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(54) **METHOD FOR PRODUCING  
POLYUNSATURATED FATTY ACIDS IN  
TRANSGENIC PLANTS**

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(58) **Field of Classification Search**  
None  
See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to a process for the production of polyunsaturated fatty acids in the seed of transgenic plants by introducing, into the organism, nucleic acids which encode polypeptides with a  $\omega$ 3-desaturase,  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 6-elongase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase and/or  $\Delta$ 4-desaturase activity. The invention furthermore relates to recombinant nucleic acid molecules comprising the nucleic acid sequences which encode the aforementioned polypeptides, either jointly or individually, and transgenic plants which comprise the aforementioned recombinant nucleic acid molecules. Furthermore, the invention relates to the generation of a transgenic plant and to oils, lipids and/or fatty acids with an elevated content of polyunsaturated fatty acids, in particular arachidonic acid, eicosapentaenoic acid and/or docosahexaenoic acid, as the result of the expression of the elongases and desaturases used in the process according to the invention.

**25 Claims, 33 Drawing Sheets**

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Figure 1: Various synthetic pathways for the biosynthesis of DHA (docosahexaenoic acid)

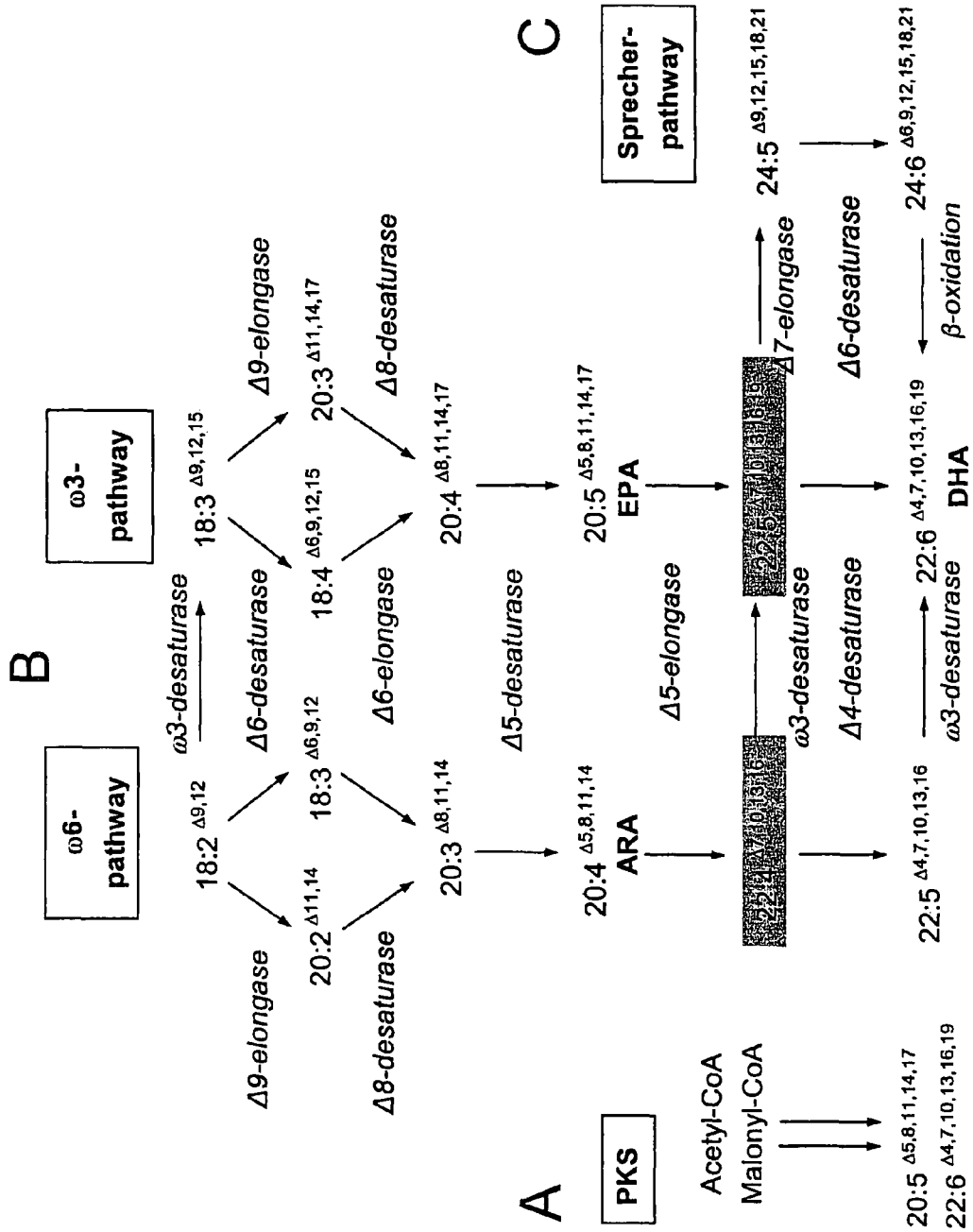


Figure 2: Substrate specificity of the  $\Delta 5$ -elongase (SEQ ID NO: 53) with regard to different fatty acids

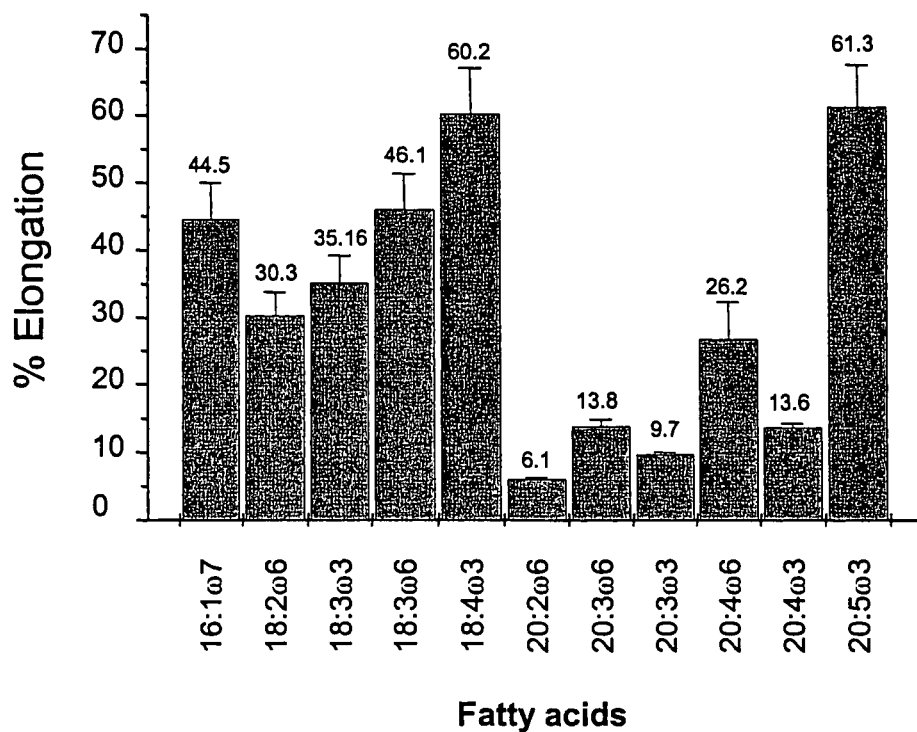


Figure 3: Reconstitution of DHA biosynthesis in yeast starting from 20:5 $\omega$ 3.

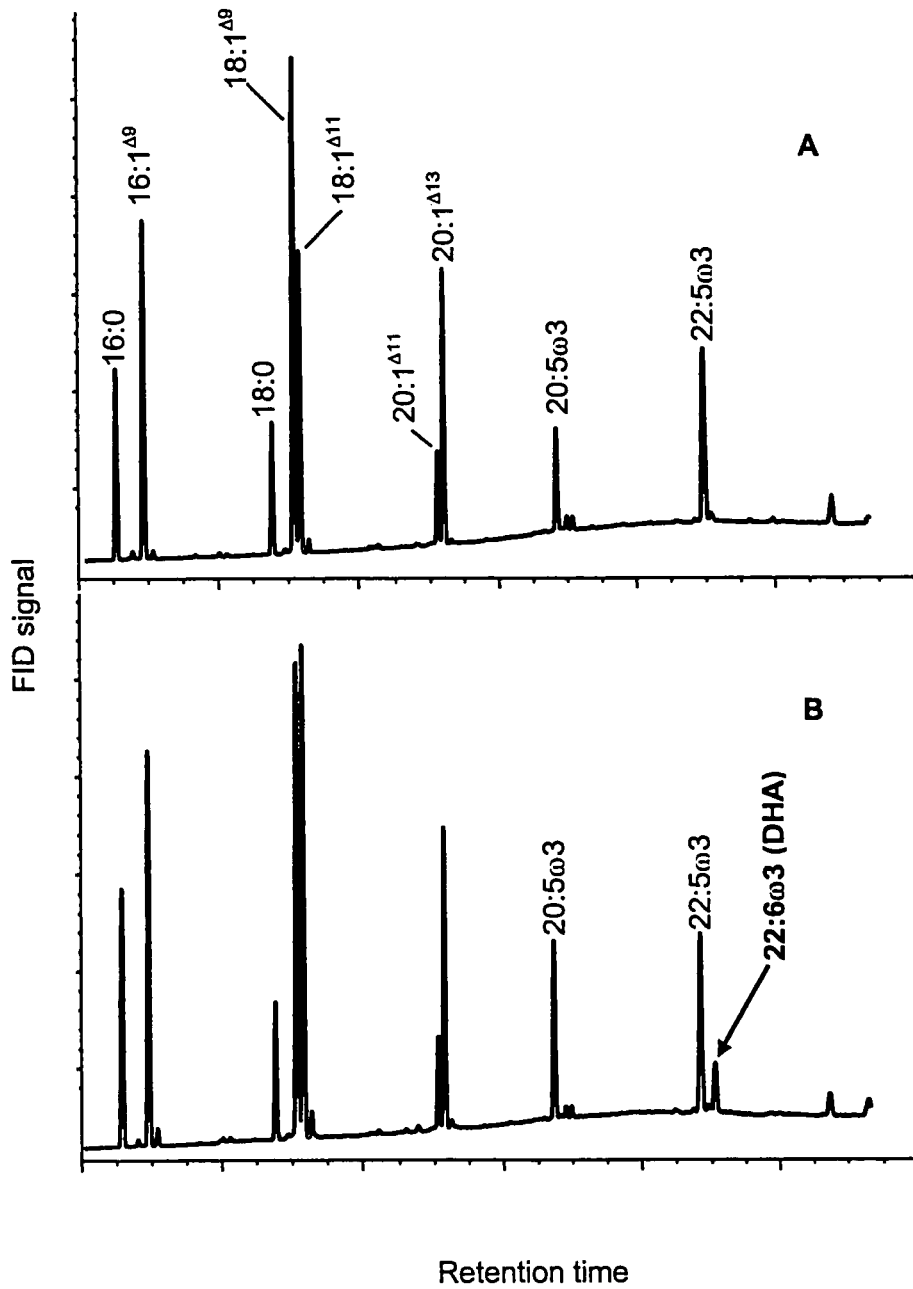


Figure 4: Reconstitution of DHA biosynthesis in yeast starting from 18:4 $\omega$ 3.

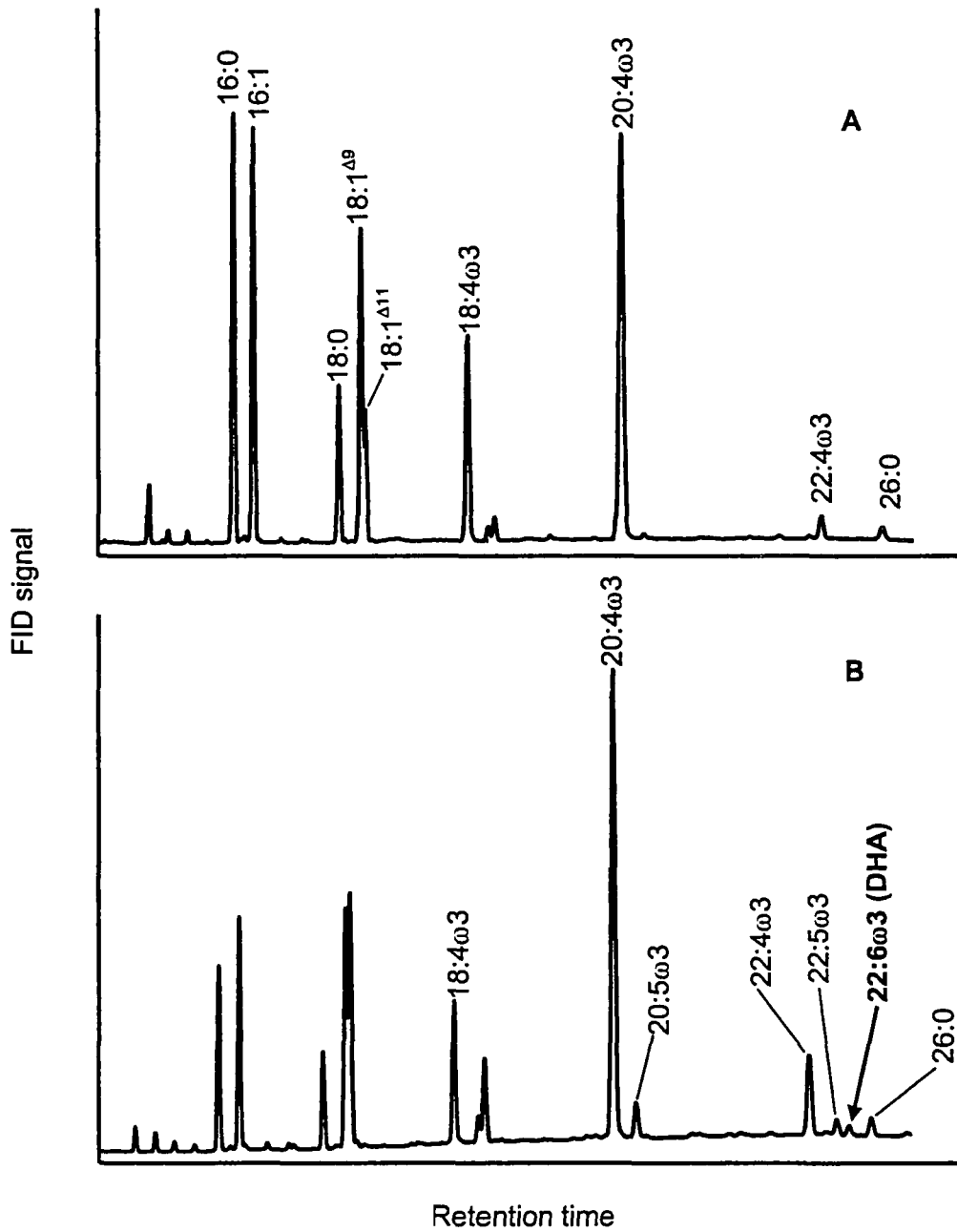


Figure 5: Fatty acid composition (in mol%) of transgenic yeasts which had been transformed with the vectors pYes3-OmELO3/pYes2-EgD4 or pYes3-OmELO3/pYes2-EgD4+pESCLeu-PtD5. The yeast cells were cultured in minimal medium without tryptophan and uracil/ and leucin in the presence of 250  $\mu$ M 20:5 <sup>$\Delta$ 5,8,11,14,17</sup> and 18:4 <sup>$\Delta$ 6,9,12,15</sup>, respectively. The fatty acid methyl esters were obtained from cell sediments by acid methanolysis and analyzed via GLC. Each value represents the mean (n=4)  $\pm$  standard deviation.

Fatty acids	pYes3-OmELO/pYes2-EgD4	pYes3-OmELO/pYes2-EgD4 EgD4 + pESCLeu-PtD5
	Feeding of 20:5 <sup><math>\Delta</math>5,8,11,14,17</sup>	Feeding of 18:4 <sup><math>\Delta</math>6,9,12,15</sup>
16:0	9.35 $\pm$ 1.61	7.35 $\pm$ 1.37
16:1 <sup><math>\Delta</math>9</sup>	14.70 $\pm$ 2.72	10.02 $\pm$ 1.81
18:0	5.11 $\pm$ 1.09	4.27 $\pm$ 1.21
18:1 <sup><math>\Delta</math>9</sup>	19.49 $\pm$ 3.01	10.81 $\pm$ 1.95
18:1 <sup><math>\Delta</math>11</sup>	18.93 $\pm$ 2.71	11.61 $\pm$ 1.48
18:4 <sup><math>\Delta</math>6,9,12,15</sup>	-	7.79 $\pm$ 1.29
20:1 <sup><math>\Delta</math>11</sup>	3.24 $\pm$ 0.41	1.56 $\pm$ 0.23
20:1 <sup><math>\Delta</math>13</sup>	11.13 $\pm$ 2.07	4.40 $\pm$ 0.78
20:4 <sup><math>\Delta</math>8,11,14,17</sup>	-	30.05 $\pm$ 3.16
20:5 <sup><math>\Delta</math>5,8,11,14,17</sup>	6.91 $\pm$ 1.10	3.72 $\pm$ 0.59
22:4 <sup><math>\Delta</math>10,13,16,17</sup>	-	5.71 $\pm$ 1.30
22:5 <sup><math>\Delta</math>7,10,13,16,19</sup>	8.77 $\pm$ 1.32	1.10 $\pm$ 0.27
22:6 <sup><math>\Delta</math>4,7,10,13,16,19</sup>	2.73 $\pm$ 0.39	0.58 $\pm$ 0.10



Figure 6: Feeding experiment for determining the functionality and substrate specificity with yeast strains

