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(54) **Process for producing a polyunsaturated fatty acid comprising arachidonic acid**

Verfahren zur Herstellung einer Arachidonsäure enthaltender mehrfach ungesättigeter Fettsäure

Procédé de préparation d'un acide gras polyinsaturé contenant l'acide archidonique

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## Description

[0001] The present invention is defined in claims 1 to 12.

[0002] Described is a nucleic acid derived from *Perkinsus marinus* which encodes a  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and a  $\Delta 5$ -desaturase enzyme. All of the coding sequences can be transcribed as a single transcript, which simplifies the process of transforming cells required to express all three proteins. Described are the individual coding sequences and proteins encoded by these sequences.

[0003] Fatty acids and triacylglycerides have a multiplicity of applications in the food industry, in animal nutrition, in cosmetics and in the pharmacological sector. Depending on whether they are free saturated or unsaturated fatty acids or else triacylglycerides with an elevated content of saturated or unsaturated fatty acids, they are suitable for very different applications. Polyunsaturated fatty acids such as linoleic acid and linolenic acid are essential for mammals, since they cannot be produced by the latter. Polyunsaturated  $\omega 3$ -fatty acids and  $\omega 6$ -fatty acids are therefore an important constituent in animal and human nutrition.

[0004] Hereinbelow, polyunsaturated fatty acids are referred to as PUFA, PUFAs, LCPUFA or LCPUFAs (poly unsaturated fatty acids, PUFA, long chain poly unsaturated fatty acids, LCPUFA).

[0005] The various fatty acids and triglycerides are mainly obtained from microorganisms such as *Mortierella* and *Schizochytrium* or from oil-producing plants such as soybean, oilseed rape, algae such as *Cryptocodinium* or *Phaeodactylum* and others, where they are obtained, as a rule, in the form of their triacylglycerides (= triglycerides = triglycerols). However, they can also be obtained from animals, such as, for example, fish. The free fatty acids are advantageously prepared by hydrolysis. Very long-chain polyunsaturated fatty acids such as docosahexaenoic acid (= DHA, C22:6 $\Delta 4,7,10,13,16,19$ ), eicosapentaenoic acid (= EPA, C20:5 $\Delta 5,8,11,14,17$ ), arachidonic acid (= ARA, C20:4 $\Delta 5,8,11,14$ ), dihomo- $\gamma$ -linolenic acid (C20:3 $\Delta 8,11,14$ ) or docosapentaenoic acid (DPA, C22:5 $\Delta 7,10,13,16,19$ ) are not synthesized in oil crops such as oilseed rape, soybean, sunflower or safflower. Conventional natural sources of these fatty acids are fish such as herring, salmon, sardine, redfish, eel, carp, trout, halibut, mackerel, zander or tuna, or algae.

[0006] Depending on the intended use, oils with saturated or unsaturated fatty acids are preferred. In human nutrition, for example, lipids with unsaturated fatty acids, specifically polyunsaturated fatty acids, are preferred. The polyunsaturated  $\omega 3$ -fatty acids are said to have a positive effect on the cholesterol level in the blood and thus on the possibility of preventing heart disease. The risk of heart disease, stroke or hypertension can be reduced markedly by adding these  $\omega 3$ -fatty acids to the food. Also,  $\omega 3$ -fatty acids have a positive effect on inflammatory, specifically on chronically inflammatory, processes in association with immunological diseases such as rheumatoid arthritis. They are therefore added to foodstuffs, specifically to dietetic foodstuffs, or are employed in medicaments.  $\omega 6$ -Fatty acids such as arachidonic acid tend to have a negative effect on these disorders in connection with these rheumatic diseases on account of our usual dietary intake.

[0007]  $\omega 3$ - and  $\omega 6$ -fatty acids are precursors of tissue hormones, known as eicosanoids, such as the prostaglandins, which are derived from dihomo- $\gamma$ -linolenic acid, arachidonic acid and eicosapentaenoic acid, and of the thromboxanes and leukotrienes, which are derived from arachidonic acid and eicosapentaenoic acid. Eicosanoids (known as the PG<sub>2</sub> series) which are formed from  $\omega 6$ -fatty acids generally promote inflammatory reactions, while eicosanoids (known as the PG<sub>3</sub> series) from  $\omega 3$ -fatty acids have little or no proinflammatory effect.

[0008] Owing to the positive characteristics of the polyunsaturated fatty acids, there has been no lack of attempts in the past to make available genes which are involved in the synthesis of these fatty acids or triglycerides for the production of oils in various organisms with a modified content of unsaturated fatty acids. Thus, WO 91/13972 and its US equivalent describes a  $\Delta 9$ -desaturase. WO 93/11245 claims a  $\Delta 15$ -desaturase and WO 94/11516 a  $\Delta 12$ -desaturase. Further desaturases are described, for example, in EP-A-0 550 162, WO 94/18337, WO 97/30582, WO 97/21340, WO 95/18222, EP-A-0 794 250, Stukey et al., J. Biol. Chem., 265, 1990: 20144-20149, Wada et al., Nature 347, 1990: 200-203 or Huang et al., Lipids 34, 1999: 649-659. However, the biochemical characterization of the various desaturases has been insufficient to date since the enzymes, being membrane-bound proteins, present great difficulty in their isolation and characterization (McKeon et al., Methods in Enzymol. 71, 1981: 12141-12147, Wang et al., Plant Physiol. Biochem., 26, 1988: 777-792). As a rule, membrane-bound desaturases are characterized by being introduced into a suitable organism which is subsequently analyzed for enzyme activity by analyzing the starting materials and the products.  $\Delta 6$ -Desaturases are described in WO 93/06712, US 5,614,393, US5614393, WO 96/21022, WO 00/21557 and WO 99/27111 and the application for the production of fatty acids in transgenic organisms is described in WO 98/46763, WO 98/46764 and WO 98/46765. In this context, the expression of various desaturases and the formation of polyunsaturated fatty acids is also described and claimed in WO 99/64616 or WO 98/46776. As regards the expression efficacy of desaturases and its effect on the formation of polyunsaturated fatty acids, it must be noted that the expression of a single desaturase as described to date has only resulted in low contents of unsaturated fatty acids/lipids such as, for example,  $\gamma$ -linolenic acid and stearidonic acid. Moreover, a mixture of  $\omega 3$ - and  $\omega 6$ -fatty acids was obtained, as a rule.

[0009] Especially suitable microorganisms for the production of PUFAs are microalgae such as *Phaeodactylum tri-comutum*, *Porphiridium* species, *Thraustochytrium* species, *Schizochytrium* species or *Cryptocodinium* species, ciliates

such as *Styloynchia* or *Colpidium*, fungae such as *Mortierella*, *Entomophthora* or *Mucor* and/or mosses such as *Physcomitrella*, *Ceratodon* and *Marchantia* (R. Vazhappilly & F. Chen (1998) *Botanica Marina* 41: 553-558; K. Totani & K. Oba (1987) *Lipids* 22: 1060-1062; M. Akimoto et al. (1998) *Appl. Biochemistry and Biotechnology* 73: 269-278). Strain selection has resulted in the development of a number of mutant strains of the microorganisms in question which produce a series of desirable compounds including PUFAs. However, the mutation and selection of strains with an improved production of a particular molecule such as the polyunsaturated fatty acids is a time-consuming and difficult process. This is why recombinant methods as described above are preferred whenever possible.

**[0010]** However, only limited amounts of the desired polyunsaturated fatty acids such as DPA, EPA or ARA can be produced with the aid of the abovementioned microorganisms, and, depending on the microorganism used, these are generally obtained as fatty acid mixtures of, for example, EPA, DPA and ARA.

**[0011]** A variety of synthetic pathways is being discussed for the synthesis of arachidonic acid, eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) (figure 1). Thus, EPA or DHA are produced in marine bacteria such as *Vibrio* sp. or *Shewanella* sp. via the polyketide pathway (Yu, R. et al. *Lipids* 35:1061-1064, 2000; Takeyama, H. et al. *Microbiology* 143:2725-2731, 1997).

**[0012]** An alternative strategy is the alternating activity of desaturases and elongases (Zank, T.K. et al. *Plant Journal* 31:255-268, 2002; Sakuradani, E. et al. *Gene* 238:445-453, 1999). A modification of the above-described pathway by  $\Delta 6$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and  $\Delta 4$ -desaturase is the Sprecher pathway (Sprecher 2000, *Biochim. Biophys. Acta* 1486:219-231) in mammals. Instead of the  $\Delta 4$ -desaturation, a further elongation step is effected here to give  $C_{24}$ , followed by a further  $\Delta 6$ -desaturation and finally  $\beta$ -oxidation to give the  $C_{22}$  chain length. Thus what is known as Sprecher pathway (see figure 1) is, however, not suitable for the production in plants and microorganisms since the regulatory mechanisms are not known.

**[0013]** Depending on their desaturation pattern, the polyunsaturated fatty acids can be divided into two large classes, viz.  $\omega 6$ - or  $\omega 3$ -fatty acids, which differ with regard to their metabolic and functional activities (fig. 1).

**[0014]** The starting material for the  $\omega 6$ -metabolic pathway is the fatty acid linoleic acid ( $18:2^{\Delta 9,12}$ ) while the  $\omega 3$ -pathway proceeds via linolenic acid ( $18:3^{\Delta 9,12,15}$ ). Linolenic acid is formed by the activity of an  $\omega 3$ -desaturase (Tocher et al. 1998, *Prog. Lipid Res.* 37, 73-117; Domergue et al. 2002, *Eur. J. Biochem.* 269, 4105-4113).

**[0015]** Mammals, and thus also humans, have no corresponding desaturase activity ( $\Delta 12$ - and  $\omega 3$ -desaturase) and must take up these fatty acids (essential fatty acids) via the food. Starting with these precursors, the physiologically important polyunsaturated fatty acids arachidonic acid (= ARA,  $20:4^{\Delta 5,8,11,14}$ ), an  $\omega 6$ -fatty acid and the two  $\omega 3$ -fatty acids eicosapentaenoic acid (= EPA,  $20:5^{\Delta 5,8,11,14,17}$ ) and docosahexaenoic acid (DHA,  $22:6^{\Delta 4,7,10,13,17,19}$ ) are synthesized via the sequence of desaturase and elongase reactions. The application of  $\omega 3$ -fatty acids shows the therapeutic activity described above in the treatment of cardiovascular diseases (Shimikawa 2001, *World Rev. Nutr. Diet.* 88, 100-108), Entzündungen (Calder 2002, *Proc. Nutr. Soc.* 61, 345-358) and Arthritis (Cleland and James 2000, *J. Rheumatol.* 27, 2305-2307).

**[0016]** The elongation of fatty acids, by elongases, by 2 or 4 C atoms is of crucial importance for the production of  $C_{20}$ - and  $C_{22}$ -PUFAs, respectively. This process proceeds via 4 steps. The first step is the condensation of malonyl-CoA with the fatty-acid-acyl-CoA by ketoacyl-CoA synthase (KCS, hereinbelow referred to as elongase). This is followed by a reduction step (ketoacyl-CoA reductase, KCR), a dehydration step (dehydratase) and a final reduction step (enoyl-CoA reductase). It has been postulated that the elongase activity affects the specificity and rate of the entire process (Millar and Kunst, 1997 *Plant Journal* 12:121-131).

**[0017]** There have been a large number of attempts in the past to obtain elongase genes. Millar and Kunst, 1997 (*Plant Journal* 12:121-131) and Millar et al. 1999, (*Plant Cell* 11:825-838) describe the characterization of plant elongases for the synthesis of monounsaturated long-chain fatty acids ( $C_{22}:1$ ) and for the synthesis of very long-chain fatty acids for the formation of waxes in plants ( $C_{28}$ - $C_{32}$ ). Descriptions regarding the synthesis of arachidonic acid and EPA are found, for example, in WO0159128, WO0012720, WO02077213 and WO0208401. The synthesis of polyunsaturated  $C_{24}$ -fatty acids is described, for example, in Tvrdik et al. 2000, *JCB* 149:707-717 or WO0244320.

**[0018]** Higher plants comprise polyunsaturated fatty acids such as linoleic acid ( $18:2^{\Delta 9,12}$ ) and linolenic acid ( $18:3^{\Delta 9,12,15}$ ). ARA, EPA and DHA are found not at all in the seed oil of higher plants, or only in miniscule amounts (E. Ucciani: *Nouveau Dictionnaire des Huiles Végétales* [New Dictionary of Vegetable Oils]. Technique & Documentation - Lavoisier, 1995. ISBN: 2-7430-0009-0). However, the production of LCPUFAs in higher plants, preferably in oil crops such as oilseed rape, linseed, sunflower and soybeans, would be advantageous since large amounts of high-quality LCPUFAs for the food industry, animal nutrition and pharmaceutical purposes might be obtained economically. To this end, it is advantageous to introduce, into oil crops, genes which encode enzymes of the LCPUFA biosynthesis via recombinant methods and to express them therein. These genes may encode for example  $\Delta 9$ -elongases,  $\Delta 8$ -desaturases and/or  $\Delta 5$ -desaturases. These genes can advantageously be isolated from microorganisms and lower plants which produce LCPUFAs and incorporate them in the membranes or triacylglycerides. Thus, it has already been possible to isolate  $\Delta 6$ -desaturase genes from the moss *Physcomitrella patens* and  $\Delta 6$ -elongase genes from *P. patens* and from the nematode *C. elegans*.

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**[0019]** The first transgenic plants which comprise and express genes encoding LCPUFA biosynthesis enzymes and which, as a consequence, produce LCPUFAs were described for the first time, for example, in DE-A-102 19 203 (process for the production of polyunsaturated fatty acids in plants). However, these plants produce LCPUFAs in amounts which require further optimization for processing the oils which are present in the plants.

As can be seen from Figure 1, products of the  $\omega$ 6-pathway can be modified using appropriate desaturases and, if necessary, elongases to give  $\omega$ 3 fatty acids. Therefore, it would be exceedingly valuable to develop a product which makes possible the production of ARA in a genetically modified organism.

The oyster protozoan parasite *Perkinsus marinus* is capable of synthesizing saturated and unsaturated fatty acids, including the essential fatty acid, arachidonic acid [20:4(n-6)], via the  $\Delta$ -8 desaturase pathway. Surprisingly the present inventors have found that *P. marinus* contains nucleic encoding a  $\Delta$ 9-elongase, a  $\Delta$ 8-desaturase and a  $\Delta$ 5-desaturase which can all be transcribed as a single transcript. The full length sequence is shown as SEQ ID NO: 1.

Described is an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 9-elongase,  $\Delta$ 8-desaturase and  $\Delta$ 5-desaturase activity and which is selected from the group consisting of:

- a) A nucleic acid sequence comprising nucleic acid residues 7668 to 12077 of SEQ ID NO: 1 or a homolog thereof;
- b) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising nucleic acid residues 7668 to 12077 of SEQ ID NO: 1;
- c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 9-elongase,  $\Delta$ 8-desaturase and  $\Delta$ 5-desaturase activity, wherein the polypeptides are selected from the group consisting of SEQ ID NOS 2, 3 and 4;
- d) A derivative of a nucleic acid sequence of SEQ ID NO: 1 which encodes polypeptides with at least 40% identity at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4; wherein said polypeptides have  $\Delta$ 9-elongase,  $\Delta$ 8-desaturase and  $\Delta$ 5-desaturase activity.

The advantage of the nucleic acid sequence is that, although it encodes three separate enzymes, it can be transcribed as a single sequence, which makes it much simpler to prepare cloning and expression vectors expressing all three enzymes.

Preferably, the isolated nucleic acid sequence is not identical to SEQ ID No 1 (sequence 1047306867) itself.

In the present context "hybridizes under stringent conditions" is intended to describe hybridization and washing conditions under which nucleotide sequences with at least 60% homology to one another usually remain hybridized with one another. Conditions are preferably such that sequences with at least approximately 65%, preferably at least approximately 70% and especially preferably at least 75% or more homology to one another usually remain hybridized to one another.

These stringent conditions are known to the skilled worker and described, for example, in Current Protocols in Molecular Biology, John Wiley & Sons, N. Y. (1989), 6.3.1-6.3.6. A preferred nonlimiting example of stringent hybridization conditions is hybridizations in 6 x sodium chloride/sodium citrate (= SSC) at approximately 45°C, followed by one or more washing steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C. The skilled worker knows that these hybridization conditions differ depending on the type of nucleic acid and, for example when organic solvents are present, regarding temperature and buffer concentration. Under "standard hybridization conditions", for example, the hybridization temperature is, depending on the type of nucleic acid, between 42°C and 58°C in aqueous buffer with a concentration of 0.1 to 5 x SSC (pH 7.2). If organic solvents, for example 50% formamide, are present in the abovementioned buffer, the temperature under standard conditions is approximately 42°C. The hybridization conditions for DNA:DNA hybrids, for example, are 0.1 x SSC and 20°C to 45°C, preferably 30°C to 45°C. The hybridization conditions for DNA:RNA hybrids are, for example, 0.1 x SSC and 30°C to 55°C, preferably 45°C to 55°C. The abovementioned hybridization conditions are determined by way of example for a nucleic acid with approximately 100 bp (= base pairs) in length and with a G + C content of 50% in the absence of formamide. The skilled worker knows how to determine the required hybridization conditions on the basis of the abovementioned textbooks or textbooks such as Sambrook et al., "Molecular Cloning", Cold Spring Harbor Laboratory, 1989; Hames and Higgins (Ed.) 1985, "Nucleic Acids Hybridization: A Practical Approach", IRL Press at Oxford University Press, Oxford; Brown (Ed.) 1991, "Essential Molecular Biology: A Practical Approach", IRL Press at Oxford University Press, Oxford.

**[0020]** Furthermore, when the present specification refers to isolated nucleic acid molecules of a nucleotide sequence which hybridize with one of the nucleotide sequences shown in SEQ ID NO: 1, SEQ ID NO: 3 or with a part thereof under stringent conditions, "a part thereof" is understood as meaning, in accordance with the invention, that at least 25 base pairs (= bp), 50 bp, 75 bp, 100 bp, 125 bp or 150 bp, preferably at least 175 bp, 200 bp, 225 bp, 250 bp, 275 bp or 300 bp, especially preferably 350 bp, 400 bp, 450 bp, 500 bp or more base pairs are used for the hybridization.

**[0021]** "Homologs" of the nucleic acid sequence with the sequence SEQ ID NO: 1 means, for example, allelic variants with at least approximately 50 or 60%, preferably at least approximately 60 or 70%, more preferably at least approximately 70 or 80%, 90% or 95% and even more preferably at least approximately 85%, 86%, 87%, 88%, 89%, 90%, 91 %, 92%, 93%, 94%, 95 %, 96%, 97%, 98%, 99% or more identity or homology with a nucleotide sequence shown in SEQ ID NO: 1.

**[0022]** "Allelic variants" comprise in particular functional variants which can be obtained by deletion, insertion or sub-

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stitution of nucleotides from/into the sequence, it being intended, however, that the enzyme activity of the resulting proteins which are synthesized is advantageously retained for the insertion of one or more genes.

"Homologs" also means bacterial, fungal and plant homologs, truncated sequences, single-stranded DNA or RNA of the coding and noncoding DNA sequence and derivatives such as, for example, promoter variants. The promoters upstream of the nucleotide sequences detailed can be modified by one or more nucleotide exchanges, by insertion(s) and/or deletion(s) without the functionality or activity of the promoters being adversely affected, however. It is furthermore possible that the modification of the promoter sequence enhances their activity or that they are replaced entirely by more active promoters, including those from heterologous organisms.

In order to determine the percentage of homology (= identity) of two amino acid sequences, the sequences are written one under the other for an optimal comparison (for example, gaps may be introduced into the sequence of a protein or of a nucleic acid in order to generate an optimal alignment with the other protein or the other nucleic acid). Then, the amino acid residue or nucleotides at the corresponding amino acid positions or nucleotide positions are compared. If a position in a sequence is occupied by the same amino acid residue or the same nucleotide as the corresponding position in the other sequence, then the molecules are homologous at this position (i.e. amino acid or nucleic acid "homology" as used in the present context corresponds to amino acid or nucleic acid "identity"). The percentage of homology between the two sequences is a function of the number of positions which the sequences share (i.e. % homology = number of identical positions/total number of positions x 100). The terms homology and identity are therefore to be considered as synonymous.

The homology was calculated over the entire amino acid or nucleic acid sequence region. The skilled worker has available a series of programs which are based on various algorithms for the comparison of various sequences. Here, the algorithms of Needleman and Wunsch or Smith and Waterman give particularly reliable results. The program PileUp (J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153) or the programs Gap and BestFit [Needleman and Wunsch (J. Mol. Biol. 48; 443-453 (1970) and Smith and Waterman (Adv. Appl. Math. 2; 482-489 (1981)), which are part of the GCG software packet [Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991)], were used for the sequence alignment. The sequence Ogy values which are indicated above as a percentage were determined over the entire sequence region using the program GAP and the following settings: Gap Weight: 50, Length Weight: 3, Average Match: 10.000 and Average Mismatch: 0.000. Unless otherwise specified, these settings were always used as standard settings for the sequence alignments. In the present context " $\Delta$ 9-elongase,  $\Delta$ 8-desaturase and  $\Delta$ 5-desaturase activity" is understood as meaning that a protein encoded by a derivative of SEQ ID NO:1 or nucleic acid residues 7668 to 12077 of SEQ ID NO: 1 retains an enzymatic activity of at least 10%, preferably 20%, especially preferably 30% and very especially 40% in comparison with the proteins/enzymes encoded by the sequence SEQ ID NO: 1 or nucleic acid residues 7668 to 12077 of SEQ ID NO: 1 and can thus catalyse the conversion of linoleic acid to arachidonic acid.

**[0023]** Although it is often extremely useful to transcribe nucleic acid encoding polypeptides with  $\Delta$ 9-elongase,  $\Delta$ 8-desaturase and  $\Delta$ 5-desaturase activity as a single sequence, there may be some circumstances in which it is preferable to make use of nucleic acid encoding a single enzyme, i.e. a  $\Delta$ 9-elongase, a  $\Delta$ 8-desaturase or a  $\Delta$ 5-desaturase.

**[0024]** Described is an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta$ 9-elongase activity and which is selected from the group consisting of:

- a) a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1, SEQ ID NO: 9 or a homolog of one of these;
- b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence comprising residues 7668 to 9200 of SEQ ID NO: 1 or SEQ ID NO: 9;
- c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 9-elongase, activity, wherein the polypeptide comprises SEQ ID NO: 2 or SEQ ID NO: 10;
- d) A derivative of a a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1 or SEQ ID NO: 9, which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 2 or SEQ ID NO: 10; wherein said polypeptide has  $\Delta$ 9-elongase activity.

**[0025]** Described is an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta$ 8-desaturase activity and which is selected from the group consisting of:

- a) a sequence comprising nucleic acid residues 9351 to 10724 of SEQ ID NO: 1 or a homolog thereof;
- b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence comprising

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residues 9351 to 10724 of SEQ ID NO: 1;

c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 8$ -desaturase activity, wherein the polypeptide comprises SEQ ID NO: 3;

d) A derivative of a a sequence comprising nucleic acid residues 9351 to 10724 of SEQ ID NO: 1 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 3; wherein said polypeptide has  $\Delta 8$ -desaturase activity.

**[0026]** Described is an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta 5$ -desaturase activity and which is selected from the group consisting of:

a) a sequence comprising nucleic acid residues 10842 to 12077 of SEQ ID NO: 1 or a homolog thereof;

b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence comprising residues 10842 to 12077 of SEQ ID NO: 1;

c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 5$ -desaturase activity, wherein the polypeptide comprises SEQ ID NO: 4;

d) A derivative of a a sequence comprising nucleic acid residues 10842 to 12077 of SEQ ID NO: 1 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 4; wherein said polypeptide has  $\Delta 5$ -desaturase activity.

