tat ttg ttg atc cgt ggt aat aag cgt cac ccg gat       192
Ile Gly Ala Ile Tyr Leu Leu Ile Arg Gly Asn Lys Arg His Pro Asp
    50                  55                  60

gca cgt tct cgc ttt ttg gaa gag atc gcg acc agc tcg gtg ttc gat       240
Ala Arg Ser Arg Phe Leu Glu Glu Ile Ala Thr Ser Ser Val Phe Asp
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cgc ctg cgt gaa gca gac tcc gag ggt ttt gac gca ttc ctg gaa gag       288
Arg Leu Arg Glu Ala Asp Ser Glu Gly Phe Asp Ala Phe Leu Glu Glu
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cgc att cac tgt gtg act ggc gag gtc acg gaa gca ggt ttt ggc atc       336
Arg Ile His Cys Val Thr Gly Glu Val Thr Glu Ala Gly Phe Gly Ile
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ggc caa gag gac tac cgc aaa ctg gcg acc gaa ttg gac gcg gtg att       384
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Gly Gln Glu Asp Tyr Arg Lys Leu Ala Thr Glu Leu Asp Ala Val Ile
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Asn Ser Ala Ala Ser Val Asn Phe Arg Glu Glu Leu Asp Lys Ala Leu
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gcg atc aac act ctg tgc ctg cgc aat atc gcg ggt atg gtg gat ctg        480
Ala Ile Asn Thr Leu Cys Leu Arg Asn Ile Ala Gly Met Val Asp Leu
145                 150                 155                 160

aat cca aaa ctg gcg gtc ctg caa gtt agc act tgc tat gtg aac ggt        528
Asn Pro Lys Leu Ala Val Leu Gln Val Ser Thr Cys Tyr Val Asn Gly
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atg aac agc ggt caa gtt acc gaa agc gtg atc aag ccg gca ggt gaa        576
Met Asn Ser Gly Gln Val Thr Glu Ser Val Ile Lys Pro Ala Gly Glu
            180                 185                 190

gcg gtt ccg cgt agc ccg gat ggt ttt tac gag att gaa gag ctg gtg        624
Ala Val Pro Arg Ser Pro Asp Gly Phe Tyr Glu Ile Glu Glu Leu Val
        195                 200                 205

cgc ctg ctg cag gac aaa atc gag gac gtt cag gct cgt tat agc ggc        672
Arg Leu Leu Gln Asp Lys Ile Glu Asp Val Gln Ala Arg Tyr Ser Gly
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Lys Val Leu Glu Arg Lys Leu Val Asp Leu Gly Ile Arg Glu Ala Asn
225                 230                 235                 240

cgt tat ggc tgg agc gac acg tac acg ttt acc aag tgg ctg ggt gag        768
Arg Tyr Gly Trp Ser Asp Thr Tyr Thr Phe Thr Lys Trp Leu Gly Glu
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cag ctg ttg atg aaa gcg ctg aat ggt cgc acc ttg acc atc ctg cgt        816
Gln Leu Leu Met Lys Ala Leu Asn Gly Arg Thr Leu Thr Ile Leu Arg
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ccg agc att att gag tct gcc ctg gaa gaa cct gcg cct ggc tgg atc        864
Pro Ser Ile Ile Glu Ser Ala Leu Glu Glu Pro Ala Pro Gly Trp Ile
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gag ggt gtg aag gtt gca gac gca atc att ctg gcc tat gcg cgt gag        912
Glu Gly Val Lys Val Ala Asp Ala Ile Ile Leu Ala Tyr Ala Arg Glu
    290                 295                 300

aag gtt acc ctg ttc ccg ggt aag cgt agc ggt att atc gat gtc atc        960
Lys Val Thr Leu Phe Pro Gly Lys Arg Ser Gly Ile Ile Asp Val Ile
305                 310                 315                 320

ccg gtt gac ctg gtc gcc aac agc att att ctg agc ctg gcg gaa gcg       1008
Pro Val Asp Leu Val Ala Asn Ser Ile Ile Leu Ser Leu Ala Glu Ala
                325                 330                 335

ctg ggc gag cca ggc cgt cgc cgc atc tat caa tgc tgt tct ggt ggt       1056
Leu Gly Glu Pro Gly Arg Arg Arg Ile Tyr Gln Cys Cys Ser Gly Gly
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ggt aac ccg atc agc ctg ggt gag ttc atc gac cat ctg atg gcc gag       1104
Gly Asn Pro Ile Ser Leu Gly Glu Phe Ile Asp His Leu Met Ala Glu
        355                 360                 365

agc aaa gca aat tac gcc gca tac gat cac ctg ttc tac cgt cag ccg       1152
Ser Lys Ala Asn Tyr Ala Ala Tyr Asp His Leu Phe Tyr Arg Gln Pro
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Ser Lys Pro Phe Leu Ala Val Asn Arg Ala Leu Phe Asp Leu Val Ile
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Ser Gly Val Arg Leu Pro Leu Ser Leu Thr Asp Arg Val Leu Lys Leu
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ttg ggt aac tcc cgt gat ctg aaa atg ctg cgc aat ctg gac acc acc       1296
Leu Gly Asn Ser Arg Asp Leu Lys Met Leu Arg Asn Leu Asp Thr Thr
            420                 425                 430

caa tcc ctg gcc acc att ttc ggc ttc tat acc gct ccg gac tac atc       1344
Gln Ser Leu Ala Thr Ile Phe Gly Phe Tyr Thr Ala Pro Asp Tyr Ile
        435                 440                 445

ttc cgt aat gat gaa ctg atg gcc ctg gcc aac cgt atg ggc gag gtc       1392
Phe Arg Asn Asp Glu Leu Met Ala Leu Ala Asn Arg Met Gly Glu Val
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gat aaa ggc ctg ttt ccg gtt gat gcg cgt ctg att gac tgg gag ctg       1440
Asp Lys Gly Leu Phe Pro Val Asp Ala Arg Leu Ile Asp Trp Glu Leu
465                 470                 475                 480

tac ctg cgt aaa atc cat ctg gct ggc ctg aac cgt tac gca ttg aaa       1488
Tyr Leu Arg Lys Ile His Leu Ala Gly Leu Asn Arg Tyr Ala Leu Lys
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gaa cgt aaa gtc tac tcg ctg aaa acc gct cgt cag cgc aaa aag gcc       1536
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gcg taa tga                                                         1545
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Phe Leu Gly Lys Val Val Leu Glu Arg Leu Ile Arg Ala Val Pro Asp
        35                  40                  45

Ile Gly Ala Ile Tyr Leu Leu Ile Arg Gly Asn Lys Arg His Pro Asp
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Ala Arg Ser Arg Phe Leu Glu Glu Ile Ala Thr Ser Ser Val Phe Asp
65                  70                  75                  80

Arg Leu Arg Glu Ala Asp Ser Glu Gly Phe Asp Ala Phe Leu Glu Glu
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Arg Ile His Cys Val Thr Gly Glu Val Thr Glu Ala Gly Phe Gly Ile
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100 105 110

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

Asn Ser Ala Ala Ser Val Asn Phe Arg Glu Glu Leu Asp Lys Ala Leu
130 135 140

Ala Ile Asn Thr Leu Cys Leu Arg Asn Ile Ala Gly Met Val Asp Leu
145 150 155 160

Asn Pro Lys Leu Ala Val Leu Gln Val Ser Thr Cys Tyr Val Asn Gly
165 170 175

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

Ala Val Pro Arg Ser Pro Asp Gly Phe Tyr Glu Ile Glu Glu Leu Val
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Arg Leu Leu Gln Asp Lys Ile Glu Asp Val Gln Ala Arg Tyr Ser Gly
210 215 220