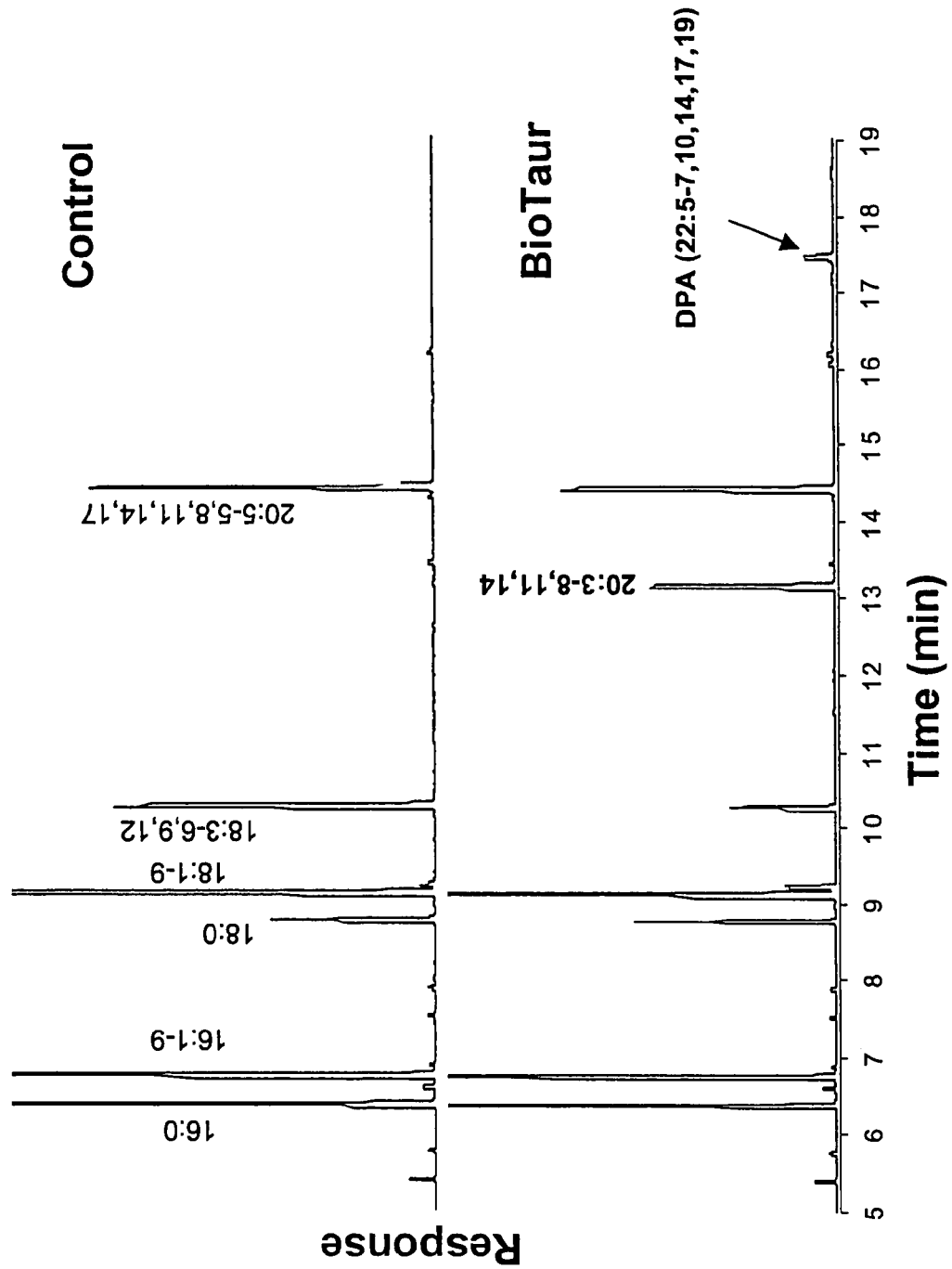


Figure 7: Elongation of eicosapentaenoic acid by OtlElo1

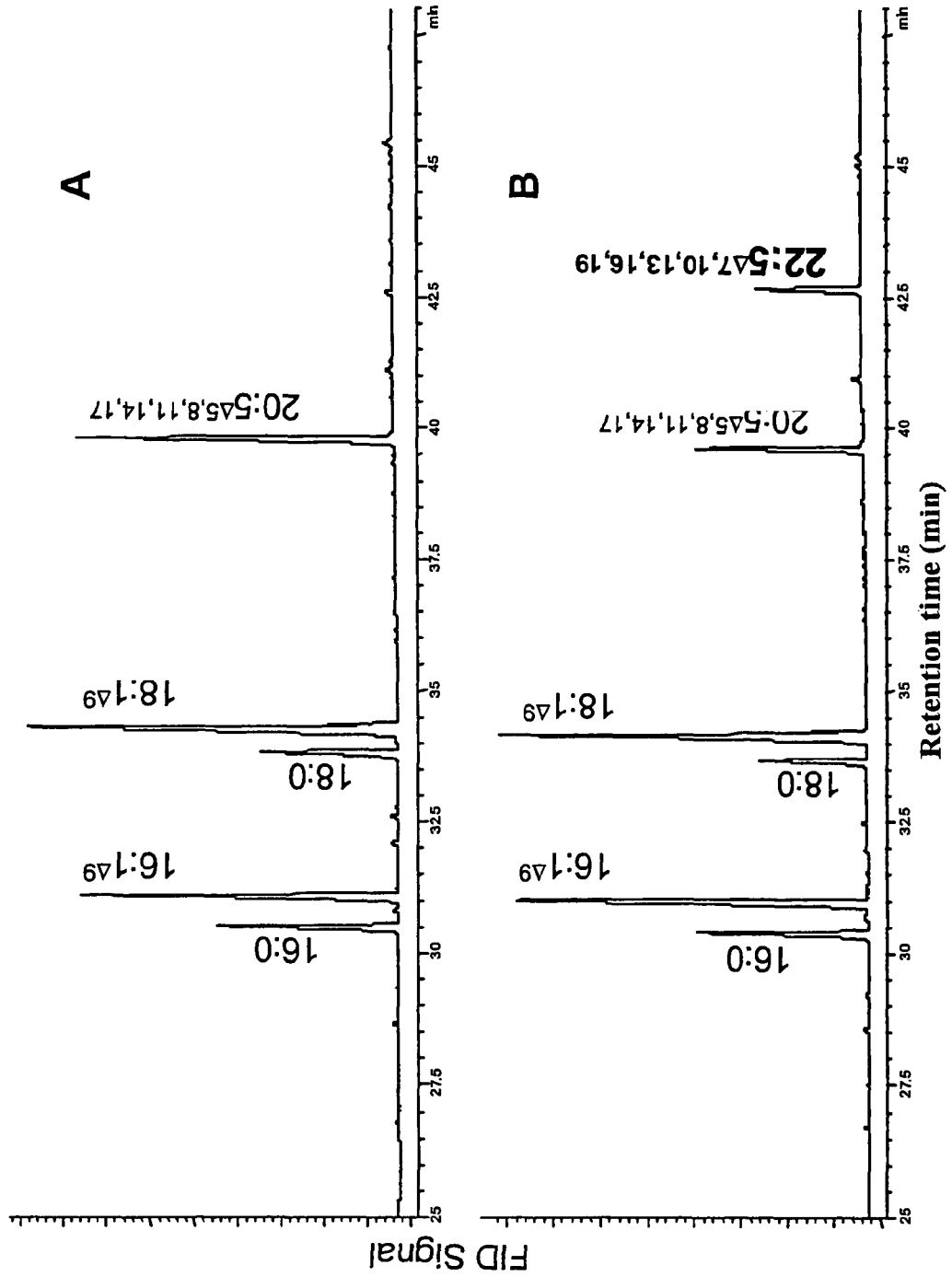


Figure 8: Elongation of arachidonic acid by OtElo1

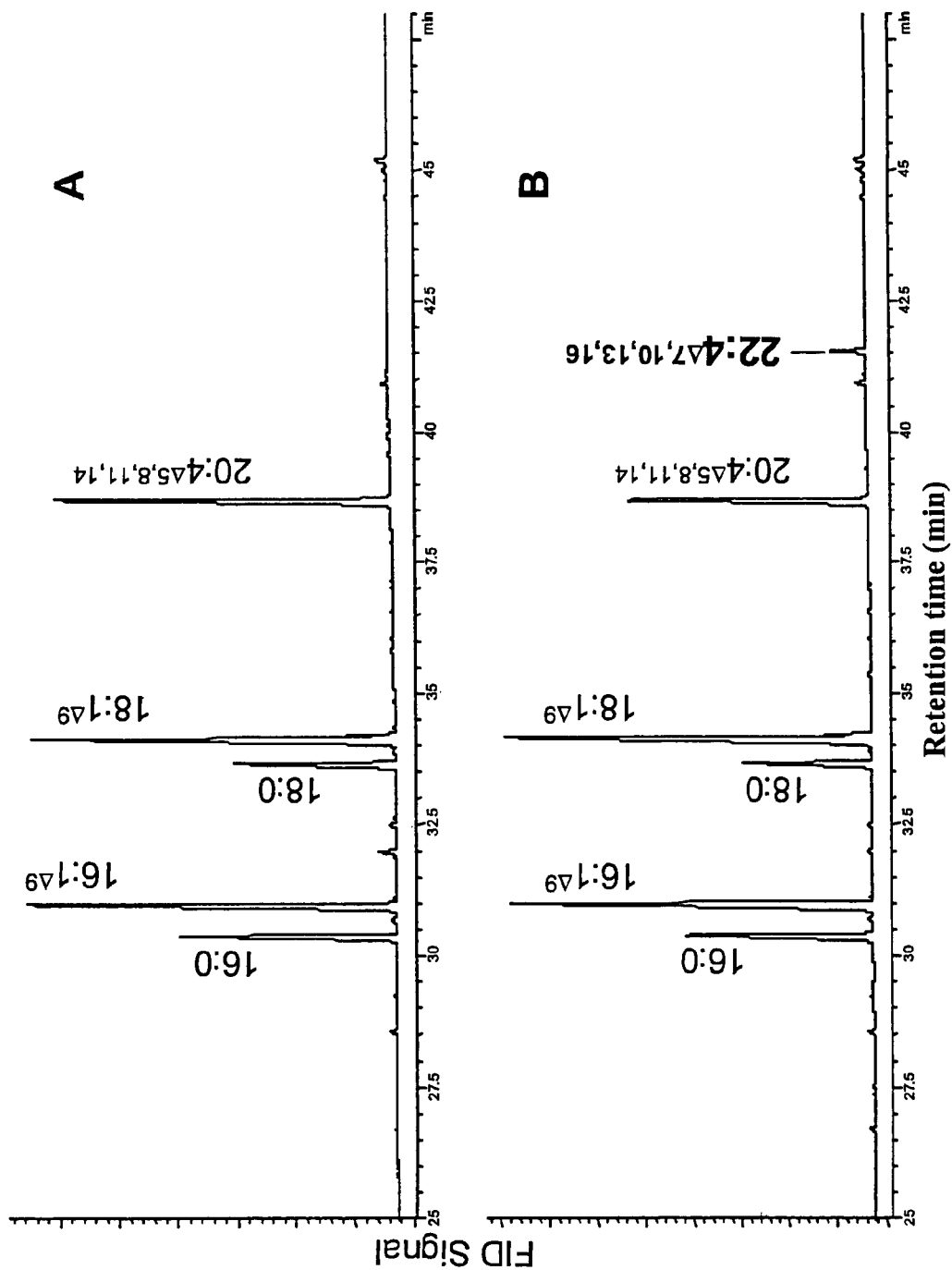


Figure 9: Expression of TpELO1 in yeast

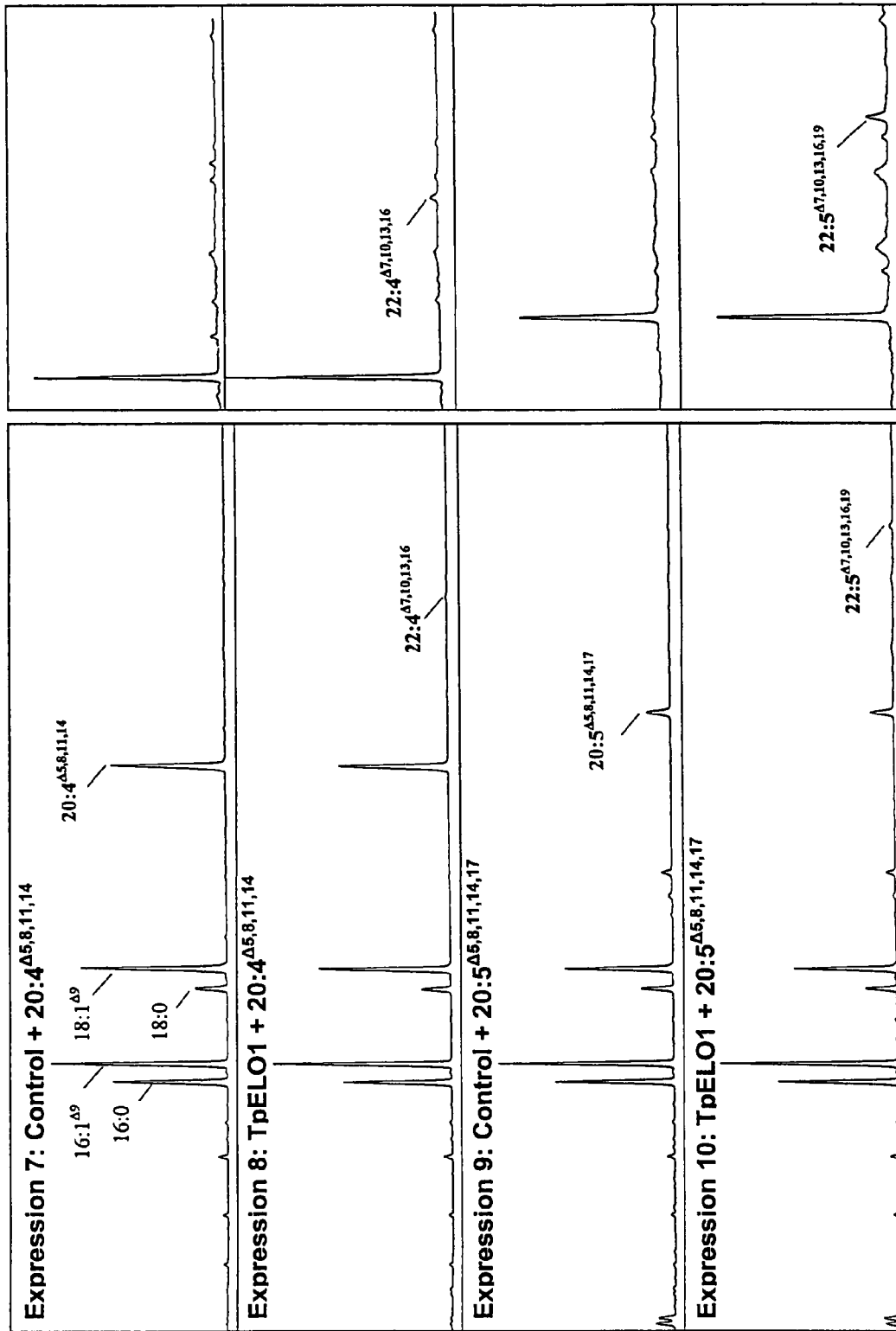


Figure 10: Expression of TpELO3 in yeast

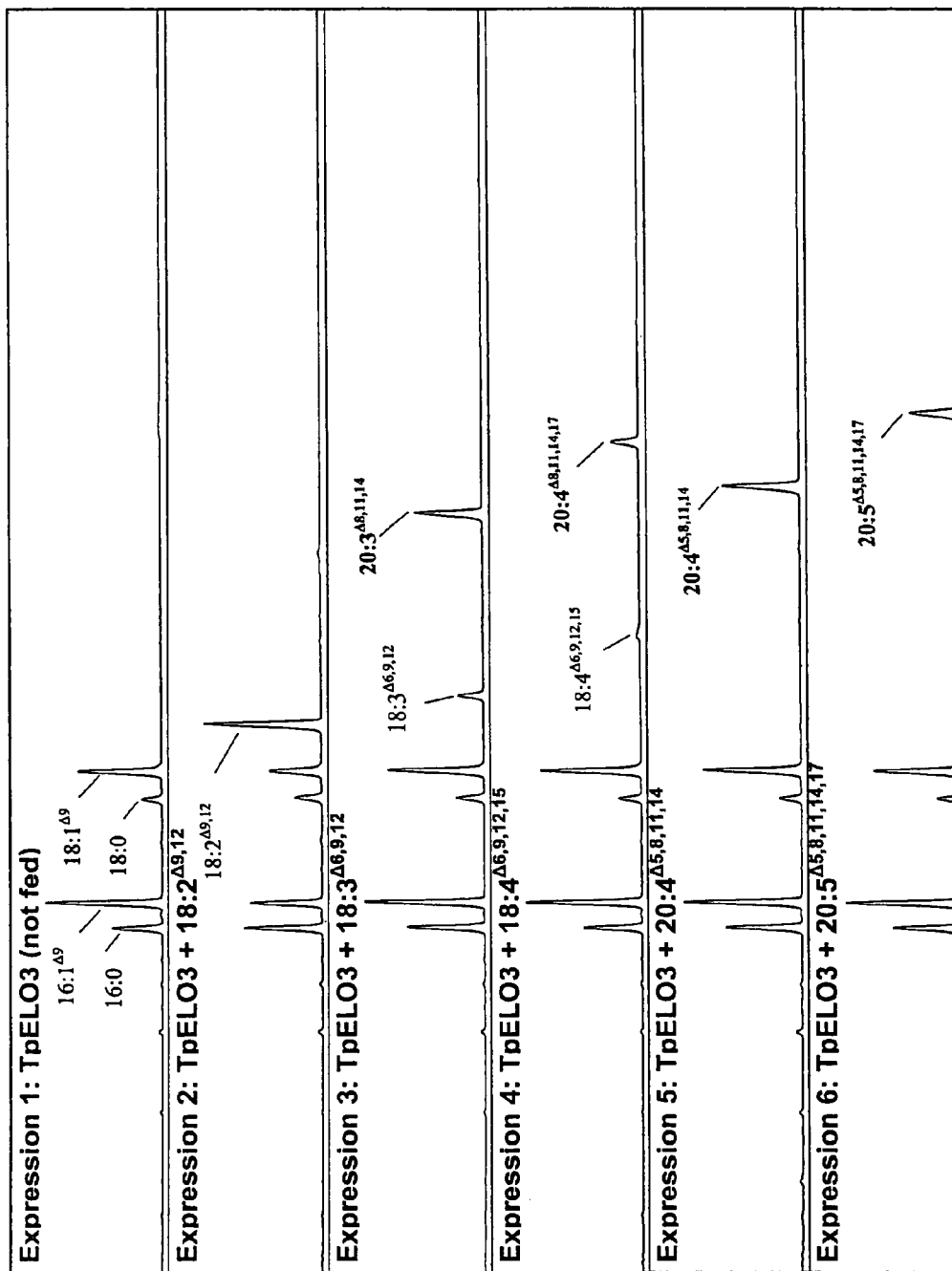


Figure 11: Expression of Thraustochytrium  $\Delta 5$ -elongase TL16/pYES2.1 in yeast

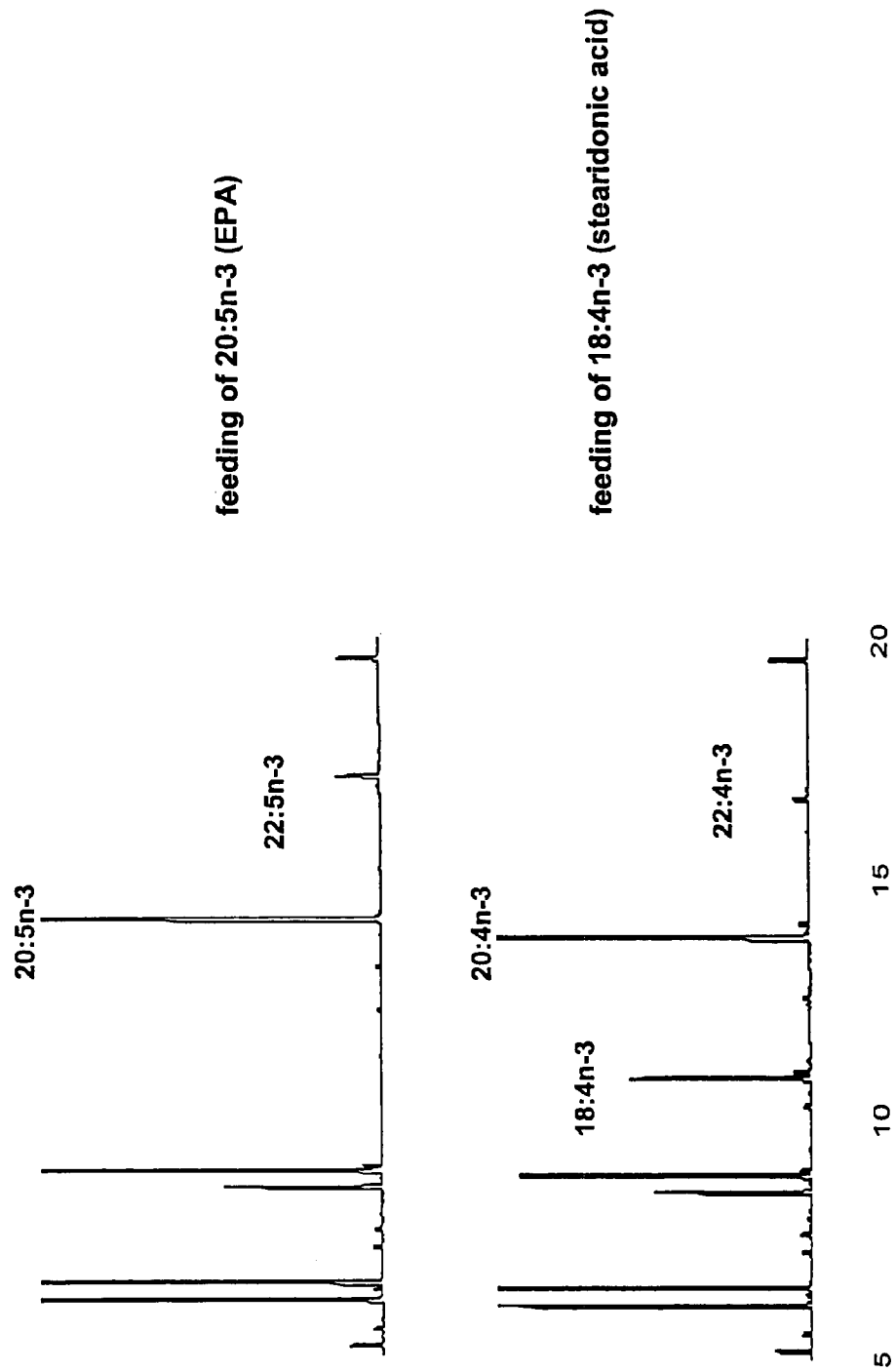


Figure 12: Desaturation of  $\gamma$ -linolenic acid (18:2  $\omega$ 6-fatty acid) to give  $\alpha$ -linolenic acid (18:3  $\omega$ 3-fatty acid) by Pi-omega3Des.