**[0027]** Described is a polypeptide which is encoded by a nucleic acid sequence described herein.

**[0028]** Advantageously, the polypeptide encoded by these nucleic acid molecules have at least approximately 50%, preferably at least approximately 60% and more preferably at least approximately 70%, 80% or 90% and most preferably at least approximately 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identity with the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 or SEQ ID NO: 9.

**[0029]** The nucleic acid sequences used in the process are advantageously introduced into an expression cassette which makes possible the expression of the nucleic acids in organisms such as microorganisms or plants.

**[0030]** Described is a gene construct comprising a nucleic acid sequence which encodes one or more polypeptides with  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase activity as set out above, operably linked with one or more regulatory sequences.

**[0031]** In the expression cassette, the nucleic acid sequence which encodes  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase, is linked operably with one or more regulatory sequences, advantageously for enhancing gene expression. These regulatory sequences are intended to make possible the specific expression of the genes and proteins. Depending on the host organism, this may mean, for example, that the gene is expressed and/or overexpressed only after induction has taken place, or else that it is expressed and/or overexpressed immediately. For example, these regulatory sequences take the form of sequences to which inducers or repressors bind, thus controlling the expression of the nucleic acid. In addition to these novel regulatory sequences, or instead of these sequences, the natural regulatory elements of these sequences may still be present before the actual structural genes and, if appropriate, may have been genetically modified in such a way that their natural regulation is eliminated and the expression of the genes is enhanced. However, the expression cassette (= expression construct = gene construct) can also be simpler in construction, that is to say no additional regulatory signals have been inserted before the nucleic acid sequence or its derivatives, and the natural promoter together with its regulation was not removed. Instead, the natural regulatory sequence has been mutated in such a way that regulation no longer takes place and/or gene expression is enhanced. These modified promoters can also be positioned on their own before the natural gene in the form of part-sequences (= promoter with parts of the nucleic acid sequences described herein) in order to enhance the activity. Moreover, the gene construct may advantageously also comprise one or more what are known as enhancer sequences in operable linkage with the promoter, which make possible an enhanced expression of the nucleic acid sequence.

**[0032]** Additional advantageous sequences, such as further regulatory elements or terminator sequences, may also be inserted at the 3' end of the DNA sequences. One or more sequences encoding enzymes which catalyse the conversion of ARA to an  $\omega 3$ -unsaturated fatty acid such as EPA or DHA may also be present. Thus, for example, sequences encoding a  $\Delta 5$ -elongase,  $\omega 3$ -desaturase and/or  $\Delta 4$ -desaturase, may be present in one or more copies of the expression cassette (= gene construct). Preferably, only one copy of the genes is present in each expression cassette. This gene construct or the gene constructs can be expressed together in the host organism. In this context, the gene construct(s) can be inserted in one or more vectors and be present in the cell in free form, or else be inserted in the genome. It is

advantageous for the insertion of further genes in the genome when the genes to be expressed are present together in one gene construct.

**[0033]** In this context, the regulatory sequences or factors can, as described above, preferably have a positive effect on the gene expression of the genes introduced, thus enhancing it. Thus, an enhancement of the regulatory elements, advantageously at the transcriptional level, may take place by using strong transcription signals such as promoters and/or enhancers. In addition, however, enhanced translation is also possible, for example by improving the stability of the mRNA.

**[0034]** The regulatory sequences include, in particular, plant sequences such as promoter and terminator sequences. The constructs can advantageously be stably propagated in microorganisms, in particular in *E. coli* and *Agrobacterium tumefaciens*, under selective conditions and make possible the transfer of heterologous DNA into plants or microorganisms.

**[0035]** Useful regulatory sequences are present, for example, in promoters such as the *cos*, *tac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIq*, *T7*, *T5*, *T3*, *gal*, *trc*, *ara*, *SP6*,  $\lambda$ -PR or  $\lambda$ -PL promoter and are advantageously employed in Gram-negative bacteria. Further advantageous regulatory sequences are, for example, present in the Gram-positive promoters *amy* and *SPO2*, in the yeast or fungal promoters *ADC1*, *MF $\alpha$* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH* or in the plant promoters *CaMV/35S* [Franck et al., Cell 21 (1980) 285-294], *PRP1* [Ward et al., Plant. Mol. Biol. 22 (1993)], *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or in the ubiquitin or phaseolin promoter. Advantageous in this context are also inducible promoters, such as the promoters described in EP-A-0 388 186 (benzenesulfonamide-inducible), Plant J. 2, 1992:397-404 (Gatz et al., tetracycline-inducible), EP-A-0 335 528 (abscissic acid-inducible) or WO 93/21334 (ethanol- or cyclohexenol-inducible) promoters. Further suitable plant promoters are the cytosolic FBPase promoter or the ST-LSI promoter of potato (Stockhaus et al., EMBO J. 8, 1989, 2445), the glycine max phosphoribosylpyrophosphate amidotransferase promoter (Genbank Accession No. U87999) or the node-specific promoter described in EP-A-0 249 676.

**[0036]** Especially advantageous promoters are promoters which make possible the expression in tissues which are involved in the biosynthesis of fatty acids. Very especially advantageous are seed-specific promoters, such as the USP promoter as described, but also other promoters such as the *LeB4*, *DC3*, phaseolin or napin promoter. Further especially advantageous promoters are seed-specific promoters which can be used for monocotyledonous or dicotyledonous plants and which are described in US 5,608,152 (oilseed rape napin promoter), WO 98/45461 (*Arabidopsis oleosin* promoter), US 5,504,200 (*Phaseolus vulgaris* phaseolin promoter), WO 91/13980 (*Brassica Bce4* promoter), by Bäumlein et al., Plant J., 2, 2, 1992:233-239 (*LeB4* promoter from a legume), these promoters being suitable for dicots. Examples of promoters which are suitable for monocots are the barley *lpt-2* or *lpt-1* promoter (WO 95/15389 and WO 95/23230), the barley hordein promoter and other suitable promoters described in WO 99/16890.

**[0037]** In principle, it is possible to use all natural promoters together with their regulatory sequences, such as those mentioned above. It is also possible and advantageous to use synthetic promoters, either in addition or alone, in particular when they mediate seed-specific expression, such as those described in WO 99/16890.

**[0038]** In order to achieve a particularly high ARA content, especially in transgenic plants, the genes should advantageously be expressed in oil crops in a seed-specific manner. To this end, seed-specific promoters can be used, or those promoters which are active in the embryo and/or in the endosperm. In principle, seed-specific promoters can be isolated both from dicotyledonous and from monocotyledonous plants. Preferred promoters are listed hereinbelow: USP (= unknown seed protein) and vicilin (*Vicia faba*) [Bäumlein et al., Mol. Gen. Genet., 1991, 225(3)], napin (oilseed rape) [US 5,608,152], acyl carrier protein (oilseed rape) [US 5,315,001 and WO 92/18634], oleosin (*Arabidopsis thaliana*) [WO 98/45461 and WO 93/20216], phaseolin (*Phaseolus vulgaris*) [US 5,504,200], *Bce4* [WO 91/13980], legumines *B4* (*LegB4* promoter) [Bäumlein et al., Plant J., 2,2, 1992], *Lpt2* and *Lpt1* (barley) [WO 95/15389 and WO95/23230], seed-specific promoters from rice, maize and wheat [WO 99/16890], *Amy32b*, *Amy 6-6* and *aleurain* [US 5,677,474], *Bce4* (oilseed rape) [US 5,530,149], *glycinin* (soybean) [EP 571 741], *phosphoenol pyruvate carboxylase* (soybean) [JP 06/62870], *ADR12-2* (soybean) [WO 98/08962], *isocitrate lyase* (oilseed rape) [US 5,689,040] or  $\alpha$ -amylase (barley) [EP 781 849].

**[0039]** Plant gene expression can also be facilitated via a chemically inducible promoter (see review in Gatz 1997, Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89-108). Chemically inducible promoters are particularly suitable when it is desired that gene expression should take place in a time-specific manner. Examples of such promoters are a salicylic acid-inducible promoter (WO 95/19443), a tetracycline-inducible promoter (Gatz et al. (1992) Plant J. 2, 397-404) and an ethanol-inducible promoter.

**[0040]** To ensure the stable integration of the biosynthesis genes into the transgenic plant over a plurality of generations, it is usually necessary for each of the nucleic acids which encodes a protein of interest to be expressed under the control of a separate promoter, preferably a promoter which differs from the other promoters, since repeating sequence motifs can lead to instability of the T-DNA, or to recombination events. This is one reason why the nucleic acid described herein is particularly advantageous since sequences encoding  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase can be transcribed as a single unit needing only one promoter. It will, of course, be necessary for other genes encoding, for example,  $\Delta 5$ -elongase,  $\omega 3$ -desaturase and/or  $\Delta 4$ -desaturase to be under the control of separate promoters.

**[0041]** In this context, the expression cassette is advantageously constructed in such a way that a promoter is followed by a suitable cleavage site, advantageously in a polylinker, for insertion of the nucleic acid to be expressed and, if appropriate, a terminator sequence is positioned behind the polylinker. This sequence is repeated several times, preferably three, four or five times, so that up to five genes can be combined in one construct and introduced into the transgenic plant in order to be expressed. Advantageously, the sequence is repeated up to three times. To express the nucleic acid sequences, the latter are inserted behind the promoter *via* a suitable cleavage site, for example in the polylinker. Advantageously, each nucleic acid sequence has its own promoter and, if appropriate, its own terminator sequence. Such advantageous constructs are disclosed, for example, in DE 101 02 337 or DE 101 02 338. However, it is also possible to insert a plurality of nucleic acid sequences behind a promoter and, if appropriate, before a terminator sequence. Here, the insertion site, or the sequence, of the inserted nucleic acids in the expression cassette is not of critical importance, that is to say a nucleic acid sequence can be inserted at the first or last position in the cassette without its expression being substantially influenced thereby. Advantageously, different promoters such as, for example, the USP, LegB4 or DC3 promoter, and different terminator sequences can be used in the expression cassette. However, it is also possible to use only one type of promoter in the cassette. This, however, may lead to undesired recombination events.

**[0042]** As described above, the transcription of the genes which have been introduced should advantageously be terminated by suitable terminator sequences at the 3' end of the biosynthesis genes which have been introduced (behind the stop codon). An example of a sequence which can be used in this context is the OCS 1 terminator sequence. As is the case with the promoters, different terminator sequences should be used for each gene.

**[0043]** The gene construct described herein may also comprise biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxigenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) and desaturase(s) such as  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 9$ -desaturase,  $\Delta 12$ -desaturase or  $\Delta 6$ -elongase.

**[0044]** These additional nucleic acids or genes can be cloned into the expression cassettes, which are then used for transforming plants with the aid of vectors such as *Agrobacterium*.

**[0045]** Here, the regulatory sequences or factors can, as described above, preferably have a positive effect on, and thus enhance, the expression genes which have been introduced. Thus, enhancement of the regulatory elements can advantageously take place at the transcriptional level by using strong transcription signals such as promoters and/or enhancers. However, an enhanced translation is also possible, for example by improving the stability of the mRNA. In principle, the expression cassettes can be used directly for introduction into the plants or else be introduced into a vector.

**[0046]** Therefore, described is a vector comprising a nucleic acid or a gene construct described above.

**[0047]** The vector may be a cloning vector.

**[0048]** The nucleic acid sequence(s) described herein may be introduced alone, or preferably, in combination with an expression cassette (nucleic acid construct) into an organism. To introduce the nucleic acids, the latter are advantageously amplified and ligated in the known manner. Preferably, a procedure following the protocol for Pfu DNA polymerase or a Pfu/Taq DNA polymerase mixture is followed. The primers are selected taking into consideration the sequence to be amplified. The primers should advantageously be chosen in such a way that the amplificate comprises the entire codogenic sequence from the start codon to the stop codon. After the amplification, the amplificate is expediently analyzed. For example, a gel-electrophoretic separation can be carried out, which is followed by a quantitative and a qualitative analysis. Thereafter, the amplificate can be purified following a standard protocol (for example Qiagen). An aliquot of the purified amplificate is then available for the subsequent cloning step.

**[0049]** Suitable cloning vectors are generally known to the skilled worker. These include, in particular, vectors which are capable of replication in microbial systems, that is to say mainly vectors which ensure efficient cloning in yeasts or fungi and which make possible the stable transformation of plants. Those which must be mentioned in particular are various binary and cointegrated vector systems which are suitable for the T-DNA-mediated transformation. Such vector systems are, as a rule, characterized in that they comprise at least the *vir* genes required for the *Agrobacterium*-mediated transformation and the T-DNA-delimiting sequences (T-DNA border). These vector systems advantageously also comprise further cis-regulatory regions such as promoters and terminator sequences and/or selection markers, by means of which suitably transformed organisms can be identified. While in the case of cointegrated vector systems *vir* genes and T-DNA sequences are arranged on the same vector, binary systems are based on at least two vectors, one of which bears *vir* genes, but no T-DNA, while a second one bears T-DNA, but no *vir* gene. Owing to this fact, the last-mentioned vectors are relatively small, easy to manipulate and to replicate both in *E. coli* and in *Agrobacterium*. These binary vectors include vectors from the series pBIB-HYG, pPZP, pBecks, pGreen. In accordance with the invention, Bin19, pBI101, pBinAR, pGPTV and pCAMBIA are used by preference. An overview of the binary vectors and their use is found in Hellens et al, Trends in Plant Science (2000) 5, 446-451. In order to prepare the vectors, the vectors can first be linearized



with restriction endonuclease(s) and then modified enzymatically in a suitable manner. Thereafter, the vector is purified, and an aliquot is employed for the cloning step. In the cloning step, the enzymatically cleaved and, if appropriate, purified amplificate is cloned with vector fragments which have been prepared in a similar manner, using ligase. In this context, a particular nucleic acid construct, or vector or plasmid construct, can have one or else more than one codogenic gene segment. The codogenic gene segments in these constructs are preferably linked operably with regulatory sequences. The regulatory sequences include, in particular, plant sequences such as the above-described promoters and terminator sequences. The constructs can advantageously be stably propagated in microorganisms, in particular in *E. coli* and *Agrobacterium tumefaciens*, under selective conditions and make possible the transfer of heterologous DNA into plants or microorganisms.

**[0050]** The nucleic acids described herein can be introduced into organisms such as microorganisms or advantageously plants, advantageously using cloning vectors, and thus be used in the transformation of plants such as those which are published and cited in: *Plant Molecular Biology and Biotechnology* (CRC Press, Boca Raton, Florida), Chapter 6/7, p. 71-119 (1993); F.F. White, *Vectors for Gene Transfer in Higher Plants*; in: *Transgenic Plants*, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press, 1993, 15-38; B. Jenès et al., *Techniques for Gene Transfer*, in: *Transgenic Plants*, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press (1993), 128-143; Potrykus, *Annu. Rev. Plant Physiol. Plant Molec. Biol.* 42 (1991), 205-225. Thus, the nucleic acids and nucleic acid constructs, and/or vectors used in the process can be used for the recombinant modification of a broad spectrum of organisms, advantageously plants, so that the latter become better and/or more efficient producers of ARA.

**[0051]** A series of mechanisms exist by which modification of the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase proteins is possible, so that the yield, production and/or production efficiency of ARA in a plant, preferably in an oil crop plant or a microorganism, can be influenced directly owing to these modified proteins. The number or activity of the proteins or genes can be increased, so that greater amounts of the gene products and, ultimately, greater amounts of the compounds of the general formula I are produced. A *de novo* synthesis in an organism which has lacked the activity and ability to biosynthesize the compounds prior to introduction of the corresponding gene(s) is also possible. This applies analogously to the combination with further desaturases or elongases or further enzymes of the fatty acid and lipid metabolism. The use of various divergent sequences, i.e. sequences which differ at the DNA sequence level, may also be advantageous in this context, or else the use of promoters for gene expression which make possible a different gene expression in the course of time, for example as a function of the degree of maturity of a seed or an oil-storing tissue.

**[0052]** Owing to the introduction of a gene encoding  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase into an organism, alone or in combination with other genes in a cell, it is not only possible to increase biosynthesis flux towards the end product, but also to increase, or to create *de novo* the corresponding triacylglycerol composition. Likewise, the number or activity of other genes which are involved in the import of nutrients which are required for the biosynthesis of one or more fatty acids, oils, polar and/or neutral lipids, can be increased, so that the concentration of these precursors, cofactors or intermediates within the cells or within the storage compartment is increased, whereby the ability of the cells to produce ARA as described below is enhanced further. By optimizing the activity or increasing the number of one or more genes encoding  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase which are involved in the biosynthesis ARA, or by destroying the activity of one or more genes which are involved in the degradation of ARA, an enhanced yield, production and/or efficiency of production of fatty acid and lipid molecules in organisms, advantageously in plants, is made possible.

**[0053]** Nucleic acids which can advantageously be used in the process are derived from bacteria, fungi, diatoms, animals such as *Caenorhabditis* or *Oncorhynchus* or plants such as algae or mosses, such as the genera *Shewanella*, *Physcomitrella*, *Thraustochytrium*, *Fusarium*, *Phytophthora*, *Ceratodon*, *Mantoniella*, *Ostreococcus*, *Isochrysis*, *Aleurita*, *Muscarioides*, *Mortierella*, *Borago*, *Phaeodactylum*, *Cryptothecodinium*, specifically from the genera and species *Oncorhynchus mykiss*, *Xenopus laevis*, *Ciona intestinalis*, *Thalassiosira pseudonona*, *Mantoniella squamata*, *Ostreococcus sp.*, *Ostreococcus tauri*, *Euglena gracilis*, *Physcomitrella patens*, *Phytophthora infestans*, *Fusarium gramineum*, *Cryptothecodinium cohnii*, *Ceratodon purpureus*, *Isochrysis galbana*, *Aleurita farinosa*, *Thraustochytrium sp.*, *Muscarioides viallii*, *Mortierella alpina*, *Borago officinalis*, *Phaeodactylum tricorutum*, *Caenorhabditis elegans* or especially advantageously from *Oncorhynchus mykiss*, *Euglena gracilis*, *Thalassiosira pseudonona* or *Cryptothecodinium cohnii*.

**[0054]** Alternatively, the vector may be an expression vector designed to transform an organism in which the nucleic acid is to be expressed and linoleic acid converted to ARA.

**[0055]** These advantageous vectors, preferably expression vectors, comprise the nucleic acid(s) which encode the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase and which are described herein.

**[0056]** As used in the present context, the term "vector" refers to a nucleic acid molecule which is capable of transporting another nucleic acid to which it is bound. One type of vector is a "plasmid", a circular double-stranded DNA loop into which additional DNA segments can be ligated. A further type of vector is a viral vector, it being possible for additional DNA segments to be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they have been introduced (for example bacterial vectors with bacterial replication origin). Other vectors are advantageously integrated into the genome of a host cell when they are introduced into the host cell, and thus replicate

together with the host genome. Moreover, certain vectors can govern the expression of genes with which they are in operable linkage. These vectors are referred to in the present context as "expression vectors". Usually, expression vectors which are suitable for DNA recombination techniques take the form of plasmids.

**[0057]** In the present description, where the term "plasmid" is used, it should be understood that plasmids can be substituted for other types of expression vector, such as viral vectors, which exert similar functions. Furthermore, the term "vector" is also intended to comprise other vectors with which the skilled worker is familiar, such as phages, viruses such as SV40, CMV, TMV, transposons, IS elements, phasmids, phagemids, cosmids, linear or circular DNA.

**[0058]** The recombinant expression vectors advantageously used in the process comprise the nucleic acids described below or the above-described gene construct in a form which is suitable for expressing the nucleic acids used in a host cell, which means that the recombinant expression vectors comprise one or more regulatory sequences, selected on the basis of the host cells used for the expression, which regulatory sequence(s) is/are linked operably with the nucleic acid sequence to be expressed. In a recombinant expression vector, "linked operably" means that the nucleotide sequence of interest is bound to the regulatory sequence(s) in such a way that the expression of the nucleotide sequence is possible and they are bound to each other in such a way that both sequences carry out the predicted function which is ascribed to the sequence (for example in an in-vitro transcription/translation system, or in a host cell if the vector is introduced into the host cell). The term "regulatory sequence" is intended to comprise promoters, enhancers and other expression control elements (for example polyadenylation signals). These regulatory sequences are described, for example, in Goeddel: Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990), or see: Gruber and Crosby, in: Methods in Plant Molecular Biology and Biotechnology, CRC Press, Boca Raton, Florida, Ed.: Glick and Thompson, Chapter 7, 89-108, including the references cited therein. Regulatory sequences comprise those which govern the constitutive expression of a nucleotide sequence in many types of host cell and those which govern the direct expression of the nucleotide sequence only in specific host cells under specific conditions. The skilled worker knows that the design of the expression vector can depend on factors such as the choice of host cell to be transformed, the desired expression level of the protein and the like.

**[0059]** The recombinant expression vectors used can be designed for the expression of  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase in prokaryotic or eukaryotic cells. This is advantageous since intermediate steps of the vector construction are frequently carried out in microorganisms for the sake of simplicity. For example, the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase gene can be expressed in bacterial cells, insect cells (using Baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A., et al. (1992) "Foreign gene expression in yeast: a review", Yeast 8:423-488; van den Hondel, C.A.M.J.J., et al. (1991) "Heterologous gene expression in filamentous fungi", in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, Ed., pp. 396-428; Academic Press: San Diego; and van den Hondel, C.A.M.J.J., & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F., et al., Ed., pp. 1-28, Cambridge University Press: Cambridge), algae (Falciatore et al., 1999, Marine Biotechnology.1, 3:239-251), ciliates of the types: Holotrichia, Peritrichia, Spirotrichia, Suctorina, Tetrahymena, Paramecium, Colpidium, Glaucoma, Platyophrya, Potomacus, Desaturaseudocohnilembus, Euplotes, Engelmaniella and Stylonychia, in particular of the genus Stylonychia lemnae, using vectors in a transformation method as described in WO 98/01572 and, preferably, in cells of multi-celled plants (see Schmidt, R. and Willmitzer, L. (1988) "High efficiency Agrobacterium tumefaciens-mediated transformation of Arabidopsis thaliana leaf and cotyledon explants" Plant Cell Rep.:583-586; Plant Molecular Biology and Biotechnology, C Press, Boca Raton, Florida, Chapter 6/7, pp.71-119 (1993); F.F. White, B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press (1993), 128-43; Potrykus, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991), 205-225 (and references cited therein)). Suitable host cells are furthermore discussed in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). As an alternative, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7-promoter regulatory sequences and T7-polymerase.

**[0060]** In most cases, the expression of proteins in prokaryotes involves the use of vectors comprising constitutive or inducible promoters which govern the expression of fusion or nonfusion proteins. Typical fusion expression vectors are, inter alia, pGEX (Pharmacia Biotech Inc; Smith, D.B., and Johnson, K.S. (1988) Gene 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ), where glutathione S-transferase (GST), maltose-E binding protein and protein A, respectively, is fused with the recombinant target protein.