Lys Val Leu Glu Arg Lys Leu Val Asp Leu Gly Ile Arg Glu Ala Asn
225 230 235 240

Arg Tyr Gly Trp Ser Asp Thr Tyr Thr Phe Thr Lys Trp Leu Gly Glu
245 250 255

Gln Leu Leu Met Lys Ala Leu Asn Gly Arg Thr Leu Thr Ile Leu Arg
260 265 270

Pro Ser Ile Ile Glu Ser Ala Leu Glu Glu Pro Ala Pro Gly Trp Ile
275 280 285

Glu Gly Val Lys Val Ala Asp Ala Ile Ile Leu Ala Tyr Ala Arg Glu
290 295 300

Lys Val Thr Leu Phe Pro Gly Lys Arg Ser Gly Ile Ile Asp Val Ile
305 310 315 320

Pro Val Asp Leu Val Ala Asn Ser Ile Ile Leu Ser Leu Ala Glu Ala
325 330 335

Leu Gly Glu Pro Gly Arg Arg Arg Ile Tyr Gln Cys Cys Ser Gly Gly
340 345 350

Gly Asn Pro Ile Ser Leu Gly Glu Phe Ile Asp His Leu Met Ala Glu
355 360 365

Ser Lys Ala Asn Tyr Ala Ala Tyr Asp His Leu Phe Tyr Arg Gln Pro

370 375 380

Ser Lys Pro Phe Leu Ala Val Asn Arg Ala Leu Phe Asp Leu Val Ile
385 390 395 400

Ser Gly Val Arg Leu Pro Leu Ser Leu Thr Asp Arg Val Leu Lys Leu
405 410 415

Leu Gly Asn Ser Arg Asp Leu Lys Met Leu Arg Asn Leu Asp Thr Thr
420 425 430

Gln Ser Leu Ala Thr Ile Phe Gly Phe Tyr Thr Ala Pro Asp Tyr Ile
435 440 445

Phe Arg Asn Asp Glu Leu Met Ala Leu Ala Asn Arg Met Gly Glu Val
450 455 460

Asp Lys Gly Leu Phe Pro Val Asp Ala Arg Leu Ile Asp Trp Glu Leu
465 470 475 480

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gtt gaa aaa ctc ctg gcc cgt ggc ggt acc gtt tac gtc ctg gtg cgc 96
Val Glu Lys Leu Leu Ala Arg Gly Gly Thr Val Tyr Val Leu Val Arg
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gaa cag tct cag gat aaa ctg gaa cgc ctg cgt gag cgt tgg ggt gcc 144
Glu Gln Ser Gln Asp Lys Leu Glu Arg Leu Arg Glu Arg Trp Gly Ala
35 40 45

gat gac aaa caa gtc aaa gcc gtt atc ggc gac ctg acc agc aag aac 192
Asp Asp Lys Gln Val Lys Ala Val Ile Gly Asp Leu Thr Ser Lys Asn
50 55 60

ctg ggc atc gac gcc aag acc ctg aaa tcg ctg aaa ggt aac att gac 240
Leu Gly Ile Asp Ala Lys Thr Leu Lys Ser Leu Lys Gly Asn Ile Asp

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His Val Phe His Leu Ala Ala Val Tyr Asp Met Gly Ala Asp Glu Glu
                85                  90                  95

gcg caa gca gcg acc aac att gag ggt acc cgt gcc gct gtc cag gca        336
Ala Gln Ala Ala Thr Asn Ile Glu Gly Thr Arg Ala Ala Val Gln Ala
            100                 105                 110

gcc gag gcg atg ggc gct aag cac ttt cat cac gtt tcc agc att gcg        384
Ala Glu Ala Met Gly Ala Lys His Phe His His Val Ser Ser Ile Ala
        115                 120                 125

gca gcc ggt ctg ttc aag ggc atc ttt cgt gag gat atg ttc gaa gag        432
Ala Ala Gly Leu Phe Lys Gly Ile Phe Arg Glu Asp Met Phe Glu Glu
    130                 135                 140

gcc gaa aag ctg gat cac ccg tat ctg cgc acc aaa cac gag agc gaa        480
Ala Glu Lys Leu Asp His Pro Tyr Leu Arg Thr Lys His Glu Ser Glu
145                 150                 155                 160

aag gtc gtc cgc gaa gag tgc aag gtt ccg ttc cgt atc tat cgt ccg        528
Lys Val Val Arg Glu Glu Cys Lys Val Pro Phe Arg Ile Tyr Arg Pro
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Gly Met Val Ile Gly His Ser Glu Thr Gly Glu Met Asp Lys Val Asp
            180                 185                 190

ggc ccg tat tac ttc ttc aaa atg atc caa aag atc cgc cac gcg ctg        624
Gly Pro Tyr Tyr Phe Phe Lys Met Ile Gln Lys Ile Arg His Ala Leu
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ccg cag tgg gtg ccg acc att ggt atc gaa ggt ggt cgt ctg aat att        672
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    210                 215                 220

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Val Pro Val Asp Phe Val Val Asp Ala Leu Asp His Ile Ala His Leu
225                 230                 235                 240

gaa ggc gag gat ggc aac tgt ttc cat ctg gtg gac agc gac cca tac        768
Glu Gly Glu Asp Gly Asn Cys Phe His Leu Val Asp Ser Asp Pro Tyr
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Lys Val Gly Glu Ile Leu Asn Ile Phe Cys Glu Ala Gly His Ala Pro
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Arg Met Gly Met Arg Ile Asp Ser Arg Met Phe Gly Phe Ile Pro Pro
        275                 280                 285

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Phe Ile Arg Gln Ser Ile Lys Asn Leu Pro Pro Val Lys Arg Ile Thr
    290                 295                 300

ggt gca ctg ctg gac gat atg ggt att ccg ccg agc gtc atg tct ttc        960
Gly Ala Leu Leu Asp Asp Met Gly Ile Pro Pro Ser Val Met Ser Phe
305                 310                 315                 320

atc aat tat ccg acg cgc ttc gat act cgt gag ctg gag cgt gtt ttg       1008
Ile Asn Tyr Pro Thr Arg Phe Asp Thr Arg Glu Leu Glu Arg Val Leu
                325                 330                 335

aag ggc acc gat atc gaa gtt ccg cgt ctg ccg agc tac gcc cct gtg       1056
Lys Gly Thr Asp Ile Glu Val Pro Arg Leu Pro Ser Tyr Ala Pro Val
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                340                 345                 350

atc tgg gac tat tgg gag cgt aac ctg gac cca gat ctg ttt aag gac      1104
Ile Trp Asp Tyr Trp Glu Arg Asn Leu Asp Pro Asp Leu Phe Lys Asp
        355                 360                 365

cgt acg ttg aaa ggt acc gtt gaa ggc aag gtg tgc gtt gtc acg ggc      1152
Arg Thr Leu Lys Gly Thr Val Glu Gly Lys Val Cys Val Val Thr Gly
    370                 375                 380

gca acc agc ggt att ggc ctg gcg acc gcc gag aag ctg gca gag gcg      1200
Ala Thr Ser Gly Ile Gly Leu Ala Thr Ala Glu Lys Leu Ala Glu Ala
385                 390                 395                 400

ggt gct atc ctg gtc att ggt gca cgt acc aaa gaa acg ctg gac gag      1248
Gly Ala Ile Leu Val Ile Gly Ala Arg Thr Lys Glu Thr Leu Asp Glu
                405                 410                 415

gtg gca gcg agc ctg gaa gcg aaa ggt ggt aac gtt cac gct tat caa      1296
Val Ala Ala Ser Leu Glu Ala Lys Gly Gly Asn Val His Ala Tyr Gln
            420                 425                 430

tgt gat ttc tct gat atg gac gat tgc gat cgc ttt gtg aaa acc gtt      1344
Cys Asp Phe Ser Asp Met Asp Asp Cys Asp Arg Phe Val Lys Thr Val
        435                 440                 445

ctg gac aat cac ggc cat gtg gat gtc ctg gtt aac aat gct ggt cgt      1392
Leu Asp Asn His Gly His Val Asp Val Leu Val Asn Asn Ala Gly Arg
    450                 455                 460

agc att cgc cgt tcc ctg gcg ctg tct ttc gac cgt ttt cac gat ttt      1440
Ser Ile Arg Arg Ser Leu Ala Leu Ser Phe Asp Arg Phe His Asp Phe
465                 470                 475                 480