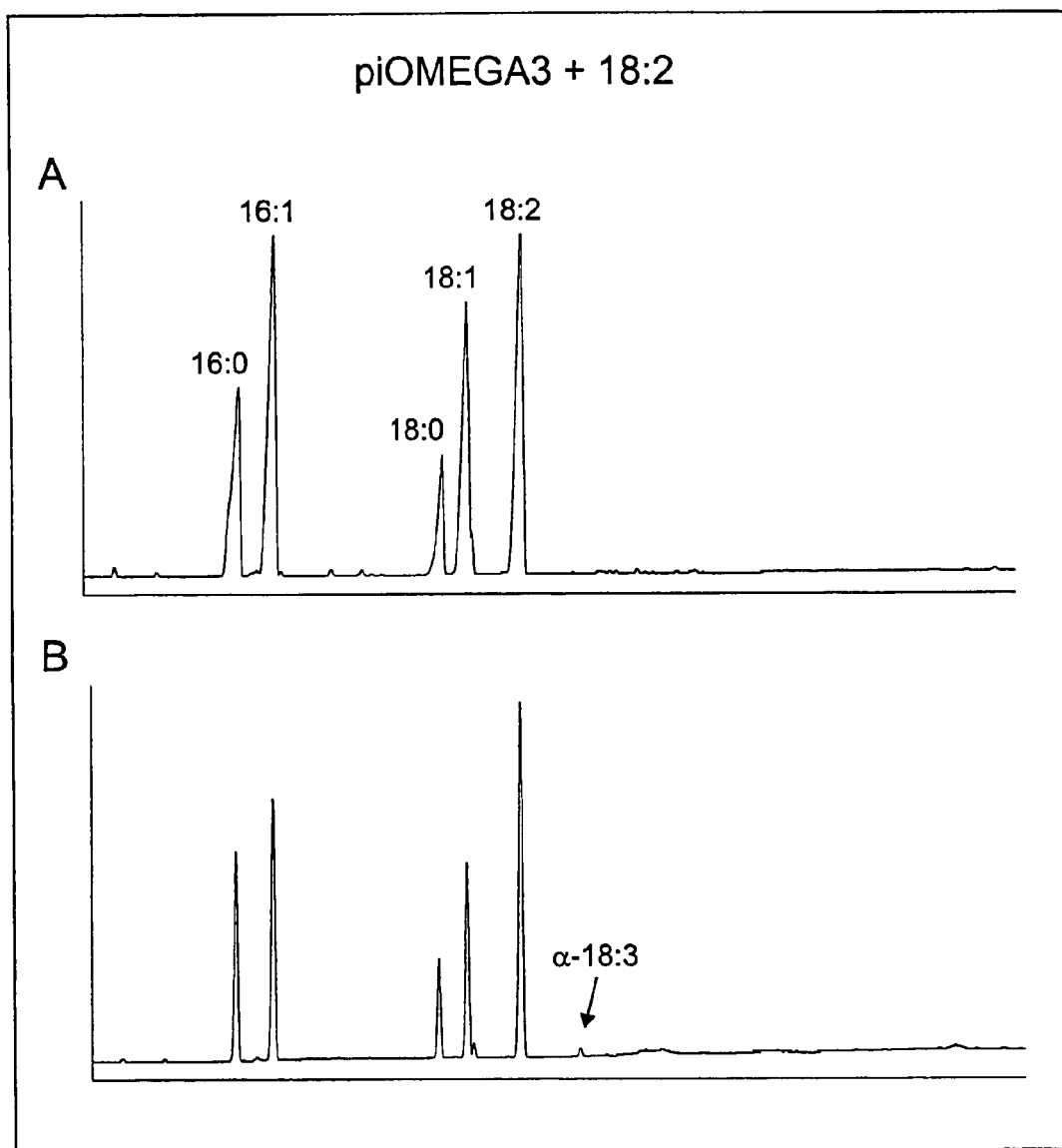


Figure 13: Desaturation of  $\gamma$ -linolenic acid (18:2  $\omega$ 6-fatty acid) to give stearidonic acid (18:4  $\omega$ 3-fatty acid) by Pi-omega3Des.

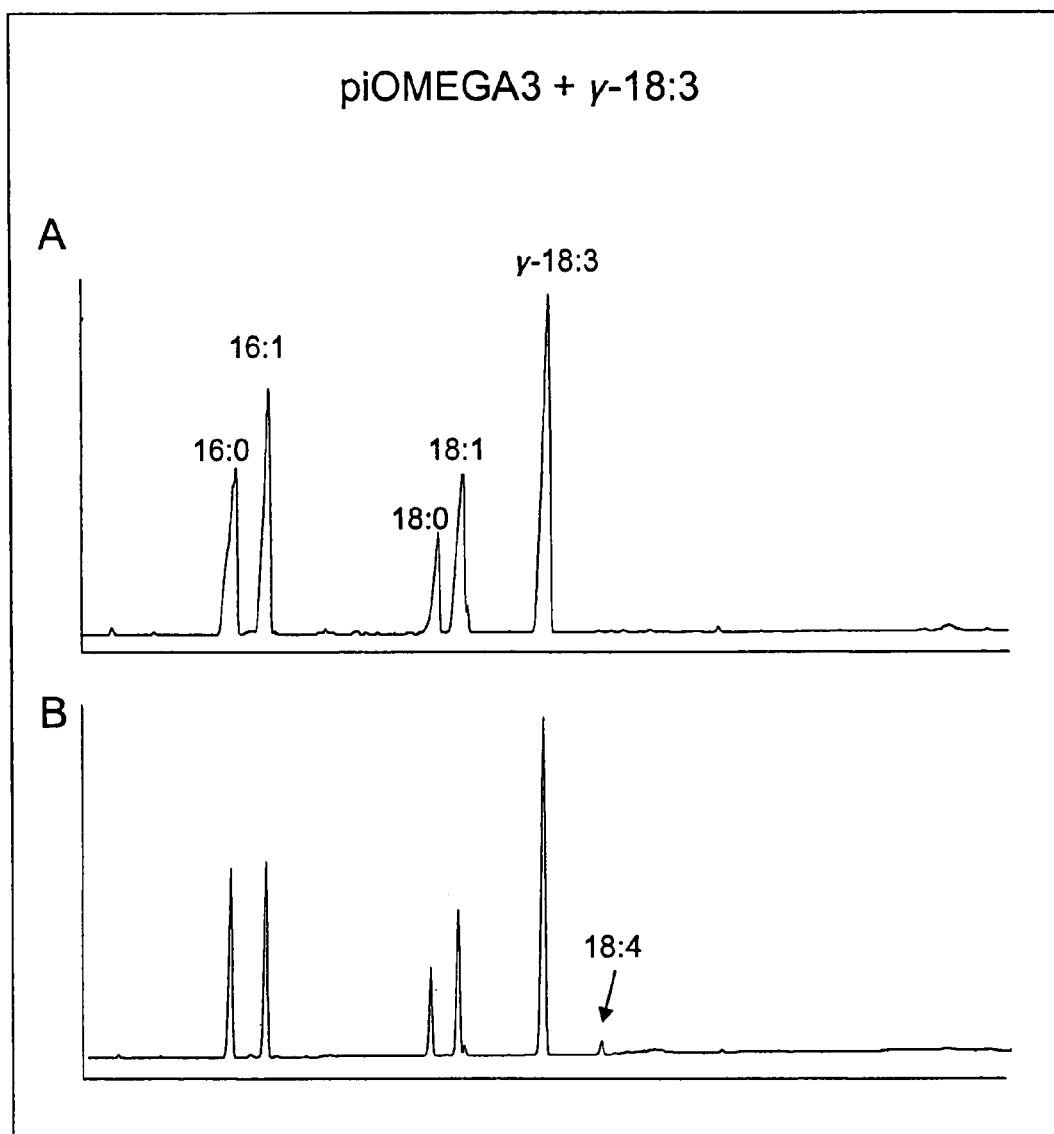




Figure 14: Desaturation of C20:2 ω6-fatty acid to give C20:3 ω3-fatty acid by Pi-omega3Des.

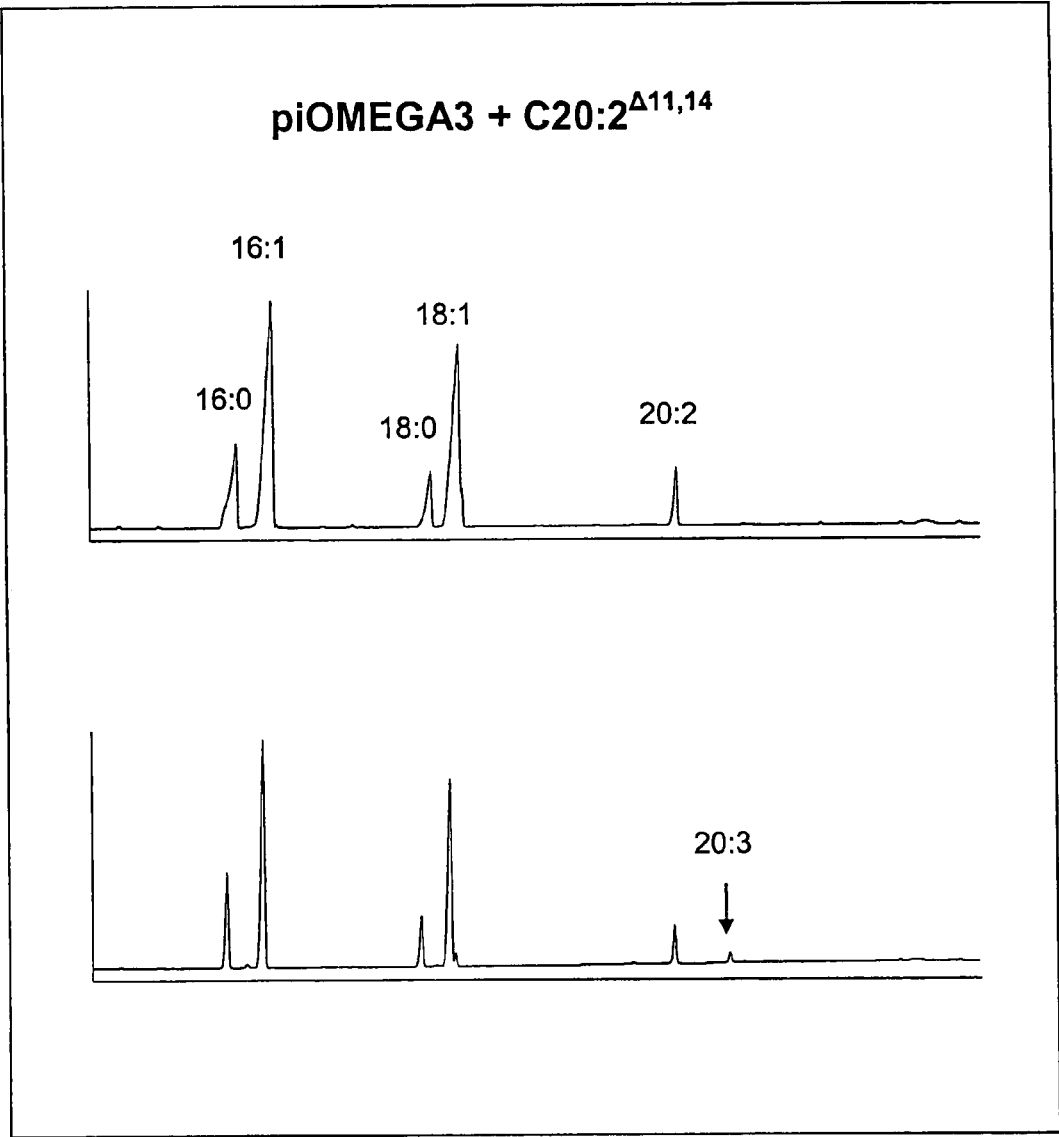


Figure 15: Desaturation of C20:3 ω6-fatty acid to give C20:4 ω3-fatty acid by Pi-omega3Des.

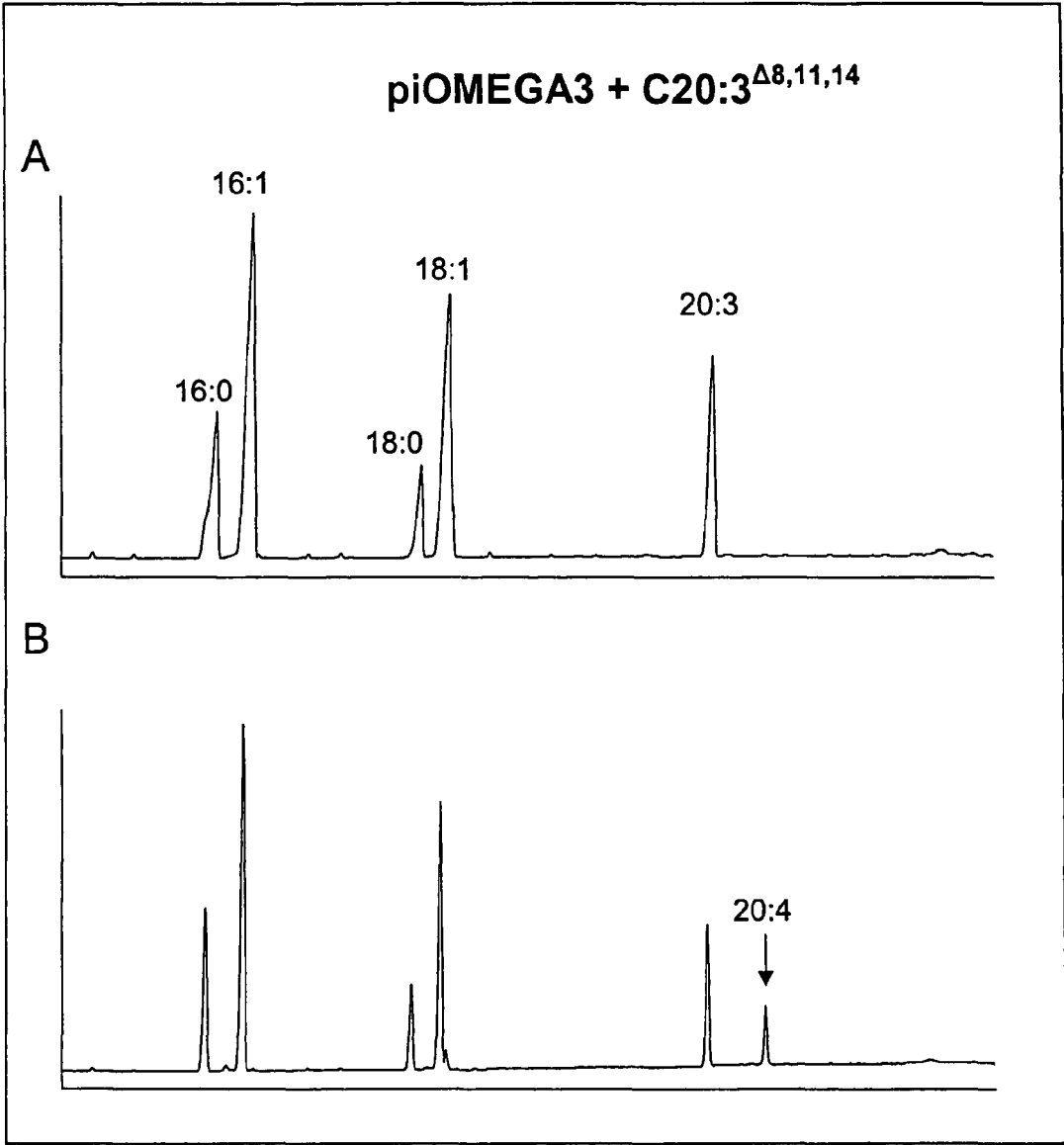


Figure 16: Desaturation of arachidonic acid (C20:4  $\omega$ 6-fatty acid) to give eicosapentaenoic acid (C20:5  $\omega$ 3-fatty acid) by Pi-omega3Des.

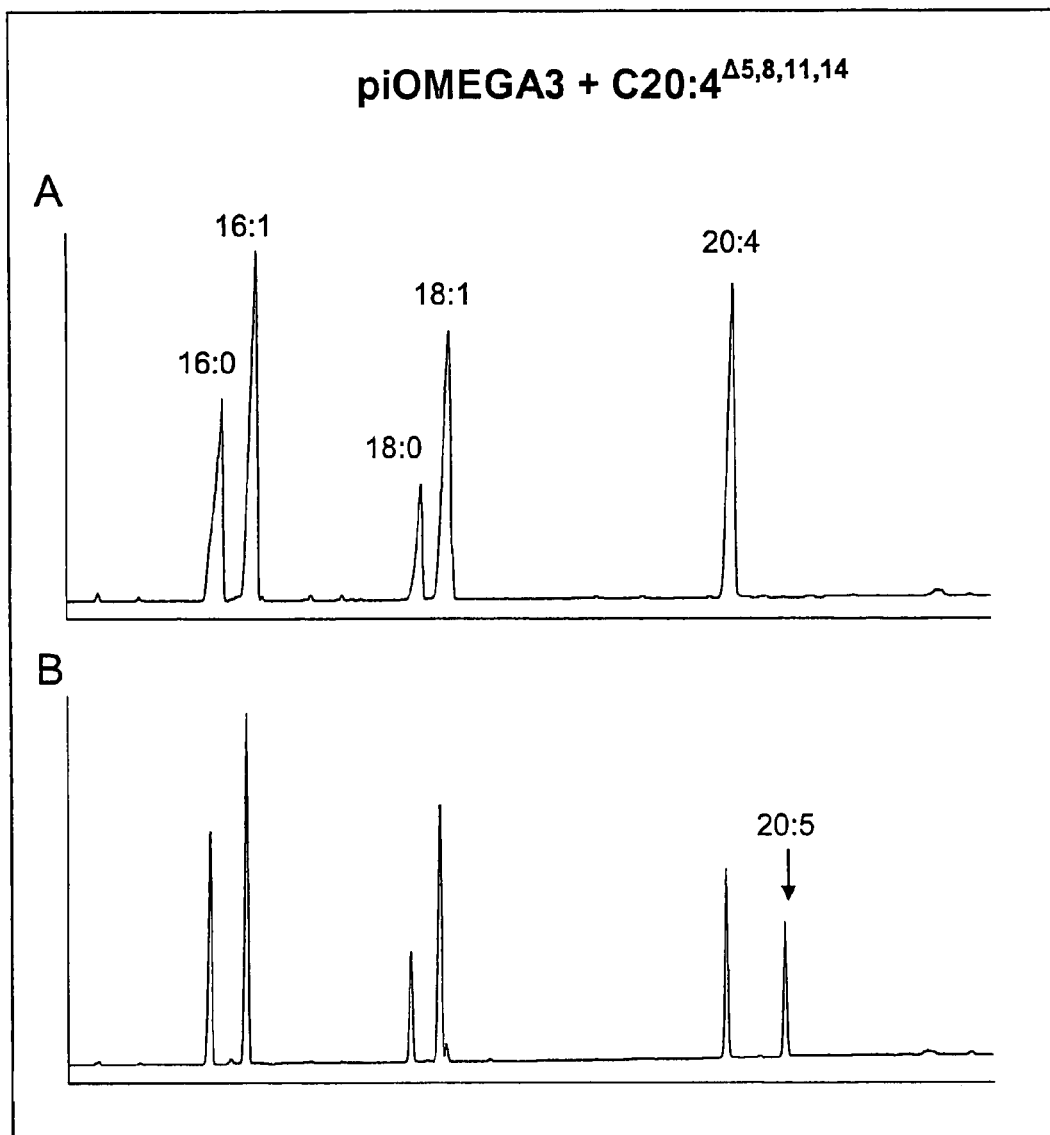


Figure 17: Desaturation of docosatetraenoic acid (C22:4 ω6-fatty acid) to give docosapentaenoic acid (C22:5 ω3-fatty acid) by Pi-omega3Des.

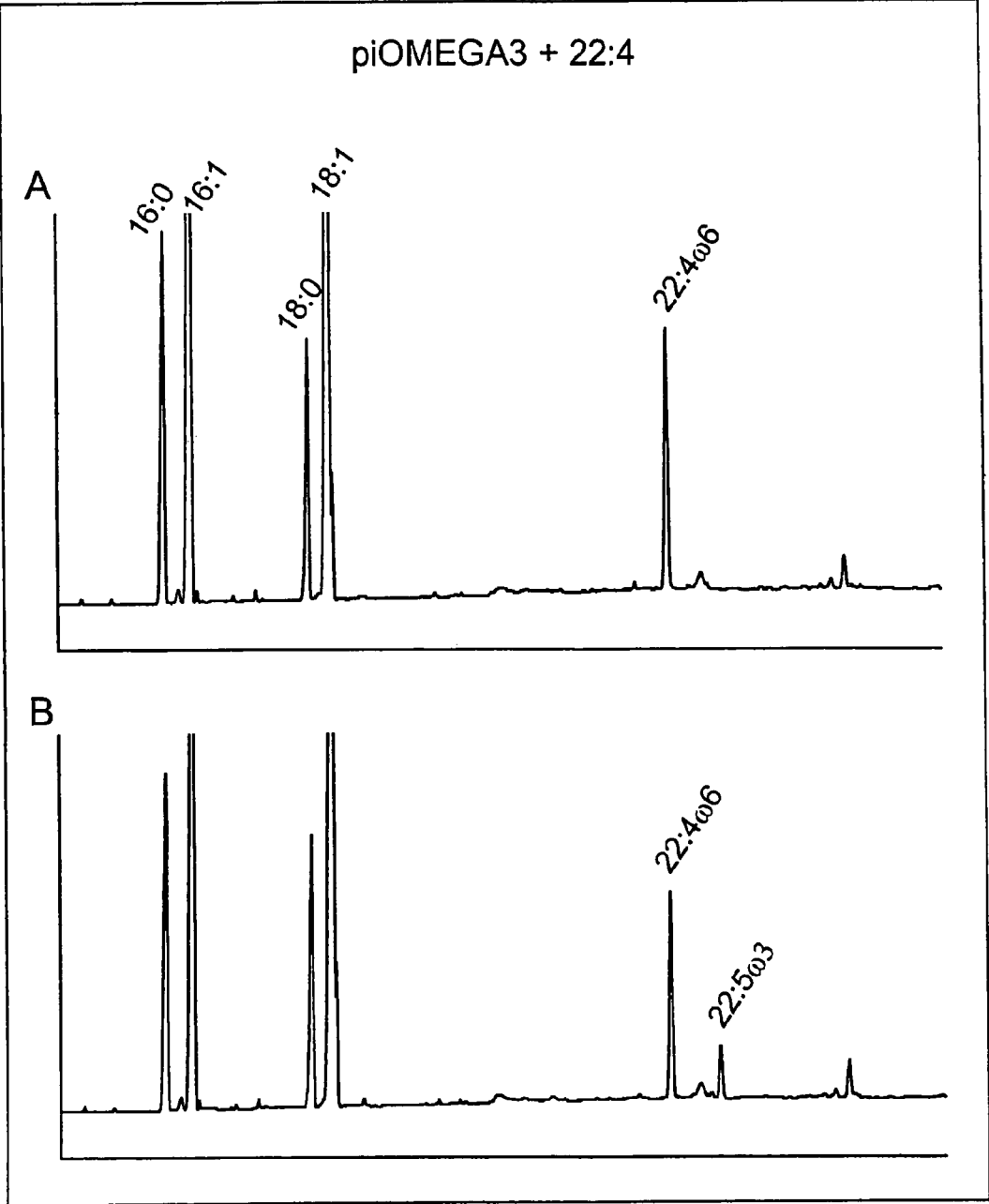


Figure 18: Substrate specificity of Pi-omega3Des with regard to different fatty acids