**[0061]** Examples of suitable inducible nonfusion *E. coli* expression vectors are, inter alia, pTrc (Amann et al. (1988) Gene 69:301-315) and pET 11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). The target gene expression from the pTrc vector is based on the transcription from a hybrid trp-lac fusion promoter by the host RNA polymerase. The target gene expression from the vector pET 11d is based on the transcription of a T7-gn10-lac fusion promoter, which is mediated by a viral RNA polymerase (T7 gn1), which is coexpressed. This viral polymerase is provided by the host strains BL21 (DE3) or HMS174 (DE3) from a resident  $\lambda$ -prophage which harbors a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

Other vectors which are suitable for prokaryotic organisms are known to the skilled worker, these vectors are, for example

in *E. coli* pLG338, pACYC184, the pBR series such as pBR322, the pUC series such as pUC18 or pUC19, the M13mp series, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1,  $\lambda$ gt11 or pBdCl, in *Streptomyces* pIJ101, pIJ364, pIJ702 or pIJ361, in *Bacillus* pUB110, pC194 or pBD214, in *Corynebacterium* pSA77 or pAJ667. The expression vector can be a yeast expression vector. Examples for vectors for expression in the yeast *S. cerevisiae* comprise pYeDesaturasec1 (Baldari et al. (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz (1982) *Cell* 30:933-943), pJRY88 (Schultz et al. (1987) *Gene* 54:113-123) and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and processes for the construction of vectors which are suitable for use in other fungi, such as the filamentous fungi, comprise those which are described in detail in: van den Hondel, C.A.M.J.J., & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of fungi*, J.F. Peberdy et al., Ed., pp. 1-28, Cambridge University Press: Cambridge, or in: *More Gene Manipulations in Fungi* [J.W. Bennet & L.L. Lasure, Ed., pp. 396-428: Academic Press: San Diego]. Further suitable yeast vectors are, for example, pAG-1, YEp6, YEp13 or pEMBLye23.

As an alternative,  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase can be expressed in insect cells using Baculovirus vectors. Baculovirus expression vectors which are available for the expression of proteins in cultured insect cells (for example Sf9 cells) comprise the pAc series (Smith et al. (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

The abovementioned vectors are only a small overview over suitable vectors which are possible. Further plasmids are known to the skilled worker and are described, for example, in: *Cloning Vectors* (Ed. Pouwels, P.H., et al., Elsevier, Amsterdam-New York-Oxford, 1985, ISBN 0 444 904018). For further suitable expression systems for prokaryotic and eukaryotic cells, see the Chapters 16 and 17 in Sambrook, J., Fritsch, E.F., and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, 2. edition, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In a further alternative of the process, the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase can be expressed in single-celled plant cells (such as algae), see Falciatore et al., 1999, *Marine Biotechnology* 1 (3):239-251 and references cited therein, and in plant cells from higher plants (for example spermatophytes such as arable crops). Examples of plant expression vectors comprise those which are described in detail in: Becker, D., Kemper, E., Schell, J., and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20:1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acids Res.* 12:8711-8721; *Vectors for Gene Transfer in Higher Plants*; in: *Transgenic Plants*, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press, 1993, p. 15-38.

**[0062]** A plant expression cassette preferably comprises regulatory sequences which are capable of governing the expression of genes in plant cells and which are linked operably so that each sequence can fulfill its function, such as transcriptional termination, for example polyadenylation signals. Preferred polyadenylation signals are those which are derived from *Agrobacterium tumefaciens* T-DNA, such as gene 3 of the Ti plasmid pTiACH5 (Gielen et al., *EMBO J.* 3 (1984) 835 et seq.), which is known as octopine synthase, or functional equivalents thereof, but all other terminator sequences which are functionally active in plants are also suitable.

**[0063]** Since plant gene expression is very often not limited to the transcriptional level, a plant expression cassette preferably comprises other sequences which are linked operably, such as translation enhancers, for example the overdrive sequence, which enhances the tobacco mosaic virus 5' - untranslated leader sequence, which increases the protein/RNA ratio (Gallie et al., 1987, *Nucl. Acids Research* 15:8693-8711).

**[0064]** As described above, plant gene expression must be linked operably with a suitable promoter which triggers gene expression with the correct timing or in a cell- or tissue-specific manner. Utilizable promoters are constitutive promoters (Benfey et al., *EMBO J.* 8 (1989) 2195-2202), such as those which are derived from plant viruses, such as 35S CaMV (Franck et al., *Cell* 21 (1980) 285-294), 19S CaMV (see also US 5352605 and WO 84/02913), or plant promoters, such as the promoter of the Rubisco subunit, which is described in US 4,962,028.

**[0065]** Other preferred sequences for use in operable linkage in plant gene expression cassettes are targeting sequences, which are required for steering the gene product into its corresponding cell compartment (see a review in Kermode, *Crit. Rev. Plant Sci.* 15, 4 (1996) 285-423 and references cited therein), for example into the vacuole, into the nucleus, all types of plastids, such as amyloplasts, chloroplasts, chromoplasts, the extracellular space, the mitochondria, the endoplasmid reticulum, elaioplasts, peroxisomes and other compartments of plant cells.

**[0066]** As described above, plant gene expression can also be achieved *via* a chemically inducible promoter (see review in Gatz 1997, *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, 48:89-108). Chemically inducible promoters are particularly suitable when it is desired that the gene expression takes place in a time-specific manner. Examples of such promoters are a salicylic-acid-inducible promoter (WO 95/19443), a tetracyclin-inducible promoter (Gatz et al. (1992) *Plant J.* 2, 397-404) and an ethanol-inducible promoter.

**[0067]** Promoters which respond to biotic or abiotic stress conditions are also suitable, for example the pathogen-induced PRP1 gene promoter (Ward et al., *Plant. Mol. Biol.* 22 (1993) 361-366), the heat-inducible tomato hsp80 promoter (US 5,187,267), the chill-inducible potato alpha-amylase promoter (WO 96/12814) or the wound-inducible pinll promoter

(EP-A-0 375 091).

**[0068]** Especially preferred are those promoters which bring about the gene expression in tissues and organs in which the biosynthesis of fatty acids, lipids and oils takes place, in seed cells, such as cells of the endosperm and of the developing embryo. Suitable promoters are the oilseed rape napin promoter (US 5,608,152), the *Vicia faba* USP promoter (Baeumlein et al., Mol Gen Genet, 1991, 225 (3):459-67), the *Arabidopsis oleosin* promoter (WO 98/45461), the *Phaseolus vulgaris* phaseolin promoter (US 5,504,200), the *Brassica Bce4* promoter (WO 91/13980) or the legumine B4 promoter (LeB4; Baeumlein et al., 1992, Plant Journal, 2 (2):233-9), and promoters which bring about the seed-specific expression in monocotyledonous plants such as maize, barley, wheat, rye, rice and the like. Suitable noteworthy promoters are the barley *lpt2* or *lpt1* gene promoter (WO 95/15389 and WO 95/23230) or the promoters from the barley hordein gene, the rice glutelin gene, the rice oryzin gene, the rice prolamine gene, the wheat gliadine gene, the wheat glutelin gene, the maize zeine gene, the oat glutelin gene, the sorghum kasirin gene or the rye secalin gene, which are described in WO 99/16890.

**[0069]** As described above, it may be advantageous to include in an expression cassette nucleic acid encoding enzymes capable of converting ARA to  $\omega$ 3-unsaturated fatty acids such as EPA or DHA. Thus, for example the expression cassette may also include nucleic acid encoding a  $\Delta$ 5-elongase,  $\omega$ 3-desaturase and/or  $\Delta$ 4-desaturase. Such expression cassettes can be introduced *via* the simultaneous transformation of a plurality of individual expression constructs or, preferably, by combining a plurality of expression cassettes on one construct. Also, a plurality of vectors can be transformed with in each case a plurality of expression cassettes and then transferred into the host cell.

**[0070]** Other promoters which are likewise especially suitable are those which bring about a plastid-specific expression, since plastids constitute the compartment in which the precursors and some end products of lipid biosynthesis are synthesized. Suitable promoters, such as the viral RNA polymerase promoter, are described in WO 95/16783 and WO 97/06250, and the *clpP* promoter from *Arabidopsis*, described in WO 99/46394.

**[0071]** Vector DNA can be introduced into prokaryotic and eukaryotic cells *via* conventional transformation or transfection techniques. The terms "transformation" and "transfection", conjugation and transduction, as used in the present context, are intended to comprise a multiplicity of methods known in the prior art for the introduction of foreign nucleic acid (for example DNA) into a host cell, including calcium phosphate or calcium chloride coprecipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemically mediated transfer, electroporation or particle bombardment. Suitable methods for the transformation or transfection of host cells, including plant cells, can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual., 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989) and other laboratory textbooks such as Methods in Molecular Biology, 1995, Vol. 44, Agrobacterium protocols, Ed.: Gartland and Davey, Humana Press, Totowa, New Jersey.

**[0072]** Described is a transgenic nonhuman organism comprising at least one nucleic acid, gene construct or vector described herein.

**[0073]** The transgenic nonhuman organism may be a microorganism, a nonhuman animal or a plant.

**[0074]** Host cells which are suitable in principle for taking up the nucleic acid described herein, the gene product or the vector described herein are all prokaryotic or eukaryotic organisms. The host organisms which are advantageously used are microorganisms such as fungi or yeasts, or plant cells, preferably plants or parts thereof. Fungi, yeasts or plants are preferably used, especially plants, for example plants such as oil crops, which are high in lipid compounds, such as oilseed rape, evening primrose, hemp, thistle, peanut, canola, linseed, soybean, safflower, sunflower, borage, or plants such as maize, wheat, rye, oats, triticale, rice, barley, cotton, cassava, pepper, *Tagetes*, *Solanacea* plants such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants (coffee, cacao, tea), *Salix* species, trees (oil palm, coconut), and perennial grasses and fodder crops. Especially preferred plants are oil crops such as soybean, peanut, oilseed rape, canola, linseed, hemp, evening primrose, sunflower, safflower, trees (oil palm, coconut).

**[0075]** The term "nucleic acid (molecule)" as used in the present context additionally comprises the untranslated sequence at the 3' and at the 5' end of the coding gene region: at least 500, preferably 200, especially preferably 100 nucleotides of the sequence upstream of the 5' end of the coding region and at least 100, preferably 50, especially preferably 20 nucleotides of the sequence downstream of the 3' end of the coding gene region. An "isolated" nucleic acid molecule is separate from other nucleic acid molecules which are present in the natural source of the nucleic acid. An "isolated" nucleic acid preferably has no sequences which naturally flank the nucleic acid in the genomic DNA of the organism from which the nucleic acid is derived (for example sequences which are located at the 5' and 3' ends of the nucleic acid). The isolated  $\Delta$ 9-elongase,  $\Delta$ 8-desaturase or  $\Delta$ 5-desaturase molecule can comprise for example fewer than approximately 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid is derived. The same applies to other nucleic acid sequences which may be included in an expression cassette, for example sequences encoding a  $\Delta$ 5-elongase,  $\omega$ 3-desaturase and/or  $\Delta$ 4-desaturase

**[0076]** The nucleic acid molecules described herein, for example a nucleic acid molecule with a nucleotide sequence of SEQ ID NO: 1 or residues 7668 to 12077 thereof, or the parts of SEQ ID NO: 1 specified herein, can be isolated using molecular-biological standard techniques and the sequence information provided herein. Also, for example a homologous

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sequence or homologous, conserved sequence regions can be identified at the DNA or amino acid level with the aid of comparative algorithms. They can be used as hybridization probe and standard hybridization techniques (such as, for example, those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989) for isolating further nucleic acid sequences which can be used in the process.

**[0077]** Moreover, a nucleic acid molecule from *Perkinsus marinus* comprising a complete sequence of SEQ ID NO: 1 or a part thereof can be isolated by polymerase chain reaction, where oligonucleotide primers which are used on the basis of this sequence or parts thereof (for example a nucleic acid molecule comprising the complete sequence or part thereof can be isolated by polymerase chain reaction using oligonucleotide primers which have been generated based on this same sequence). For example, mRNA can be isolated from cells (for example by means of the guanidinium thiocyanate extraction method of Chirgwin et al. (1979) *Biochemistry* 18:5294-5299) and cDNA by means of reverse transcriptase (for example Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD, or AMV reverse transcriptase, available from Seikagaku America, Inc., St.Petersburg, FL).

**[0078]** Synthetic oligonucleotide primers for the amplification by means of polymerase chain reaction can be generated based on one of the sequences shown in SEQ ID NO: 1 or with the aid of the amino acid sequences detailed in SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4. Particularly suitable primers are shown in the Examples as SEQ ID NO: 5 and SEQ ID NO: 6.

**[0079]** A nucleic acid as described herein can be amplified by standard PCR amplification techniques using cDNA or, alternatively, genomic DNA as template (SEQ ID NO 9) and suitable oligonucleotide primers (SEQ ID NO: 5 and SEQ ID NO: 6). The nucleic acid amplified thus can be cloned into a suitable vector and characterized by means of DNA sequence analysis. Oligonucleotides which correspond to a desaturase or elongase nucleotide sequence can be generated by standard synthetic methods, for example using an automatic DNA synthesizer.

**[0080]** The abovementioned nucleic acids and protein molecules with  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or  $\Delta 5$ -desaturase activity may be used in a process for the production of ARA from linoleic acid in transgenic organisms.

**[0081]** Therefore, in a first aspect of the invention, there is provided a process for producing a polyunsaturated fatty acid (PUFA) comprising arachidonic acid (ARA) wherein the process comprises the conversion of linoleic acid to arachidonic acid in a non-human transgenic organism, the process comprising

(i) providing a non-human transgenic organism comprising, as heterologous nucleic acid sequence, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 9$ -elongase activity and which is selected from the group consisting of:

a) a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1;

b) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising residues 7668 to 9200 of SEQ ID NO: 1, wherein hybridization is in 6 x sodium chloride/sodium citrate (SSC) at approximately 45°C, followed by one or more washing steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C;

c) a nucleic acid sequence which encodes a polypeptide comprising SEQ ID NO: 2;

d) a nucleic acid sequence which encodes a polypeptide with at least 85% identity at the amino acid level with SEQ ID NO: 2; and

at least one nucleic acid sequence encoding a  $\Delta 8$  desaturase and at least one nucleic acid sequence encoding a  $\Delta 5$  desaturase; and

(ii) expressing said nucleic acid sequence.

**[0082]** Described is a process for the conversion of linoleic acid or a derivative thereof to arachidonic acid or a derivative thereof in an organism, the process comprising introducing into an organism which comprises linoleic acid at least one nucleic acid sequence comprising :

a) SEQ ID NO: 1 (Full sequence 1047306867), sequence comprising nucleic acid residues 7668 to 12077 of SEQ ID NO: 1 or a homolog of one of these;

b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence of SEQ ID NO: 1 or a sequence comprising nucleic acid residues 7668 to 12077 of SEQ ID NO: 1;

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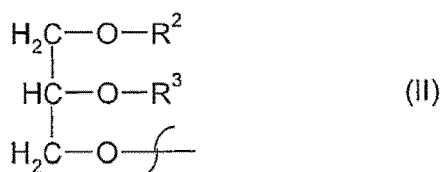
c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase activity, wherein the polypeptides are selected from the group consisting of SEQ ID NOS 2, 3 and 4;

d) A derivative of a nucleic acid sequence of SEQ ID NO: 1 which encodes polypeptides with at least 40% identity at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4; wherein said polypeptides have  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase activity.

and expressing said nucleic acid sequence.

**[0083]** A "derivative" of linoleic or arachidonic acid is a compound in which the OH of the carboxylic acid moiety is replaced by a moiety  $R^1$ , wherein:

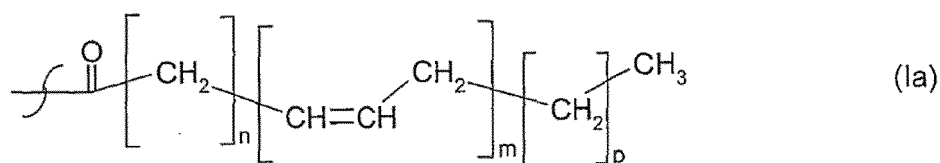
$R^1$  is coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the formula II



in which

$R^2 =$  hydrogen, lysophosphatidyl choline, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated  $C_2$ - $C_{24}$ -alkyl-carbonyl,

$R^3 =$  hydrogen, saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl, or  $R^2$  and  $R^3$  independently of one another are a radical of the formula Ia:



in which

$n = 2, 3, 4, 5, 6, 7$  or  $9$ ,  $m = 2, 3, 4, 5$  or  $6$  and  $p = 0$  or  $3$ ;

and wherein an oxygen in the  $R^1$  radical may be replaced by sulphur such that  $R^1$  is bonded to the remainder of the molecule *via* a thioester linkage.

**[0084]** The process according to the invention preferably yields total ARA in a content of at least 1% by weight, advantageously at least 3% by weight, based on the total fatty acids in the non-human transgenic organisms, preferably in a transgenic plant.

**[0085]** Since a plurality of reaction steps are performed by the starting compounds linoleic acid ( $18:2^{\Delta 9,12}$ ) in the process according to the invention, ARA ( $20:4^{\Delta 5,8,11,14}$ ) is not obtained as a pure product; minor traces of the precursors are always present in the end product.

**[0086]** Chemically pure ARA can also be synthesized by the process described above. To this end, ARA is isolated from the organisms, such as the microorganisms or the plants or the culture medium in or on which the organisms have been grown, or from the organism and the culture medium, in the known manner, for example *via* extraction, distillation, crystallization, chromatography or a combination of these methods. This chemical ARA is advantageous for applications in the food industry sector, the cosmetic sector and especially the pharmacological industry sector.

**[0087]** The process may include additional steps of converting the ARA to an  $\omega$ -3 fatty acid by introducing into the organism nucleic acid encoding a  $\omega$ -3 desaturase and optionally a  $\Delta 5$ -elongase and/or a  $\Delta 4$ -elongase and/or a  $\Delta 4$ -

desaturase.

**[0088]** Described is a process for the conversion of 18:2 $\Delta^{9,12}$  (linoleic acid) to 20:2 $\Delta^{11,14}$ , the process comprising introducing into an organism which comprises linoleic acid at least one nucleic acid sequence which encodes a polypeptide having  $\Delta 9$ -elongase activity and which comprises:

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a) a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1, SEQ ID NO: 9 or a homolog of one of these;

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b) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising residues 7668 to 9200 of SEQ ID NO: 1 or SEQ ID NO: 9;

c) an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta 9$ -elongase activity, wherein the polypeptide comprises SEQ ID NO: 2 or SEQ ID NO: 10;

15

d) A derivative of a a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1 or SEQ ID NO: 9 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 2 or SEQ ID NO: 10; wherein said polypeptide has  $\Delta 9$ -elongase activity;

and expressing said nucleic acid sequence.

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**[0089]** Further described is a process for the conversion of 20:2 $\Delta^{11,14}$  to 20:3 $\Delta^{8,11,14}$ , the process comprising introducing into an organism which comprises 20:2 $\Delta^{11,14}$ , or which comprises linoleic acid and a  $\Delta 9$  elongase, an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta 8$ -desaturase activity and which is selected from the group consisting of:

25

a) a sequence comprising nucleic acid residues 9351 to 10724 of SEQ ID NO: 1 or a homolog thereof;

b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence comprising residues 9351 to 10724 of SEQ ID NO: 1;

30

c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 8$ -desaturase activity, wherein the polypeptide comprises SEQ ID NO: 3;

d) A derivative of a a sequence comprising nucleic acid residues 9351 to 10724 of SEQ ID NO: 1 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 3; wherein said polypeptide has  $\Delta 8$ -desaturase activity; and

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expressing said nucleic acid sequence.

**[0090]** Also described is a process for the conversion of 20:3 $\Delta^{8,11,14}$  to 20:4 $\Delta^{5,8,11,14}$  (ARA), the process comprising introducing into an organism which comprises 20:3 $\Delta^{8,11,14}$  or which comprises 20:2 $\Delta^{11,14}$  and a  $\Delta 8$ -desaturase, or which comprises linoleic acid, a  $\Delta 9$  elongase and a  $\Delta 8$ -desaturase, an isolated nucleic acid sequence which encodes a polypeptide with  $\Delta 5$ -desaturase activity and which is selected from the group consisting of:

40

a) a sequence comprising nucleic acid residues 10842 to 12077 of SEQ ID NO: 1 or a homolog thereof;

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b) nucleic acid sequences which hybridize under stringent conditions with a nucleic acid sequence comprising residues 10842 to 12077 of SEQ ID NO: 1;

c) an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 5$ -desaturase activity, wherein the polypeptide comprises SEQ ID NO: 4;

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d) A derivative of a a sequence comprising nucleic acid residues 10842 to 12077 of SEQ ID NO: 1 which encodes a polypeptide with at least 40% identity at the amino acid level with SEQ ID NO: 4; wherein said polypeptide has  $\Delta 5$ -desaturase activity.

and expressing said nucleic acid sequence.

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**[0091]** The process may include additional steps of converting the ARA to an  $\omega$ -3 fatty acid by introducing into the organism nucleic acid encoding a  $\omega$ -3 desaturase and optionally a  $\Delta 5$ -elongase and/or a  $\Delta 4$ -elongase and/or a  $\Delta 4$ -desaturase.

**[0092]** For the processes set out above, it has been found that expression has been most effectively achieved using

induction with galactose.

**[0093]** Suitable organisms for the production in the process according to the invention are, in principle, any organisms such as microorganisms, nonhuman animals or plants.

**[0094]** Plants which are suitable are, in principle, all those plants which are capable of synthesizing fatty acids, such as all dicotyledonous or monocotyledonous plants, algae or mosses. Advantageous plants are selected from the group of the plant families Adelotheceaceae, Anacardiaceae, Asteraceae, Apiaceae, Betulaceae, Boraginaceae, Brassicaceae, Bromeliaceae, Caricaceae, Cannabaceae, Convolvulaceae, Chenopodiaceae, Crypthecodiniaceae, Cucurbitaceae, Ditrichaceae, Elaeagnaceae, Ericaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Juglandaceae, Lauraceae, Leguminosae, Linaceae, Euglenaceae, Prasinophyceae or vegetable plants or ornamentals such as *Tagetes*.