gag cgc acg atg cag ctg aat tac ttt ggc agc gtg cgt ctg att atg      1488
Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly Ser Val Arg Leu Ile Met
                485                 490                 495

ggt ttc gcc cct gcg atg ttg gag cgc cgt cgc ggt cat gtg gtg aac      1536
Gly Phe Ala Pro Ala Met Leu Glu Arg Arg Arg Gly His Val Val Asn
            500                 505                 510

atc agc agc att ggc gtc ttg acc aat gca ccg cgc ttc agc gca tac      1584
Ile Ser Ser Ile Gly Val Leu Thr Asn Ala Pro Arg Phe Ser Ala Tyr
        515                 520                 525

gtt agc agc aag agc gcg ctg gac gcc ttc tct cgt tgc gcg gca gct      1632
Val Ser Ser Lys Ser Ala Leu Asp Ala Phe Ser Arg Cys Ala Ala Ala
    530                 535                 540

gag tgg agc gac cgc aat gtg acc ttt acg acg atc aac atg ccg ttg      1680
Glu Trp Ser Asp Arg Asn Val Thr Phe Thr Thr Ile Asn Met Pro Leu
545                 550                 555                 560

gtc aaa acc ccg atg att gcg ccg acc aaa atc tac gac tcc gtg ccg      1728
Val Lys Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Asp Ser Val Pro
                565                 570                 575

acc ctg acc ccg gac gag gcg gct caa atg gtg gcg gac gcg att gtc      1776
Thr Leu Thr Pro Asp Glu Ala Ala Gln Met Val Ala Asp Ala Ile Val
            580                 585                 590

tac cgt ccg aag cgt atc gcg acg cgt ctg ggt gtg ttt gcg caa gtg      1824
Tyr Arg Pro Lys Arg Ile Ala Thr Arg Leu Gly Val Phe Ala Gln Val
        595                 600                 605

ctg cac gcg ttg gca ccg aaa atg ggt gag att atc atg aat act ggc      1872
Leu His Ala Leu Ala Pro Lys Met Gly Glu Ile Ile Met Asn Thr Gly
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610 615 620

tac cgt atg ttc ccg gac agc ccg gca gca gcg ggt tcg aaa agc ggt 1920
Tyr Arg Met Phe Pro Asp Ser Pro Ala Ala Ala Gly Ser Lys Ser Gly
625 630 635 640

gag aaa ccg aaa gtt agc acg gaa cag gtc gct ttt gcg gca att atg 1968
Glu Lys Pro Lys Val Ser Thr Glu Gln Val Ala Phe Ala Ala Ile Met
645 650 655

cgt ggt att tac tgg taa 1986
Arg Gly Ile Tyr Trp
660

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<212> PRT
<213> Marinobacter aquaeolei

<400> 140

Met Asn Tyr Phe Leu Thr Gly Gly Thr Gly Phe Ile Gly Arg Phe Leu
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Val Glu Lys Leu Leu Ala Arg Gly Gly Thr Val Tyr Val Leu Val Arg
20 25 30

Glu Gln Ser Gln Asp Lys Leu Glu Arg Leu Arg Glu Arg Trp Gly Ala
35 40 45

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

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

His Val Phe His Leu Ala Ala Val Tyr Asp Met Gly Ala Asp Glu Glu
85 90 95

Ala Gln Ala Ala Thr Asn Ile Glu Gly Thr Arg Ala Ala Val Gln Ala
100 105 110

Ala Glu Ala Met Gly Ala Lys His Phe His His Val Ser Ser Ile Ala
115 120 125

Ala Ala Gly Leu Phe Lys Gly Ile Phe Arg Glu Asp Met Phe Glu Glu
130 135 140

Ala Glu Lys Leu Asp His Pro Tyr Leu Arg Thr Lys His Glu Ser Glu
145 150 155 160

Lys Val Val Arg Glu Glu Cys Lys Val Pro Phe Arg Ile Tyr Arg Pro
165 170 175

Gly Met Val Ile Gly His Ser Glu Thr Gly Glu Met Asp Lys Val Asp
180 185 190

Gly Pro Tyr Tyr Phe Phe Lys Met Ile Gln Lys Ile Arg His Ala Leu
195 200 205

Pro Gln Trp Val Pro Thr Ile Gly Ile Glu Gly Gly Arg Leu Asn Ile
210 215 220

Val Pro Val Asp Phe Val Val Asp Ala Leu Asp His Ile Ala His Leu
225 230 235 240

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

Lys Val Gly Glu Ile Leu Asn Ile Phe Cys Glu Ala Gly His Ala Pro
260 265 270

Arg Met Gly Met Arg Ile Asp Ser Arg Met Phe Gly Phe Ile Pro Pro
275 280 285

Phe Ile Arg Gln Ser Ile Lys Asn Leu Pro Pro Val Lys Arg Ile Thr
290 295 300

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

Ile Asn Tyr Pro Thr Arg Phe Asp Thr Arg Glu Leu Glu Arg Val Leu
325 330 335

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

Ile Trp Asp Tyr Trp Glu Arg Asn Leu Asp Pro Asp Leu Phe Lys Asp
355 360 365

Arg Thr Leu Lys Gly Thr Val Glu Gly Lys Val Cys Val Val Thr Gly
370 375 380

Ala Thr Ser Gly Ile Gly Leu Ala Thr Ala Glu Lys Leu Ala Glu Ala
385 390 395 400

Gly Ala Ile Leu Val Ile Gly Ala Arg Thr Lys Glu Thr Leu Asp Glu
405 410 415

Val Ala Ala Ser Leu Glu Ala Lys Gly Gly Asn Val His Ala Tyr Gln
420 425 430

Cys Asp Phe Ser Asp Met Asp Asp Cys Asp Arg Phe Val Lys Thr Val
435 440 445

Leu Asp Asn His Gly His Val Asp Val Leu Val Asn Asn Ala Gly Arg
450 455 460

Ser Ile Arg Arg Ser Leu Ala Leu Ser Phe Asp Arg Phe His Asp Phe
465 470 475 480

Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly Ser Val Arg Leu Ile Met
485 490 495

Gly Phe Ala Pro Ala Met Leu Glu Arg Arg Arg Gly His Val Val Asn
500 505 510

Ile Ser Ser Ile Gly Val Leu Thr Asn Ala Pro Arg Phe Ser Ala Tyr
515 520 525

Val Ser Ser Lys Ser Ala Leu Asp Ala Phe Ser Arg Cys Ala Ala Ala
530 535 540

Glu Trp Ser Asp Arg Asn Val Thr Phe Thr Thr Ile Asn Met Pro Leu
545 550 555 560

Val Lys Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Asp Ser Val Pro
565 570 575

Thr Leu Thr Pro Asp Glu Ala Ala Gln Met Val Ala Asp Ala Ile Val
580 585 590

Tyr Arg Pro Lys Arg Ile Ala Thr Arg Leu Gly Val Phe Ala Gln Val
595 600 605

Leu His Ala Leu Ala Pro Lys Met Gly Glu Ile Ile Met Asn Thr Gly
610 615 620

Tyr Arg Met Phe Pro Asp Ser Pro Ala Ala Ala Gly Ser Lys Ser Gly
625 630 635 640

Glu Lys Pro Lys Val Ser Thr Glu Gln Val Ala Phe Ala Ala Ile Met
645 650 655

Arg Gly Ile Tyr Trp
660

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<211> 1647
<212> DNA
<213> Arabidopsis thaliana

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<222> (1)..(1647)

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Met Ala Thr Thr Asn Val Leu Ala Thr Ser His Ala Phe Lys Leu Asn
1 5 10 15