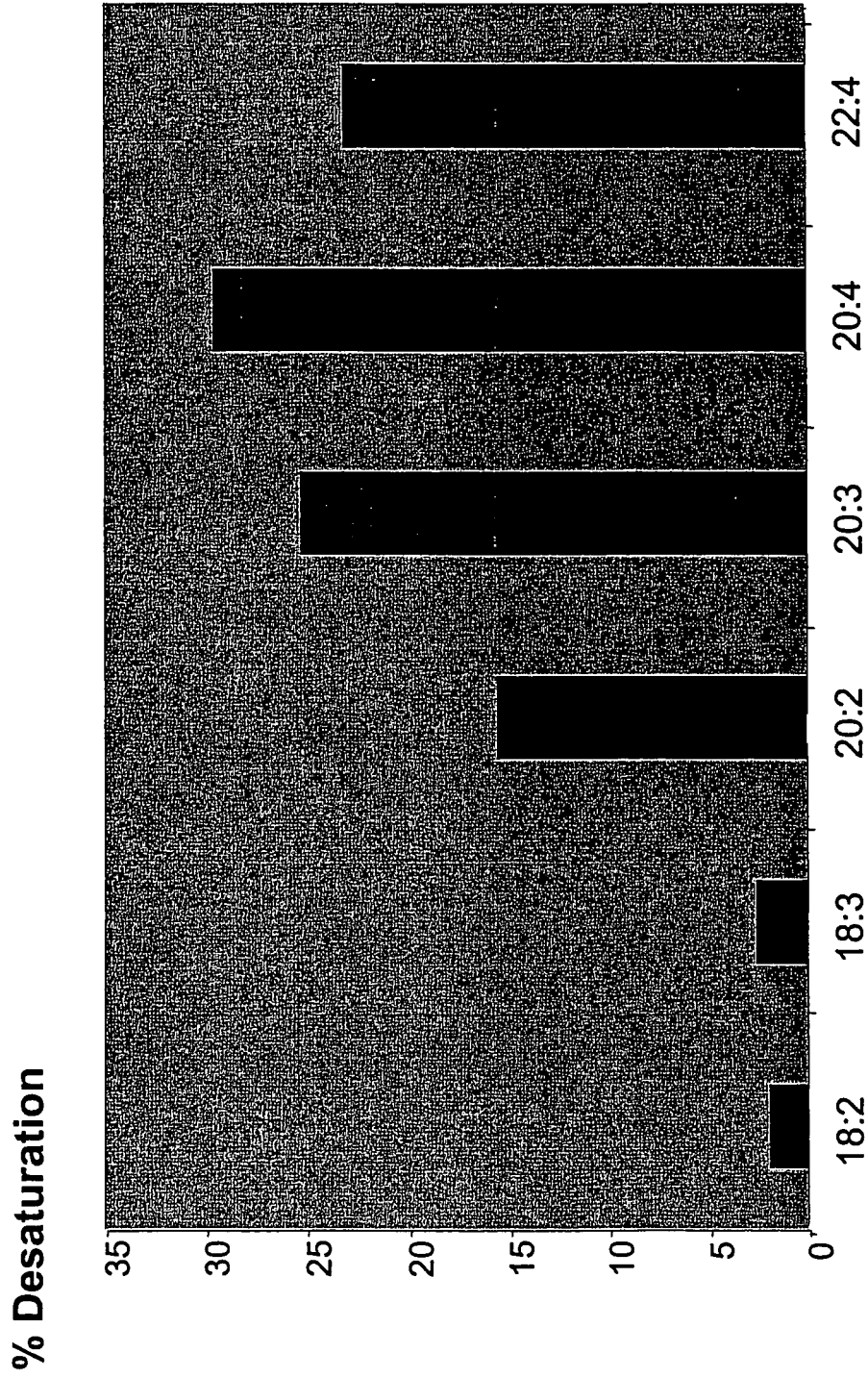


Figure 19: Desaturation of phospholipid-bound arachidonic acid to give EPA by Pi-Omega3Des

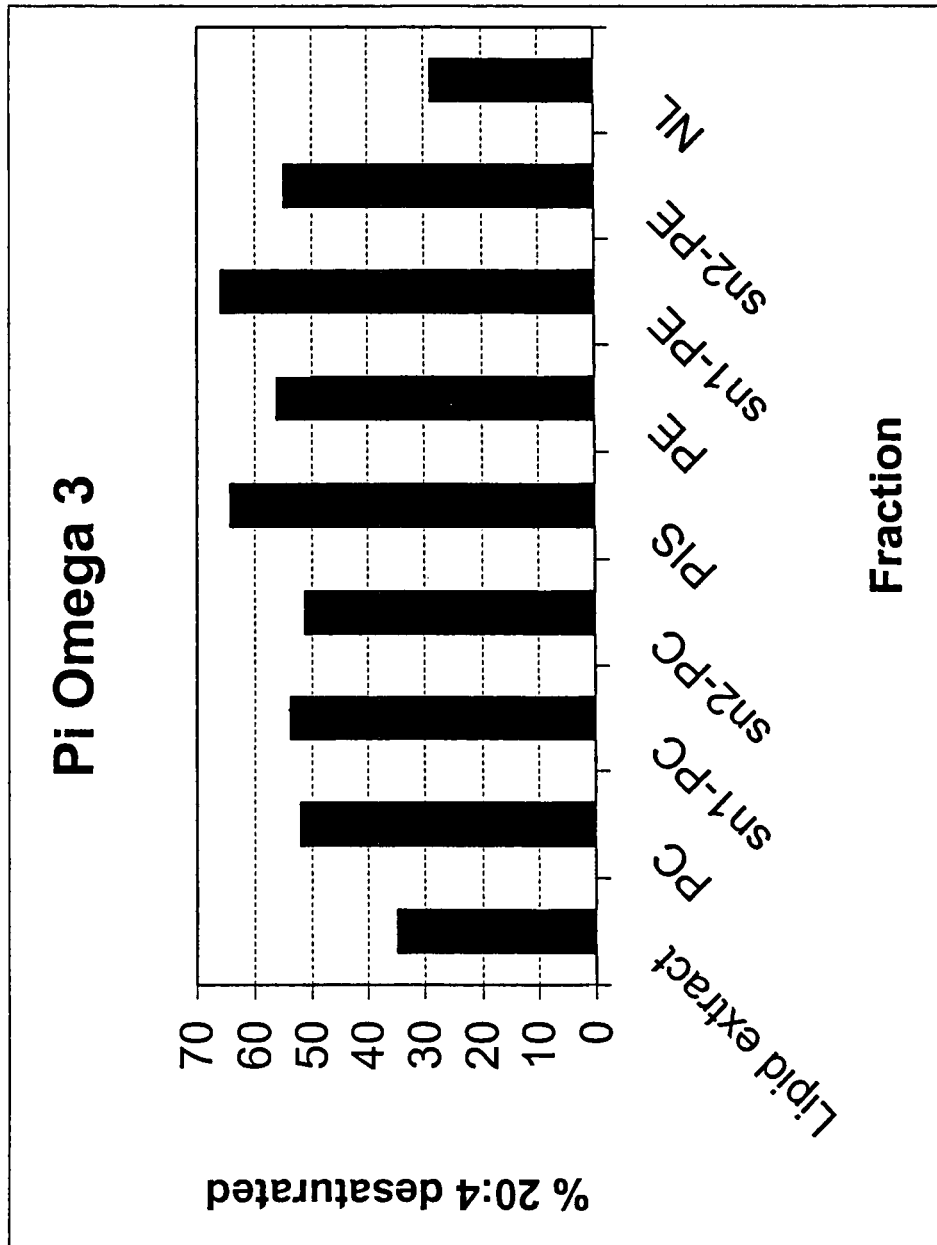
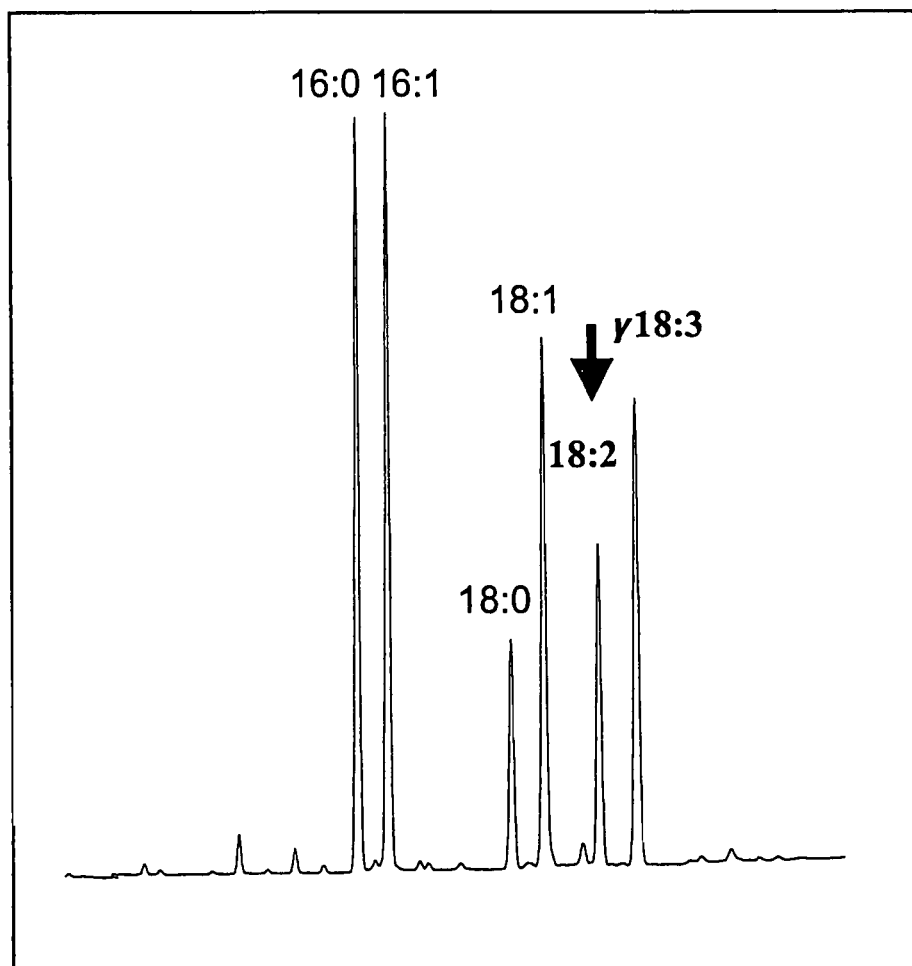


Figure 20: Conversion of linoleic acid (arrow) to give  $\gamma$ -linolenic acid ( $\gamma$ -18:3) by Ot-Des6.1.

Absorption mAU



Retention time

Figure 21: Conversion of linoleic acid and  $\alpha$ -linolenic acid (A and C), and reconstitution of the ARA and EPA synthetic pathways, respectively, in yeast (B and D) in the presence of OtD6.1.

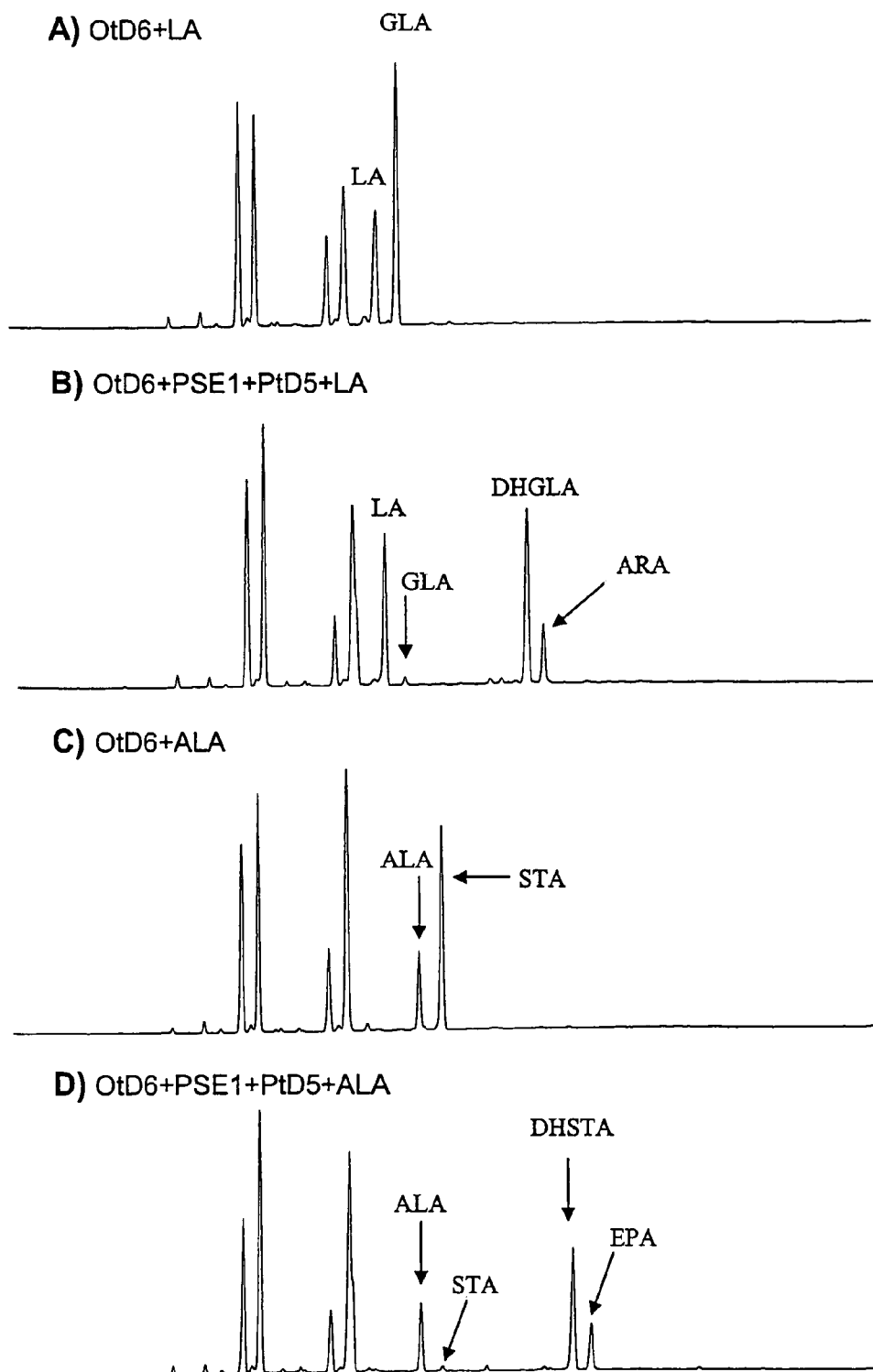




Figure 22: Expression of ELO(XI) in yeast

Absorption in mA

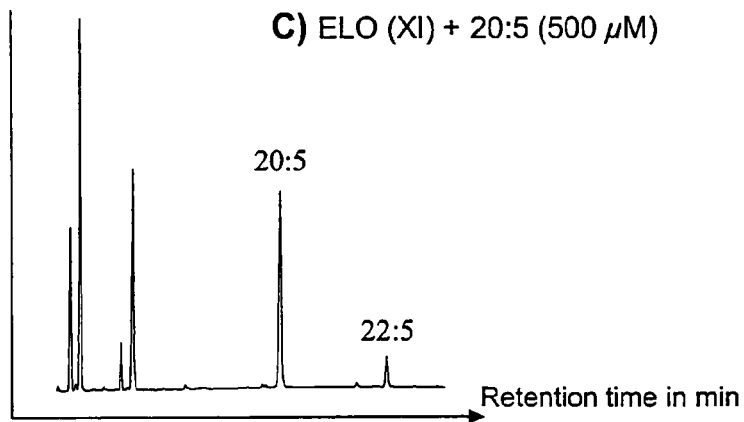
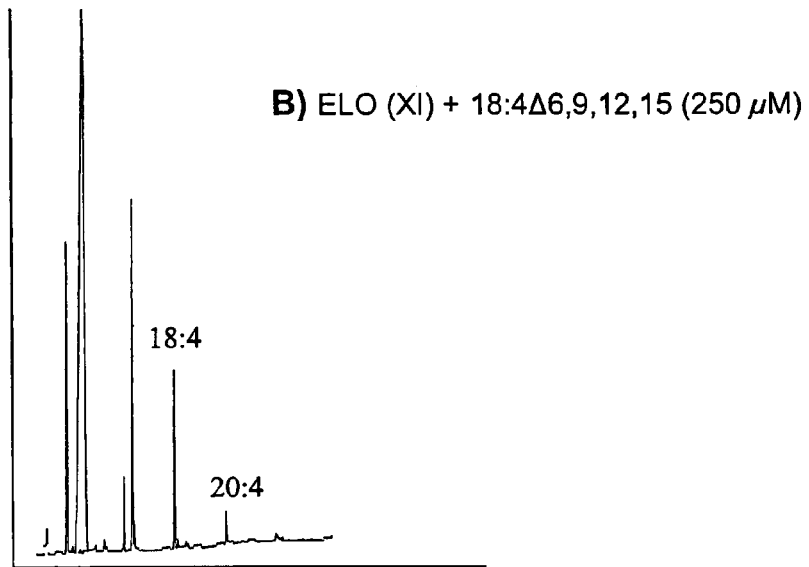
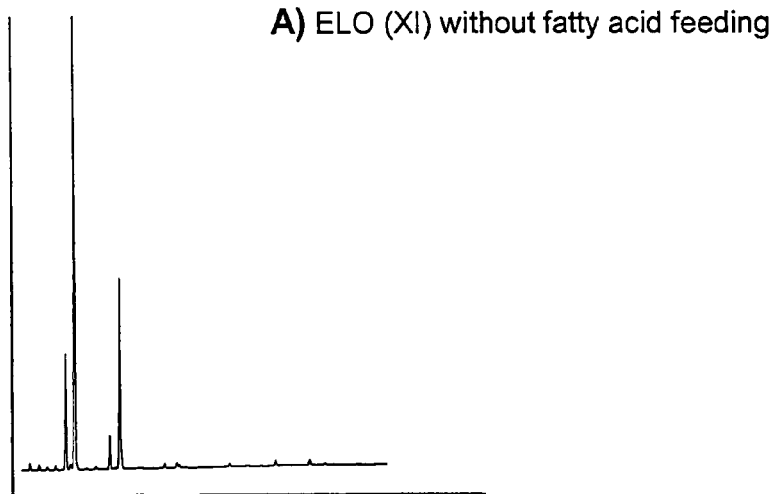


Figure 23:

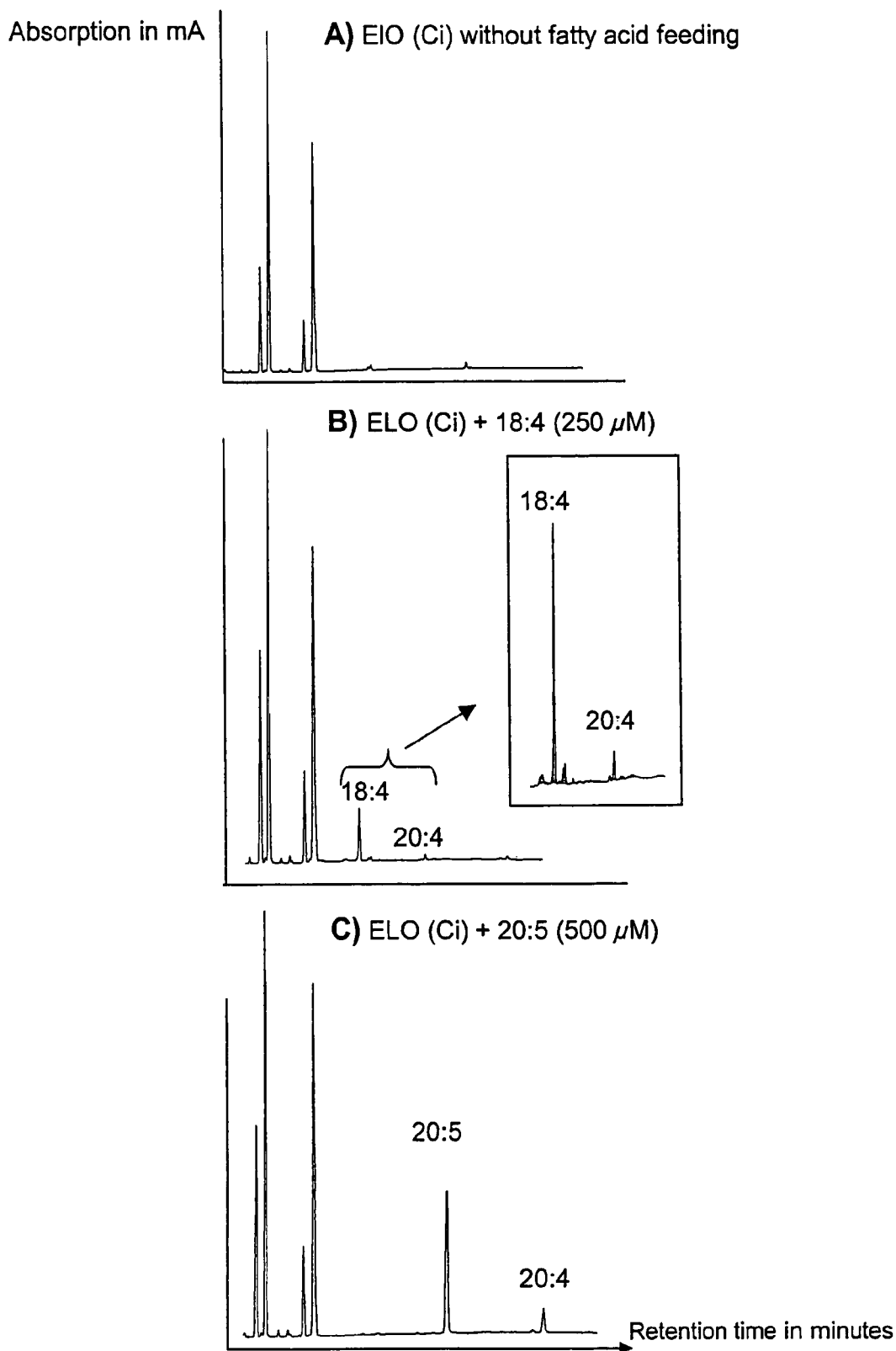


Figure 24: Elongation of eicosapentaenoic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:5 $\omega$ 3).