**[0095]** Examples which may be mentioned are the following plants selected from the group consisting of: Adelotheceaceae such as the genera *Physcomitrella*, for example the genus and species *Physcomitrella patens*, Anacardiaceae such as the genera *Pistacia*, *Mangifera*, *Anacardium*, for example the genus and species *Pistacia vera* [pistachio], *Mangifera indica* [mango] or *Anacardium occidentale* [cashew], Asteraceae, such as the genera *Calendula*, *Carthamus*, *Centaurea*, *Cichorium*, *Cynara*, *Helianthus*, *Lactuca*, *Locusta*, *Tagetes*, *Valeriana*, for example the genus and species *Calendula officinalis* [common marigold], *Carthamus tinctorius* [safflower], *Centaurea cyanus* [cornflower], *Cichorium intybus* [chicory], *Cynara scolymus* [artichoke], *Helianthus annuus* [sunflower], *Lactuca sativa*, *Lactuca crispa*, *Lactuca esculenta*, *Lactuca scariola* L. ssp. *sativa*, *Lactuca scariola* L. var. *integrata*, *Lactuca scariola* L. var. *integrifolia*, *Lactuca sativa* subsp. *romana*, *Locusta communis*, *Valeriana locusta* [salad vegetables], *Tagetes lucida*, *Tagetes erecta* or *Tagetes tenuifolia* [african or french marigold], Apiaceae, such as the genus *Daucus*, for example the genus and species *Daucus carota* [carrot], Betulaceae, such as the genus *Corylus*, for example the genera and species *Corylus avellana* or *Corylus colurna* [hazelnut], Boraginaceae, such as the genus *Borago*, for example the genus and species *Borago officinalis* [borage], Brassicaceae, such as the genera *Brassica*, *Camelina*, *Melanosinapis*, *Sinapis*, *Arabadopsis*, for example the genera and species *Brassica napus*, *Brassica rapa* ssp. [oilseed rape], *Sinapis arvensis* *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapioides*, *Camelina sativa*, *Melanosinapis communis* [mustard], *Brassica oleracea* [fodder beet] or *Arabidopsis thaliana*, Bromeliaceae, such as the genera *Anana*, *Bromelia* (pineapple), for example the genera and species *Anana comosus*, *Ananas ananas* or *Bromelia comosa* [pineapple], Caricaceae, such as the genus *Carica*, such as the genus and species *Carica papaya* [pawpaw], Cannabaceae, such as the genus *Cannabis*, such as the genus and species *Cannabis sativa* [hemp], Convolvulaceae, such as the genera *Ipomea*, *Convolvulus*, for example the genera and species *Ipomoea batatas*, *Ipomoea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomoea fastigiata*, *Ipomoea tiliacea*, *Ipomoea triloba* or *Convolvulus panduratus* [sweet potato, batate], Chenopodiaceae, such as the genus *Beta*, such as the genera and species *Beta vulgaris*, *Beta vulgaris* var. *altissima*, *Beta vulgaris* var. *vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva* or *Beta vulgaris* var. *esculenta* [sugarbeet], Crypthecodiniaceae, such as the genus *Crypthecodinium*, for example the genus and species *Crypthecodinium cohnii*, Cucurbitaceae, such as the genus *Cucurbita*, for example the genera and species *Cucurbita maxima*, *Cucurbita mixta*, *Cucurbita pepo* or *Cucurbita moschata* [pumpkin/squash], Cymbeliaceae, such as the genera *Amphora*, *Cymbella*, *Okedenia*, *Phaeodactylum*, *Reimeria*, for example the genus and species *Phaeodactylum tricornutum*, Ditrichaceae, such as the genera *Ditrichaceae*, *Astomiopsis*, *Ceratodon*, *Chrysoblastella*, *Ditrichum*, *Distichium*, *Eccremidium*, *Lophidion*, *Philibertiella*, *Pleuridium*, *Saelania*, *Trichodon*, *Skottsbergia*, for example the genera and species *Ceratodon antarcticus*, *Ceratodon columbiae*, *Ceratodon heterophyllum*, *Ceratodon purpurascens*, *Ceratodon purpureus*, *Ceratodon purpureus* ssp. *convolutus*, *Ceratodon purpureus* ssp. *stenocarpus*, *Ceratodon purpureus* var. *rotundifolius*, *Ceratodon ratodon*, *Ceratodon stenocarpus*, *Chrysoblastella chilensis*, *Ditrichum ambiguum*, *Ditrichum brevisetum*, *Ditrichum crispatisimum*, *Ditrichum difficile*, *Ditrichum falcifolium*, *Ditrichum flexicaule*, *Ditrichum giganteum*, *Ditrichum heteromallum*, *Ditrichum lineare*, *Ditrichum lineare*, *Ditrichum montanum*, *Ditrichum montanum*, *Ditrichum pallidum*, *Ditrichum punctulatum*, *Ditrichum pusillum*, *Ditrichum pusillum* var. *tortile*, *Ditrichum rhynchostegium*, *Ditrichum schimperii*, *Ditrichum tortile*, *Distichium capillaceum*, *Distichium hagenii*, *Distichium inclinatum*, *Distichium macounii*, *Eccremidium floridanum*, *Eccremidium whiteleggei*, *Lophidion strictus*, *Pleuridium acuminatum*, *Pleuridium alternifolium*, *Pleuridium holdridgei*, *Pleuridium mexicanum*, *Pleuridium ravenelii*, *Pleuridium subulatum*, *Saelania glaucescens*, *Trichodon borealis*, *Trichodon cylindricus* or *Trichodon cylindricus* var. *oblongus*, Elaeagnaceae, such as the genus *Elaeagnus*, for example the genus and species *Olea europaea* [olive], Ericaceae, such as the genus *Kalmia*, for example the genera and species *Kalmia latifolia*, *Kalmia angustifolia*, *Kalmia microphylla*, *Kalmia polifolia*, *Kalmia occidentalis*, *Cistus chamaerhodendros* or *Kalmia lucida* [mountain laurel], Euglenaceae, such as the genera *Ascoglena*, *Astasia*, *Colacium*, *Cyclidiopsis*, *Euglena*, *Euglenopsis*, *Hyalaphacus*, *Khawkinaea*, *Lepocinclis*, *Phacus*, *Strombomonas*, *Trachelomonas*, for example the genus and species *Euglena gracilis*; Euphorbiaceae, such as the genera *Manihot*, *Janipha*, *Jatropha*, *Ricinus*, for example the genera and species *Manihot utilissima*, *Janipha manihot*, *Jatropha manihot*, *Manihot aipil*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot esculenta* [cassava] or *Ricinus communis* [castor-oil plant], Fabaceae, such as the genera *Pisum*, *Albizia*, *Cathormion*, *Feuillea*, *Inga*, *Pithecolobium*, *Acacia*, *Mimosa*, *Medicago*, *Glycine*, *Dolichos*, *Phaseolus*, soybean, for example the genera and species *Pisum sativum*, *Pisum arvense*, *Pisum humile* [pea], *Albizia berteriana*, *Albizia julibrissin*, *Albizia lebeck*,



*Acacia berteriana*, *Acacia littoralis*, *Albizia berteriana*, *Albizzia berteriana*, *Cathormion berteriana*, *Feuillea berteriana*,  
*Inga fragrans*, *Pithecellobium berterianum*, *Pithecellobium fragrans*, *Pithecolobium berterianum*, *Pseudalbizzia berteri-*  
*ana*, *Acacia julibrissin*, *Acacia nemu*, *Albizia nemu*, *Feuillea julibrissin*, *Mimosa julibrissin*, *Mimosa speciosa*, *Sericanrda*  
*julibrissin*, *Acacia lebbeck*, *Acacia macrophylla*, *Albizia lebbeck*, *Feuillea lebbeck*, *Mimosa lebbeck*, *Mimosa speciosa*,  
5 *Medicago sativa*, *Medicago falcata*, *Medicago varia* [alfalfa] *Glycine max* *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*,  
*Phaseolus max*, *Soja hispida* or *Soja max* [soybean], Funariaceae, such as the genera *Aphanorrhagma*, *Entosthodon*,  
*Funaria*, *Physcomitrella*, *Physcomitrium*, for example the genera and species *Aphanorrhagma serratum*, *Entosthodon*  
*attenuatus*, *Entosthodon bolanderi*, *Entosthodon bonplandii*, *Entosthodon californicus*, *Entosthodon drummondii*, *Ento-*  
*sthodon jamesonii*, *Entosthodon leibergii*, *Entosthodon neoscoticus*, *Entosthodon rubrisetus*, *Entosthodon spathulifolius*,  
10 *Entosthodon tucsoni*, *Funaria americana*, *Funaria bolanderi*, *Funaria calcarea*, *Funaria californica*, *Funaria calvescens*,  
*Funaria convoluta*, *Funaria flavicans*, *Funaria groutiana*, *Funaria hygrometrica*, *Funaria hygrometrica* var. *arctica*, *Funaria*  
*hygrometrica* var. *calvescens*, *Funaria hygrometrica* var. *convoluta*, *Funaria hygrometrica* var.  *muralis*, *Funaria hygrom-*  
*etrica* var. *utahensis*, *Funaria microstoma*, *Funaria microstoma* var. *obtusifolia*, *Funaria muhlenbergii*, *Funaria orcuttii*,  
15 *Funaria plano-convexa*, *Funaria polaris*, *Funaria ravenelii*, *Funaria rubriseta*, *Funaria serrata*, *Funaria sonora*, *Funaria*  
*sublimbatus*, *Funaria tucsoni*, *Physcomitrella californica*, *Physcomitrella patens*, *Physcomitrella readeri*, *Physcomitrium*  
*australe*, *Physcomitrium californicum*, *Physcomitrium collenchymatum*, *Physcomitrium coloradense*, *Physcomitrium cu-*  
*puliferum*, *Physcomitrium drummondii*, *Physcomitrium eurystomum*, *Physcomitrium flexifolium*, *Physcomitrium hookeri*,  
*Physcomitrium hookeri* var. *serratum*, *Physcomitrium immersum*, *Physcomitrium kellermanii*, *Physcomitrium megaloc-*  
*carpum*, *Physcomitrium pyriforme*, *Physcomitrium pyriforme* var. *serratum*, *Physcomitrium rufipes*, *Physcomitrium sand-*  
20 *bergii*, *Physcomitrium subsphaericum*, *Physcomitrium washingtoniense*, Geraniaceae, such as the genera *Pelargonium*,  
*Cocos*, *Oleum*, for example the genera and species *Cocos nucifera*, *Pelargonium grossularioides* or *Oleum cocois*  
[coconut], Gramineae, such as the genus *Saccharum*, for example the genus and species *Saccharum officinarum*,  
Juglandaceae, such as the genera *Juglans*, *Wallia*, for example the genera and species *Juglans regia*, *Juglans ailan-*  
*thifolia*, *Juglans sieboldiana*, *Juglans cinerea*, *Wallia cinerea*, *Juglans bixbyi*, *Juglans californica*, *Juglans hindsii*, *Juglans*  
25 *intermedia*, *Juglans jamaicensis*, *Juglans major*, *Juglans microcarpa*, *Juglans nigra* or *Wallia nigra* [walnut], Lauraceae,  
such as the genera *Persea*, *Laurus*, for example the genera and species *Laurus nobilis* [bay], *Persea americana*, *Persea*  
*gratissima* or *Persea persea* [avocado], Leguminosae, such as the genus *Arachis*, for example the genus and species  
*Arachis hypogaea* [peanut], Linaceae, such as the genera *Adenolinum*, for example the genera and species *Linum*  
*usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*,  
30 *Linum grandiflorum*, *Adenolinum grandiflorum*, *Linum lewisii*, *Linum narbonense*, *Linum perenne*, *Linum perenne* var.  
*lewisii*, *Linum pratense* or *Linum trigynum* [linseed], Lythraeae, such as the genus *Punica*, for example the genus and  
species *Punica granatum* [pomegranate], Malvaceae, such as the genus *Gossypium*, for example the genera and species  
*Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum* or *Gossypium thurberi*  
[cotton], Marchantiaceae, such as the genus *Marchantia*, for example the genera and species *Marchantia berteroana*,  
35 *Marchantia foliacea*, *Marchantia macropora*, Musaceae, such as the genus *Musa*, for example the genera and species  
*Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp. [banana], Onagraceae, such as the genera *Camissonia*,  
*Oenothera*, for example the genera and species *Oenothera biennis* or *Camissonia brevipes* [evening primrose], Palmae,  
such as the genus *Elaeis*, for example the genus and species *Elaeis guineensis* [oil palm], Papaveraceae, such as, for  
example, the genus *Papaver*, for example the genera and species *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium*  
40 [poppy], Pedaliaceae, such as the genus *Sesamum*, for example the genus and species *Sesamum indicum* [sesame],  
Piperaceae, such as the genera *Piper*, *Artanthe*, *Peperomia*, *Steffensia*, for example the genera and species *Piper*  
*aduncum*, *Piper amalago*, *Piper angustifolium*, *Piper auritum*, *Piper betel*, *Piper cubeba*, *Piper longum*, *Piper nigrum*,  
*Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper elongatum*, *Steffensia elongata*  
[cayenne pepper], Poaceae, such as the genera *Hordeum*, *Secale*, *Avena*, *Sorghum*, *Andropogon*, *Holcus*, *Panicum*,  
45 *Oryza*, *Zea* (maize), *Triticum*, for example the genera and species *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum*  
*murinum*, *Hordeum secalinum*, *Hordeum distichon* *Hordeum aegiceras*, *Hordeum hexastichon*, *Hordeum hexastichum*,  
*Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum* [barley], *Secale cereale* [rye], *Avena sativa*, *Avena fatua*,  
*Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* [oats], *Sorghum bicolor*, *Sorghum halepense*, *Sorghum sac-*  
*charatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum*  
50 *arundinaceum*, *Sorghum caffrorum*, *Sorghum cernuum*, *Sorghum dochna*, *Sorghum drummondii*, *Sorghum durra*, *Sor-*  
*ghum guineense*, *Sorghum lanceolatum*, *Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sor-*  
*ghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum miliaceum*, *Panicum militaceum* [millet], *Oryza*  
*sativa*, *Oryza latifolia* [rice], *Zea mays* [maize] *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*,  
*Triticum macha*, *Triticum sativum* or *Triticum vulgare* [wheat], Porphyridiaceae, such as the genera *Chroothoece*, *Flintiella*,  
55 *Petrovanella*, *Porphyridium*, *Rhodella*, *Rhodosorus*, *Vanhoeffenia*, for example the genus and species *Porphyridium*  
*cruentum*, Proteaceae, such as the genus *Macadamia*, for example the genus and species *Macadamia intergrifolia*  
[macadamia], Prasinophyceae, such as the genera *Nephroselmis*, *Prasinococcus*, *Scherffelia*, *Tetraselmis*, *Mantoniella*,  
*Ostreococcus*, for example the genera and species *Nephroselmis olivacea*, *Prasinococcus capsulatus*, *Scherffelia dubia*,

*Tetraselmis chui*, *Tetraselmis suecica*, *Mantoniella squamata*, *Ostreococcus tauri*, Rubiaceae, such as the genus *Coffea*, for example the genera and species *Coffea* spp., *Coffea arabica*, *Coffea canephora* or *Coffea liberica* [coffee], Scrophulariaceae, such as the genus *Verbascum*, for example the genera and species *Verbascum blattaria*, *Verbascum chaixii*, *Verbascum densiflorum*, *Verbascum lagurus*, *Verbascum longifolium*, *Verbascum lychnitis*, *Verbascum nigrum*, *Verbascum olympicum*, *Verbascum phlomoides*, *Verbascum phoenicum*, *Verbascum pulverulentum* or *Verbascum thapsus* [verbascum], Solanaceae, such as the genera *Capsicum*, *Nicotiana*, *Solanum*, *Lycopersicon*, for example the genera and species *Capsicum annuum*, *Capsicum annuum* var. *glabriusculum*, *Capsicum frutescens* [pepper], *Capsicum annuum* [paprika], *Nicotiana tabacum*, *Nicotiana alata*, *Nicotiana attenuata*, *Nicotiana glauca*, *Nicotiana langsdorffii*, *Nicotiana obtusifolia*, *Nicotiana quadrivalvis*, *Nicotiana repanda*, *Nicotiana rustica*, *Nicotiana sylvestris* [tobacco], *Solanum tuberosum* [potato], *Solanum melongena* [eggplant] *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium* or *Solanum lycopersicum* [tomato], Sterculiaceae, such as the genus *Theobroma*, for example the genus and species *Theobroma cacao* [cacao] or Theaceae, such as the genus *Camellia*, for example the genus and species *Camellia sinensis* [tea].

**[0096]** Advantageous microorganisms are, for example, fungi selected from the group of the families Chaetomiaceae, Choanephoraceae, Cryptococcaceae, Cunninghamellaceae, Dematiaceae, Moniliaceae, Mortierellaceae, Mucoraceae, Pythiaceae, Saccharomycetaceae, Saprolegniaceae, Schizosaccharomycetaceae, Sodariaceae or Tuberculariaceae.

**[0097]** Examples of microorganisms which may be mentioned are those from the groups: Choanephoraceae, such as the genera *Blakeslea*, *Choanephora*, for example the genera and species *Blakeslea trispora*, *Choanephora cucurbitarum*, *Choanephora infundibulifera* var. *cucurbitarum*, Mortierellaceae, such as the genus *Mortierella*, for example the genera and species *Mortierella isabellina*, *Mortierella polycephala*, *Mortierella ramanniana*, *Mortierella vinacea*, *Mortierella zonata*, Pythiaceae, such as the genera *Pythium*, *Phytophthora*, for example the genera and species *Pythium debaryanum*, *Pythium intermedium*, *Pythium irregulare*, *Pythium megalacanthum*, *Pythium paroecandrum*, *Pythium sylvaticum*, *Pythium ultimum*, *Phytophthora cactorum*, *Phytophthora cinnamomi*, *Phytophthora citricola*, *Phytophthora citrophthora*, *Phytophthora cryptogea*, *Phytophthora drechsleri*, *Phytophthora erythroseptica*, *Phytophthora lateralis*, *Phytophthora megasperma*, *Phytophthora nicotianae*, *Phytophthora nicotianae* var. *parasitica*, *Phytophthora palmivora*, *Phytophthora parasitica*, *Phytophthora syringae*, Saccharomycetaceae, such as the genera *Hansenula*, *Pichia*, *Saccharomyces*, *Saccharomycodes*, *Yarrowia*, for example the genera and species *Hansenula anomala*, *Hansenula californica*, *Hansenula canadensis*, *Hansenula capsulata*, *Hansenula ciferrii*, *Hansenula glucozyma*, *Hansenula henricii*, *Hansenula holstii*, *Hansenula minuta*, *Hansenula nonfermentans*, *Hansenula philodendri*, *Hansenula polymorpha*, *Hansenula saturnus*, *Hansenula subpelliculosa*, *Hansenula wickerhamii*, *Hansenula wingei*, *Pichia alcoholophila*, *Pichia angusta*, *Pichia anomala*, *Pichia bisporea*, *Pichia burtonii*, *Pichia canadensis*, *Pichia capsulata*, *Pichia carsonii*, *Pichia cellobiosa*, *Pichia ciferrii*, *Pichia farinosa*, *Pichia fermentans*, *Pichia finlandica*, *Pichia glucozyma*, *Pichia guilliermondii*, *Pichia haplophila*, *Pichia henricii*, *Pichia holstii*, *Pichia jadinii*, *Pichia lindnerii*, *Pichia membranaefaciens*, *Pichia methanolica*, *Pichia minuta* var. *minuta*, *Pichia minuta* var. *nonfermentans*, *Pichia norvegensis*, *Pichia ohmeri*, *Pichia pastoris*, *Pichia philodendri*, *Pichia pini*, *Pichia polymorpha*, *Pichia quercuum*, *Pichia rhodanensis*, *Pichia sargentensis*, *Pichia stipitis*, *Pichia strasburgensis*, *Pichia subpelliculosa*, *Pichia toletana*, *Pichia trehalophila*, *Pichia vini*, *Pichia xylosa*, *Saccharomyces acetii*, *Saccharomyces bailii*, *Saccharomyces bayanus*, *Saccharomyces bisporeus*, *Saccharomyces capensis*, *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces cerevisiae* var. *ellipsoideus*, *Saccharomyces chevalieri*, *Saccharomyces delbrueckii*, *Saccharomyces diastaticus*, *Saccharomyces drosophilum*, *Saccharomyces elegans*, *Saccharomyces ellipsoideus*, *Saccharomyces fermentati*, *Saccharomyces florentinus*, *Saccharomyces fragilis*, *Saccharomyces heterogenicus*, *Saccharomyces hienipiensis*, *Saccharomyces inusitatus*, *Saccharomyces italicus*, *Saccharomyces kluyveri*, *Saccharomyces krusei*, *Saccharomyces lactis*, *Saccharomyces marxianus*, *Saccharomyces microellipsoides*, *Saccharomyces montanus*, *Saccharomyces norbensis*, *Saccharomyces oleaceus*, *Saccharomyces paradoxus*, *Saccharomyces pastorianus*, *Saccharomyces pretoriensis*, *Saccharomyces rosei*, *Saccharomyces rouxii*, *Saccharomyces uvarum*, *Saccharomycodes ludwigii*, *Yarrowia lipolytica*, Schizosaccharomycetaceae such as the genera *Schizosaccharomyces* e.g. the species *Schizosaccharomyces japonicus* var. *japonicus*, *Schizosaccharomyces japonicus* var. *versatilis*, *Schizosaccharomyces malidevorans*, *Schizosaccharomyces octosporus*, *Schizosaccharomyces pombe* var. *malidevorans*, *Schizosaccharomyces pombe* var. *pombe*, Thraustochytriaceae such as the genera *Althornia*, *Aplanochytrium*, *Japonochytrium*, *Schizochytrium*, *Thraustochytrium* e.g. the species *Schizochytrium aggregatum*, *Schizochytrium limacinum*, *Schizochytrium mangrovei*, *Schizochytrium minutum*, *Schizochytrium octosporum*, *Thraustochytrium aggregatum*, *Thraustochytrium amoeboidum*, *Thraustochytrium antacticum*, *Thraustochytrium arudimentale*, *Thraustochytrium aureum*, *Thraustochytrium benthicola*, *Thraustochytrium globosum*, *Thraustochytrium indicum*, *Thraustochytrium kerguelense*, *Thraustochytrium kinnei*, *Thraustochytrium motivum*, *Thraustochytrium multirudimentale*, *Thraustochytrium pachydermum*, *Thraustochytrium proliferum*, *Thraustochytrium roseum*, *Thraustochytrium rossii*, *Thraustochytrium striatum* or *Thraustochytrium visurgense*.

**[0098]** Further advantageous microorganisms are, for example, bacteria selected from the group of the families Bacillaceae, Enterobacteriaceae or Rhizobiaceae.