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ggt gtt agc tac ttt agc agc ttc ccg cgc aag ccg aat cac tac atg          96
Gly Val Ser Tyr Phe Ser Ser Phe Pro Arg Lys Pro Asn His Tyr Met
            20                  25                  30

ccg cgt cgc cgt ctg agc cat acc acg cgc cgt gtt caa acg agc tgc         144
Pro Arg Arg Arg Leu Ser His Thr Thr Arg Arg Val Gln Thr Ser Cys
        35                  40                  45

ttt tac ggt gaa acc agc ttt gaa gcg gtg acc agc ctg gtt acc cct         192
Phe Tyr Gly Glu Thr Ser Phe Glu Ala Val Thr Ser Leu Val Thr Pro
    50                  55                  60

aag acc gaa acc agc cgt aat agc gac ggc att ggc att gtt cgt ttc         240
Lys Thr Glu Thr Ser Arg Asn Ser Asp Gly Ile Gly Ile Val Arg Phe
65                  70                  75                  80

ctg gaa ggc aaa agc tat ctg gtg acc ggc gca acc ggt ttt ctg gcc         288
Leu Glu Gly Lys Ser Tyr Leu Val Thr Gly Ala Thr Gly Phe Leu Ala
                85                  90                  95

aag gtg ctg atc gag aaa ctg ctg cgt gag agc ctg gaa att ggc aag         336
Lys Val Leu Ile Glu Lys Leu Leu Arg Glu Ser Leu Glu Ile Gly Lys
            100                 105                 110

att ttc ttg ctg atg cgt agc aag gat caa gag agc gcg aat aag cgt         384
Ile Phe Leu Leu Met Arg Ser Lys Asp Gln Glu Ser Ala Asn Lys Arg
        115                 120                 125

ctg tac gac gag atc att agc agc gac ctg ttc aaa ctg ctg aag caa         432
Leu Tyr Asp Glu Ile Ile Ser Ser Asp Leu Phe Lys Leu Leu Lys Gln
    130                 135                 140

atg cat ggc agc tct tat gag gcc ttc atg aaa cgc aaa ttg atc ccg         480
Met His Gly Ser Ser Tyr Glu Ala Phe Met Lys Arg Lys Leu Ile Pro
145                 150                 155                 160

gtt atc ggt gat atc gaa gaa gat aac ctg ggt atc aag tcc gaa atc         528
Val Ile Gly Asp Ile Glu Glu Asp Asn Leu Gly Ile Lys Ser Glu Ile
                165                 170                 175

gcg aac atg atc tcc gaa gag atc gac gtt atc atc agc tgt ggt ggt         576
Ala Asn Met Ile Ser Glu Glu Ile Asp Val Ile Ile Ser Cys Gly Gly
            180                 185                 190

cgc acc acc ttt gat gac cgt tat gac tcg gcc ctg agc gtc aac gcc         624
Arg Thr Thr Phe Asp Asp Arg Tyr Asp Ser Ala Leu Ser Val Asn Ala
        195                 200                 205

ttg ggt cca ggt cgt ctg ttg agc ttc ggc aaa ggc tgc cgt aag ttg         672
Leu Gly Pro Gly Arg Leu Leu Ser Phe Gly Lys Gly Cys Arg Lys Leu
    210                 215                 220

aaa ctg ttc ctg cac ttt tcc act gct tat gtc acc ggc aag cgt gaa         720
Lys Leu Phe Leu His Phe Ser Thr Ala Tyr Val Thr Gly Lys Arg Glu
225                 230                 235                 240

ggc acg gtc ttg gaa acc ccg ctg tgc atc ggc gag aac att acc tct         768
Gly Thr Val Leu Glu Thr Pro Leu Cys Ile Gly Glu Asn Ile Thr Ser
                245                 250                 255

gac ctg aac atc aaa tcc gag ctg aaa ctg gca agc gag gca gtg cgt         816
Asp Leu Asn Ile Lys Ser Glu Leu Lys Leu Ala Ser Glu Ala Val Arg
            260                 265                 270

aaa ttc cgt ggc cgt gaa gag att aag aag ctg aaa gag ctg ggt ttt         864
Lys Phe Arg Gly Arg Glu Glu Ile Lys Lys Leu Lys Glu Leu Gly Phe
        275                 280                 285
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gag cgc gca cag cat tat ggt tgg gag aat tcg tat acg ttt acc aag        912
Glu Arg Ala Gln His Tyr Gly Trp Glu Asn Ser Tyr Thr Phe Thr Lys
    290                 295                 300

gcg att ggc gaa gcg gtc att cac agc aag cgc ggt aat ctg ccg gtg        960
Ala Ile Gly Glu Ala Val Ile His Ser Lys Arg Gly Asn Leu Pro Val
305                 310                 315                 320

gtc att att cgc ccg agc atc atc gag agc agc tac aat gaa ccg ttc       1008
Val Ile Ile Arg Pro Ser Ile Ile Glu Ser Ser Tyr Asn Glu Pro Phe
                325                 330                 335

ccg ggc tgg att cag ggt acg cgt atg gcg gac ccg att atc ctg gct       1056
Pro Gly Trp Ile Gln Gly Thr Arg Met Ala Asp Pro Ile Ile Leu Ala
            340                 345                 350

tac gcg aaa ggt cag atc agc gat ttc tgg gcc gac cca cag tcc ctg       1104
Tyr Ala Lys Gly Gln Ile Ser Asp Phe Trp Ala Asp Pro Gln Ser Leu
        355                 360                 365

atg gac atc atc ccg gtt gat atg gtt gcg aac gcg gcg att gct gcg       1152
Met Asp Ile Ile Pro Val Asp Met Val Ala Asn Ala Ala Ile Ala Ala
    370                 375                 380

atg gca aaa cac ggt tgt ggt gtt ccg gag ttt aag gtc tac aac ctg       1200
Met Ala Lys His Gly Cys Gly Val Pro Glu Phe Lys Val Tyr Asn Leu
385                 390                 395                 400

acg agc agc agc cac gtg aac ccg atg cgt gca ggt aaa ctg atc gat       1248
Thr Ser Ser Ser His Val Asn Pro Met Arg Ala Gly Lys Leu Ile Asp
                405                 410                 415

ctg tcc cat caa cac ctg tgt gat ttc cct ctg gaa gaa acc gtc att       1296
Leu Ser His Gln His Leu Cys Asp Phe Pro Leu Glu Glu Thr Val Ile
            420                 425                 430

gac ttg gag cac atg aag att cat tcc agc ctg gaa ggt ttt acg tct       1344
Asp Leu Glu His Met Lys Ile His Ser Ser Leu Glu Gly Phe Thr Ser
        435                 440                 445

gcg ctg tct aat acc att atc aaa cag gag cgc gtg atc gat aac gag       1392
Ala Leu Ser Asn Thr Ile Ile Lys Gln Glu Arg Val Ile Asp Asn Glu
    450                 455                 460

ggt ggt ggt ctg agc acg aaa ggc aag cgt aaa ctg aac tat ttc gtg       1440
Gly Gly Gly Leu Ser Thr Lys Gly Lys Arg Lys Leu Asn Tyr Phe Val
465                 470                 475                 480

agc ctg gcc aaa acg tac gag ccg tac acc ttc ttt cag gct cgc ttc       1488
Ser Leu Ala Lys Thr Tyr Glu Pro Tyr Thr Phe Phe Gln Ala Arg Phe
                485                 490                 495

gat aat acc aac acg act agc ctg att caa gag atg agc atg gaa gaa       1536
Asp Asn Thr Asn Thr Thr Ser Leu Ile Gln Glu Met Ser Met Glu Glu
            500                 505                 510

aag aaa acc ttc ggt ttt gac att aag ggc att gac tgg gag cac tac       1584
Lys Lys Thr Phe Gly Phe Asp Ile Lys Gly Ile Asp Trp Glu His Tyr
        515                 520                 525

att gtc aat gtg cat ctg ccg ggt ctg aag aaa gag ttc ctg agc aag       1632
Ile Val Asn Val His Leu Pro Gly Leu Lys Lys Glu Phe Leu Ser Lys
    530                 535                 540

aag aaa acc gag taa                                                  1647
Lys Lys Thr Glu
545
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<210> 142
<211> 548
<212> PRT
<213> Arabidopsis thaliana