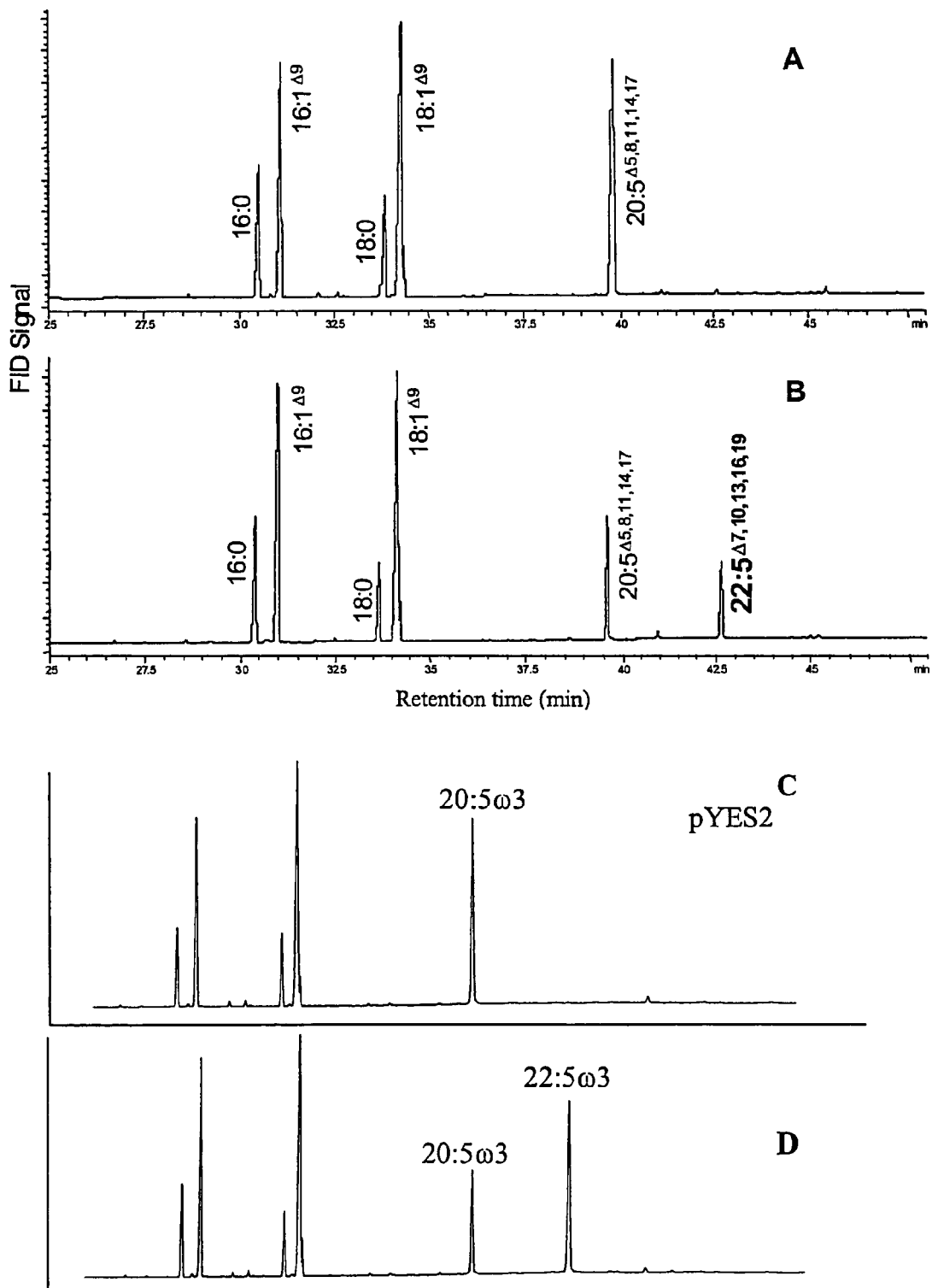


Figure 25: Elongation of arachidonic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:4 $\omega$ 6).

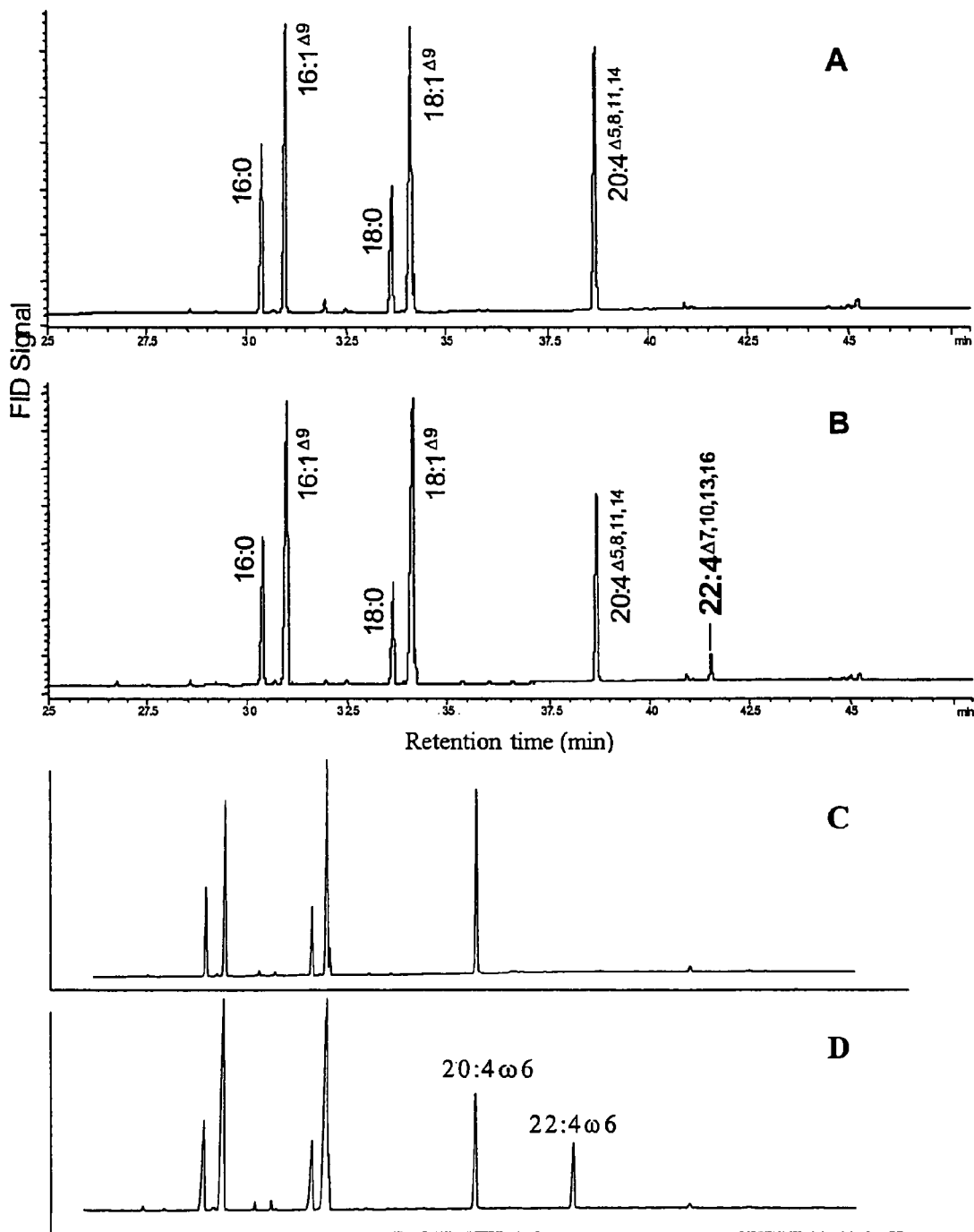


Figure 26: Elongation of 20:5n-3 by the elongases At3g06470.

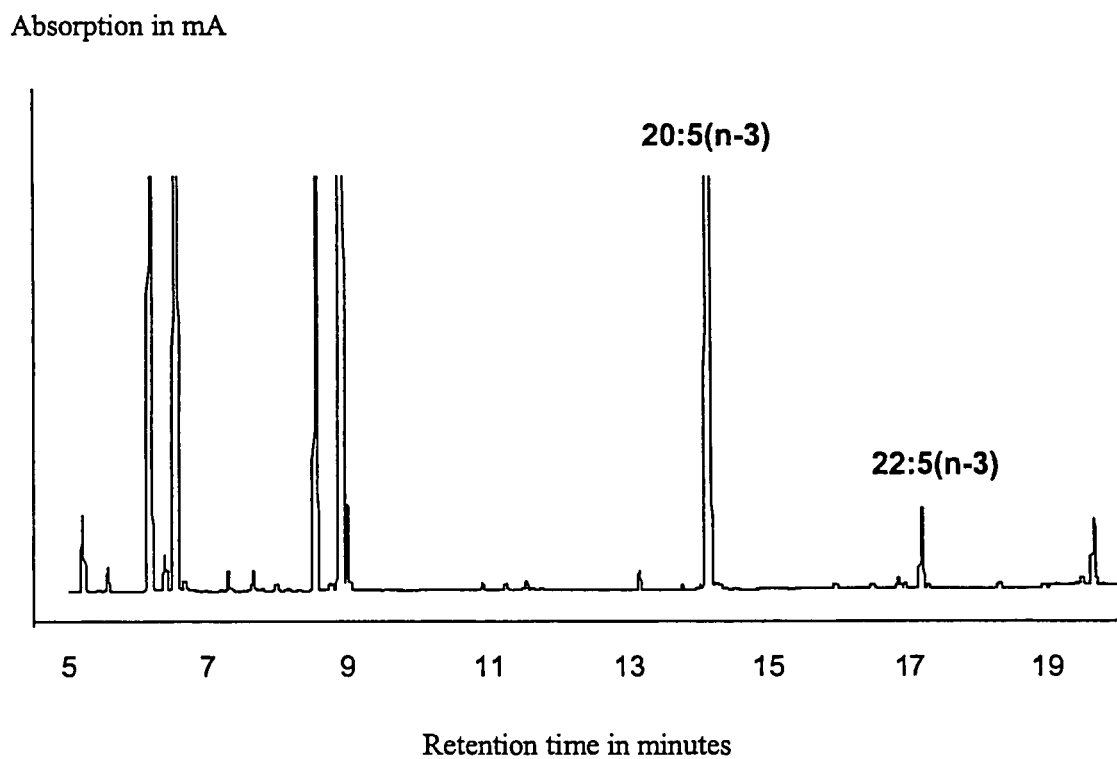


Figure 27: Substrate specificity of the *Xenopus* Elongase (A), *Ciona* Elongase (B) and *Oncorhynchus* Elongase (C)

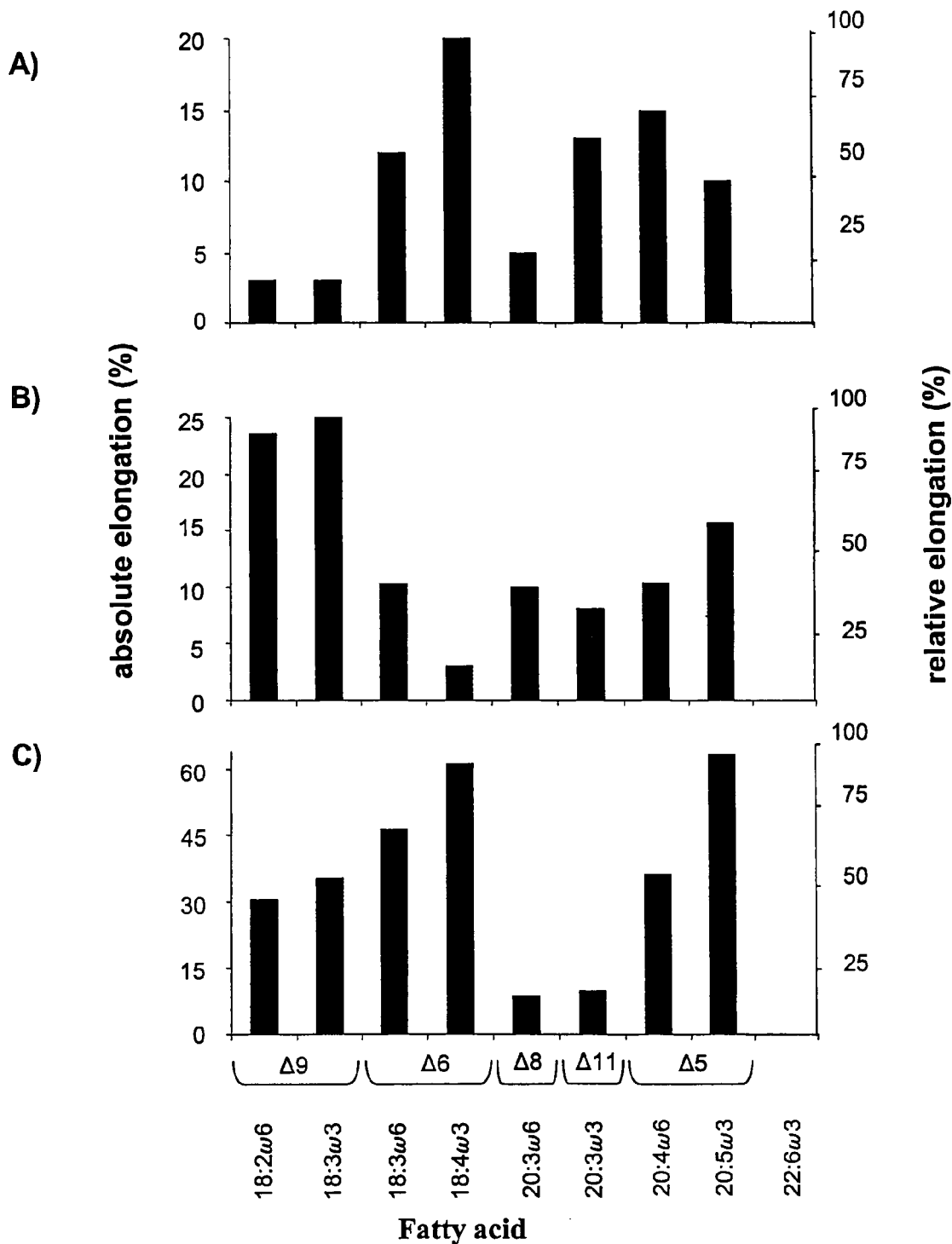


Figure 28: Substrate specificity of the *Ostreococcus*  $\Delta 5$ -elongase (A), the *Ostreococcus*  $\Delta 6$ -elongase (B), the *Thalassiosira*  $\Delta 5$ -elongase (C) and the *Thalassiosira* *Ostreococcus*  $\Delta 6$ -elongase (D)

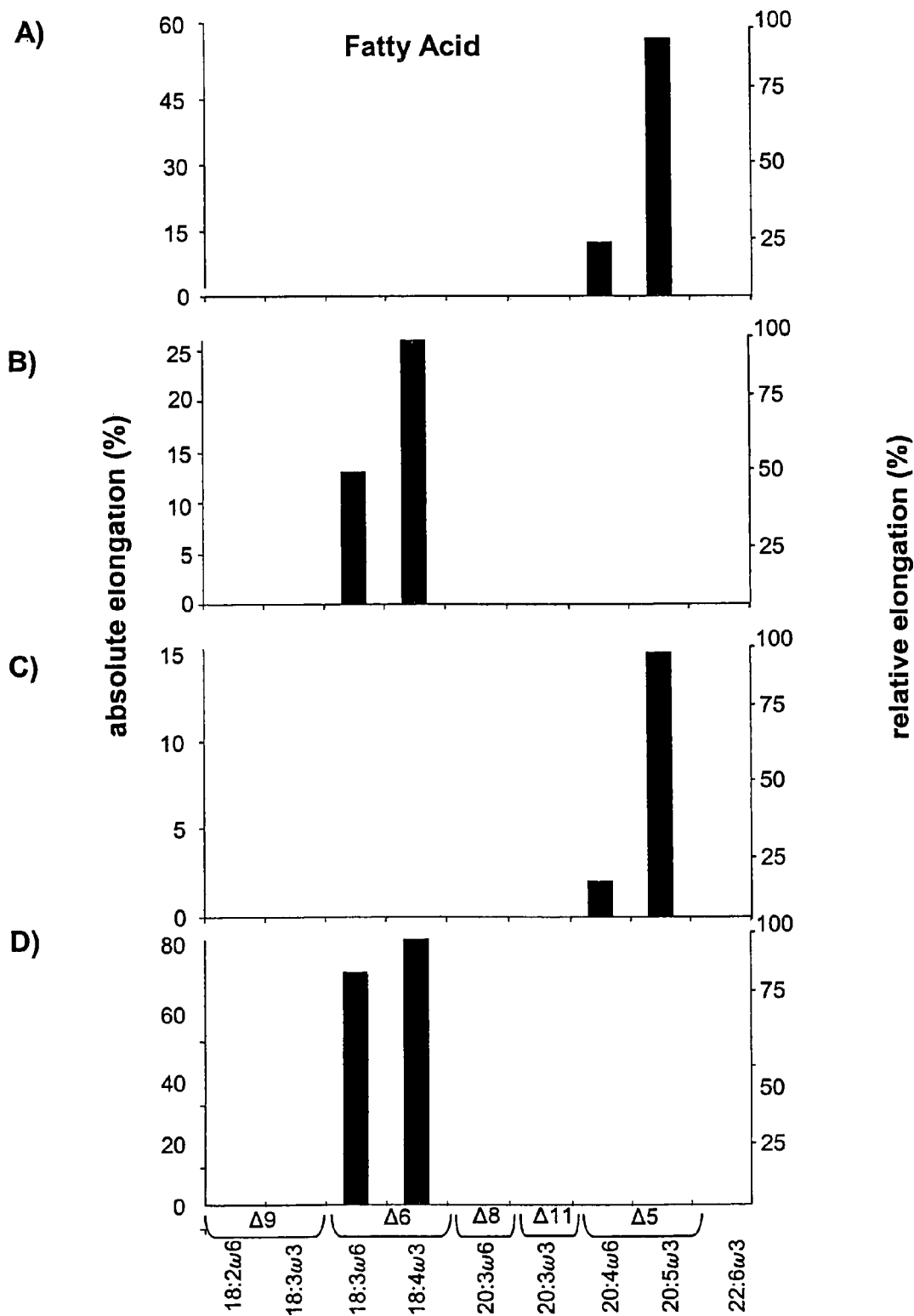


Figure 29: Expression of the *Phaeodactylum tricornutum*  $\Delta 6$ -elongase (PtELO6) in yeast. A) shows the elongation of the C18:3 <sup>$\Delta 6,9,12$</sup>  fatty acid and B) the elongation of the C18:3 <sup>$\Delta 6,9,12,15$</sup>  fatty acid

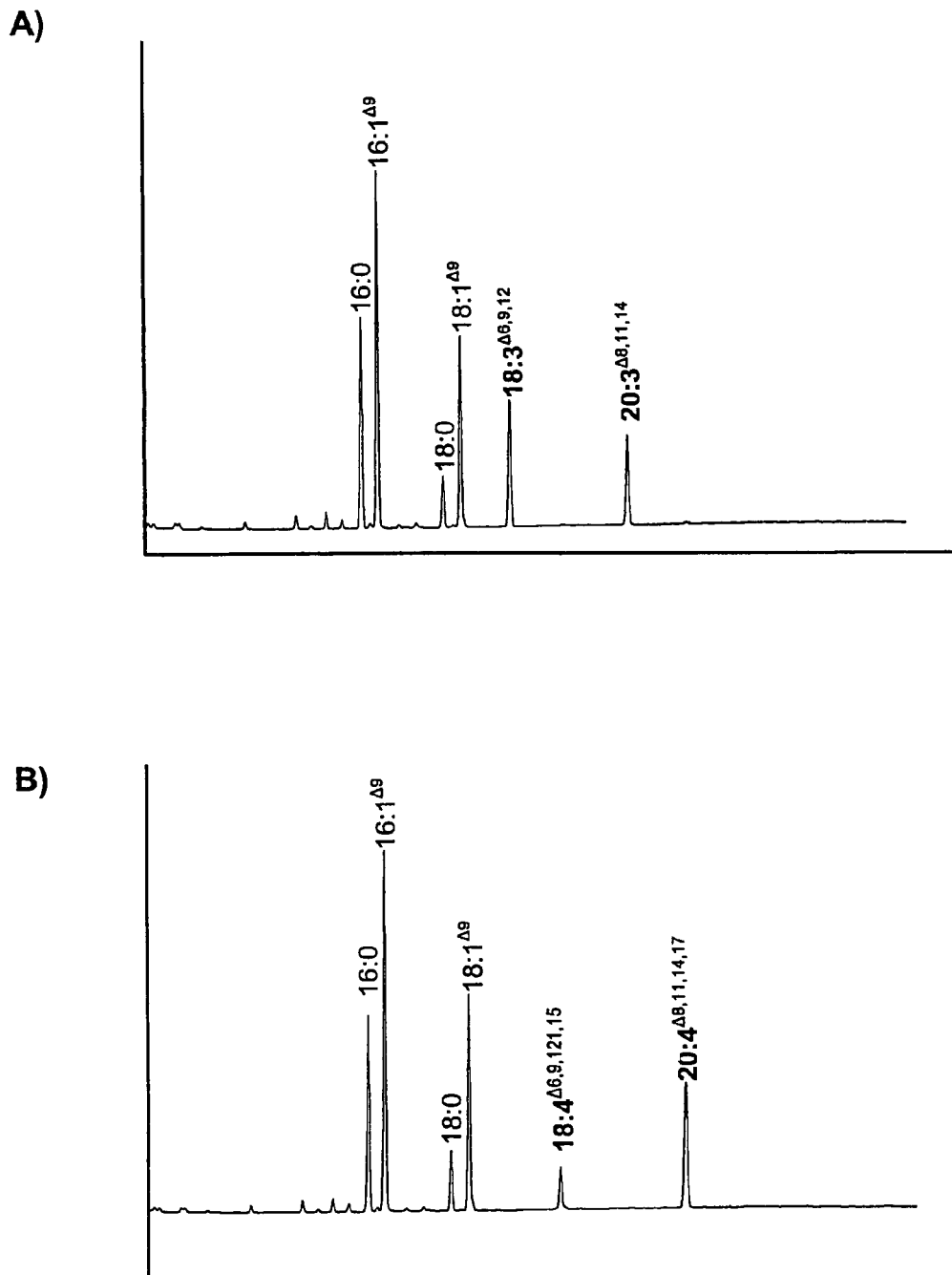




Figure 30: Figure 30 shows the substrate specificity of PtELO6 with regard to the substrates fed.