**[0099]** Examples which may be mentioned are the following microorganisms selected from the group consisting of:

Bacillaceae, such as the genus *Bacillus*, for example the genera and species *Bacillus acidocaldarius*, *Bacillus acidoterrestris*, *Bacillus alcalophilus*, *Bacillus amyloliquefaciens*, *Bacillus amylovorus*, *Bacillus brevis*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus sphaericus* subsp. *fusiformis*, *Bacillus galactophilus*, *Bacillus globisporus*, *Bacillus globisporus* subsp. *marinus*, *Bacillus halophilus*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus polymyxa*, *Bacillus psychrosaccharolyticus*, *Bacillus pumilus*, *Bacillus sphaericus*, *Bacillus subtilis* subsp. *spizizenii*, *Bacillus subtilis* subsp. *subtilis* or *Bacillus thuringiensis*; Enterobacteriaceae such as the genera *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Erwinia*, *Escherichia*, *Klebsiella*, *Salmonella* or *Serratia*, for example the genera and species *Citrobacter amalonaticus*, *Citrobacter diversus*, *Citrobacter freundii*, *Citrobacter genomospecies*, *Citrobacter gillenii*, *Citrobacter intermedium*, *Citrobacter koseri*, *Citrobacter murlinae*, *Citrobacter* sp., *Edwardsiella hoshinae*, *Edwardsiella ictaluri*, *Edwardsiella tarda*, *Erwinia alni*, *Erwinia amylovora*, *Erwinia ananatis*, *Erwinia aphidicola*, *Erwinia billingiae*, *Erwinia cacticida*, *Erwinia cancerogena*, *Erwinia camegieana*, *Erwinia carotovora* subsp. *atroseptica*, *Erwinia carotovora* subsp. *betavasculorum*, *Erwinia carotovora* subsp. *odorifera*, *Erwinia carotovora* subsp. *wasabiae*, *Erwinia chrysanthemi*, *Erwinia cyripedii*, *Erwinia dissolvens*, *Erwinia herbicola*, *Erwinia mallotivora*, *Erwinia milletiae*, *Erwinia nigrifluens*, *Erwinia nimipressuralis*, *Erwinia persicina*, *Erwinia psidii*, *Erwinia pyrifoliae*, *Erwinia quercina*, *Erwinia rhapontici*, *Erwinia rubrifaciens*, *Erwinia salicis*, *Erwinia stewartii*, *Erwinia tracheiphila*, *Erwinia uredovora*, *Escherichia adecarboxylata*, *Escherichia anindolica*, *Escherichia aurescens*, *Escherichia blattae*, *Escherichia coli*, *Escherichia coli* var. *communior*, *Escherichia coli*-*mutabile*, *Escherichia fergusonii*, *Escherichia hermannii*, *Escherichia* sp., *Escherichia vulneris*, *Klebsiella aerogenes*, *Klebsiella edwardsii* subsp. *atlantae*, *Klebsiella ornithinolytica*, *Klebsiella oxytoca*, *Klebsiella planticola*, *Klebsiella pneumoniae*, *Klebsiella pneumoniae* subsp. *pneumoniae*, *Klebsiella* sp., *Klebsiella terrigena*, *Klebsiella trevisanii*, *Salmonella abony*, *Salmonella arizonae*, *Salmonella bongori*, *Salmonella choleraesuis* subsp. *arizonae*, *Salmonella choleraesuis* subsp. *bongori*, *Salmonella choleraesuis* subsp. *choleraesuis*, *Salmonella choleraesuis* subsp. *diarizonae*, *Salmonella choleraesuis* subsp. *houtenae*, *Salmonella choleraesuis* subsp. *indica*, *Salmonella choleraesuis* subsp. *salamae*, *Salmonella daressalaam*, *Salmonella enterica* subsp. *houtenae*, *Salmonella enterica* subsp. *salamae*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella heidelberg*, *Salmonella panama*, *Salmonella senftenberg*, *Salmonella typhimurium*, *Serratia entomophila*, *Serratia ficaria*, *Serratia fonticola*, *Serratia grimesii*, *Serratia liquefaciens*, *Serratia marcescens*, *Serratia marcescens* subsp. *marcescens*, *Serratia marinorubra*, *Serratia odorifera*, *Serratia plymouthensis*, *Serratia plymuthica*, *Serratia proteamaculans*, *Serratia proteamaculans* subsp. *quinovora*, *Serratia quinivorans* or *Serratia rubidaea*; Rhizobiaceae, such as the genera *Agrobacterium*, *Carbophilus*, *Chelatobacter*, *Ensifer*, *Rhizobium*, *Sinorhizobium*, for example the genera and species *Agrobacterium atlanticum*, *Agrobacterium ferrugineum*, *Agrobacterium gelatinovorum*, *Agrobacterium larrymoorei*, *Agrobacterium meteorii*, *Agrobacterium radiobacter*, *Agrobacterium rhizogenes*, *Agrobacterium rubi*, *Agrobacterium steiluiatum*, *Agrobacterium tumefaciens*, *Agrobacterium vitis*, *Carbophilus carboxidus*, *Chelatobacter heintzii*, *Ensifer adhaerens*, *Ensifer arboris*, *Ensifer fredii*, *Ensifer kostiensis*, *Ensifer kummerowiae*, *Ensifer medicae*, *Ensifer meliloti*, *Ensifer sahelii*, *Ensifer terangae*, *Ensifer xinjiangensis*, *Rhizobium ciceri*, *Rhizobium etli*, *Rhizobium fredii*, *Rhizobium galegae*, *Rhizobium gallicum*, *Rhizobium giardinii*, *Rhizobium hainanense*, *Rhizobium huakuii*, *Rhizobium huautlense*, *Rhizobium indigoferae*, *Rhizobium japonicum*, *Rhizobium leguminosarum*, *Rhizobium loessense*, *Rhizobium loti*, *Rhizobium lupini*, *Rhizobium mediterraneum*, *Rhizobium meliloti*, *Rhizobium mongolense*, *Rhizobium phaseoli*, *Rhizobium radiobacter*, *Rhizobium rhizogenes*, *Rhizobium rubi*, *Rhizobium suilae*, *Rhizobium tianshanense*, *Rhizobium trifolii*, *Rhizobium tropici*, *Rhizobium undicola*, *Rhizobium vitis*, *Sinorhizobium adhaerens*, *Sinorhizobium arboris*, *Sinorhizobium fredii*, *Sinorhizobium kostiense*, *Sinorhizobium kummerowiae*, *Sinorhizobium medicae*, *Sinorhizobium meliloti*, *Sinorhizobium morelense*, *Sinorhizobium sahelii* or *Sinorhizobium xinjiangense*.

**[0100]** Further examples of advantageous microorganisms for the process according to the invention are protists or diatoms selected from the group of the families Dinophyceae, Turaniellidae or Oxytrichidae, such as the genera and species: *Crypthecodinium cohnii*, *Phaeodactylum tricornutum*, *Stylonychia mytilus*, *Stylonychia pustulata*, *Stylonychia putrina*, *Stylonychia notophora*, *Stylonychia* sp., *Colpidium campylum* or *Colpidium* sp.

**[0101]** Those which are advantageously applied in the process according to the invention are transgenic organisms such as fungi, such as *Mortierella* or *Thraustochytrium*, yeasts such as *Saccharomyces* or *Schizosaccharomyces*, mosses such as *Physcomitrella* or *Ceratodon*, nonhuman animals such as *Caenorhabditis*, algae such as *Nephroselmis*, *Pseudoscourfielda*, *Prasinococcus*, *Scherffelia*, *Tetraselmis*, *Mantoniella*, *Ostreococcus*, *Crypthecodinium* or *Phaeodactylum* or plants such as dicotyledonous or monocotyledonous plants. Organisms which are especially advantageously used in the process according to the invention are organisms which belong to the oil-producing organisms, that is to say which are used for the production of oil, such as fungi, such as *Mortierella* or *Thraustochytrium*, algae such as *Nephroselmis*, *Pseudoscourfielda*, *Prasinococcus*, *Scherffelia*, *Tetraselmis*, *Mantoniella*, *Ostreococcus*, *Crypthecodinium*, *Phaeodactylum*, or plants, in particular plants, preferably oilseed or oil crop plants which comprise large amounts of lipid compounds, such as peanut, oilseed rape, canola, sunflower, safflower (*Carthamus tinctoria*), poppy, mustard, hemp, castor-oil plant, olive, sesame, *Calendula*, *Punica*, evening primrose, *Verbascum*, thistle, wild roses, hazelnut, almond, macadamia, avocado, bay, pumpkin/squash, linseed, soybean, pistachios, borage, trees (oil palm, coconut or walnut) or arable crops such as maize, wheat, rye, oats, triticale, rice, barley, cotton, cassava, pepper, *Tagetes*, *Solanaceae*

plants such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa or bushy plants (coffee, cacao, tea), *Salix* species, and perennial grasses and fodder crops. Preferred plants according to the invention are oil crop plants such as peanut, oilseed rape, canola, sunflower, safflower, poppy, mustard, hemp, castor-oil plant, olive, *Calendula*, *Punica*, evening primrose, pumpkin/squash, linseed, soybean, borage, trees (oil palm, coconut). Especially preferred for the process are plants which are high in C18:2-fatty acids, such as sunflower, safflower, tobacco, verbascum, sesame, cotton, pumpkin/squash, poppy, evening primrose, walnut, linseed, hemp or thistle. Very especially preferred plants are plants such as safflower, sunflower, poppy, evening primrose, walnut, linseed or hemp.

**[0102]** It is also be advantageous for the above-described method according to the invention additionally to introduce, into the organism, further nucleic acids which encode enzymes of the fatty acid or lipid metabolism, in addition to the nucleic acids described herein.

**[0103]** Such nucleic acids are advantageously derived from plants such as algae, for example algae of the family of the Prasinophyceae such as the genera *Heteromastix*, *Mammella*, *Mantoniella*, *Micromonas*, *Nephroselmis*, *Ostreococcus*, *Prasinocladus*, *Prasinococcus*, *Pseudoscourfieldia*, *Pycnococcus*, *Pyramimonas*, *Scherffelia* or *Tetraselmis* such as the genera and species *Heteromastix longifillilis*, *Mamiella gilva*, *Mantoniella squamata*, *Micromonas pusilla*, *Nephroselmis olivacea*, *Nephroselmis pyriformis*, *Nephroselmis rotunda*, *Ostreococcus tauri*, *Ostreococcus* sp. *Prasinocladus ascus*, *Prasinocladus lubricus*, *Pycnococcus provasolii*, *Pyramimonas amyliifera*, *Pyramimonas disomata*, *Pyramimonas obovata*, *Pyramimonas orientalis*, *Pyramimonas parkeae*, *Pyramimonas spinifera*, *Pyramimonas* sp., *Tetraselmis apiculata*, *Tetraselmis carteriaformis*, *Tetraselmis chui*, *Tetraselmis convolutae*, *Tetraselmis desikacharyi*, *Tetraselmis gracilis*, *Tetraselmis hazeni*, *Tetraselmis impellucida*, *Tetraselmis inconspicua*, *Tetraselmis levis*, *Tetraselmis maculata*, *Tetraselmis marina*, *Tetraselmis striata*, *Tetraselmis subcordiformis*, *Tetraselmis suecica*, *Tetraselmis tetrabrachia*, *Tetraselmis tetrathele*, *Tetraselmis verrucosa*, *Tetraselmis verrucosa* fo. *rubens* or *Tetraselmis* sp. or from algae of the family Euglenaceae such as the genera *Ascoglena*, *Astasia*, *Colacium*, *Cyclidiopsis*, *Euglena*, *Euglenopsis*, *Hyalophacus*, *Khawkinea*, *Lepocinclis*, *Phacus*, *Strombomonas* or *Trachelomonas*, such as the genera and species *Euglena acus*, *Euglena geniculata*, *Euglena gracilis*, *Euglena mixocylindracea*, *Euglena rostrifera*, *Euglena viridis*, *Colacium stentorium*, *Trachelomonas cylindrica* or *Trachelomonas volvocina*. The nucleic acids used are advantageously derived from algae of the genera *Euglena*, *Mantoniella* or *Ostreococcus*.

**[0104]** Further advantageous plants are algae such as *Isochrysis* or *Cryptothecodinium*, algae/diatoms such as *Thalassiosira* or *Phaeodactylum*, mosses such as *Physcomitrella* or *Ceratodon*, or higher plants such as the Primulaceae such as *Aleuritia*, *Calendula stellata*, *Osteospermum spinescens* or *Osteospermum hyoseroides*, microorganisms such as fungi, such as *Aspergillus*, *Thraustochytrium*, *Phytophthora*, *Entomophthora*, *Mucor* or *Mortierella*, bacteria such as *Shewanella*, yeasts or animals such as nematodes such as *Caenorhabditis*, insects, frogs, abalone, or fish. The isolated nucleic acid sequences described herein are advantageously derived from an animal of the order of the vertebrates. Preferably, the nucleic acid sequences are derived from the classes of the Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei, Protacanthopterygii, Salmoniformes; Salmonidae or *Oncorhynchus* or Vertebrata, Amphibia, Anura, Pipidae, *Xenopus* or Evertebrata such as Protochordata, Tunicata, Holothuroidea, Cionidae such as *Amaroucium constellatum*, *Botryllus schlosseri*, *Ciona intestinalis*, *Molgula citrina*, *Molgula manhattensis*, *Perophora viridis* or *Styela partita*. The nucleic acids are especially advantageously derived from fungi, animals, or from plants such as algae or mosses, preferably from the order of the Salmoniformes, such as the family of the Salmonidae, such as the genus *Salmo*, for example from the genera and species *Oncorhynchus mykiss*, *Trutta trutta* or *Salmo trutta fario*, from algae, such as the genera *Mantoniella* or *Ostreococcus*, or from the diatoms such as the genera *Thalassiosira* or *Phaeodactylum* or from algae such as *Cryptothecodinium*. The process furthermore may comprise the step of obtaining a cell or an intact organism which comprises the nucleic acid sequences used in the process, where the cell and/or the organism is transformed with a nucleic acid sequence which encodes the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and/or the  $\Delta 5$ -desaturase, a gene construct or a vector as described above, alone or in combination with further nucleic acid sequences which encode proteins of the fatty acid or lipid metabolism. In a further preferred alternative described herein, this process furthermore comprises the step of obtaining the oils, lipids or free fatty acids from the organism or from the culture. The culture can, for example, take the form of a fermentation culture, for example in the case of the cultivation of microorganisms, such as, for example, *Mortierella*, *Thalassiosira*, *Mantoniella*, *Ostreococcus*, *Saccharomyces* or *Thraustochytrium*, or a greenhouse- or field-grown culture of a plant. The cell or the organism produced thus is advantageously a cell of an oil-producing organism, such as an oil crop, such as, for example, peanut, oilseed rape, canola, linseed, hemp, peanut, soybean, safflower, hemp, sunflowers or borage.

In the case of plant cells, plant tissue or plant organs, "growing" is understood as meaning, for example, the cultivation on or in a nutrient medium, or of the intact plant on or in a substrate, for example in a hydroponic culture, potting compost or on arable land.

For the purposes of the invention, "transgenic" or "recombinant" means with regard to, for example, a nucleic acid sequence, an expression cassette (= gene construct) or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors described herein, all those constructions brought about by recombinant methods in which either

a) the nucleic acid sequence described herein, or

b) a genetic control sequence which is operably linked with the nucleic acid sequence described herein, for example a promoter, or

c) a) and b)

are not located in their natural genetic environment or have been modified by recombinant methods, it being possible for the modification to take the form of, for example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. The natural genetic environment is understood as meaning the natural genomic or chromosomal locus in the original organism or the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette - for example the naturally occurring combination of the natural promoter of the nucleic acid sequences with the corresponding  $\Delta 5$ -desaturase gene - becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial") methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in US 5,565,350 or WO 00/15815.

**[0105]** A transgenic organism or transgenic plant for the purposes of the invention is therefore understood as meaning, as above, that the nucleic acids used in the process are not at their natural locus in the genome of an organism, it being possible for the nucleic acids to be expressed homologously or heterologously. However, as mentioned, transgenic also means that, while the nucleic acids according to the invention are at their natural position in the genome of an organism, the sequence has been modified with regard to the natural sequence, and/or that the regulatory sequences of the natural sequences have been modified. Transgenic is preferably understood as meaning the expression of the nucleic acids described herein at an unnatural locus in the genome, i.e. homologous or, preferably, heterologous expression of the nucleic acids takes place. Preferred transgenic organisms are fungi such as *Mortierella* or *Phytophthora*, mosses such as *Physcomitrella*, algae such as *Mantoniella*, *Euglena*, *Cryptocodium* or *Ostreococcus*, diatoms such as *Thalassiosira* or *Phaeodactylum*, or plants such as the oil crops.

**[0106]** Organisms or host organisms for the nucleic acids, the expression cassette or the vector used in the process according to the invention are, in principle, advantageously all organisms which are capable of synthesizing fatty acids, specifically unsaturated fatty acids, and/or which are suitable for the expression of recombinant genes. Examples which may be mentioned are plants such as *Arabidopsis*, Asteraceae such as *Calendula* or crop plants such as soybean, peanut, castor-oil plant, sunflower, maize, cotton, flax, oilseed rape, coconut, oil palm, safflower (*Carthamus tinctorius*) or cacao bean, microorganisms, such as fungi, for example the genus *Mortierella*, *Thraustochytrium*, *Saprolegnia*, *Phytophthora* or *Pythium*, bacteria, such as the genus *Escherichia* or *Shewanella*, yeasts, such as the genus *Saccharomyces*, cyanobacteria, ciliates, algae such as *Mantoniella*, *Euglena*, *Thalassiosira* or *Ostreococcus*, or protozoans such as dinoflagellates, such as *Cryptocodium*. Preferred organisms are those which are naturally capable of synthesizing substantial amounts of oil, such as fungi, such as *Mortierella alpina*, *Pythium insidiosum*, *Phytophthora infestans*, or plants such as soybean, oilseed rape, coconut, oil palm, safflower, flax, hemp, castor-oil plant, *Calendula*, peanut, cacao bean or sunflower, or yeasts such as *Saccharomyces cerevisiae* with soybean, flax, oilseed rape, safflower, sunflower, *Calendula*, *Mortierella* or *Saccharomyces cerevisiae* being especially preferred. In principle, host organisms are, in addition to the abovementioned transgenic organisms, also transgenic animals, advantageously nonhuman animals, for example *C. elegans*, *Ciona intestinalis* or *Xenopus laevis*.

**[0107]** Further utilizable host cells are detailed in: Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).

**[0108]** Expression strains which can be used, for example those with a lower protease activity, are described in: Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128.

**[0109]** These include plant cells and certain tissues, organs and parts of plants in all their phenotypic forms such as anthers, fibers, root hairs, stalks, embryos, calli, cotyledons, petioles, harvested material, plant tissue, reproductive tissue and cell cultures which are derived from the actual transgenic plant and/or can be used for bringing about the transgenic plant.

**[0110]** Transgenic plants which comprise the polyunsaturated fatty acids synthesized in the process according to the invention can advantageously be marketed directly without there being any need for the oils, lipids or fatty acids synthesized to be isolated. Plants for the process according to the invention are listed as meaning intact plants and all plant parts, plant organs or plant parts such as leaf, stem, seeds, root, tubers, anthers, fibers, root hairs, stalks, embryos, calli, cotyledons, petioles, harvested material, plant tissue, reproductive tissue and cell cultures which are derived from the actual transgenic plant and/or can be used for bringing about the transgenic plant. In this context, the seed comprises

all parts of the seed such as the seed coats, epidermal cells, seed cells, endosperm or embryonic tissue. However, the compounds produced in the process according to the invention can also be isolated from the organisms, advantageously plants, in the form of their oils, fats, lipids and/or free fatty acids. Polyunsaturated fatty acids produced by this process can be obtained by harvesting the organisms, either from the crop in which they grow, or from the field. This can be done *via* pressing or extraction of the plant parts, preferably the plant seeds. In this context, the oils, fats, lipids and/or free fatty acids can be obtained by what is known as cold-beating or cold-pressing without applying heat. To allow for greater ease of disruption of the plant parts, specifically the seeds, they are previously comminuted, steamed or roasted. The seeds which have been pretreated in this manner can subsequently be pressed or extracted with solvents such as warm hexane. The solvent is subsequently removed. In the case of microorganisms, the latter are, after harvesting, for example extracted directly without further processing steps or else, after disruption, extracted *via* various methods with which the skilled worker is familiar. In this manner, more than 96% of the compounds produced in the process can be isolated. Thereafter, the resulting products are processed further, i.e. refined. In this process, substances such as the plant mucilages and suspended matter are first removed. What is known as desliming can be effected enzymatically or, for example, chemico-physically by addition of acid such as phosphoric acid. Thereafter, the free fatty acids are removed by treatment with a base, for example sodium hydroxide solution. The resulting product is washed thoroughly with water to remove the alkali remaining in the product and then dried. To remove the pigment remaining in the product, the products are subjected to bleaching, for example using filler's earth or active charcoal. At the end, the product is deodorized, for example using steam.

**[0111]** The fatty acids produced by the processes of the present invention can be isolated from the organism in the form of an oil, a lipid or a free fatty acid. Suitable organisms are, for example, those mentioned above. Preferred organisms are transgenic plants.

**[0112]** Described are therefore oils, lipids or fatty acids of formula I or fractions thereof which have been produced by the above-described process, especially preferably oil, lipid or a fatty acid composition comprising a compound of formula I and being derived from transgenic plants.

**[0113]** Further described is the use of the oil, lipid, the fatty acids and/or the fatty acid composition in feedstuffs, foodstuffs, cosmetics or pharmaceuticals. The oils, lipids, fatty acids or fatty acid mixtures can be used in the manner with which the skilled worker is familiar for mixing with other oils, lipids, fatty acids or fatty acid mixtures of animal origin, such as, for example, fish oils. These oils, lipids, fatty acids or fatty acid mixtures, which are composed of vegetable and animal constituents, may also be used for the preparation of feedstuffs, foodstuffs, cosmetics or pharmacologicals.

**[0114]** The term "oil", "lipid" or "fat" is understood as meaning a fatty acid mixture comprising unsaturated, saturated, preferably esterified, fatty acid(s). The oil, lipid or fat is preferably high in polyunsaturated free or, advantageously, esterified fatty acid(s), in particular linoleic acid,  $\gamma$ -linolenic acid, dihomo- $\gamma$ -linolenic acid, arachidonic acid,  $\alpha$ -linolenic acid, stearidonic acid, eicosatetraenoic acid, eicosapentaenoic acid, docosapentaenoic acid or docosahexaenoic acid.

**[0115]** The amount of unsaturated esterified fatty acids preferably amounts to approximately 30%, a content of 50% is more preferred, a content of 60%, 70%, 80% or more is even more preferred. For the analysis, the fatty acid content can, for example, be determined by gas chromatography after converting the fatty acids into the methyl esters by transesterification. The oil, lipid or fat can comprise various other saturated or unsaturated fatty acids, for example calendulic acid, palmitic acid, palmitoleic acid, stearic acid, oleic acid and the like. The content of the various fatty acids in the oil or fat can vary, in particular depending on the starting organism.

**[0116]** The ARA produced in the process may be, as described above, in the form of fatty acid derivatives, for example sphingolipids, phosphoglycerides, lipids, glycolipids, phospholipids, monoacylglycerol, diacylglycerol, triacylglycerol or other fatty acid esters.

**[0117]** The ARA and other polyunsaturated fatty acids which are present can be liberated for example *via* treatment with alkali, for example aqueous KOH or NaOH, or acid hydrolysis, advantageously in the presence of an alcohol such as methanol or ethanol, or *via* enzymatic cleavage, and isolated *via*, for example, phase separation and subsequent acidification *via*, for example, H<sub>2</sub>SO<sub>4</sub>. The fatty acids can also be liberated directly without the above-described processing step.

**[0118]** After their introduction into an organism, advantageously a plant cell or plant, the nucleic acids used in the process can either be present on a separate plasmid or, advantageously, integrated into the genome of the host cell. In the case of integration into the genome, integration can be random or else be effected by recombination such that the native gene is replaced by the copy introduced, whereby the production of the desired compound by the cell is modulated, or by the use of a gene in trans, so that the gene is linked operably with a functional expression unit which comprises at least one sequence which ensures the expression of a gene and at least one sequence which ensures the polyadenylation of a functionally transcribed gene. The nucleic acids are advantageously introduced into the organisms *via* multiexpression cassettes or constructs for multiparallel expression, advantageously into the plants for the multiparallel seed-specific expression of genes.

**[0119]** If microorganisms such as yeasts, such as *Saccharomyces* or *Schizosaccharomyces*, fungi such as *Mortierella*, *Aspergillus*, *Phytophthora*, *Entomophthora*, *Mucor* or *Thraustochytrium*, algae such as *Isochrysis*, *Mantoniella*, *Euglena*,

Ostreococcus, Phaeodactylum or Cryptocodinium are used as organisms in the process according to the invention, these organisms are advantageously grown in fermentation cultures.

**[0120]** If microorganisms are used as organisms in the process according to the invention, they are grown or cultured in the manner with which the skilled worker is familiar, depending on the host organism. As a rule, microorganisms are grown in a liquid medium comprising a carbon source, usually in the form of sugars, a nitrogen source, usually in the form of organic nitrogen sources such as yeast extract or salts such as ammonium sulfate, trace elements such as salts of iron, manganese and magnesium and, if appropriate, vitamins, at temperatures of between 0°C and 100°C, preferably between 10°C and 60°C, while passing in oxygen. The pH of the liquid medium can either be kept constant, that is to say regulated during the culturing period, or not. The cultures can be grown batchwise, semi-batchwise or continuously. Nutrients can be provided at the beginning of the fermentation or fed in semicontinuously or continuously. The polyunsaturated fatty acids produced can be isolated from the organisms as described above by processes known to the skilled worker, for example by extraction, distillation, crystallization, if appropriate precipitation with salt, and/or chromatography. To this end, the organisms can advantageously be disrupted beforehand.