<400> 142

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Met Ala Thr Thr Asn Val Leu Ala Thr Ser His Ala Phe Lys Leu Asn
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Gly Val Ser Tyr Phe Ser Ser Phe Pro Arg Lys Pro Asn His Tyr Met
            20                  25                  30

Pro Arg Arg Arg Leu Ser His Thr Thr Arg Arg Val Gln Thr Ser Cys
        35                  40                  45

Phe Tyr Gly Glu Thr Ser Phe Glu Ala Val Thr Ser Leu Val Thr Pro
    50                  55                  60

Lys Thr Glu Thr Ser Arg Asn Ser Asp Gly Ile Gly Ile Val Arg Phe
65                  70                  75                  80

Leu Glu Gly Lys Ser Tyr Leu Val Thr Gly Ala Thr Gly Phe Leu Ala
                85                  90                  95

Lys Val Leu Ile Glu Lys Leu Leu Arg Glu Ser Leu Glu Ile Gly Lys
            100                 105                 110

Ile Phe Leu Leu Met Arg Ser Lys Asp Gln Glu Ser Ala Asn Lys Arg
        115                 120                 125

Leu Tyr Asp Glu Ile Ile Ser Ser Asp Leu Phe Lys Leu Leu Lys Gln
    130                 135                 140

Met His Gly Ser Ser Tyr Glu Ala Phe Met Lys Arg Lys Leu Ile Pro
145                 150                 155                 160

Val Ile Gly Asp Ile Glu Glu Asp Asn Leu Gly Ile Lys Ser Glu Ile
                165                 170                 175

Ala Asn Met Ile Ser Glu Glu Ile Asp Val Ile Ile Ser Cys Gly Gly
            180                 185                 190

Arg Thr Thr Phe Asp Asp Arg Tyr Asp Ser Ala Leu Ser Val Asn Ala
        195                 200                 205

Leu Gly Pro Gly Arg Leu Leu Ser Phe Gly Lys Gly Cys Arg Lys Leu
    210                 215                 220

Lys Leu Phe Leu His Phe Ser Thr Ala Tyr Val Thr Gly Lys Arg Glu
225                 230                 235                 240
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Gly Thr Val Leu Glu Thr Pro Leu Cys Ile Gly Glu Asn Ile Thr Ser
245 250 255

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

Lys Phe Arg Gly Arg Glu Glu Ile Lys Lys Leu Lys Glu Leu Gly Phe
275 280 285

Glu Arg Ala Gln His Tyr Gly Trp Glu Asn Ser Tyr Thr Phe Thr Lys
290 295 300

Ala Ile Gly Glu Ala Val Ile His Ser Lys Arg Gly Asn Leu Pro Val
305 310 315 320

Val Ile Ile Arg Pro Ser Ile Ile Glu Ser Ser Tyr Asn Glu Pro Phe
325 330 335

Pro Gly Trp Ile Gln Gly Thr Arg Met Ala Asp Pro Ile Ile Leu Ala
340 345 350

Tyr Ala Lys Gly Gln Ile Ser Asp Phe Trp Ala Asp Pro Gln Ser Leu
355 360 365

Met Asp Ile Ile Pro Val Asp Met Val Ala Asn Ala Ala Ile Ala Ala
370 375 380

Met Ala Lys His Gly Cys Gly Val Pro Glu Phe Lys Val Tyr Asn Leu
385 390 395 400

Thr Ser Ser Ser His Val Asn Pro Met Arg Ala Gly Lys Leu Ile Asp
405 410 415

Leu Ser His Gln His Leu Cys Asp Phe Pro Leu Glu Glu Thr Val Ile
420 425 430

Asp Leu Glu His Met Lys Ile His Ser Ser Leu Glu Gly Phe Thr Ser
435 440 445

Ala Leu Ser Asn Thr Ile Ile Lys Gln Glu Arg Val Ile Asp Asn Glu
450 455 460

Gly Gly Gly Leu Ser Thr Lys Gly Lys Arg Lys Leu Asn Tyr Phe Val
465 470 475 480

Ser Leu Ala Lys Thr Tyr Glu Pro Tyr Thr Phe Phe Gln Ala Arg Phe
485 490 495

Asp Asn Thr Asn Thr Thr Ser Leu Ile Gln Glu Met Ser Met Glu Glu
500 505 510

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Lys Lys Thr Phe Gly Phe Asp Ile Lys Gly Ile Asp Trp Glu His Tyr
        515                 520                 525


Ile Val Asn Val His Leu Pro Gly Leu Lys Lys Glu Phe Leu Ser Lys
    530                 535                 540


Lys Lys Thr Glu
545


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<211>  888
<212>  DNA
<213>  Acinetobacter sp. M-1


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<222>  (1)..(888)

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Met Asn Ala Lys Leu Lys Lys Leu Phe Gln Gln Lys Val Asp Gly Lys
1               5                   10                  15

aca atc att gtc aca gga gca tca agt ggt att ggt tta acg gtt tca          96
Thr Ile Ile Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Thr Val Ser
            20                  25                  30

aaa tac ctt gct caa gca ggt gct cat gtc tta ttg ctc gct cgt act         144
Lys Tyr Leu Ala Gln Ala Gly Ala His Val Leu Leu Leu Ala Arg Thr
        35                  40                  45

aaa gag aag tta gat gag gtc aaa gca gag atc gag gct gaa ggt gga         192
Lys Glu Lys Leu Asp Glu Val Lys Ala Glu Ile Glu Ala Glu Gly Gly
    50                  55                  60

aaa gcg acc gta ttt cca tgt gat ctc aat gat atg gaa tct att gat         240
Lys Ala Thr Val Phe Pro Cys Asp Leu Asn Asp Met Glu Ser Ile Asp
65                  70                  75                  80

gcc gtt tca aaa gaa atc tta gca gca gta gat cac att gat att ctt         288
Ala Val Ser Lys Glu Ile Leu Ala Ala Val Asp His Ile Asp Ile Leu
                85                  90                  95

gta aat aac gca gga cgt tca atc cgt cgt gcg gta cat gag tca gtt         336
Val Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Val
            100                 105                 110

gat cgt ttc cat gac ttc gaa cgt acc atg cag tta aat tac ttt ggt         384
Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

gca gta cgt tta gtc ttg aat gtt tta ccg cac atg atg cag cgt aaa         432
Ala Val Arg Leu Val Leu Asn Val Leu Pro His Met Met Gln Arg Lys
    130                 135                 140

gac ggt caa atc att aac atc agc tca att ggt gtt ctt gcc aac gca         480
Asp Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

act cgc ttt tct gct tac gtt gcg tct aaa gct gca ttg gat gca ttt         528
Thr Arg Phe Ser Ala Tyr Val Ala Ser Lys Ala Ala Leu Asp Ala Phe
                165                 170                 175
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agt cgt tgt tta tct gcg gaa gtt cac tca cac aaa att gcg att acc        576
Ser Arg Cys Leu Ser Ala Glu Val His Ser His Lys Ile Ala Ile Thr
            180                 185                 190

tct att tat atg cct ttg gtc cgc aca cca atg att gca cca acc aaa        624
Ser Ile Tyr Met Pro Leu Val Arg Thr Pro Met Ile Ala Pro Thr Lys
        195                 200                 205

att tat aaa tat gta cca acg ctt tca cct gaa gaa gca gcc gat tta        672
Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

att gct tat gca atc gtg aag cgt ccg aaa aag atc gcg acg aac tta        720
Ile Ala Tyr Ala Ile Val Lys Arg Pro Lys Lys Ile Ala Thr Asn Leu
225                 230                 235                 240

ggt cgc ctt gct tcg att act tat gcg att gca cca gac att aac aac        768
Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

att tta atg tcg att ggt ttc aac tta ttc cca agt tct acc gcg tct        816
Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ser
            260                 265                 270

gtt ggt gag caa gag aag ttg aat tta att caa cgt gcc tat gca cgt        864
Val Gly Glu Gln Glu Lys Leu Asn Leu Ile Gln Arg Ala Tyr Ala Arg
        275                 280                 285

ttg ttc cca ggc gaa cac tgg taa                                      888
Leu Phe Pro Gly Glu His Trp
    290                 295
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<210> 144
<211> 295
<212> PRT
<213> Acinetobacter sp. M-1