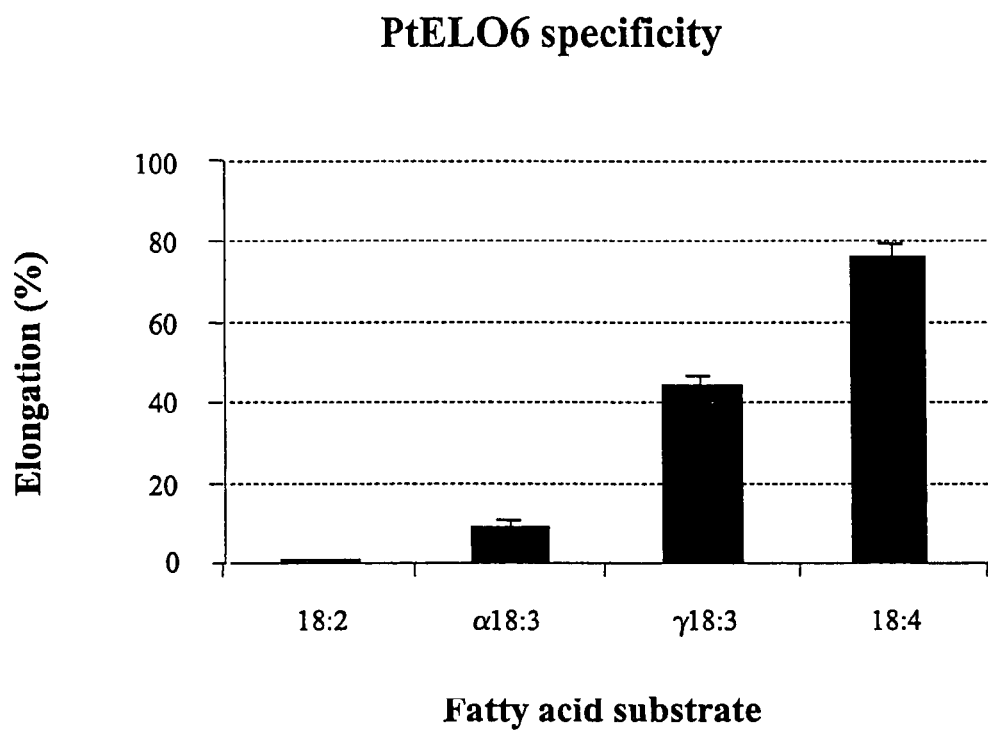


Figure 31: Gas-chromatographic analysis of the seed of a transgenic plant, transformed with pSUN-5G.

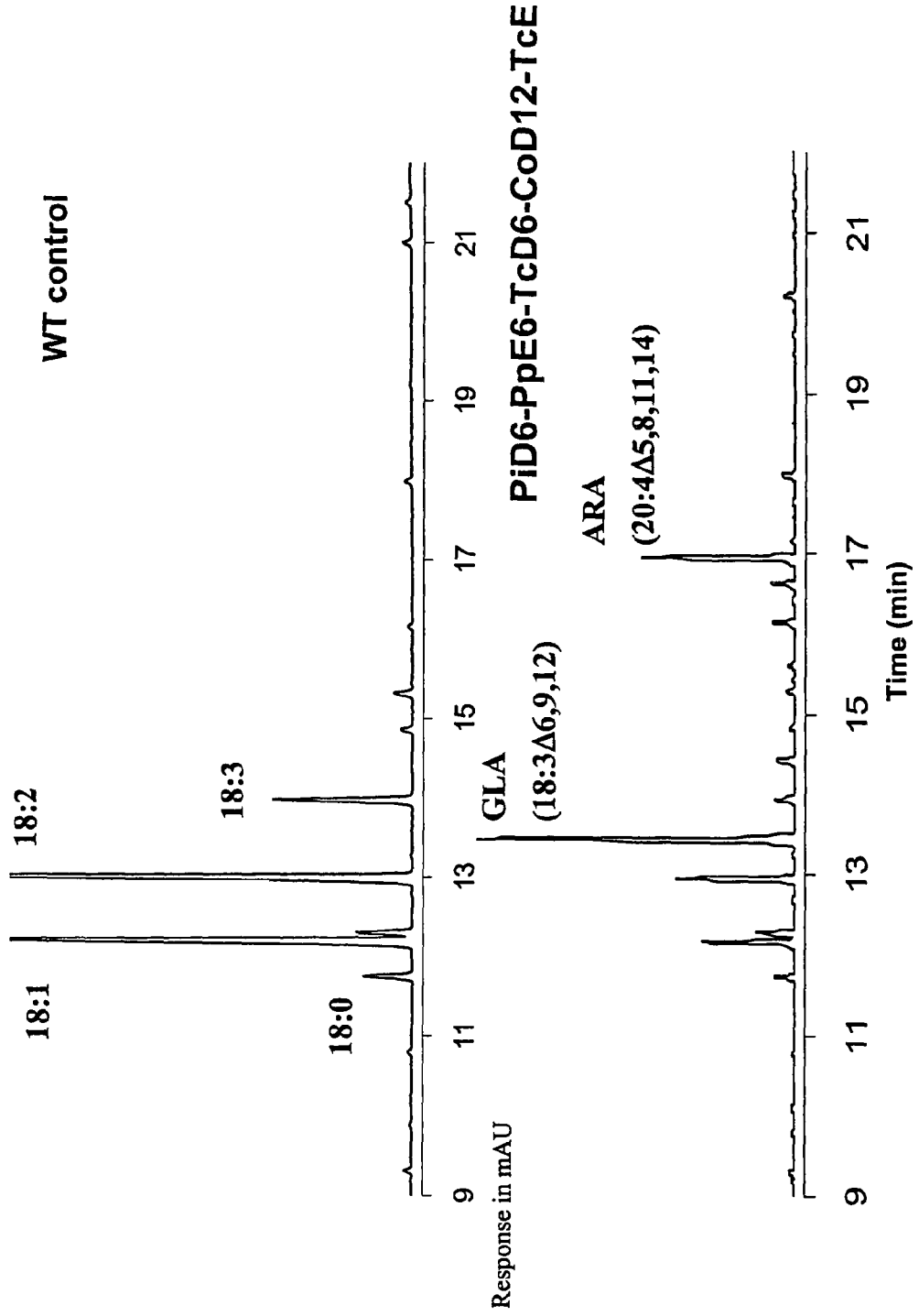


Figure 32: Gas-chromatographic analysis of the seed of a transgenic plant, transformed with pGPTV-D6Des(Pir)\_D5Des(Tc)\_D6Elo(PP)\_12Des(Co)

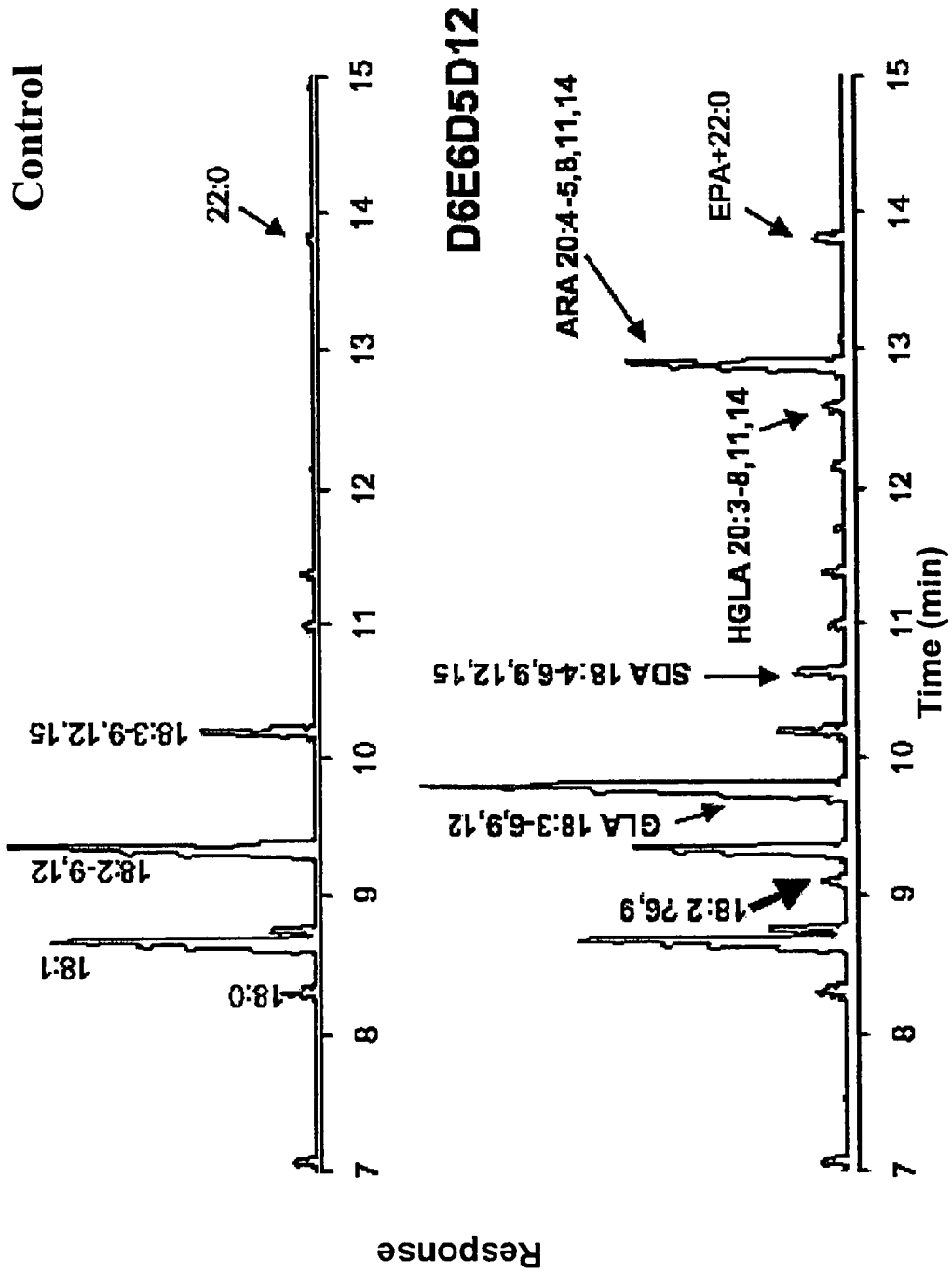
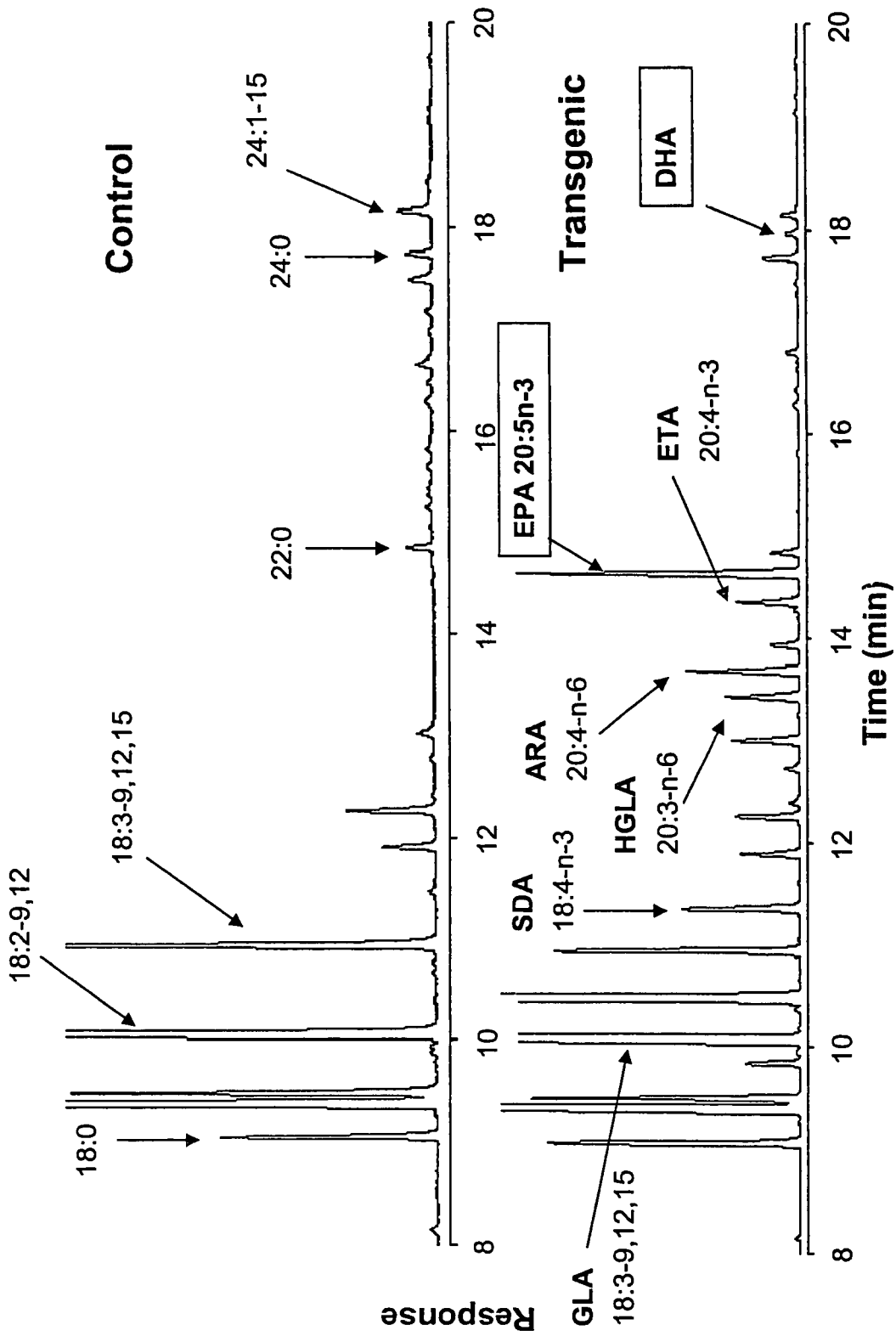


Figure 33: DHA in transgenic seeds of Brassica juncea. The plants were transformed with the construct pSUN-8G.



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## METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN TRANSGENIC PLANTS

### RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2005/001863 filed Feb. 23, 2005, and claims benefit of German application 10 2004 009 457.8 filed Feb. 27, 2004; German application 10 2004 012 370.5 filed Mar. 13, 2004; German application 10 2004 017 518.7 filed Apr. 8, 2004; German application 10 2004 024 014.0 filed May 14, 2004; PCT application PCT/EP2004/07957 filed Jun. 16, 2004; and German application 10 2004 062 543.3 filed Dec. 24, 2004.

### SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc, each containing: file name: "Sequence Listing-13987-00020-US", date recorded: May 9, 2007, size: 613 KB.

### FIELD OF THE INVENTION

The present invention relates to a process for the production of polyunsaturated fatty acids in the seed of transgenic plants by introducing, into the organism, nucleic acids which encode polypeptides with  $\omega$ 3-desaturase,  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 6-elongase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase and/or  $\Delta$ 4-desaturase activity, preferably polypeptides with  $\Delta$ 6-desaturase,  $\Delta$ 6-elongase and  $\Delta$ 5-desaturase activity.

The nucleic acid sequences are the sequences shown in SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 and SEQ ID NO: 201. Preferably, a further nucleic acid sequence which encodes a polypeptide with a  $\Delta$ 12-desaturase activity is additionally introduced into the plant, in addition to these nucleic acid sequences, and also expressed simultaneously. Especially preferably, this is the nucleic acid sequence shown in SEQ ID NO: 195.

These nucleic acid sequences can advantageously be expressed in the organism, if appropriate together with further nucleic acid sequences which encode polypeptides of the biosynthesis of the fatty acid or lipid metabolism. Especially advantageous are nucleic acid sequences which encode a  $\Delta$ 6-desaturase, a  $\Delta$ 5-desaturase,  $\Delta$ 4-desaturase,  $\Delta$ 12-desaturase and/or  $\Delta$ 6-elongase activity. These desaturases and elongases originate advantageously from *Thalassiosira*, *Euglena* or *Ostreococcus*. Furthermore, the invention relates to a process for the production of oils and/or triacylglycerides with an elevated content of long-chain polyunsaturated fatty acids.

In a preferred embodiment, the invention furthermore relates to a process for the production of arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid and to a process for the production of triglycerides with an elevated content of unsaturated fatty acids, in particular arachidonic acid, eicosapentaenoic acid and/or docosahexaenoic acid, in transgenic plants, advantageously in the seed of the transgenic plant. The invention relates to the generation of a transgenic plant with an elevated content of polyunsaturated fatty acids, in particular arachidonic acid, eicosapentaenoic acid and/or docosahexaenoic acid, as the result of the

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expression of the elongases and desaturases used in the process according to the invention.

The invention furthermore relates to recombinant nucleic acid molecules comprising the nucleic acid sequences which encode the polypeptides with  $\Delta$ 6-desaturase,  $\Delta$ 6-elongase,  $\Delta$ 5-desaturase and  $\Delta$ 5-elongase activity, either jointly or individually, and transgenic plants which comprise the abovementioned recombinant nucleic acid molecules.

A further part of the invention relates to oils, lipids and/or fatty acids which have been produced by the process according to the invention, and to their use. Moreover, the invention relates to unsaturated fatty acids and to triglycerides with an elevated content of unsaturated fatty acids and to their use.

### DESCRIPTION OF RELATED ART

Lipid synthesis can be divided into two sections: the synthesis of fatty acids and their binding to sn-glycerol-3-phosphate, and the addition or modification of a polar head group. Usual lipids which are used in membranes comprise phospholipids, glycolipids, sphingolipids and phosphoglycerides. Fatty acid synthesis starts with the conversion of acetyl-CoA into malonyl-CoA by acetyl-CoA carboxylase or into acetyl-ACP by acetyl transacylase. After condensation reaction, these two product molecules together form acetoacetyl-ACP, which is converted via a series of condensation, reduction and dehydration reactions so that a saturated fatty acid molecule with the desired chain length is obtained. The production of the unsaturated fatty acids from these molecules is catalyzed by specific desaturases, either aerobically by means of molecular oxygen or anaerobically (regarding the fatty acid synthesis in microorganisms, see F. C. Neidhardt et al. (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 612-636 and references cited therein; Lengeler et al. (Ed.) (1999) *Biology of Prokaryotes*. Thieme: Stuttgart, New York, and the references therein, and Magnuson, K., et al. (1993) *Microbiological Reviews* 57:522-542 and the references therein). To undergo the further elongation steps, the resulting phospholipid-bound fatty acids must be returned to the fatty acid CoA ester pool. This is made possibly by acyl-CoA:lysophospholipid acyltransferases. Moreover, these enzymes are capable of transferring the elongated fatty acids from the CoA esters back to the phospholipids. If appropriate, this reaction sequence can be followed repeatedly.