**[0121]** If the host organisms are microorganisms, the process according to the invention is advantageously carried out at a temperature of between 0°C and 95°C, preferably between 10°C and 85°C, especially preferably between 15°C and 75°C, very especially preferably between 15°C and 45°C.

**[0122]** In this process, the pH value is advantageously kept between pH 4 and 12, preferably between pH 6 and 9, especially preferably between pH 7 and 8.

**[0123]** The process according to the invention can be operated batchwise, semibatchwise or continuously. An overview over known cultivation methods can be found in the textbook by Chmiel (Bioprozeßtechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess technology 1. Introduction to Bioprocess technology] (Gustav Fischer Verlag, Stuttgart, 1991)) or in the textbook by Storhas (Bioreaktoren und periphere Einrichtungen [Bioreactors and peripheral equipment] (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)).

**[0124]** The culture medium to be used must suitably meet the requirements of the strains in question. Descriptions of culture media for various microorganisms can be found in the textbook "Manual of Methods für General Bacteriology" of the American Society for Bacteriology (Washington D. C., USA, 1981).

**[0125]** As described above, these media which can be employed in accordance with the invention usually comprise one or more carbon sources, nitrogen sources, inorganic salts, vitamins and/or trace elements.

**[0126]** Preferred carbon sources are sugars, such as mono-, di- or polysaccharides. Examples of very good carbon sources are glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose. Sugars can also be added to the media *via* complex compounds such as molasses or other byproducts from sugar refining. The addition of mixtures of a variety of carbon sources may also be advantageous. Other possible carbon sources are oils and fats such as, for example, soya oil, sunflower oil, peanut oil and/or coconut fat, fatty acids such as, for example, palmitic acid, stearic acid and/or linoleic acid, alcohols and/or polyalcohols such as, for example, glycerol, methanol and/or ethanol, and/or organic acids such as, for example, acetic acid and/or lactic acid.

**[0127]** Nitrogen sources are usually organic or inorganic nitrogen compounds or materials comprising these compounds. Examples of nitrogen sources comprise ammonia in liquid or gaseous form or ammonium salts such as ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate or ammonium nitrate, nitrates, urea, amino acids or complex nitrogen sources such as cornsteep liquor, soya meal, soya protein, yeast extract, meat extract and others. The nitrogen sources can be used individually or as a mixture.

**[0128]** Inorganic salt compounds which may be present in the media comprise the chloride, phosphorus and sulfate salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron.

**[0129]** Inorganic sulfur-containing compounds such as, for example, sulfates, sulfites, dithionites, tetrathionates, thiosulfates, sulfides, or else organic sulfur compounds such as mercaptans and thiols may be used as sources of sulfur for the production of sulfur-containing fine chemicals, in particular of methionine.

**[0130]** Phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts may be used as sources of phosphorus.

**[0131]** Chelating agents may be added to the medium in order to keep the metal ions in solution. Particularly suitable chelating agents include dihydroxyphenols such as catechol or protocatechuic acid and organic acids such as citric acid.

**[0132]** The fermentation media used according to the invention for culturing microorganisms usually also comprise other growth factors such as vitamins or growth promoters, which include, for example, biotin, riboflavin, thiamine, folic acid, nicotinic acid, pantothenate and pyridoxine. Growth factors and salts are frequently derived from complex media components such as yeast extract, molasses, cornsteep liquor and the like. It is moreover possible to add suitable precursors to the culture medium. The exact composition of the media compounds heavily depends on the particular experiment and is decided upon individually for each specific case. Information on the optimization of media can be found in the textbook "Applied Microbiol. Physiology, A Practical Approach" (Editors P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). Growth media can also be obtained from commercial suppliers, for example Standard 1 (Merck) or BHI (brain heart infusion, DIFCO) and the like.

[0133] All media components are sterilized, either by heat (20 min at 1.5 bar and 121°C) or by filter sterilization. The components may be sterilized either together or, if required, separately. All media components may be present at the start of the cultivation or added continuously or batchwise, as desired.

[0134] The culture temperature is normally between 15°C and 45°C, preferably at from 25°C to 40°C, and may be kept constant or may be altered during the experiment. The pH of the medium should be in the range from 5 to 8.5, preferably around 7.0. The pH for cultivation can be controlled during cultivation by adding basic compounds such as sodium hydroxide, potassium hydroxide, ammonia and aqueous ammonia or acidic compounds such as phosphoric acid or sulfuric acid. Foaming can be controlled by employing antifoams such as, for example, fatty acid polyglycol esters. To maintain the stability of plasmids it is possible to add to the medium suitable substances having a selective effect, for example antibiotics. Aerobic conditions are maintained by introducing oxygen or oxygen-containing gas mixtures such as, for example, ambient air into the culture. The temperature of the culture is normally 20° to 40°C and preferably 25°C to 40°C. The culture is continued until formation of the desired product is at a maximum. This aim is normally achieved within 10 to 160 hours.

The fermentation broths obtained in this way, in particular those containing polyunsaturated fatty acids, usually contain a dry mass of from 7.5 to 25% by weight. The fermentation broth can then be processed further. The biomass may, according to requirement, be removed completely or partially from the fermentation broth by separation methods such as, for example, centrifugation, filtration, decanting or a combination of these methods or be left completely in said broth. It is advantageous to process the biomass after its separation.

However, the fermentation broth can also be thickened or concentrated without separating the cells, using known methods such as, for example, with the aid of a rotary evaporator, thin-film evaporator, falling-film evaporator, by reverse osmosis or by nanofiltration. Finally, this concentrated fermentation broth can be processed to obtain the fatty acids present therein. The fatty acids obtained in the process are also suitable as starting material for the chemical synthesis of further products of interest. For example, they can be used in combination with one another or alone for the preparation of pharmaceuticals, foodstuffs, animal feeds or cosmetics.

All of the nucleic acid sequences used in the process according to the invention are advantageously derived from a eukaryotic organism such as a plant, a microorganism or an animal. The nucleic acid sequences are preferably derived from the order Salmoniformes, algae such as *Mantoniella*, *Cryptocodinium*, *Euglena* or *Ostreococcus*, fungi such as the genus *Phytophthora* or from diatoms such as the genera *Thalassiosira* or *Phaeodactylum*. The specification will now be described in greater detail with reference to the following Examples and to the drawings in which:

FIGURE 1 shows various synthetic pathways for the biosynthesis of  $\omega$ -6 and  $\omega$ -3 fatty acids.

FIGURE 2 is a gas chromatography trace showing the conversion of  $\Delta$ 9, 12-18:2 (linoleic acid) to  $\Delta$ 11, 14-20:2 by heterologous expression of the *P. marinus*  $\Delta$ 9-elongase sequence (SEQ ID NO: 1, residues 7668 to 9200) in yeast induced either by galactose (Figure 2A) or glucose (Figure 2B).

### Example 1 - Cloning of a FAE1 elongase from *Perkinsus marinus*

[0135] *Perkinsus marinus* is an oyster protozoan parasite capable of synthesizing saturated and unsaturated fatty acids including the essential fatty acid, arachidonic acid [20:4(n-6)]. *P. marinus* employs the delta-8 ( $\Delta$ -8) desaturase pathway to synthesize arachidonic acid.

#### Materials and Methods.

##### *Growth and harvesting of P. marinus.*

[0136] *Perkinsus marinus* meronts were cultivated at 28°C in a medium prepared as described by La Peyre et al. (J Eukaryot Microbiol 1993;40:304-10) and contained amino acids, nucleotides, carbohydrates, and vitamins, but no fetal bovine serum.

##### *Nucleic acid manipulation and PCR-based cloning.*

[0137] DNA was extracted from cells using a DNeasy DNA mini kit (Qiagen). DNA were amplified with primers specific to delta5 desaturase gene as follows: the reactions were heated to 95 C for 2 min followed by 35 cycles at 95 C for 1 min, 2 min at 52 and 72 C for 4 min, then a single step at 72 C for 5 min. PCR amplification products were cloned into TOPO vector (Invitrogen) and verified by sequencing. FAE elongase gen was amplified with gene-specific primers (Table I) designed to the 5' and 3' ends of the coding region, with restriction sites to facilitate cloning into the yeast vector (Table I). Forward primers for cloning into yeast expression vector pYES2 (Invitrogen) were designed to contain a G/A at position -3 and a G at position +4 to improve translation initiation in eukaryotic cells.



**Oligonucleotide primers used in this study.**

**[0138]** Transcripts of *Perkinsus marinus* were analyzed by reverse transcriptase PCR (RT-PCR). Total RNA was extracted from cells using an RNeasy plant mini kit (Qiagen). First strand cDNA was synthesised from total RNA using the SMART RACE cDNA Amplification kit (BD-Clontech, Basingstoke, UK) according to the manufacture's instructions. Single -stranded cDNAs were amplified with following primers.

FAEoperon forward 5'-GGAATTCGAGGAGTAGGATCTTATCTGAGGATAGTCACACTAGTCGTACT-3' FAEoperon reverse 5'-CATCTGCGAATACTAACCATACATT

**[0139]** The reactions were heated to 95 C for 2 min followed by 30 cycles at 94 C for 30 s, 30 s at temperatures ranging from 55 to 72 according to the primer design and 72 C for 2 min, then a single step at 72 C for 10 min. PCR amplification products were cloned into TOPO vector (Invitrogen) and verified by sequencing. Surprisingly it was shown that the transcripts of the  $\Delta 9$ -elongase,  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase are all found on the the same mRNA. This is the first example showing PUFA genes to be organized in an operon-like structure.

**[0140]** In a further investigation the specificity of the  $\Delta 9$ -elongase was analyzed. For this purpose the coding sequence of this gene was amplified by RT-PCR as described above using following primers.

Elo2For: 5'- ATGCAAGTTCCCGCGGAGCATCACTCC -3'  
Elo2Rev: 5'- CGTTACGCATCAATATTATGCATAGCCAACC -3'

**[0141]** The amplified PCR product was then cloned into a pCRscript vector according to manufacture's recommendations (Stratagen). In a second PCR step the modified sequences for yeast expression were introduced using following primers.

*Yeast expression.*

**[0142]**

Kpn Elo2For 5'- TTGG**TACCAT**GGGATTTCTGCGGAG -3'  
Sac Elo1Rev 5'- GGGAGCTCTTACGCATCAATATTATGCATAGC-3'

**[0143]** Sequence of the primers is given in the 5' to 3' orientation  
Restriction sites used for cloning are in bold.

**RESULTS****Isolation of FAE1 elongase from *P. marinus*.**

**[0144]** Using publicly available data derived from an *P. marinus* genome sequencing project carried out by TIGR (<http://www.tigr.org/tdb/e2k1/pmg/>) we identified one contig (1047306867) which showed significant homology to known elongases, with the target sequence (designated Elo1For, SEQ ID NO: 9) consisting of an open reading frame of 511 residues and no introns. The putative amino acid derived from the target sequence is SEQ ID NO: 10.

**Functional characterisation in *Saccharomyces cerevisiae*.**

**[0145]** The full-length cDNA corresponding to putative  $\Delta 9$  fatty acid elongase (SEQ ID NO: 9) was cloned into yeast expression vector pYES2 to give a construct designated pYPmFAE. *S. cerevisiae* strain W<sub>303-1A</sub> was transformed with the pYPmFAE or the empty vector as a control. Transformed cell were grown in a minimal medium containing raffinose and induced with 2% galactose. After 48h of growth total yeast fatty acids were extracted and the resulting FAMES analysed by GC.

**[0146]** GC analysis (Figure 2) revealed that yeast cells transformed with pYPmFAE produced an additional fatty acid, which was identified as eicosadienoic acid indicating that the gene we had cloned encoded a delta 9 fatty acid elongase. Yeast cells expressing the *P. marinus* delta 9 fatty acid elongase is capable of recognizing C18:2 (c9,12) substrate with a 8.2% percentage of conversion rate.

**[0147]** Table 1 shows the fatty acid content of the yeast cells after transformation with pYPmFAE (+) or with the empty vector pYES2 (-) and induction with 2% galactose. The percentage conversion for **18:2 <sup>$\Delta 9,12$</sup>  to 20:2 <sup>$\Delta 11,14$</sup> , for example is calculated by the equation:**

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$$\% \text{ conversion} = \frac{[20:2^{\Delta 11,14}]}{[18:2^{\Delta 9,12}] + [20:2^{\Delta 11,14}]}$$

5

TABLE 1

		FATTY ACIDS										
%	16:0	16:1 <sup>Δ9</sup>	18:0	18:1 <sup>Δ9</sup>	18:2 <sup>Δ9,12</sup>	20:2 <sup>Δ11,14</sup>	18:3 <sup>Δ6,9,12</sup>	20:3 <sup>Δ8,11,14</sup>	20:4 <sup>Δ5,8,11,14</sup>	22:4 <sup>Δ7,10,13,16</sup>	% conv	
FAE 18:2+	19.05	22.79	5.15	12.54	37.14	3.33	0.00	0.00	0.00	0.00	8.2	
FAE 18:2-	20.81	19.50	5.50	12.11	42.07	0.00	0.00	0.00	0.00	0.00	0.0	
FAE 18:3+	18.86	19.77	4.81	11.15	0.00	0.00	44.93	0.48	0.00	0.00	1.1	
FAE 18:3-	20.35	18.15	4.84	10.33	0.00	0.00	46.27	0.07	0.00	0.00	0.1	
FAE 20:4+	20.84	31.09	5.48	15.91	0.00	0.00	0.00	0.00	26.68	0.00	0.0	
FAE 20:4-	22.13	31.00	4.55	14.65	0.00	0.00	0.00	0.00	27.67	0.00	0.0	

30

[0148] The results presented in Table 1 show that no elongase activity was detected with 20:4<sup>Δ5,8,11,14</sup>, and a minimal activity (1% conversion) for 18:3<sup>Δ6,9,12</sup>. It therefore appears that the Δ9 fatty acid elongase is selective for linoleic acid and does not act to elongate other PUFAs.

35 SEQUENCE LISTING

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6420

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35

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6600

40

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6720

45

aagataaatg cgcatagtaa agtcgactcc gthctgagagt agacatgcca thctccgagct  
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taactgcgac atgctatctt ctccaggagag actctgacga gtatthctt ggtaatthct  
6840

50

agtggagagt ggacactgaa cacagacctc tgaccccgcg cagtactcac aagatgacgc  
6900

55

tccgactgag aaaagattga thcttactaac tgtgaagcag acatacgaaa ggtgtattcc  
6960

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aatccttgctg ttgttggtat tgttgtagt ctccgtgtgg gagtgaaccg catcccattg  
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 5 tcgagtgaat cgagcggcgc accgaaagat gagcaatact cagactgatg tgcattgatg  
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 7200  
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 7560  
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 7676  
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 40 Pro Ala Glu His His Ser Thr Arg Val Ile Ser Ile Cys Asp Ile Val  
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 7772  
 45 Ile Ser Gly Pro Phe Gly Met Cys Asn His Asp Tyr Ser Ala Ser Ile  
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 7820  
 50 Pro Ala Ser Ser Ser Gly Ser Thr Arg Arg Met Arg Leu Val Ala Tyr  
 40 45 50  
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 7868  
 55 Ile Thr Leu Val Ser Ile His Tyr Gln Gln Leu Leu Phe Tyr Ser Ser  
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7916  
Ile Ile Thr Ile Ile Thr Gly Tyr His Tyr Tyr Val Ala Ala Leu Pro  
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ctt tac gac atc tca att gct cta tct gtg ctt tcg gga cta aca cta  
7964  
Leu Tyr Asp Ile Ser Ile Ala Leu Ser Val Leu Ser Gly Leu Thr Leu  
85 90 95

10  
ctg tgg tta tgt aat tgc tat tac aac agc aag ccc aat gta ttc tgc  
8012  
Leu Trp Leu Cys Asn Cys Tyr Tyr Asn Ser Lys Pro Asn Val Phe Cys  
100 105 110 115

15  
atc gat cat gtt gag ttt gac gct cct ccc tct tgg aag gtc agt cat  
8060  
Ile Asp His Val Glu Phe Asp Ala Pro Pro Ser Trp Lys Val Ser His  
120 125 130

20  
gaa gac atc atc aac att gcc aag ata caa ggt tgc tac acg gaa gat  
8108  
Glu Asp Ile Ile Asn Ile Ala Lys Ile Gln Gly Cys Tyr Thr Glu Asp  
135 140 145

25  
tca ctc aac ttc atg cag cgt ctt ctc gag agg tct ggt act tgc cct  
8156  
Ser Leu Asn Phe Met Gln Arg Leu Leu Glu Arg Ser Gly Thr Cys Pro  
150 155 160

30  
gat aag agt gct gct tac cct cca gtg gtt gtt gag tca ctg agg act  
8204  
Asp Lys Ser Ala Ala Tyr Pro Pro Val Val Val Glu Ser Leu Arg Thr  
165 170 175

35  
aac gcc ccc gcc gat gcc tct gct gtc aat act aga gag gaa gcg agg  
8252  
Asn Ala Pro Ala Asp Ala Ser Ala Val Asn Thr Arg Glu Glu Ala Arg  
180 185 190 195

40  
gaa gtg atc ata act acg gtc aaa gat ctg ctc aag aaa act ggt gtg  
8300  
Glu Val Ile Ile Thr Thr Val Lys Asp Leu Leu Lys Lys Thr Gly Val  
200 205 210

45  
cat cct aaa tct atc gac tac atc atc gtc aat tgc gcc atg tac aac  
8348  
His Pro Lys Ser Ile Asp Tyr Ile Ile Val Asn Cys Ala Met Tyr Asn  
215 220 225

50  
ccg aca ccg tca cat gct gct atg ata gtg aat gaa gtc ggt atg agg  
8396  
Pro Thr Pro Ser His Ala Ala Met Ile Val Asn Glu Val Gly Met Arg  
230 235 240

55  
aat gac gtt atc acc tat aac ctc agt ggt atg ggg tgt agt gcc ggt  
8444  
Asn Asp Val Ile Thr Tyr Asn Leu Ser Gly Met Gly Cys Ser Ala Gly  
245 250 255

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5 gtt atc aca att gat cta gca acg cgt ctg ttg aga gag acc aga ggt  
 8492  
 Val Ile Thr Ile Asp Leu Ala Thr Arg Leu Leu Arg Glu Thr Arg Gly  
 260 265 270 275

10 agg gca ctg att gtc tca act gag ata cta act cgt tgc ttc tat cgt  
 8540  
 Arg Ala Leu Ile Val Ser Thr Glu Ile Leu Thr Arg Cys Phe Tyr Arg  
 280 285 290

15 ggt aat gat cgt gaa cca ctg atg ggt aac aca tta ttc aga tgt ggt  
 8588  
 Gly Asn Asp Arg Glu Pro Leu Met Gly Asn Thr Leu Phe Arg Cys Gly  
 295 300 305

20 ggt gct gct gct ttg cta tcg tca ttg cct aaa gac cta tct cgt gcc  
 8636  
 Gly Ala Ala Ala Leu Leu Ser Ser Leu Pro Lys Asp Leu Ser Arg Ala  
 310 315 320

25 aaa tat aag ttg tta cat acc gta aga acg caa gtt ctc ggt aat gag  
 8684  
 Lys Tyr Lys Leu Leu His Thr Val Arg Thr Gln Val Leu Gly Asn Glu  
 325 330 335

30 agt ttt gaa acg att atg gag act gat gac agt acc aag ccc aac agt  
 8732  
 Ser Phe Glu Thr Ile Met Glu Thr Asp Asp Ser Thr Lys Pro Asn Ser  
 340 345 350 355

35 att gtt aca cta agg ctc cag aag agc atc atc aaa gtt gct gct gtt  
 8780  
 Ile Val Thr Leu Arg Leu Gln Lys Ser Ile Ile Lys Val Ala Ala Val  
 360 365 370

40 gct att aaa caa aat ttt act aag ctt gct tat atg gtt ctc cct ctg  
 8828  
 Ala Ile Lys Gln Asn Phe Thr Lys Leu Ala Tyr Met Val Leu Pro Leu  
 375 380 385

45 aga gaa ctg ttg aag gtc tta tac tcg atg gtg acg atg aaa atg aga  
 8876  
 Arg Glu Leu Leu Lys Val Leu Tyr Ser Met Val Thr Met Lys Met Arg  
 390 395 400

50 aga aag tcg tca aaa gaa ggt cgc gag ttg tac gta cct gat ttt aga  
 8924  
 Arg Lys Ser Ser Lys Glu Gly Arg Glu Leu Tyr Val Pro Asp Phe Arg  
 405 410 415

55 aag ggt act gat cat tgg tgt att cat gct ggt ggc cgt ggt gta ttg  
 8972  
 Lys Gly Thr Asp His Trp Cys Ile His Ala Gly Gly Arg Gly Val Leu  
 420 425 430 435

gat acc tta caa gat tct ctc cag ctg tca gac tac gat atc caa gca  
 9020  
 Asp Thr Leu Gln Asp Ser Leu Gln Leu Ser Asp Tyr Asp Ile Gln Ala  
 440 445 450

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agc cgt agt gtt ctc tat gag aga ggc aac acc agt agc agt agc ata  
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 Ser Arg Ser Val Leu Tyr Glu Arg Gly Asn Thr Ser Ser Ser Ser Ile  
 455 460 465  
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 tgg tat gag ttg gca tgg ctc gaa cgt gac caa cgt att aag cgt gga  
 9116  
 Trp Tyr Glu Leu Ala Trp Leu Glu Arg Asp Gln Arg Ile Lys Arg Gly  
 470 475 480  
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 gat agg gta tta cag ttg gct ttt ggt agt ggt ttc aaa tgt aac tca  
 9164  
 Asp Arg Val Leu Gln Leu Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser  
 485 490 495  
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 9210  
 Ser Val Trp Leu Ala Met His Asn Ile Asp Ala  
 500 505 510  
 20  
 tttttctcac tatgagttgg ctccaccgta atcaatggcc atcatctcct tttctagtta  
 9270  
 ttatcgatga ttatagtcag tgccgatgtg tgctagtgtt ttactcttta tcaacttgtg  
 9330  
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 9383  
 Met Thr Thr Ser Thr Thr Thr Val Gln Leu Gln  
 515 520  
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 gaa gac ctg tca agt ggt gac cag aac gcc cac ccc agt cca agc cga  
 9431  
 Glu Asp Leu Ser Ser Gly Asp Gln Asn Ala His Pro Ser Pro Ser Arg  
 525 530 535  
 35  
 gct act cct agt gtt ggt gat act aag gag gat gcg agg gtt gtg atc  
 9479  
 Ala Thr Pro Ser Val Gly Asp Thr Lys Glu Asp Ala Arg Val Val Ile  
 540 545 550  
 40  
 aaa cta ttt ggt aca tgg gtt gat gtt aca gct tgg ttg aat gac cat  
 9527  
 Lys Leu Phe Gly Thr Trp Val Asp Val Thr Ala Trp Leu Asn Asp His  
 555 560 565  
 45  
 cct ggt ggt tct aaa gtg ctc aga gca ttc aac aag aag gac gcg act  
 9575  
 Pro Gly Gly Ser Lys Val Leu Arg Ala Phe Asn Lys Lys Asp Ala Thr  
 570 575 580 585  
 50  
 gat gct gtt atg gcc atg cac act gat gaa gct atc aag cgc atc atc  
 9623  
 Asp Ala Val Met Ala Met His Thr Asp Glu Ala Ile Lys Arg Ile Ile  
 590 595 600  
 55  
 aga ttt tca aat gtg gtc tcc tog gcc ccc atc aac gcc tct att ggt  
 9671