<400> 144

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Met Asn Ala Lys Leu Lys Lys Leu Phe Gln Gln Lys Val Asp Gly Lys
1               5                   10                  15

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

Lys Tyr Leu Ala Gln Ala Gly Ala His Val Leu Leu Leu Ala Arg Thr
        35                  40                  45

Lys Glu Lys Leu Asp Glu Val Lys Ala Glu Ile Glu Ala Glu Gly Gly
    50                  55                  60

Lys Ala Thr Val Phe Pro Cys Asp Leu Asn Asp Met Glu Ser Ile Asp
65                  70                  75                  80

Ala Val Ser Lys Glu Ile Leu Ala Ala Val Asp His Ile Asp Ile Leu
                85                  90                  95

Val Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Val
            100                 105                 110
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```
Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

Ala Val Arg Leu Val Leu Asn Val Leu Pro His Met Met Gln Arg Lys
    130                 135                 140

Asp Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160

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

Ser Arg Cys Leu Ser Ala Glu Val His Ser His Lys Ile Ala Ile Thr
            180                 185                 190

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

Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

Ile Ala Tyr Ala Ile Val Lys Arg Pro Lys Lys Ile Ala Thr Asn Leu
225                 230                 235                 240

Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ser
            260                 265                 270

Val Gly Glu Gln Glu Lys Leu Asn Leu Ile Gln Arg Ala Tyr Ala Arg
        275                 280                 285

Leu Phe Pro Gly Glu His Trp
    290                 295


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<212>  DNA
<213>  Acinetobacter sp. ADP1


<220>
<221>  CDS
<222>  (1)..(915)

<400>  145
ttg atc tcg atc cgt gaa aaa cgt gtt aac aag aaa ttg gag gcc ctg         48
Leu Ile Ser Ile Arg Glu Lys Arg Val Asn Lys Lys Leu Glu Ala Leu
1               5                   10                  15

ttt cgt gag aat gtc aaa ggc aag gtt gcc ctg atc acg ggt gct agc         96
Phe Arg Glu Asn Val Lys Gly Lys Val Ala Leu Ile Thr Gly Ala Ser
            20                  25                  30

agc ggc atc ggc ctg acg att gcc aaa cgc att gct gcg gca ggt gca        144
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Ser Gly Ile Gly Leu Thr Ile Ala Lys Arg Ile Ala Ala Ala Gly Ala
        35                  40                  45

cat gtt ctg ttg gtc gcg cgc acc cag gaa acc ctg gaa gaa gtg aag        192
His Val Leu Leu Val Ala Arg Thr Gln Glu Thr Leu Glu Glu Val Lys
    50                  55                  60

gca gca atc gag caa cag ggt ggc cag gcc agc att ttc ccg tgt gac        240
Ala Ala Ile Glu Gln Gln Gly Gly Gln Ala Ser Ile Phe Pro Cys Asp
65                  70                  75                  80

ctg acc gat atg aat gcg att gat cag ctg agc caa cag att atg gca        288
Leu Thr Asp Met Asn Ala Ile Asp Gln Leu Ser Gln Gln Ile Met Ala
                85                  90                  95

tcc gtc gac cac gta gat ttt ctg atc aac aat gcc ggt cgc agc att        336
Ser Val Asp His Val Asp Phe Leu Ile Asn Asn Ala Gly Arg Ser Ile
            100                 105                 110

cgt cgc gca gtg cac gaa agc ttc gac cgt ttt cat gat ttc gag cgt        384
Arg Arg Ala Val His Glu Ser Phe Asp Arg Phe His Asp Phe Glu Arg
        115                 120                 125

acg atg caa ttg aac tac ttc ggt gcg gtg cgt ctg gtc ctg aac ctg        432
Thr Met Gln Leu Asn Tyr Phe Gly Ala Val Arg Leu Val Leu Asn Leu
    130                 135                 140

ctg ccg cac atg atc aaa cgt aag aac ggt caa atc atc aat atc agc        480
Leu Pro His Met Ile Lys Arg Lys Asn Gly Gln Ile Ile Asn Ile Ser
145                 150                 155                 160

agc atc ggc gtg ctg gcg aat gcg act cgc ttt agc gcg tac gtt gcg        528
Ser Ile Gly Val Leu Ala Asn Ala Thr Arg Phe Ser Ala Tyr Val Ala
                165                 170                 175

agc aaa gca gcg ctg gat gcg ttt tct cgt tgc ctg agc gca gaa gtt        576
Ser Lys Ala Ala Leu Asp Ala Phe Ser Arg Cys Leu Ser Ala Glu Val
            180                 185                 190

ttg aaa cat aag att agc atc acg agc att tac atg ccg ttg gtg cgt        624
Leu Lys His Lys Ile Ser Ile Thr Ser Ile Tyr Met Pro Leu Val Arg
        195                 200                 205

acc ccg atg atc gcc ccg acc aaa atc tat aag tat gtg ccg acg ctg        672
Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Lys Tyr Val Pro Thr Leu
    210                 215                 220

agc ccg gaa gag gca gct gac ctg att gtc tac gct att gtt aaa cgt        720
Ser Pro Glu Glu Ala Ala Asp Leu Ile Val Tyr Ala Ile Val Lys Arg
225                 230                 235                 240

cca aag cgt att gcg acc cac ctg ggt cgc ttg gcg tcc atc acc tac        768
Pro Lys Arg Ile Ala Thr His Leu Gly Arg Leu Ala Ser Ile Thr Tyr
                245                 250                 255

gcg att gcg ccg gac att aac aat att ctg atg tcc att ggt ttc aac        816
Ala Ile Ala Pro Asp Ile Asn Asn Ile Leu Met Ser Ile Gly Phe Asn
            260                 265                 270

ctg ttc cct agc tct acc gcg gct ctg ggc gag cag gag aag ctg aat        864
Leu Phe Pro Ser Ser Thr Ala Ala Leu Gly Glu Gln Glu Lys Leu Asn
        275                 280                 285

ctg ctg caa cgt gcc tat gcg cgc ctg ttc ccg ggt gag cac tgg tga        912
Leu Leu Gln Arg Ala Tyr Ala Arg Leu Phe Pro Gly Glu His Trp
    290                 295                 300

taa                                                                    915
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<210> 146
<211> 303
<212> PRT
<213> Acinetobacter sp. ADP1

<400> 146

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

Phe Arg Glu Asn Val Lys Gly Lys Val Ala Leu Ile Thr Gly Ala Ser
            20                  25                  30

Ser Gly Ile Gly Leu Thr Ile Ala Lys Arg Ile Ala Ala Ala Gly Ala
        35                  40                  45

His Val Leu Leu Val Ala Arg Thr Gln Glu Thr Leu Glu Glu Val Lys
    50                  55                  60

Ala Ala Ile Glu Gln Gln Gly Gly Gln Ala Ser Ile Phe Pro Cys Asp
65                  70                  75                  80

Leu Thr Asp Met Asn Ala Ile Asp Gln Leu Ser Gln Gln Ile Met Ala
                85                  90                  95

Ser Val Asp His Val Asp Phe Leu Ile Asn Asn Ala Gly Arg Ser Ile
            100                 105                 110

Arg Arg Ala Val His Glu Ser Phe Asp Arg Phe His Asp Phe Glu Arg
        115                 120                 125

Thr Met Gln Leu Asn Tyr Phe Gly Ala Val Arg Leu Val Leu Asn Leu
    130                 135                 140

Leu Pro His Met Ile Lys Arg Lys Asn Gly Gln Ile Ile Asn Ile Ser
145                 150                 155                 160

Ser Ile Gly Val Leu Ala Asn Ala Thr Arg Phe Ser Ala Tyr Val Ala
                165                 170                 175

Ser Lys Ala Ala Leu Asp Ala Phe Ser Arg Cys Leu Ser Ala Glu Val
            180                 185                 190