Furthermore, fatty acids must subsequently be transported to various modification sites and incorporated into the triacylglycerol storage lipid. A further important step during lipid synthesis is the transfer of fatty acids to the polar head groups, for example by glycerol fatty acid acyltransferase (see Frentzen, 1998, *Lipid*, 100(4-5): 161-166).

With regard to publications on the biosynthesis of fatty acids in plants, desaturation, the lipid metabolism and the membrane transport of lipidic compounds, beta-oxidation, the modification of fatty acids and cofactors and the storage and assembly of triacylglycerol, including the references cited therein, see the following papers: Kinney, 1997, *Genetic Engineering*, Ed.: J K Setlow, 19:149-166; Ohlrogge and Browse, 1995, *Plant Cell* 7:957-970; Shanklin and Cahoon, 1998, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:611-641; Voelker, 1996, *Genetic Engineering*, Ed.: J K Setlow, 18:111-13; Gerhardt, 1992, *Prog. Lipid R.* 31:397-417; Gühnemann-Schäfer & Kindl, 1995, *Biochim. Biophys. Acta* 1256:181-186; Kunau et al., 1995, *Prog. Lipid Res.* 34:267-342; Stymne et al., 1993, in: *Biochemistry and Molecular Biology of Membrane and Storage Lipids of*

Plants, Eds.: Murata and Somerville, Rockville, American Society of Plant Physiologists, 150-158, Murphy & Ross 1998, Plant Journal. 13(1): 1-16.

In the text which follows, polyunsaturated fatty acids are referred to as PUFA, PUFAs, LCPUFA or LCPUFAs (poly unsaturated fatty acids, PUFA, long chain poly unsaturated fatty acids, LCPUFA).

Fatty acids and triacylglycerides have a multiplicity of applications in the food industry, in animal nutrition, in cosmetics and 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 and linolenic acid are essential for mammals since they cannot be produced by the latter. This is why polyunsaturated  $\omega$ 3-fatty acids and  $\omega$ 6-fatty acids are an important constituent of human and animal food. Thus, for example, lipids with unsaturated fatty acids, specifically with polyunsaturated fatty acids, are preferred in human nutrition. The polyunsaturated  $\omega$ 3-fatty acids are supposed to have a positive effect on the cholesterol level in the blood and thus on the prevention of heart disease. The risk of heart disease, strokes or hypertension can be reduced markedly by adding these  $\omega$ 3-fatty acids to the food (Shimikawa 2001, World Rev. Nutr. Diet. 88, 100-108).

$\omega$ 3-fatty acids also have a positive effect on inflammatory, specifically on chronically inflammatory, processes in association with immunological diseases such as rheumatoid arthritis (Calder 2002, Proc. Nutr. Soc. 61, 345-358; Cleland and James 2000, J. Rheumatol. 27, 2305-2307). 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 in connection with these rheumatological diseases.

$\omega$ 3- and  $\omega$ 6-fatty acids are precursors of tissue hormones, known as eicosanoids, such as the prostaglandins, which are derived from dihomono- $\gamma$ -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 the  $\omega$ 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.

Polyunsaturated long-chain  $\omega$ 3-fatty acids such as eicosapentaenoic acid (=EPA, C20:5 <sup>$\Delta$ 5,8,11,14,17</sup>) or docosahexaenoic acid (=DHA, C22:6 <sup>$\Delta$ 4,7,10,13,16,19</sup>) are important components of human nutrition owing to their various roles in health aspects, including the development of the child brain, the functionality of the eyes, the synthesis of hormones and other signal substances, and the prevention of cardiovascular disorders, cancer and diabetes (Poulos, A Lipids 30:1-14, 1995; Horrocks, L A and Yeo Y K Pharmacol Res 40:211-225, 1999). There is therefore a demand for the production of polyunsaturated long-chain fatty acids.

Owing to the present-day composition of human food, an addition of polyunsaturated  $\omega$ 3-fatty acids, which are preferentially found in fish oils, to the food is particularly important. Thus, for example, polyunsaturated fatty acids such as docosahexaenoic acid (=DHA, C22:6 <sup>$\Delta$ 4,7,10,13,16,19</sup>) or eicosapentaenoic acid (=EPA, C20:5 <sup>$\Delta$ 5,8,11,14,17</sup>) are added to infant formula to improve the nutritional value. The unsaturated fatty acid DHA is supposed to have a positive effect on the development and maintenance of brain function. There is therefore a demand for the production of polyunsaturated long-chain fatty acids.

The various fatty acids and triglycerides are mainly obtained from microorganisms such as *Mortierella* or *Schizochytrium* or from oil-producing plants such as soybeans, oilseed rape, algae such as *Cryptocodinium* or *Phaeodactylum* and others, being obtained, as a rule, in the form, of their triacylglycerides (=triglycerides=triglycerols). However, they can also be obtained from animals, for example, fish. The free fatty acids are advantageously prepared by hydrolysis. Very long-chain polyunsaturated fatty acids such as DHA, EPA, arachidonic acid (ARA, C20:4 <sup>$\Delta$ 5,8,11,14</sup>), dihomono- $\gamma$ -linolenic acid (C20:3 <sup>$\Delta$ 8,11,14</sup>) or docosapentaenoic acid (DPA, C22:5 <sup>$\Delta$ 7,10,13,16,19</sup>) are, however, not synthesized in oil crops such as oilseed rape, soybeans, sunflowers and 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.

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.  $\omega$ 3-fatty acids such as arachidonic acid tend to have an adverse effect on these disorders in connection with these rheumatic diseases on account of our usual dietary intake.

Owing to their positive characteristics, 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 describe 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, U.S. Pat. No. 5,614,393, U.S. Pat. No. 5,614,393 WO 96/21022, WO 00/21557 and WO 99/27111. The application of this enzyme for the production of fatty acids in transgenic organisms is described in WO 98/46763, WO 98/46764 and WO 98/46765. The expression of various desaturases is 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

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contents of unsaturated fatty acids/lipids such as, for example,  $\gamma$ -linolenic acid and stearidonic acid.

There have been a 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 (C22:1) and for the synthesis of very long-chain fatty acids for the formation of waxes in plants (C<sub>28</sub>-C<sub>32</sub>). The synthesis of arachidonic acid and EPA is described, for example, in WO 01/59128, WO 00/12720, WO 02/077213 and WO 02/08401. The synthesis of polyunsaturated C24-fatty acids is described, for example, in Tvrdik et al. 2000, J. Cell Biol. 149:707-718 or WO 02/44320.

Especially suitable microorganisms for the production of PUFAs are microorganisms such as microalgae such as *Phaeodactylum tricornutum*, *Porphyridium* species, *Thraustochytrium* species, *Schizochytrium* species or *Cryptocodinium* species, ciliates such as *Stylonychia* or *Colpidium*, fungi 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, which is why as described above, recombinant methods are preferred. 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; where, as a rule, they are generally obtained as fatty acid mixtures, depending on the microorganisms used.

Higher plants comprise polyunsaturated fatty acids such as linoleic acid (C18:2) and linolenic acid (C18:3). 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 the Vegetable Oils]. Technique & Documentation—Lavoisier, 1995. ISBN: 2-7430-0009-0). However, the production of LCPUFAs in higher plants, preferably in oilseed crops such as oilseed rape, linseed, sunflowers 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 oilseed crops, genes which encode enzymes of the LCPUFA biosynthesis via recombinant methods and to express them therein. These genes encode for example  $\Delta 6$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases or  $\Delta 4$ -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*. A variety of synthetic pathways is being discussed for the synthesis of arachidonic acid, eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) (FIG. 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).

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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 C24, followed by a further  $\Delta 6$ -desaturation and finally  $\beta$ -oxidation to give the C<sub>22</sub> chain length. Thus what is known as Sprecher pathway (see FIG. 1) is, however, not suitable for the production in plants and microorganisms since the regulatory mechanisms are not known.

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).

The starting material for the  $\omega 6$ -metabolic pathway is the fatty acid linoleic acid (18:2<sup>A9,12</sup>) while the  $\omega 3$ -pathway proceeds via linolenic acid (18:3<sup>A9,12,15</sup>). 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).

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<sup>A5,8,11,14</sup>), an  $\omega 6$ -fatty acid and the two  $\omega 3$ -fatty acids eicosapentaenoic acid (=EPA, 20:5<sup>A5,8,11,14,17</sup>) and docosahexaenoic acid (DHA, 22:6<sup>A4,7,10,13,17,19</sup>) 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), inflammations (Calder 2002, Proc. Nutr. Soc. 61, 345-358) and arthritis (Cleland and James 2000, J. Rheumatol. 27, 2305-2307).

From the angle of nutritional physiology, it is therefore advantageous to achieve a shift between the  $\omega 6$ -synthetic pathway and the  $\omega 3$ -synthetic pathway (see FIG. 1) so that more  $\omega 3$ -fatty acids are produced. The enzymatic activities of various  $\omega 3$ -desaturases which desaturate C<sub>18:2</sub>, C<sub>22:4</sub> or C<sub>22:5</sub>-fatty acids have been described in the literature (see FIG. 1). However, none of the desaturases whose biochemistry has been described converts a broad range of substrates of the  $\omega 6$ -synthetic pathway into the corresponding fatty acids of the  $\omega 3$ -synthetic pathway.

The elongation of fatty acids, by elongases, by 2 or 4 C atoms is of crucial importance for the production of C<sub>20</sub>- and C<sub>22</sub>-PUFAs, respectively. This process proceeds via 4 steps. The first step is the condensation of malonyl-CoA onto 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).

No specific elongase has been described to date for the production of DHA (C22:6 n-3) in organisms which do not naturally produce this fatty acid. Only elongases which provide C<sub>20</sub>- or C<sub>24</sub>-fatty acids have been described to date. A  $\Delta 5$ -elongase activity has not been described to date.

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) or in WO 2004/071467. However, these plants produce LCPUFAs in amounts which require further optimization for processing the oils which are present in the plants. Thus, ARA content in the plants described in DE-A-102 19 203 only amounts to 0.4 to 2% and the EPA content only to 0.5 to 1%, in each case based on the total lipid content of the plants. WO 2004/071467 discloses higher contents of polyunsaturated C<sub>20</sub>- and C<sub>22</sub>-fatty acids such as ARA, EPA or DHA. However, the process disclosed has a series of grave disadvantages. It seems that DHA cannot be detected at all in the seeds in the process disclosed. To produce PUFAs, soybean is less suitable, owing to its low oil content of approximately only 20% by weight. Soybean is an advantageous protein source and is therefore grown on a large scale. However, the oil content of soybeans is rather low. Moreover, the dihomo- $\gamma$ -linolenic acid (=DGHL or HGLA) content obtained in the production process is much too high. HGLA is hardly detectable in fish oils or algal oils or microbial oils. A further disadvantage is that the plants disclosed in WO 2004/071467 were generated by cotransformation, which leads to the segregation of the characteristics in the subsequent generations, and thus to an increased selection effort.

To make possible the fortification of food and/or of feed with these polyunsaturated fatty acids, there is therefore a great need for a simple, inexpensive process for the production of these polyunsaturated fatty acids in plant systems, especially in the seed of transgenic plants.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows various synthetic pathways for the biosynthesis of DHA (docosahexaenoic acid).

FIG. 2 shows substrate specificity of the 5-elongase (SEQ ID NO: 53) with regard to different fatty acids.

FIG. 3 shows reconstitution of DHA biosynthesis in yeast starting from 20:5 $\omega$ 3.

FIG. 4 shows reconstitution of DHA biosynthesis in yeast starting from 18:4 $\omega$ 3.

FIG. 5 shows fatty acid composition (in mol %) of transgenic yeasts which had been transformed with the vectors pYes3-OmELO3/pYes2-EgD4 or pYes3-OmELO3/pYes2-EgD4+pESCLEu-PtD5. The yeast cells were cultured in minimal medium without tryptophan and uracil/and leucine in the presence of 250M 20:5 $\Delta^{5,8,11,14,17}$  and 18:4 $\Delta^{6,9,12,15}$ , respectively. The fatty acid methyl esters were obtained from cell sediments by acid methanolysis and analyzed via GLC. Each value represents the mean (n=4) $\pm$ standard deviation.

FIG. 6 shows feeding experiment for determining the functionality and substrate specificity with yeast strains.

FIG. 7 shows elongation of eicosapentaenoic acid by OtElo1.

FIG. 8 shows elongation of arachidonic acid by OtElo1.

FIG. 9 shows expression of TpELO1 in yeast.

FIG. 10 shows expression of TpELO3 in yeast.

FIG. 11 shows expression of *Thraustochytrium* 5-elongase TL16/pYES2.1 in yeast.

FIG. 12 shows desaturation of  $\gamma$ -linolenic acid (18:2  $\omega$ 6-fatty acid) to give  $\alpha$ -linolenic acid (18:3  $\omega$ 3-fatty acid) by Pi-omega3Des.

FIG. 13 shows desaturation of  $\gamma$ -linolenic acid (18:2  $\omega$ 6-fatty acid) to give stearidonic acid (18:4  $\omega$ 3-fatty acid) by Pi-omega3Des.

FIG. 14 shows desaturation of C20:2  $\omega$ 6-fatty acid to give C20:3  $\omega$ 3-fatty acid by Pi-omega3Des.

FIG. 15 shows desaturation of C20:3  $\omega$ 6-fatty acid to give C20:4  $\omega$ 3-fatty acid by Pi-omega3Des.

FIG. 16 shows desaturation of arachidonic acid (C20:4  $\omega$ 6-fatty acid) to give eicosapentaenoic acid (C20:5  $\omega$ 3-fatty acid) by Pi-omega3Des.

FIG. 17 shows desaturation of docosatetraenoic acid (C22:4  $\omega$ 6-fatty acid) to give docosapentaenoic acid (C22:5  $\omega$ 3-fatty acid) by Pi-omega3Des.

FIG. 18 shows substrate specificity of Pi-omega3Des with different fatty acids.

FIG. 19 shows desaturation of phospholipid-bound arachidonic acid to give EPA by Pi-Omega3Des.

FIG. 20 shows conversion of linoleic acid (arrow) to give  $\gamma$ -linolenic acid ( $\gamma$ -18:3) by OtDes6.1.

FIG. 21 shows conversion of linoleic acid and  $\alpha$ -linolenic acid (A and C), and reconstitution of the ARA and EPA synthetic pathways, respectively, in yeast (B and D) in the presence of OtD6.1.

FIG. 22 shows expression of ELO(XI) in yeast.

FIG. 23 shows substrate specificity of ELO(Ci).

FIG. 24 shows elongation of eicosapentaenoic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:5 $\omega$ 3).

FIG. 25 shows elongation of arachidonic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:4 $\omega$ 6).

FIG. 26 shows elongation of 20:5n-3 by the elongases At3g06470.

FIG. 27 shows substrate specificity of the *Xenopus* Elongase (A), *Ciona* Elongase (B) and *Oncorhynchus* Elongase (C).

FIG. 28 shows substrate specificity of the *Ostreococcus*  $\Delta$ 5-elongase (A), the *Ostreococcus*  $\Delta$ 6-elongase (B), the *Thalassiosira*  $\Delta$ 5-elongase (C) and the *Thalassiosira*  $\Delta$ 6-elongase (D).

FIG. 29 shows expression of the *Phaeodactylum tricoratum*  $\Delta$ 6-elongase (PtELO6) in yeast. A) shows the elongation of the C18:3 $\Delta^{6,9,12}$  fatty acid and B) the elongation of the C18:3 $\Delta^{6,9,12,15}$  fatty acid.

FIG. 30 shows the substrate specificity of PtELO6 with regard to the substrates fed.

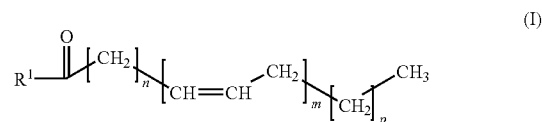
FIG. 31 shows gas-chromatographic analysis of the seed of a transgenic plant, transformed with pSUN-5G.

FIG. 32 shows gas-chromatographic analysis of the seed of a transgenic plant, transformed with pGPTV-D6Des (Pir)\_D5Des(Tc)\_D6Elo(PP)\_12Des(Co).

FIG. 33 shows DHA in transgenic seeds of *Brassica juncea*. The plants were transformed with the construct pSUN-8G.

#### DETAILED DESCRIPTION OF THE INVENTION

The object of the invention was therefore to develop a process for the production of large amounts of polyunsaturated fatty acids, specifically ARA, EPA and DHA, in the seed of a transgenic plant. This object was achieved by the process according to the invention for the production of compounds of the general formula I

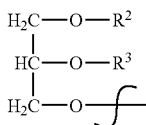




in the seeds of transgenic plants with a content of at least 20% by weight based on the total lipid content, which comprises the following process steps:

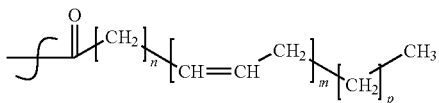
- a) introducing, into the organism, at least one nucleic acid sequence which encodes a  $\Delta 9$ -elongase and  $\Delta 6$ -desaturase activity, and
  - b) introducing, into the organism, at least one nucleic acid sequence which encodes a  $\Delta 8$ -desaturase and  $\Delta 6$ -elongase activity, and
  - c) introducing, into the organism, at least one nucleic acid sequence which encodes a  $\Delta 5$ -desaturase activity, and
  - d) introducing, into the organism, at least one nucleic acid sequence which encodes a  $\Delta 5$ -elongase activity, and
  - e) introducing, into the organism, at least one nucleic acid sequence which encodes a  $\Delta 4$ -desaturase activity, and
- where the variables and substituents in formula I have the following meanings:

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



$R^2$ =hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl,

$R^3$ =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:



$n=2, 3, 4, 5, 6, 7$  or  $9$ ,  $m=2, 3, 4, 5$  or  $6$  and  $p=0$  or  $3$ . Advantageously, the variables  $n$ ,  $m$  and  $p$  in the abovementioned formula I and Ia denote the following:  $n=2, 3$  or  $5$ ,  $m=4, 5$  or  $6$  and  $p=0$  or  $3$ . In an especially advantageous embodiment of the process; the variables  $n$ ,  $m$  and  $p$  in the formulae I and Ia denote the following:  $m=4$ ,  $n=3$ ,  $p=3$  and the compounds of the general formula I and Ia thus denote arachidonic acid, and/or  $m=5$ ,  $n=3$ ,  $p=0$  and the compounds of the general formula I and Ia thus denote eicosapentaenoic acid, and/or  $m=5$ ,  $n=5$ ,  $p=0$  and the compounds of the general formula I and Ia thus denote docosapentaenoic acid is and/or  $m=6$ ,  $n=3$ ,  $p=0$  and the compounds of the general formula I and Ia thus denote docosahexaenoic acid is.

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



The abovementioned radicals of  $R^1$  are always bonded to the compounds of the general formula I in the form of their thioesters.

$R^2$  in the general formula II is hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl.

Alkyl radicals which may be mentioned are substituted or unsubstituted, saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl chains such as ethylcarbonyl, n-propylcarbonyl, n-butylcarbonyl, n-pentylcarbonyl, n-hexylcarbonyl, n-heptylcarbonyl, n-octylcarbonyl, n-nonylcarbonyl, n-decylcarbonyl, n-undecylcarbonyl, n-dodecylcarbonyl, n-tridecylcarbonyl, n-tetradecylcarbonyl, n-pentadecylcarbonyl, n-hexadecylcarbonyl, n-heptadecylcarbonyl, n-octadecylcarbonyl, n-nonadecylcarbonyl, n-eicosylcarbonyl, n-docosanylcarbonyl- or n-tetracosanylcarbonyl, which comprise one or more double bonds. Saturated or unsaturated  $C_{10}$ - $C_{22}$ -alkylcarbonyl radicals such as n-decylcarbonyl, n-undecylcarbonyl, n-dodecylcarbonyl, n-tridecylcarbonyl, n-tetradecylcarbonyl, n-pentadecylcarbonyl, n-hexadecylcarbonyl, n-heptadecylcarbonyl, n-octadecylcarbonyl, n-nonadecylcarbonyl, n-eicosylcarbonyl, n-docosanylcarbonyl or n-tetracosanylcarbonyl, which comprise one or more double bonds are preferred. Especially preferred are saturated and/or unsaturated  $C_{10}$ - $C_{22}$ -alkylcarbonyl radicals such as  $C_{10}$ -alkylcarbonyl,  $C_{11}$ -alkylcarbonyl,  $C_{12}$ -alkylcarbonyl,  $C_{13}$ -alkylcarbonyl,  $C_{14}$ -alkylcarbonyl,  $C_{16}$ -alkylcarbonyl,  $C_{18}$ -alkylcarbonyl,  $C_{20}$ -alkylcarbonyl or  $C_{22}$ -alkylcarbonyl radicals which comprise one or more double bonds. Very especially preferred are saturated or unsaturated  $C_{16}$ - $C_{22}$ -alkylcarbonyl radicals such as  $C_{16}$ -alkylcarbonyl,  $C_{18}$ -alkylcarbonyl,  $C_{20}$ -alkylcarbonyl or  $C_{22}$ -alkylcarbonyl radicals which comprise one or more double bonds. These advantageous radicals can comprise two, three, four, five or six double bonds. The especially preferred radicals with 20 or 22 carbon atoms in the fatty acid chain comprise up to six double bonds, advantageously three, four, five or six double bonds, especially preferably five or six. All the abovementioned radicals are derived from the corresponding fatty acids.