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Arg Phe Ser Asn Val Val Ser Ser Ala Pro Ile Asn Ala Ser Ile Gly  
 605 610 615  
 gat gtc cag gtt att gag aaa tct cta tcg aga gaa cag ttg atg tat  
 5 9719  
 Asp Val Gln Val Ile Glu Lys Ser Leu Ser Arg Glu Gln Leu Met Tyr  
 620 625 630  
 tac aag ctc cgc act ctt gct aga aac cag ggc tgg ttt caa agc aat  
 10 9767  
 Tyr Lys Leu Arg Thr Leu Ala Arg Asn Gln Gly Trp Phe Gln Ser Asn  
 635 640 645  
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 15 9815  
 Leu Leu Tyr Glu Gly Val Lys Ala Met Ile Ala Phe Gly Leu Leu Ile  
 650 655 660 665  
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 20 9863  
 Ile Gly Phe Ala Thr Leu Tyr Phe Asp Tyr Gly Ile Trp Ser Thr Ala  
 670 675 680  
 ctg ata ggt ttc gct tgg ttt cag ctg ggg tgg ttg gga cat gac tgg  
 25 9911  
 Leu Ile Gly Phe Ala Trp Phe Gln Leu Gly Trp Leu Gly His Asp Trp  
 685 690 695  
 tca cat cat aca gct cta cct aag tct act act aac tgt gcg aac tac  
 30 9959  
 Ser His His Thr Ala Leu Pro Lys Ser Thr Thr Asn Cys Ala Asn Tyr  
 700 705 710  
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 35 10007  
 Asn Asp Tyr Leu Gly Trp Leu Thr Gly Leu Ala Arg Gly Asn Thr Leu  
 715 720 725  
 ctg tgg tgg aaa ctg agg cac aat act cat cac gtg ctg acc aat cag  
 40 10055  
 Leu Trp Trp Lys Leu Arg His Asn Thr His His Val Leu Thr Asn Gln  
 730 735 740 745  
 tac gag aat gat cct gat att cta act caa cca ccg ttg cat ttt ttc  
 45 10103  
 Tyr Glu Asn Asp Pro Asp Ile Leu Thr Gln Pro Pro Leu His Phe Phe  
 750 755 760  
 gag gac ttc gat gtt ggt aat gtg aac aga tat caa gct gtc tac tac  
 10151  
 Glu Asp Phe Asp Val Gly Asn Val Asn Arg Tyr Gln Ala Val Tyr Tyr  
 50 765 770 775  
 cta cca atg tta act cta ctg cat cta ttt tgg ttg tac gag tcg gta  
 10199  
 Leu Pro Met Leu Thr Leu Leu His Leu Phe Trp Leu Tyr Glu Ser Val  
 55 780 785 790  
 ttg gtt tgc ttg aga caa agt agg tct att aat aga tac aac cgt atg

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10247  
 Leu Val Cys Leu Arg Gln Ser Arg Ser Ile Asn Arg Tyr Asn Arg Met  
 795 800 805

5 cat gcc agg agg gat acc gta gct ttg gta ctt cac ata ctc att gtt  
 10295  
 His Ala Arg Arg Asp Thr Val Ala Leu Val Leu His Ile Leu Ile Val  
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10 ggc atc ata tcg tac acc agt ggt aag tat ttg ctc atc ctt ctg gcc  
 10343  
 Gly Ile Ile Ser Tyr Thr Ser Gly Lys Tyr Leu Leu Ile Leu Leu Ala  
 830 835 840

15 tac atg ctt agt ggc ttt cta act gct gtt gtt gta ttt gcc agc cac  
 10391  
 Tyr Met Leu Ser Gly Phe Leu Thr Ala Val Val Val Phe Ala Ser His  
 845 850 855

20 tac aac gag cct agg gta gct tct ggt gaa tcc tta tca ctc gtt cgt  
 10439  
 Tyr Asn Glu Pro Arg Val Ala Ser Gly Glu Ser Leu Ser Leu Val Arg  
 860 865 870

25 cag aca ttg tta acc act atc aat ata ggc tca ttc agt gat act cat  
 10487  
 Gln Thr Leu Leu Thr Thr Ile Asn Ile Gly Ser Phe Ser Asp Thr His  
 875 880 885

30 tgg gag aag aag ttg tgg ttc tat cta act ggt ggt ctt aat atg caa  
 10535  
 Trp Glu Lys Lys Leu Trp Phe Tyr Leu Thr Gly Gly Leu Asn Met Gln  
 890 895 900 905

35 atc gag cat cat ctc ttc cca aca atg ccc cgc cat aat ctt ccg aag  
 10583  
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Pro Lys  
 910 915 920

40 aca act ttt ctg gtc aag tca cta gcc cag gag cta gga ctg cca tac  
 10631  
 Thr Thr Phe Leu Val Lys Ser Leu Ala Gln Glu Leu Gly Leu Pro Tyr  
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45 aag gaa acc aac att gtc agt tta acc aag gcg gcc gtt act act ttg  
 10679  
 Lys Glu Thr Asn Ile Val Ser Leu Thr Lys Ala Ala Val Thr Thr Leu  
 940 945 950

50 cat cat aat gct ctg cgt aac atc gag aga ttg ctt gct agg tag  
 10724  
 His His Asn Ala Leu Arg Asn Ile Glu Arg Leu Leu Ala Arg  
 955 960 965

55 ttctcatcat tgcaaccgca acaagaacat ggtcaactcg tagtgggtggg agaggattgt  
 10784  
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 10841

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atg tct tct ctt acc ctc tac aga ggc ccc ttt tcc cga atg gtg ctc  
 10889  
 Met Ser Ser Leu Thr Leu Tyr Arg Gly Pro Phe Ser Arg Met Val Leu  
 5                   970                   975                   980

cct cgt cag gaa atc tgc atc aat ggt cgc ata tac gat gtc act gag  
 10937  
 Pro Arg Gln Glu Ile Cys Ile Asn Gly Arg Ile Tyr Asp Val Thr Glu  
 10                   985                   990                   995

ttc atc aat cgt cat cca ggt ggt aag att atc ctc ttc caa gtt  
 10982  
 Phe Ile Asn Arg His Pro Gly Gly Lys Ile Ile Leu Phe Gln Val  
 15                   1000                   1005                   1010

ggt gct gat gcc act gat gct ttt cgt gag ttt cat gct ggc agt  
 11027  
 Gly Ala Asp Ala Thr Asp Ala Phe Arg Glu Phe His Ala Gly Ser  
 20                   1015                   1020                   1025

gag aag gca gag aag atc ctc aaa acc cta cca tcc cgt gat gat  
 11072  
 Glu Lys Ala Glu Lys Ile Leu Lys Thr Leu Pro Ser Arg Asp Asp  
 25                   1030                   1035                   1040

gac ggt act ttc ctt cct tca acc caa cgc tcc atc atg gat gat  
 11117  
 Asp Gly Thr Phe Leu Pro Ser Thr Gln Arg Ser Ile Met Asp Asp  
 30                   1045                   1050                   1055

ttc aaa cgc cta aga gat gac ctc gtc agc aga ggt gtc ttc aag  
 11162  
 Phe Lys Arg Leu Arg Asp Asp Leu Val Ser Arg Gly Val Phe Lys  
 35                   1060                   1065                   1070

cca agc gtc atg cat gtt gta tac cgc tgc ttg gaa gtc gtt gct  
 11207  
 Pro Ser Val Met His Val Val Tyr Arg Cys Leu Glu Val Val Ala  
 40                   1075                   1080                   1085

ctc tat ctc att ggc ttc tat ttg gct ctg tgc acc agt aat gtg  
 11252  
 Leu Tyr Leu Ile Gly Phe Tyr Leu Ala Leu Cys Thr Ser Asn Val  
 45                   1090                   1095                   1100

tac gtt ggg tgt gct gta ctt ggt gta gct caa ggt cgt gct ggt  
 11297  
 Tyr Val Gly Cys Ala Val Leu Gly Val Ala Gln Gly Arg Ala Gly  
 50                   1105                   1110                   1115

tgg ttg atg cat gaa gga ggt cat cac tct ctg act ggt aac tgg  
 11342  
 Trp Leu Met His Glu Gly Gly His His Ser Leu Thr Gly Asn Trp  
 55                   1120                   1125                   1130

aaa gtt gac cag ttc ctc caa gaa cta ttt ttc ggc att ggt tgt  
 11387  
 Lys Val Asp Gln Phe Leu Gln Glu Leu Phe Phe Gly Ile Gly Cys



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	1135		1140		1145									
	ggt atg tca gct gcg tgg		tgg cgc aat gca cac		aac aag cat cac									
5	11432 Gly Met Ser Ala Ala Trp		Trp Arg Asn Ala His		Asn Lys His His									
	1150		1155		1160									
	gct gct cct cag cat tta		ggg aaa gat gtt gat		ctc gag aca ttg									
10	11477 Ala Ala Pro Gln His Leu		Gly Lys Asp Val Asp		Leu Glu Thr Leu									
	1165		1170		1175									
	cct ctg gtc gcc ttc aat		aag gcc gta ctt cga		ggc cgt cta ccg									
15	11522 Pro Leu Val Ala Phe Asn		Lys Ala Val Leu Arg		Gly Arg Leu Pro									
	1180		1185		1190									
	tct gtc tgg atc aga tca		caa gct gtg tgc ttt		gca ccg ata tca									
20	11567 Ser Val Trp Ile Arg Ser		Gln Ala Val Cys Phe		Ala Pro Ile Ser									
	1195		1200		1205									
	aca cta ctg gta tcg ttc		ttt tgg caa ttc tac		cta cac ccg agg									
25	11612 Thr Leu Leu Val Ser Phe		Phe Trp Gln Phe Tyr		Leu His Pro Arg									
	1210		1215		1220									
	cat att att agg aca ggt		cga cga atg gag tct		ttc tgg cta ctc									
30	11657 His Ile Ile Arg Thr Gly		Arg Arg Met Glu Ser		Phe Trp Leu Leu									
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	gta cgc tac tta gtt att		gtg tac ctc ggg ttc		agc tat gga ttg									
35	11702 Val Arg Tyr Leu Val Ile		Val Tyr Leu Gly Phe		Ser Tyr Gly Leu									
	1240		1245		1250									
	gta tcg gtc ttg tta tgt		tac atc gca agt gtg		cat gtt ggt ggt									
40	11747 Val Ser Val Leu Leu Cys		Tyr Ile Ala Ser Val		His Val Gly Gly									
	1255		1260		1265									
	atg tac atc ttt gta cac		ttc gct cta tca cat		aca cat tta cct									
45	11792 Met Tyr Ile Phe Val His		Phe Ala Leu Ser His		Thr His Leu Pro									
	1270		1275		1280									
	gtc att aac cag cat ggt		aga gct aac tgg ttg		gaa tac gca tct									
50	11837 Val Ile Asn Gln His Gly		Arg Ala Asn Trp Leu		Glu Tyr Ala Ser									
	1285		1290		1295									
	aag cac aca gtt aat gtg		tca act aac aat tat		ttc gtc aca tgg									
55	11882 Lys His Thr Val Asn Val		Ser Thr Asn Asn Tyr		Phe Val Thr Trp									
	1300		1305		1310									
	ctc atg agt tat ttg aat		tat caa ata gag cat		cat ctc ttc ccg									
	11927													

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Leu Met Ser Tyr Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro  
 1315 1320 1325  
 tca tgt ccc cag ttt aga ttc cct ggt tac gtc agt atg agg gtt  
 5 11972  
 Ser Cys Pro Gln Phe Arg Phe Pro Gly Tyr Val Ser Met Arg Val  
 1330 1335 1340  
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 10 12017  
 Arg Glu Phe Phe His Lys His Gly Leu Lys Tyr Asn Glu Val Gly  
 1345 1350 1355  
 tat cta cat gca ctc aat ctc aca ttt tca aat ctg gct gct gtt  
 15 12062  
 Tyr Leu His Ala Leu Asn Leu Thr Phe Ser Asn Leu Ala Ala Val  
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 Ala Ile Val Glu  
 1375  
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 25 12177  
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 12357  
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 55 12837

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12897

5 acaggaacag tggagcagta tgtaggcgtg gacctcccat attaatgctt accatcatat  
12957

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Thr Cys Pro Asp Lys Ser Ala Ala Tyr Pro Pro Val Val Val Glu Ser  
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Glu Ala Arg Glu Val Ile Ile Thr Thr Val Lys Asp Leu Leu Lys Lys  
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Thr Gly Val His Pro Lys Ser Ile Asp Tyr Ile Ile Val Asn Cys Ala  
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Met Tyr Asn Pro Thr Pro Ser His Ala Ala Met Ile Val Asn Glu Val  
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Gly Met Arg Asn Asp Val Ile Thr Tyr Asn Leu Ser Gly Met Gly Cys  
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Ser Ala Gly Val Ile Thr Ile Asp Leu Ala Thr Arg Leu Leu Arg Glu



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25 Trp Val Asp Val Thr Ala Trp Leu Asn Asp His Pro Gly Gly Ser Lys  
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30 Val Leu Arg Ala Phe Asn Lys Lys Asp Ala Thr Asp Ala Val Met Ala  
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35 Met His Thr Asp Glu Ala Ile Lys Arg Ile Ile Arg Phe Ser Asn Val  
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45 Glu Lys Ser Leu Ser Arg Glu Gln Leu Met Tyr Tyr Lys Leu Arg Thr  
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Leu Tyr Phe Asp Tyr Gly Ile Trp Ser Thr Ala Leu Ile Gly Phe Ala  
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Trp Phe Gln Leu Gly Trp Leu Gly His Asp Trp Ser His His Thr Ala  
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Leu Pro Lys Ser Thr Thr Asn Cys Ala Asn Tyr Asn Asp Tyr Leu Gly  
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Trp Leu Thr Gly Leu Ala Arg Gly Asn Thr Leu Leu Trp Trp Lys Leu  
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Arg His Asn Thr His His Val Leu Thr Asn Gln Tyr Glu Asn Asp Pro  
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Asp Ile Leu Thr Gln Pro Pro Leu His Phe Phe Glu Asp Phe Asp Val  
 245 250 255

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Gly Asn Val Asn Arg Tyr Gln Ala Val Tyr Tyr Leu Pro Met Leu Thr  
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Leu Leu His Leu Phe Trp Leu Tyr Glu Ser Val Leu Val Cys Leu Arg  
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Gln Ser Arg Ser Ile Asn Arg Tyr Asn Arg Met His Ala Arg Arg Asp  
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Thr Val Ala Leu Val Leu His Ile Leu Ile Val Gly Ile Ile Ser Tyr  
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Thr Ser Gly Lys Tyr Leu Leu Ile Leu Leu Ala Tyr Met Leu Ser Gly  
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Phe Leu Thr Ala Val Val Val Phe Ala Ser His Tyr Asn Glu Pro Arg  
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55

Val Ala Ser Gly Glu Ser Leu Ser Leu Val Arg Gln Thr Leu Leu Thr  
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Thr Ile Asn Ile Gly Ser Phe Ser Asp Thr His Trp Glu Lys Lys Leu  
 370 375 380

Trp Phe Tyr Leu Thr Gly Gly Leu Asn Met Gln Ile Glu His His Leu  
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Phe Pro Thr Met Pro Arg His Asn Leu Pro Lys Thr Thr Phe Leu Val  
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Lys Ser Leu Ala Gln Glu Leu Gly Leu Pro Tyr Lys Glu Thr Asn Ile  
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Arg Asp Asp Leu Val Ser Arg Gly Val Phe Lys Pro Ser Val Met His  
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50 Tyr Leu Ala Leu Cys Thr Ser Asn Val Tyr Val Gly Cys Ala Val Leu

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EP 2 380 984 B1

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35

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 180 185 190

55 gaa gcg agg gaa gtg atc ata act acg gtc aaa gat ctg ctt aag aag  
 624  
 Glu Ala Arg Glu Val Ile Ile Thr Thr Val Lys Asp Leu Leu Lys Lys  
 195 200 205

act ggt gtg cat cct aaa tct att gac tat atc atc gtc aat tgc gcc



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672  
 Thr Gly Val His Pro Lys Ser Ile Asp Tyr Ile Ile Val Asn Cys Ala  
 210 215 220

5  
 atg tac aac ccg aca ccg tca cat gct gct atg ata gtg aat gaa gtc  
 720  
 Met Tyr Asn Pro Thr Pro Ser His Ala Ala Met Ile Val Asn Glu Val  
 225 230 235 240

10  
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 768  
 Gly Met Arg Asn Asp Val Ile Thr Tyr Asn Leu Ser Gly Met Gly Cys  
 245 250 255

15  
 agt gcc ggt gtt atc aca att gat cta gca acg cgt ctg ttg aga gag  
 816  
 Ser Ala Gly Val Ile Thr Ile Asp Leu Ala Thr Arg Leu Leu Arg Glu  
 260 265 270

20  
 acc aga ggt agg gca ctg att gtg tca act gag ata cta act cgt tgc  
 864  
 Thr Arg Gly Arg Ala Leu Ile Val Ser Thr Glu Ile Leu Thr Arg Cys  
 275 280 285

25  
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 912  
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30  
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 960  
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 305 310 315 320

35  
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 1008  
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40  
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 1056  
 Gly Asn Glu Ser Phe Glu Thr Ile Met Glu Thr Asp Asp Ser Thr Lys  
 340 345 350

45  
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 1104  
 Pro Asn Ser Ile Val Thr Leu Arg Leu Gln Lys Ser Ile Ile Lys Val  
 355 360 365

50  
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 1152  
 Ala Ala Val Ala Ile Lys Gln Asn Phe Thr Lys Leu Ala Tyr Val Val  
 370 375 380

55  
 ctg cct ctg aga gaa ctg ttg aag gtc gta tat tcg atg gtg atg atg  
 1200  
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 385 390 395 400

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aag atg agg agg aag tcg tca aaa gaa ggt cgt gag ttg tac gta cct  
 1248  
 Lys Met Arg Arg Lys Ser Ser Lys Glu Gly Arg Glu Leu Tyr Val Pro  
 405 410 415  
 5  
 gat ttt aga aag ggc att gat cat tgg tgt att cat gct ggt ggc cgt  
 1296  
 Asp Phe Arg Lys Gly Ile Asp His Trp Cys Ile His Ala Gly Gly Arg  
 420 425 430  
 10  
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 1344  
 Gly Val Leu Asp Thr Leu Gln Asp Ser Leu Gln Leu Ser Asp Tyr Asp  
 435 440 445  
 15  
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 1392  
 Ile Gln Ala Ser Arg Ser Val Leu Tyr Glu Arg Gly Asn Thr Ser Ser  
 450 455 460  
 20  
 agt agc ata tgg tat gag ttg gca tgg ctc gaa cgt gac caa cgt att  
 1440  
 Ser Ser Ile Trp Tyr Glu Leu Ala Trp Leu Glu Arg Asp Gln Arg Ile  
 465 470 475 480  
 25  
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 1488  
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 1 5 10 15  
 Asp Ile Ile Ile Ser Gly Pro Phe Gly Met Cys Asn His Asp Tyr Ser  
 20 25 30  
 50  
 Ser Ser Ile Pro Ala Ser Cys Ser Gly Ser Thr Arg Arg Met Arg Leu  
 55

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

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Thr Arg Gly Arg Ala Leu Ile Val Ser Thr Glu Ile Leu Thr Arg Cys  
 275 280 285

5 Phe Tyr Arg Gly Asn Asp Arg Glu Pro Leu Met Gly Asn Thr Leu Phe  
 290 295 300

10 Arg Cys Gly Gly Ala Ala Ala Leu Leu Ser Ser Leu Pro Lys Asp Leu  
 305 310 315 320

15 Ser Arg Gly Lys Tyr Lys Leu Leu His Thr Val Arg Thr Gln Val Leu  
 325 330 335

Gly Asn Glu Ser Phe Glu Thr Ile Met Glu Thr Asp Asp Ser Thr Lys  
 340 345 350

20 Pro Asn Ser Ile Val Thr Leu Arg Leu Gln Lys Ser Ile Ile Lys Val  
 355 360 365

25 Ala Ala Val Ala Ile Lys Gln Asn Phe Thr Lys Leu Ala Tyr Val Val  
 370 375 380

30 Leu Pro Leu Arg Glu Leu Leu Lys Val Val Tyr Ser Met Val Met Met  
 385 390 395 400

Lys Met Arg Arg Lys Ser Ser Lys Glu Gly Arg Glu Leu Tyr Val Pro  
 405 410 415

35 Asp Phe Arg Lys Gly Ile Asp His Trp Cys Ile His Ala Gly Gly Arg  
 420 425 430

40 Gly Val Leu Asp Thr Leu Gln Asp Ser Leu Gln Leu Ser Asp Tyr Asp  
 435 440 445

45 Ile Gln Ala Ser Arg Ser Val Leu Tyr Glu Arg Gly Asn Thr Ser Ser  
 450 455 460

Ser Ser Ile Trp Tyr Glu Leu Ala Trp Leu Glu Arg Asp Gln Arg Ile  
 465 470 475 480

50 Lys Arg Gly Asp Arg Val Leu Gln Val Ala Phe Gly Ser Gly Phe Lys  
 485 490 495

55 Cys Asn Ser Ser Val Trp Leu Ala Met His Asn Ile Asp Ala  
 500 505 510

## Claims

- 5 1. A process for producing a polyunsaturated fatty acid (PUFA) comprising arachidonic acid (ARA) wherein the process comprises the conversion of linoleic acid to arachidonic acid in a non-human transgenic organism, the process comprising
- 10 (i) providing a non-human transgenic organism comprising, as heterologous nucleic acid sequence, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 9$ -elongase activity and which is selected from the group consisting of:
- 15 a) a sequence comprising nucleic acid residues 7668 to 9200 of SEQ ID NO: 1;  
 b) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising residues 7668 to 9200 of SEQ ID NO: 1, wherein hybridization is in 6 x sodium chloride/sodium citrate (SSC) at approximately 45°C, followed by one or more washing steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C;  
 c) a nucleic acid sequence which encodes a polypeptide comprising SEQ ID NO: 2;  
 d) a nucleic acid sequence which encodes a polypeptide with at least 85% identity at the amino acid level with SEQ ID NO: 2; and
- 20 at least one nucleic acid sequence encoding a  $\Delta 8$  desaturase and at least one nucleic acid sequence encoding a  $\Delta 5$  desaturase; and  
 (ii) expressing said nucleic acid sequence.
- 25 2. The process according to claim 1, wherein the nucleic acid encoding the  $\Delta 8$ -desaturase is selected from the group consisting of:
- 30 a) a sequence comprising nucleic acid residues 9351 to 10724 of SEQ ID NO: 1;  
 b) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising residues 9351 to 10724 of SEQ ID NO: 1, wherein hybridization is in 6 x sodium chloride/sodium citrate (SSC) at approximately 45°C, followed by one or more washing steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C;  
 c) a nucleic acid sequence which encodes a polypeptide comprising SEQ ID NO: 3;  
 d) a nucleic acid sequence which encodes a polypeptide with at least 85% identity at the amino acid level with SEQ ID NO: 3;
- 35 and wherein the nucleic acid encoding the  $\Delta 5$ -desaturase is selected from the group consisting of:
- 40 e) a sequence comprising nucleic acid residues 10842 to 12077 of SEQ ID NO: 1;  
 f) a nucleic acid sequence which hybridizes under stringent conditions with a nucleic acid sequence comprising residues 10842 to 12077 of SEQ ID NO: 1, wherein hybridization is in 6 x sodium chloride/sodium citrate (SSC) at approximately 45°C, followed by one or more washing steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C;  
 g) a nucleic acid sequence which encodes a polypeptide comprising SEQ ID NO: 4;  
 h) a nucleic acid sequence which encodes a polypeptide with at least 85% identity at the amino acid level with SEQ ID NO: 4.
- 45 3. The process according to claim 1, wherein the nucleic acid comprises a nucleic acid sequence which encodes polypeptides with at least 85% identity at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4, respectively; wherein said polypeptides have  $\Delta 9$ -elongase;  $\Delta 8$ -desaturase and  $\Delta 5$ -desaturase activity, respectively.
- 50 4. The process according to any of claims 1 to 3 including the additional step of converting the ARA to an  $\omega$ -3 fatty acid.
5. The process according to claim 4, wherein the process includes the additional step of introducing into the organism an  $\omega$ -3 desaturase and optionally a  $\Delta 5$ -elongase and/or a  $\Delta 4$ -elongase and/or a  $\Delta 4$ -desaturase.
- 55 6. The process according to claim 4 or 5, wherein the  $\omega$ -3 fatty acid is eicosapentaenoic acid (EPA) and/or docosahexaenoic acid (DHA).
7. The process according to any one of claims 1 to 6, further including the additional step of introducing into the

organism one or more biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxigenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) and desaturase(s).