Leu Lys His Lys Ile Ser Ile Thr Ser Ile Tyr Met Pro Leu Val Arg
        195                 200                 205

Thr Pro Met Ile Ala Pro Thr Lys Ile Tyr Lys Tyr Val Pro Thr Leu
    210                 215                 220

Ser Pro Glu Glu Ala Ala Asp Leu Ile Val Tyr Ala Ile Val Lys Arg
225                 230                 235                 240
```

```
Pro Lys Arg Ile Ala Thr His Leu Gly Arg Leu Ala Ser Ile Thr Tyr
                245                 250                 255

Ala Ile Ala Pro Asp Ile Asn Asn Ile Leu Met Ser Ile Gly Phe Asn
            260                 265                 270

Leu Phe Pro Ser Ser Thr Ala Ala Leu Gly Glu Gln Glu Lys Leu Asn
        275                 280                 285

Leu Leu Gln Arg Ala Tyr Ala Arg Leu Phe Pro Gly Glu His Trp
    290                 295                 300
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<210> 147
<211> 888
<212> DNA
<213> Acinetobacter sp. ADP1

<220>
<221> CDS
<222> (1)..(888)

<400> 147

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Val Asn Lys Lys Leu Glu Ala Leu Phe Arg Glu Asn Val Lys Gly Lys
1               5                   10                  15

gtg gct ttg atc act ggt gca tct agt gga atc ggt ttg acg att gca          96
Val Ala Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Thr Ile Ala
            20                  25                  30

aaa aga att gct gcg gca ggt gct cat gta tta ttg gtt gcc cga acc         144
Lys Arg Ile Ala Ala Ala Gly Ala His Val Leu Leu Val Ala Arg Thr
        35                  40                  45

caa gaa aca ctg gaa gaa gtg aaa gct gca att gaa cag caa ggg gga         192
Gln Glu Thr Leu Glu Glu Val Lys Ala Ala Ile Glu Gln Gln Gly Gly
    50                  55                  60

cag gcc tct att ttt cct tgt gac ctg act gac atg aat gcg att gac         240
Gln Ala Ser Ile Phe Pro Cys Asp Leu Thr Asp Met Asn Ala Ile Asp
65                  70                  75                  80

cag tta tca caa caa att atg gcc agt gtc gat cat gtc gat ttc ctg         288
Gln Leu Ser Gln Gln Ile Met Ala Ser Val Asp His Val Asp Phe Leu
                85                  90                  95

atc aat aat gca ggg cgt tcg att cgc cgt gcc gta cac gag tcg ttt         336
Ile Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Phe
            100                 105                 110

gat cgc ttc cat gat ttt gaa cgc acc atg cag ctg aat tac ttt ggt         384
Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
        115                 120                 125

gcg gta cgt tta gtg tta aat tta ctg cca cat atg att aag cgt aaa         432
Ala Val Arg Leu Val Leu Asn Leu Leu Pro His Met Ile Lys Arg Lys
    130                 135                 140

aat ggc cag atc atc aat atc agc tct att ggt gta ttg gcc aat gcg         480
Asn Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145                 150                 155                 160
```

```
acc cgt ttt tct gct tat gtc gcg tct aaa gct gcg ctg gat gcc ttc        528
Thr Arg Phe Ser Ala Tyr Val Ala Ser Lys Ala Ala Leu Asp Ala Phe
                165                 170                 175

agt cgc tgt ctt tca gcc gag gta ctc aag cat aaa atc tca att acc        576
Ser Arg Cys Leu Ser Ala Glu Val Leu Lys His Lys Ile Ser Ile Thr
            180                 185                 190

tcg att tat atg cca ttg gtg cgt acc cca atg atc gca ccc acc aaa        624
Ser Ile Tyr Met Pro Leu Val Arg Thr Pro Met Ile Ala Pro Thr Lys
        195                 200                 205

att tat aaa tac gtg ccc acg ctt tcc cca gaa gaa gcc gca gat ctc        672
Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
    210                 215                 220

att gtc tac gcc att gtg aaa cgt cca aaa cgt att gcg acg cac ttg        720
Ile Val Tyr Ala Ile Val Lys Arg Pro Lys Arg Ile Ala Thr His Leu
225                 230                 235                 240

ggt cgt ctg gcg tca att acc tat gcc atc gca cca gac atc aat aat        768
Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
                245                 250                 255

att ctg atg tcg att gga ttt aac cta ttc cca agc tca acg gct gca        816
Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ala
            260                 265                 270

ctg ggt gaa cag gaa aaa ttg aat ctg cta caa cgt gcc tat gcc cgc        864
Leu Gly Glu Gln Glu Lys Leu Asn Leu Leu Gln Arg Ala Tyr Ala Arg
        275                 280                 285

ttg ttc cca ggc gaa cac tgg taa                                      888
Leu Phe Pro Gly Glu His Trp
    290                 295
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<210> 148
<211> 295
<212> PRT
<213> Acinetobacter sp. ADP1

<400> 148

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Val Asn Lys Lys Leu Glu Ala Leu Phe Arg Glu Asn Val Lys Gly Lys
1               5                  10                  15

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

Lys Arg Ile Ala Ala Ala Gly Ala His Val Leu Leu Val Ala Arg Thr
        35                  40                  45

Gln Glu Thr Leu Glu Glu Val Lys Ala Ala Ile Glu Gln Gln Gly Gly
    50                  55                  60

Gln Ala Ser Ile Phe Pro Cys Asp Leu Thr Asp Met Asn Ala Ile Asp
65                  70                  75                  80

Gln Leu Ser Gln Gln Ile Met Ala Ser Val Asp His Val Asp Phe Leu
                85                  90                  95
```

Ile Asn Asn Ala Gly Arg Ser Ile Arg Arg Ala Val His Glu Ser Phe
100 105 110

Asp Arg Phe His Asp Phe Glu Arg Thr Met Gln Leu Asn Tyr Phe Gly
115 120 125

Ala Val Arg Leu Val Leu Asn Leu Leu Pro His Met Ile Lys Arg Lys
130 135 140

Asn Gly Gln Ile Ile Asn Ile Ser Ser Ile Gly Val Leu Ala Asn Ala
145 150 155 160

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

Ser Arg Cys Leu Ser Ala Glu Val Leu Lys His Lys Ile Ser Ile Thr
180 185 190

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

Ile Tyr Lys Tyr Val Pro Thr Leu Ser Pro Glu Glu Ala Ala Asp Leu
210 215 220

Ile Val Tyr Ala Ile Val Lys Arg Pro Lys Arg Ile Ala Thr His Leu
225 230 235 240

Gly Arg Leu Ala Ser Ile Thr Tyr Ala Ile Ala Pro Asp Ile Asn Asn
245 250 255

Ile Leu Met Ser Ile Gly Phe Asn Leu Phe Pro Ser Ser Thr Ala Ala
260 265 270

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

Leu Phe Pro Gly Glu His Trp
290 295

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<213> Artificial Sequence

<220>
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<400> 149
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atgcttccgg ctcgtatgtt gtgtggatgt ggaattgtga gcgctcacaa ttccacaacg 120

gtttcccctct agaaataatt ttgtttaaca ggaggtaaaa ca 162

<210> 150
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 150
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<210> 151
<211> 34
<212> DNA
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<220>
<223> primer

<400> 151
tatatagcgg ccgctcatta cgcggccttt ttgc 34

<210> 152
<211> 38
<212> DNA
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<220>
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<400> 152
tatatacata tgaactattt tcttacaggc ggtacagg 38

<210> 153
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 153
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<210> 154
<211> 32
<212> DNA
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<220>
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<400> 154
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<212> DNA
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<400> 155
tatatagcgg ccgcttatta ctcggttttc ttcttgctca gg 42

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<400> 156
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<212> DNA
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gcgctgcgat gataccgcga gaaccacgct caccggctcc ggatttatca gcaataaacc 180

agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 240

ctattaattg ttgccgggaa gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg 300

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<211> 6008
<212> DNA
<213> Artificial Sequence

<220>
<223> vector

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gcgctgcgat gataccgcga gaaccacgct caccggctcc ggatttatca gcaataaacc 180

agccagccgg aagggccgag cgcagaagtg gtcctgcaac tttatccgcc tccatccagt 240

ctattaattg ttgccgggaa gctagagtaa gtagttcgcc agttaatagt ttgcgcaacg 300

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Glu Leu Thr Arg Thr Leu Trp His Ala Asn Thr Gln Arg Met Glu Ser
        115                 120                 125

atg gat gag gtc aac atc tat cgc gaa agc att gtc ctg ttg acg aaa        432
Met Asp Glu Val Asn Ile Tyr Arg Glu Ser Ile Val Leu Leu Thr Lys
    130                 135                 140

gtc ggt acc cgc tgg gcg ggt gtg cag gct ccg cct gag gac atc gag        480
Val Gly Thr Arg Trp Ala Gly Val Gln Ala Pro Pro Glu Asp Ile Glu
145                 150                 155                 160

cgt att gca acg gat atg gac atc atg atc gat agc ttc cgt gcc ctg        528
Arg Ile Ala Thr Asp Met Asp Ile Met Ile Asp Ser Phe Arg Ala Leu
                165                 170                 175

ggc ggt gcc ttc aaa ggt tac aaa gcc agc aaa gaa gct cgt cgt cgc        576
Gly Gly Ala Phe Lys Gly Tyr Lys Ala Ser Lys Glu Ala Arg Arg Arg
            180                 185                 190

gtg gag gac tgg ctg gag gag cag atc att gaa acc cgt aag ggt aac        624
Val Glu Asp Trp Leu Glu Glu Gln Ile Ile Glu Thr Arg Lys Gly Asn
        195                 200                 205

atc cat ccg ccg gag ggt acg gcg ttg tac gaa ttc gcg cac tgg gag        672
Ile His Pro Pro Glu Gly Thr Ala Leu Tyr Glu Phe Ala His Trp Glu
    210                 215                 220

gat tac ctg ggc aat cca atg gac tcc cgt acg tgc gca att gat ctg        720
Asp Tyr Leu Gly Asn Pro Met Asp Ser Arg Thr Cys Ala Ile Asp Leu
225                 230                 235                 240

atg aat acc ttt cgt cca ctg att gcg att aac cgt ttc gtg agc ttt        768
Met Asn Thr Phe Arg Pro Leu Ile Ala Ile Asn Arg Phe Val Ser Phe
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ggt ctg cat gcg atg aac gag aac ccg att acc cgc gag aaa atc aag        816
Gly Leu His Ala Met Asn Glu Asn Pro Ile Thr Arg Glu Lys Ile Lys
            260                 265                 270

agc gag ccg gac tat gcg tac aaa ttt gcg caa gag gtc cgt cgt tac        864
Ser Glu Pro Asp Tyr Ala Tyr Lys Phe Ala Gln Glu Val Arg Arg Tyr
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tat ccg ttt gtg ccg ttc ctg ccg ggc aag gcc aaa gtt gat att gac        912
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Tyr Pro Phe Val Pro Phe Leu Pro Gly Lys Ala Lys Val Asp Ile Asp
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Phe Gln Gly Val Thr Ile Pro Ala Gly Val Gly Leu Ala Leu Asp Val
305                 310                 315                 320

tac ggt acc acg cat gat gaa agc ctg tgg gac gat ccg aac gaa ttt       1008
Tyr Gly Thr Thr His Asp Glu Ser Leu Trp Asp Asp Pro Asn Glu Phe
                325                 330                 335

cgt ccg gag cgc ttc gaa acg tgg gac ggt tct ccg ttc gat ttg att       1056
Arg Pro Glu Arg Phe Glu Thr Trp Asp Gly Ser Pro Phe Asp Leu Ile
            340                 345                 350

ccg cag ggt ggc ggt gac tat tgg acg aac cac cgt tgt gcg ggt gag       1104
Pro Gln Gly Gly Gly Asp Tyr Trp Thr Asn His Arg Cys Ala Gly Glu
        355                 360                 365

tgg att act gtg atc atc atg gag gag act atg aag tat ttt gca gag       1152
Trp Ile Thr Val Ile Ile Met Glu Glu Thr Met Lys Tyr Phe Ala Glu
    370                 375                 380

aag atc acc tac gat gtt cct gaa cag gac ttg gag gtg gac ctg aat       1200
Lys Ile Thr Tyr Asp Val Pro Glu Gln Asp Leu Glu Val Asp Leu Asn
385                 390                 395                 400

agc att ccg ggc tat gtt aaa agc ggt ttt gtc atc aag aat gtt cgc       1248
Ser Ile Pro Gly Tyr Val Lys Ser Gly Phe Val Ile Lys Asn Val Arg
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gaa gtc gtg gat cgc acc taa tga                                      1272
Glu Val Val Asp Arg Thr
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Leu Lys Gln Gly Tyr Leu Tyr Thr Thr Asn Gln Arg Asn Arg Leu Asn
            20                  25                  30

Thr Ser Val Phe Gln Thr Lys Ala Leu Gly Gly Lys Pro Phe Val Val
        35                  40                  45

Val Thr Gly Lys Glu Gly Ala Glu Met Phe Tyr Asn Asn Asp Val Val
    50                  55                  60

Gln Arg Glu Gly Met Leu Pro Lys Arg Ile Val Asn Thr Leu Phe Gly
65                  70                  75                  80

Lys Gly Ala Ile His Thr Val Asp Gly Lys Lys His Val Asp Arg Lys
                85                  90                  95

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

Glu Leu Thr Arg Thr Leu Trp His Ala Asn Thr Gln Arg Met Glu Ser
115 120 125

Met Asp Glu Val Asn Ile Tyr Arg Glu Ser Ile Val Leu Leu Thr Lys
130 135 140

Val Gly Thr Arg Trp Ala Gly Val Gln Ala Pro Pro Glu Asp Ile Glu
145 150 155 160

Arg Ile Ala Thr Asp Met Asp Ile Met Ile Asp Ser Phe Arg Ala Leu
165 170 175

Gly Gly Ala Phe Lys Gly Tyr Lys Ala Ser Lys Glu Ala Arg Arg Arg
180 185 190

Val Glu Asp Trp Leu Glu Glu Gln Ile Ile Glu Thr Arg Lys Gly Asn
195 200 205

Ile His Pro Pro Glu Gly Thr Ala Leu Tyr Glu Phe Ala His Trp Glu
210 215 220

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

Met Asn Thr Phe Arg Pro Leu Ile Ala Ile Asn Arg Phe Val Ser Phe
245 250 255

Gly Leu His Ala Met Asn Glu Asn Pro Ile Thr Arg Glu Lys Ile Lys
260 265 270

Ser Glu Pro Asp Tyr Ala Tyr Lys Phe Ala Gln Glu Val Arg Arg Tyr
275 280 285

Tyr Pro Phe Val Pro Phe Leu Pro Gly Lys Ala Lys Val Asp Ile Asp
290 295 300

Phe Gln Gly Val Thr Ile Pro Ala Gly Val Gly Leu Ala Leu Asp Val
305 310 315 320

Tyr Gly Thr Thr His Asp Glu Ser Leu Trp Asp Asp Pro Asn Glu Phe
325 330 335

Arg Pro Glu Arg Phe Glu Thr Trp Asp Gly Ser Pro Phe Asp Leu Ile
340 345 350

Pro Gln Gly Gly Gly Asp Tyr Trp Thr Asn His Arg Cys Ala Gly Glu
355 360 365

Trp Ile Thr Val Ile Ile Met Glu Glu Thr Met Lys Tyr Phe Ala Glu

370 375 380

Lys Ile Thr Tyr Asp Val Pro Glu Gln Asp Leu Glu Val Asp Leu Asn
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Ser Ile Pro Gly Tyr Val Lys Ser Gly Phe Val Ile Lys Asn Val Arg
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Glu Val Val Asp Arg Thr
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