8. The process for producing ARA, EPA or DHA or a derivative thereof comprising growing the non-human transgenic organism as defined in any one of claims 1 to 7 and harvesting said ARA, EPA or DHA or a derivative thereof.
9. The process according to any one of claims 1 to 8, wherein the non-human transgenic organism is a microorganism, a non-human animal or a plant.
10. The process according to claim 9, wherein the non-human transgenic organism is a plant.
11. The process for producing ARA according to any one of claims 1 to 10, wherein the process yields ARA in a content of at least 1% by weight of the total fatty acids in the non-human transgenic organism.
12. The process for producing ARA according to claims 1 to 10, wherein the process yields ARA in a content of at least 3% by weight of the total fatty acids in the non-human transgenic organism.

### Patentansprüche

1. Verfahren zur Herstellung einer mehrfach ungesättigten Fettsäure (Polyunsaturated Fatty Acid, PUFA), die Arachidonsäure (ARA) umfasst, wobei das Verfahren die Umwandlung von Linolsäure in Arachidonsäure in einem nicht-menschlichen transgenen Organismus umfasst, wobei das Verfahren Folgendes umfasst:

(i) Bereitstellen eines nichtmenschlichen transgenen Organismus, der, als eine heterologe Nukleinsäuresequenz, wenigstens eine Nukleinsäuresequenz, die ein Polypeptid mit  $\Delta 9$ -Elongase-Aktivität codiert und die aus der aus

- a) einer Nukleinsäurereste 7668 bis 9200 der SEQ ID NO: 1 umfassenden Sequenz;
- b) einer Nukleinsäuresequenz, die unter stringenten Bedingungen mit einer Reste 7668 bis 9200 der SEQ ID NO: 1 umfassenden Nukleinsäuresequenz hybridisiert, wobei die Hybridisierung in 6 x Natriumchlorid/Natriumcitrat (SSC) bei etwa 45 °C erfolgt, gefolgt von einem oder mehreren Waschschrinen in 0,2 x SSC, 0,1% SDS bei 50 bis 65 °C;
- c) einer Nukleinsäuresequenz, die ein SEQ ID NO: 2 umfassendes Polypeptid codiert;
- d) einer Nukleinsäuresequenz, die ein Polypeptid mit einer Identität auf der Aminosäureebene von wenigstens 85% mit SEQ ID NO: 2 codiert, bestehenden Gruppe ausgewählt ist; und

wenigstens eine Nukleinsäuresequenz, die eine  $\Delta 8$ -Desaturase codiert, und wenigstens eine Nukleinsäuresequenz, die eine  $\Delta 5$ -Desaturase codiert, umfasst; und

(ii) Exprimieren der Nukleinsäuresequenz.

2. Verfahren nach Anspruch 1, wobei die die  $\Delta 8$ -Desaturase codierende Nukleinsäure aus der aus

- a) einer Nukleinsäurereste 9351 bis 10724 der SEQ ID NO: 1 umfassenden Sequenz;
- b) einer Nukleinsäuresequenz, die unter stringenten Bedingungen mit einer Reste 9351 bis 10724 der SEQ ID NO: 1 umfassenden Nukleinsäuresequenz hybridisiert, wobei die Hybridisierung in 6 x Natriumchlorid/Natriumcitrat (SSC) bei etwa 45 °C erfolgt, gefolgt von einem oder mehreren Waschschrinen in 0,2 x SSC, 0,1% SDS bei 50 bis 65 °C;
- c) einer Nukleinsäuresequenz, die ein SEQ ID NO: 3 umfassendes Polypeptid codiert;
- d) einer Nukleinsäuresequenz, die ein Polypeptid mit einer Identität auf der Aminosäureebene von wenigstens 85% mit SEQ ID NO: 3 codiert, bestehenden Gruppe ausgewählt ist; und wobei die die  $\Delta 5$ -Desaturase codierende Nukleinsäure aus der aus
- e) einer Nukleinsäurereste 10842 bis 12077 der SEQ ID NO: 1 umfassenden Sequenz;
- f) einer Nukleinsäuresequenz, die unter stringenten Bedingungen mit einer Reste 10842 bis 12077 der SEQ

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ID NO: 1 umfassenden Nukleinsäuresequenz hybridisiert, wobei die Hybridisierung in 6 x Natriumchlorid/Natriumcitrat (SSC) bei etwa 45 °C erfolgt, gefolgt von einem oder mehreren Waschschritten in 0,2 x SSC, 0,1% SDS bei 50 bis 65 °C;

g) einer Nukleinsäuresequenz, die ein SEQ ID NO: 4 umfassendes Polypeptid codiert;

h) einer Nukleinsäuresequenz, die ein Polypeptid mit einer Identität auf der Aminosäureebene von wenigstens 85% mit SEQ ID NO: 4 codiert, bestehenden Gruppe ausgewählt ist.

3. Verfahren nach Anspruch 1, wobei die Nukleinsäure eine Nukleinsäuresequenz umfasst, die Polypeptide mit einer Identität auf der Aminosäureebene von wenigstens 85% mit SEQ ID NO: 2, SEQ ID NO: 3 bzw. SEQ ID NO: 4, codiert; wobei die Polypeptide  $\Delta 9$ -Elongase-;  $\Delta 8$ -Desaturase- bzw.  $\Delta 5$ -Desaturase-Aktivität aufweisen.

4. Verfahren nach einem der Ansprüche 1 bis 3, umfassend den zusätzlichen Schritt der Umwandlung der ARA in eine  $\omega$ -3-Fettsäure.

5. Verfahren nach Anspruch 4, wobei das Verfahren den zusätzlichen Schritt der Einführung einer  $\omega$ -3-Desaturase und gegebenenfalls einer  $\Delta 5$ -Elongase und/oder einer  $\Delta 4$ -Elongase und/oder einer  $\Delta 4$ -Desaturase in den Organismus umfasst.

6. Verfahren nach Anspruch 4 oder 5, wobei es sich bei der  $\omega$ -3-Fettsäure um Eicosapentaensäure (EPA) und/oder Docosahexaensäure (DHA) handelt.

7. Verfahren nach einem der Ansprüche 1 bis 6, ferner umfassend den zusätzlichen Schritt der Einführung eines oder mehrerer Biosynthesegene des Fettsäure- oder Lipidstoffwechsels, ausgewählt aus der Gruppe Acyl-CoA-Dehydrogenase(n), Acyl-ACP[= Acyl Carrier Protein]-Desaturase(n), Acyl-ACP-Thioesterase(n), Fettsäure-Acyltransferase(n), Acyl-CoA:Lysophospholipid-Acyltransferase(n), Fettsäure-Synthase(n), Fettsäure-Hydroxylase(n), Acetyl-Coenzym-A-Carboxylase(n), Acyl-Coenzym-A-Oxidase(n), Fettsäure-Desaturase(n), Fettsäure-Acetylenasen, Lipoxygenasen, Triacylglycerin-Lipasen, Allenoxid-Synthasen, Hydroperoxid-Lyasen oder Fettsäure-Elongase(n) und Desaturase(n), in den Organismus umfasst.

8. Verfahren zur Herstellung von ARA, EPA oder DHA oder einem Derivat davon, umfassend Kultivieren des nichtmenschlichen transgenen Organismus mit der in einem der Ansprüche 1 bis 7 angegebenen Bedeutung und Ernten der ARA, EPA bzw. DHA oder eines Derivats davon.

9. Verfahren nach einem der Ansprüche 1 bis 8, wobei es sich bei dem nichtmenschlichen transgenen Organismus um einen Mikroorganismus, ein nichtmenschliches Tier oder eine Pflanze handelt.

10. Verfahren nach Anspruch 9, wobei es sich bei dem nichtmenschlichen transgenen Organismus um eine Pflanze handelt.

11. Verfahren zur Herstellung von ARA nach einem der Ansprüche 1 bis 10, wobei das Verfahren ARA bei einem Gehalt von wenigstens 1 Gew.-% der gesamten Fettsäuren im nichtmenschlichen transgenen Organismus erbringt.

12. Verfahren zur Herstellung von ARA nach einem der Ansprüche 1 bis 10, wobei das Verfahren ARA bei einem Gehalt von wenigstens 3 Gew.-% der gesamten Fettsäuren im nichtmenschlichen transgenen Organismus erbringt.

### Revendications

1. Procédé de production d'un acide gras polyinsaturé (PUFA) comprenant l'acide arachidonique (ARA), le procédé comprenant la conversion d'acide linoléique en acide arachidonique dans un organisme transgénique non humain, le procédé comprenant

(i) la fourniture d'un organisme transgénique non humain comprenant, en tant que séquence d'acide nucléique hétérologue, au moins une séquence d'acide nucléique qui code pour un polypeptide ayant une activité  $\Delta 9$ -élongase et qui est choisie dans le groupe constitué de :

a) une séquence comprenant les résidus d'acide nucléique 7668 à 9200 de SEQ ID NO: 1 ;

b) une séquence d'acide nucléique qui s'hybride dans des conditions stringentes avec une séquence d'acide

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nucléique comprenant les résidus 7668 à 9200 de SEQ ID NO: 1, l'hybridation étant conduite dans 6 x chlorure de sodium/citrate de sodium (SSC) à approximativement 45 °C, suivie d'une ou plusieurs étapes de lavage dans 0,2 x SSC, 0,1 % SDS à 50 à 65 °C ;

c) une séquence d'acide nucléique qui code pour un polypeptide comprenant SEQ ID NO: 2 ;

d) une séquence d'acide nucléique qui code pour un polypeptide ayant au moins 85 % d'identité au niveau des acides aminés avec SEQ ID NO: 2 ; et

au moins une séquence d'acide nucléique codant pour une  $\Delta 8$ -désaturase et au moins une séquence d'acide nucléique codant pour une  $\Delta 5$ -désaturase ; et

(ii) l'expression de ladite séquence d'acide nucléique.

2. Procédé selon la revendication 1, dans lequel l'acide nucléique codant pour la  $\Delta 8$ -désaturase est choisi dans le groupe constitué de :

a) une séquence comprenant les résidus d'acide nucléique 9351 à 10724 de SEQ ID NO: 1 ;

b) une séquence d'acide nucléique qui s'hybride dans des conditions stringentes avec une séquence d'acide nucléique comprenant les résidus 9351 à 10724 de SEQ ID NO: 1, l'hybridation étant conduite dans 6 x chlorure de sodium/citrate de sodium (SSC) à approximativement 45 °C, suivie d'une ou plusieurs étapes de lavage dans 0,2 x SSC, 0,1 % SDS à 50 à 65 °C ;

c) une séquence d'acide nucléique qui code pour un polypeptide comprenant SEQ ID NO: 3 ;

d) une séquence d'acide nucléique qui code pour un polypeptide ayant au moins 85 % d'identité au niveau des acides aminés avec SEQ ID NO: 3 ;

et dans lequel l'acide nucléique codant pour la  $\Delta 5$ -désaturase est choisi dans le groupe constitué de :

e) une séquence comprenant les résidus d'acide nucléique 10842 à 12077 de SEQ ID NO: 1 ;

f) une séquence d'acide nucléique qui s'hybride dans des conditions stringentes avec une séquence d'acide nucléique comprenant les résidus 10842 à 12077 de SEQ ID NO: 1, l'hybridation étant conduite dans 6 x chlorure de sodium/citrate de sodium (SSC) à approximativement 45 °C, suivie d'une ou plusieurs étapes de lavage dans 0,2 x SSC, 0,1 % SDS à 50 à 65 °C ;

g) une séquence d'acide nucléique qui code pour un polypeptide comprenant SEQ ID NO: 4 ;

h) une séquence d'acide nucléique qui code pour un polypeptide ayant au moins 85 % d'identité au niveau des acides aminés avec SEQ ID NO: 4.

3. Procédé selon la revendication 1, dans lequel l'acide nucléique comprend une séquence d'acide nucléique qui code pour des polypeptides ayant au moins 85 % d'identité au niveau des acides aminés avec SEQ ID NO: 2, SEQ ID NO: 3 et SEQ ID NO: 4, respectivement ; dans lequel lesdits polypeptides ont une activité  $\Delta 9$ -élongase ;  $\Delta 8$ -désaturase et  $\Delta 5$ -désaturase, respectivement.

4. Procédé selon l'une quelconque des revendications 1 à 3 comprenant l'étape additionnelle de conversion d'ARA en acide gras  $\omega$ -3.

5. Procédé selon la revendication 4, le procédé comprenant l'étape additionnelle d'introduction dans l'organisme d'une  $\omega$ -3 désaturase et facultativement d'une  $\Delta 5$ -élongase et/ou d'une  $\Delta 4$ -élongase et/ou d'une  $\Delta 4$ -désaturase.

6. Procédé selon la revendication 4 ou 5, dans lequel l'acide gras  $\omega$ -3 est l'acide eicosapentaénoïque (EPA) et/ou l'acide docosahexaénoïque (DHA).

7. Procédé selon l'une quelconque des revendications 1 à 6, comprenant en outre l'étape additionnelle d'introduction dans l'organisme d'un ou plusieurs gènes de biosynthèse du métabolisme des acides gras ou des lipides choisis dans le groupe des acyl-CoA déshydrogénase(s), acyl-ACP [= protéine de transport d'acyle] désaturase(s), acyl-ACP thioestérase(s), acide gras acyltransférase(s), acyl-CoA:lysophospholipide acyltransférase(s), acide gras synthase(s), acide gras hydroxylase(s), acétyl-coenzyme A carboxylase(s), acyl-coenzyme A oxydase(s), acide gras désaturase(s), acide gras acétylénases, lipoxigénases, triacylglycérol lipases, allénoxyde synthases, hydroperoxyde lyases ou acide gras élongase(s) et désaturase(s).

8. Procédé de production d'ARA, EPA ou DHA ou d'un dérivé de celui-ci, comprenant la culture de l'organisme transgénique non humain tel que défini dans l'une quelconque des revendications 1 à 7 et la collecte dudit ARA, EPA



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ou DHA ou un dérivé de celui-ci.

9. Procédé selon l'une quelconque des revendications 1 à 8, dans lequel l'organisme transgénique non humain est un micro-organisme, un animal non humain ou une plante.

5

10. Procédé selon la revendication 9, dans lequel l'organisme transgénique non humain est une plante.

11. Procédé de production d'ARA selon l'une quelconque des revendications 1 à 10, le procédé produisant ARA à une teneur d'au moins 1 % en poids des acides gras totaux dans l'organisme transgénique non humain.

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12. Procédé de production d'ARA selon les revendications 1 à 10, le procédé produisant ARA à une teneur d'au moins 3 % en poids des acides gras totaux dans l'organisme transgénique non humain.

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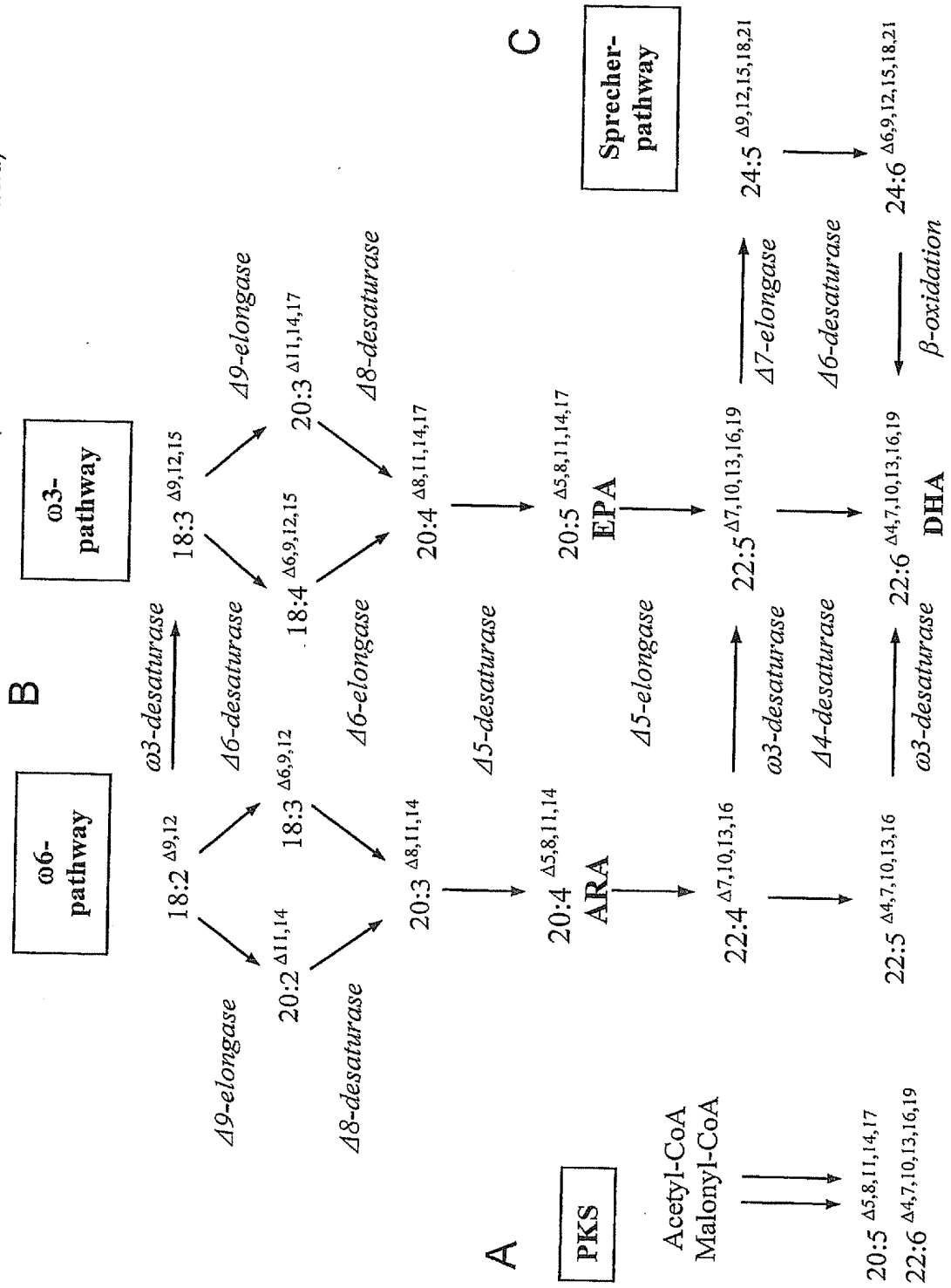
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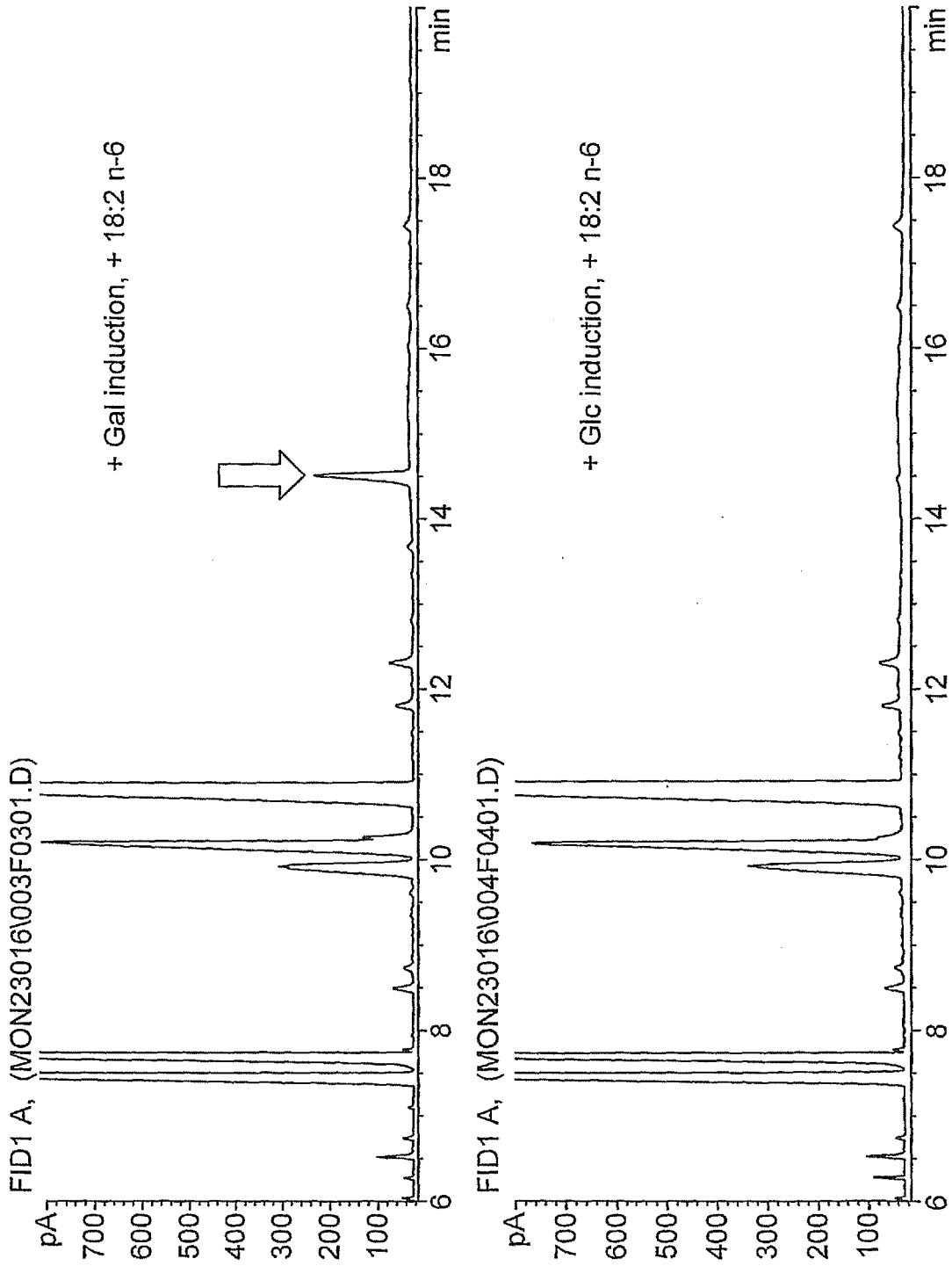
**FIG. 1**

Various synthetic pathways for the biosynthesis of DHA (docosahexaenoic acid)



# FIG. 2

Conversion of 18:2 n-6 to 20:2 n-6 by heterologous expression of the *P. marinus* sequence PmFAE in yeast



## REFERENCES CITED IN THE DESCRIPTION

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