$R^3$  in the formula II is hydrogen, saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl.

Alkyl radicals which may be mentioned are substituted or unsubstituted, saturated or unsaturated  $C_2$ - $C_{24}$ -alkylcarbonyl chains such as ethylcarbonyl, n-propylcarbonyl, n-butylcarbonyl, n-pentylcarbonyl, n-hexylcarbonyl, n-heptylcarbonyl, n-octylcarbonyl, n-nonylcarbonyl, n-decylcarbonyl, n-undecylcarbonyl, n-dodecylcarbonyl, n-tridecylcarbonyl, n-tetradecylcarbonyl, n-pentadecylcarbonyl, n-hexadecylcarbonyl, n-heptadecylcarbonyl, n-octadecylcarbonyl, n-nonadecylcarbonyl, n-eicosylcarbonyl, n-docosanylcarbonyl- or n-tetracosanylcarbonyl, which comprise one or more double bonds. Saturated or unsaturated  $C_{10}$ - $C_{22}$ -alkylcarbonyl radicals such as n-decylcarbonyl, n-undecylcarbonyl, n-dodecylcarbonyl, n-tridecylcarbonyl, n-tetradecylcarbonyl, n-pentadecylcarbonyl,

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n-hexadecylcarbonyl, n-heptadecylcarbonyl, n-octadecylcarbonyl, n-nonadecylcarbonyl, n-eicosylcarbonyl, n-docosanylcarbonyl or n-tetracosanylcarbonyl, which comprise one or more double bonds are preferred. Especially preferred are saturated and/or unsaturated C<sub>10</sub>-C<sub>22</sub>-alkylcarbonyl radicals such as C<sub>10</sub>-alkylcarbonyl, C<sub>11</sub>-alkylcarbonyl, C<sub>12</sub>-alkylcarbonyl, C<sub>13</sub>-alkylcarbonyl, C<sub>14</sub>-alkylcarbonyl, C<sub>16</sub>-alkylcarbonyl, C<sub>18</sub>-alkylcarbonyl, C<sub>20</sub>-alkylcarbonyl or C<sub>22</sub>-alkylcarbonyl radicals which comprise one or more double bonds. Very especially preferred are saturated or unsaturated C<sub>16</sub>-C<sub>22</sub>-alkylcarbonyl radicals such as C<sub>16</sub>-alkylcarbonyl, C<sub>18</sub>-alkylcarbonyl, C<sub>20</sub>-alkylcarbonyl or C<sub>22</sub>-alkylcarbonyl radicals which comprise one or more double bonds. These advantageous radicals can comprise two, three, four, five or six double bonds. The especially preferred radicals with 20 or 22 carbon atoms in the fatty acid chain comprise up to six double bonds, advantageously three, four, five or six double bonds, especially preferably four, five or six double bonds, very especially preferably five or six. All the abovementioned radicals are derived from the corresponding fatty acids.

The abovementioned radicals of R<sup>1</sup>, R<sup>2</sup> and R<sup>3</sup> can be substituted by hydroxyl and/or epoxy groups and/or can comprise triple bonds.

The polyunsaturated fatty acids produced in the process according to the invention advantageously comprise at least two, advantageously three, four, five or six, double bonds. The fatty acids especially advantageously comprise four, five or six double bonds. Fatty acids produced in the process advantageously have 18, 20 or 22 C atoms in the fatty acid chain; the fatty acids preferably comprise 20 or 22 carbon atoms in the fatty acid chain. Saturated fatty acids are advantageously reacted to a minor degree, or not at all, by the nucleic acids used in the process. To a minor degree is to be understood as meaning that the saturated fatty acids are reacted with less than 5% of the activity, advantageously less than 3%, especially advantageously with less than 2%, very especially preferably with less than 1, 0.5, 0.25 or 0.125% of the activity in comparison with polyunsaturated fatty acids. These fatty acids which have been produced can be produced in the process as a single product or be present in a fatty acid mixture.

The nucleic acid sequences used in the process according to the invention take the form of isolated nucleic acid sequences which encode polypeptides with  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase activity.

Nucleic acid sequences which are advantageously used in the process according to the invention are nucleic acid sequences which encode polypeptides with  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase activity selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49; SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91,

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SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, or

b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202, or

c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193; SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, which encode polypeptides with at least 40% identity at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120,

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SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202 and which have a  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase activity.

Advantageously, the substituents R<sup>2</sup> or R<sup>3</sup> in the general formulae I and II independently of one another are saturated or unsaturated C<sub>18</sub>-C<sub>22</sub>-alkylcarbonyl; especially advantageously, are independently of one another C<sub>18</sub>-, C<sub>20</sub>- or C<sub>22</sub>-alkylcarbonyl with at least two double bonds, advantageously with at least three, four, five or six double bonds, especially advantageously with at least four, five or six double bonds.

In a preferred embodiment of the process, a nucleic acid sequence which encodes polypeptides with  $\omega 3$ -desaturase activity, selected from the group consisting of:

- a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or
- nucleic acid sequences which can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106 as the result of the degeneracy of the genetic code, or
- derivatives of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and which have  $\omega 3$ -desaturase activity

is additionally introduced into the transgenic plant.

In a further preferred embodiment of the process, that a nucleic acid sequence which encodes polypeptides with  $\Delta 12$ -desaturase activity, selected from the group consisting of:

- a nucleic acid sequence with the sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, or
  - nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196, or
  - derivatives of the nucleic acid sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, which encode polypeptides with at least 60% at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have  $\Delta 12$ -desaturase activity
- is additionally introduced into the transgenic plant.

These abovementioned  $\Delta 12$ -desaturase sequences can be used alone or in combination with  $\omega 3$ -desaturase sequences together with the nucleic acid sequences used in the process which encode  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases or  $\Delta 4$ -desaturases.

Table 1 shows the nucleic acid sequences, the organism of origin and the sequence ID number.

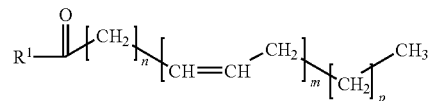
No.	Organism	Activity	Sequence number
1.	<i>Euglena gracilis</i>	$\Delta 8$ -Desaturase	SEQ ID NO: 1
2.	<i>Isochrysis galbana</i>	$\Delta 9$ -Elongase	SEQ ID NO: 3
3.	<i>Phaeodactylum tricoratum</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 5
4.	<i>Ceratodon purpureus</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 7
5.	<i>Physcomitrella patens</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 9
6.	<i>Thraustochytrium sp.</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 11
7.	<i>Mortierella alpina</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 13
8.	<i>Caenorhabditis elegans</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 15
9.	<i>Borago officinalis</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 17
10.	<i>Ceratodon purpureus</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 19
11.	<i>Phaeodactylum tricoratum</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 21

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-continued

No.	Organism	Activity	Sequence number
12.	<i>Physcomitrella patens</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 23
13.	<i>Caenorhabditis elegans</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 25
14.	<i>Physcomitrella patens</i>	$\Delta 6$ -Elongase	SEQ ID NO: 27
15.	<i>Thraustochytrium sp.</i>	$\Delta 6$ -Elongase	SEQ ID NO: 29
16.	<i>Phytophthora infestans</i>	$\Delta 6$ -Elongase	SEQ ID NO: 31
17.	<i>Mortierella alpina</i>	$\Delta 6$ -Elongase	SEQ ID NO: 33
18.	<i>Mortierella alpina</i>	$\Delta 6$ -Elongase	SEQ ID NO: 35
19.	<i>Caenorhabditis elegans</i>	$\Delta 6$ -Elongase	SEQ ID NO: 37
20.	<i>Euglena gracilis</i>	$\Delta 4$ -Desaturase	SEQ ID NO: 39
21.	<i>Thraustochytrium sp.</i>	$\Delta 4$ -Desaturase	SEQ ID NO: 41
22.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 43
23.	<i>Thalassiosira pseudonana</i>	$\Delta 6$ -Elongase	SEQ ID NO: 45
24.	<i>Cryptocodinium cohnii</i>	$\Delta 5$ -Elongase	SEQ ID NO: 47
25.	<i>Cryptocodinium cohnii</i>	$\Delta 5$ -Elongase	SEQ ID NO: 49
26.	<i>Oncorhynchus mykiss</i>	$\Delta 5$ -Elongase	SEQ ID NO: 51
27.	<i>Oncorhynchus mykiss</i>	$\Delta 5$ -Elongase	SEQ ID NO: 53
28.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 59
29.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 61
30.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 63
31.	<i>Thraustochytrium aureum</i>	$\Delta 5$ -Elongase	SEQ ID NO: 65
32.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 67
33.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Elongase	SEQ ID NO: 69
34.	<i>Primula farinosa</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 71
35.	<i>Primula vialii</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 73
36.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 75
37.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 77
38.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 79
39.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Elongase	SEQ ID NO: 81
40.	<i>Thraustochytrium sp.</i>	$\Delta 5$ -Elongase	SEQ ID NO: 83
41.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 85
42.	<i>Phytophthora infestans</i>	$\omega 3$ -Desaturase	SEQ ID NO: 87
43.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 89
44.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 91
45.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 93
46.	<i>Ostreococcus tauri</i>	$\Delta 4$ -Desaturase	SEQ ID NO: 95
47.	<i>Thalassiosira pseudonana</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 97
48.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 99
49.	<i>Thalassiosira pseudonana</i>	$\Delta 5$ -Desaturase	SEQ ID NO: 101
50.	<i>Thalassiosira pseudonana</i>	$\Delta 4$ -Desaturase	SEQ ID NO: 103
51.	<i>Thalassiosira pseudonana</i>	$\omega 3$ -Desaturase	SEQ ID NO: 105
52.	<i>Ostreococcus tauri</i>	$\Delta 12$ -Desaturase	SEQ ID NO: 107
53.	<i>Thalassiosira pseudonana</i>	$\Delta 12$ -Desaturase	SEQ ID NO: 109
54.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Elongase	SEQ ID NO: 111
55.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 113
56.	<i>Xenopus laevis</i> (BC044967)	$\Delta 5$ -Elongase	SEQ ID NO: 117
57.	<i>Ciona intestinalis</i> (AK112719)	$\Delta 5$ -Elongase	SEQ ID NO: 119
58.	<i>Euglena gracilis</i>	$\Delta 5$ -Elongase	SEQ ID NO: 131
59.	<i>Euglena gracilis</i>	$\Delta 5$ -Elongase	SEQ ID NO: 133
60.	<i>Arabidopsis thaliana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 135
61.	<i>Arabidopsis thaliana</i>	$\Delta 5$ -Elongase	SEQ ID NO: 137
62.	<i>Phaeodactylum tricoratum</i>	$\Delta 6$ -Elongase	SEQ ID NO: 183
63.	<i>Phytium irregulare</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 193
64.	<i>Calendula officinalis</i>	$\Delta 12$ -Desaturase	SEQ ID NO: 195
65.	<i>Ostreococcus tauri</i>	$\Delta 5$ -Elongase	SEQ ID NO: 197
66.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Elongase	SEQ ID NO: 199
67.	<i>Ostreococcus tauri</i>	$\Delta 6$ -Desaturase	SEQ ID NO: 201

In a further embodiment of the invention, a process to be developed for the production of large amounts of polyunsaturated fatty acids, specifically ARA and EPA, in a transgenic plant. This process is also suitable for the production of DHA. Thus, ARA, EPA, DHA or their mixtures can be produced in the process. A further embodiment of the invention is thus a process for the compounds of the general formula I



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in transgenic plants, the process comprising:

- a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a  $\Delta 6$ -desaturase activity and is selected from the group consisting of:
    - i) a nucleic acid with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,
    - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 194 or SEQ ID NO: 202,
    - iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201, and
    - iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,
  - b) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a  $\Delta 6$ -elongase activity and is selected from the group consisting of:
    - i) a nucleic acid with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199,
    - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 28 or SEQ ID NO: 200,
    - iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199, and
    - iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199,
  - c) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a  $\Delta 5$ -desaturase activity and is selected from the group consisting of:
    - i) a nucleic acid with the sequence shown in SEQ ID NO: 11,
    - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 12,
    - iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 11, and
    - iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 11,
- where the variables and substituents in the formula I have the meaning given above.

The nucleic acid sequences which can be used in the process are described in WO 02/26946 ( $\Delta 5$ -desaturase from *Thraustochytrium* ssp., SEQ ID NO: 11 and  $\Delta 6$ -desaturase from *Phytium irregulare*, SEQ ID NO: 193) and in WO 01/59128 ( $\Delta 6$ -elongase from *Physcomitrella patens*, SEQ ID NO: 27), which is expressly referred to here. However, in these cases, the formation of ARA and EPA was studied either not in transgenic plants, but only in microorganisms, or else no increase ARA and EPA synthesis was detected in the transgenic plants. Moreover, the nucleic acids according to the invention were not combined, in these applications, with nucleic acids which encode other enzymes of the fatty acid biosynthetic pathway.

Surprisingly, it has now been found that the coexpression of the nucleic acids with the sequences shown in SEQ ID NO: 11, 27, 193, 199 and 201 leads, in transgenic plants, to a greatly increased ARA content to up to more than 8%, advantageously up to more than 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19% or 20%, especially advantageously to more than 21%, 22%, 23%, 24% or 25%, based

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on the total lipid content of the plant (cf. Table 2, Table 3, Table 4 and FIG. 31). The abovementioned percentages are percent by weight.

To further increase the yields in the process described for the production of oils and/or triglycerides with a content of polyunsaturated fatty acids, especially ARA, EPA or DHA or their mixtures, which is advantageously increased in comparison with oils and/or triglycerides from wild-type plants, it may be advantageous to increase the amount of the starting material for the fatty acid biosynthesis. This can be achieved for example by introducing a nucleic acid which encodes a polypeptide with the activity of a  $\Delta 12$ -desaturase, and coexpressing it in the organism.

This is especially advantageously in oil-producing organisms such as the family Brassicaceae, such as the genus *Brassica*, for example oilseed rape, turnip rape or Indian mustard; the family Elaeagnaceae, such as the genus *Elaeagnus*, for the example the genus and species *Olea europaea* or the family Fabaceae, such as the genus *Glycine*, for example the genus and species *Glycine max*, which has a high oleic acid content, but only a low linoleic acid content (Mikoklajczak et al., Journal of the American Oil Chemical Society, 38, 1961, 678-681).

This is why, in a preferred embodiment of the present invention, a nucleic acid sequence which encodes a polypeptide with  $\Delta 12$ -desaturase activity is additionally introduced into the transgenic plant.

Especially preferably, this nucleic acid sequence is selected from the group consisting of:

- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 195,
- b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 196,
- c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 195, and
- d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 195.

The nucleic acid sequence with the SEQ ID NO: 195 is derived from *Calendula officinalis* and described in WO 01/85968, the disclosure of which is likewise incorporated in the present application by reference.

The  $\Delta 12$ -desaturases used in the process according to the invention advantageously convert oleic acid (C18:1<sup>A9</sup>) into linoleic acid (C18:2<sup>A9,12</sup>) or C18:2<sup>A6,9</sup> into C18:3<sup>A6,9,12</sup> (gamma-linolenic acid=GLA), the starting materials for the synthesis of ARA, EPA and DHA. The  $\Delta 12$ -desaturases advantageously convert fatty acids bound to phospholipids or CoA-fatty acid esters, advantageously bound to CoA-fatty acid esters. If an elongation step has taken place beforehand, this advantageously leads to higher yields of synthetic products since, as a rule, elongation takes place at CoA-fatty acid esters, while desaturation predominantly takes place at the phospholipid or at the triglycerides. An exchange between the CoA-fatty acid esters and the phospholipids or triglycerides, which would require a further, potentially limiting, enzyme reaction, is thus not required.

The additional expression of the  $\Delta 12$ -desaturase in the transgenic plants leads to a further increase in the ARA content up to more than 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19% and 20%, especially advantageously to more than 21%, 22%, 23%, 24% or 25%, based on the total lipid content of the plant (cf. Tables 3 and 4 and FIG. 32). The abovementioned percentages are percent by weight.

Further nucleic acid sequences which encode a polypeptide with a  $\Delta 5$ -elongase activity can advantageously be introduced into the plants in the process according to the invention.

Preference is given to those nucleic acid sequences which encode a  $\Delta 5$ -elongase activity is chosen from the group consisting of:

- a) a nucleic acid sequence was the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197,
- b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 44, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 86, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138 or SEQ ID NO: 198,
- c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown, in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197, and
- d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197.

In a preferred embodiment of the process, the  $\Delta 5$ -elongase genes are expressed under the control of a seed-specific promoter.

In a further advantageous embodiment of the process, all nucleic acid sequences are introduced into the plants on a shared recombinant nucleic acid molecule, it being possible for each nucleic acid sequence to be under the control of its own promoter and it being possible for this own promoter to take the form of a seed-specific promoter.

However, it is not only the nucleic acids detailed in the sequence listing which can successfully be employed in the invention to carry out the conversion; rather, even sequences which deviate to a certain degree from these sequences and which encode proteins with the essentially identical enzymatic activity can be employed. These take the form of nucleic acids which have a certain degree of identity or homology with the sequences specified in the sequence listing. An essentially identical enzymatic activity denotes proteins which have at least 20%, 30%, 40%, 50% or 60%, advantageously at least 70%, 80%, 90% or 95%, especially advantageously at least 96%, 97%, 98% or 99% of the enzymatic activity of the wild-type enzymes.

In order to determine the percentage of homology (=identity) of two amino acid sequences or of two nucleic acids, the sequences are written one under the other (for example, gaps may be introduced into the sequence of a protein or of a nucleic acid in order to generate optimal alignment with the other protein or the other nucleic acid). Then, the amino acid radicals 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 radical 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  $\times 100$ ). 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. To compare various sequences, the skilled worker has available a series of programs which are based on various algorithms. 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, Wis., USA 53711 (1991)], were used to carry out the sequence comparisons. The sequence homology data given above in percent were determined over the entire sequence region using the program GAP with 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 sequence comparisons.

The skilled worker will recognize that DNA sequence polymorphisms which lead to modifications of the amino acid sequence of SEQ ID NO: 12, 28, 194, 196, 198, 200 and/or 202 may occur within a population. These natural variants usually cause a variance of from 1 to 5% in the nucleotide sequence of the  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 6$ -elongase gene. The scope of the invention is to comprise each and all of these nucleotide variation(s) and resulting amino acid polymorphisms in the  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 6$ -elongase which are the result of natural variation and which do not essentially modify the enzymatic activity.

Essential enzymatic activity of the  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -elongase or  $\Delta 5$ -desaturase used in the process according to the invention is understood as meaning that they retain an enzymatic activity of at least 10%, preferably of at least 20%, especially preferably of at least 30%, 40%, 50% or at least 60% and most preferably at least 70%; 80%, 90%, 95%, 96%, 97%, 98% or 99% in comparison with the proteins/enzymes encoded by the sequence and its derivatives and that they are thus capable of participating in the metabolism of compounds which are required for the synthesis of fatty acids, fatty acid esters such as diacylglycerides and/or triacylglycerides in a plant or plant cell or in the transport of molecules across membranes,

meaning C<sub>18</sub>-, C<sub>20</sub>- or C<sub>22</sub>-carbon chains in the fatty acid molecule with double bonds at least two, advantageously three, four or five, positions.

Likewise, the scope of the invention comprises nucleic acid molecules which hybridize under stringent conditions with the complementary strand of the  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase and/or  $\Delta$ 6-elongase nucleic acids used. The term "hybridizes under stringent conditions" as used in the present context is 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%, 70%, 80% or 90%, preferably at least approximately 91%, 92%, 93%, 94% or 95%, and especially preferably at least approximately 96%, 97%, 98%, 99% 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 $\times$  sodium chloride/sodium citrate (=SSC) at approximately 45° C., followed by one or more washing steps in 0.2 $\times$ 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 $\times$ 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. Preferably the hybridization conditions for DNA:DNA hybrids, for example, are 0.1 $\times$ SSC and 20° C. to 45° C., preferably 30° C. to 45° C. Preferably the hybridization conditions for DNA:RNA hybrids are, for example, 0.1 $\times$ SSC and 30° C. to 55° C., preferably 45° C. to 55° C. The abovementioned hybridization temperatures are determined 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 textbooks such as Sambrook et al., "Molecular Cloning", Cold Spring Harbor Laboratory, 1989; Hames and Higgins (Eds.) 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.

By introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence, it is possible to generate an isolated nucleic acid molecule which encodes a  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase and/or  $\Delta$ 6-elongase with one or more amino acid substitutions, additions or deletions. Mutations can be introduced into one of the sequences by means of standard techniques, such as site-specific mutagenesis and PCR-mediated mutagenesis. It is preferred to generate conservative amino acid substitutions in one or more of the above nonessential amino acid radicals. In a "conservative amino acid substitution", the amino acid radical is replaced by an amino acid radical with a similar side chain. Families of amino acid radicals with similar side chains have been defined in the art. These families comprise amino acids with basic side chains (for example lysine, arginine, histidine),

acidic side chains (for example aspartic acid, glutamic acid), uncharged polar side chains (for example glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), uncharged nonpolar side chains (for example alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (for example threonine, valine, isoleucine) and aromatic side chains (for example tyrosine, phenylalanine, tryptophan, histidine). A predicted nonessential amino acid radical in a  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase or  $\Delta$ 6-elongase is thus preferably replaced by another amino acid radical from the same family of side chains. In another embodiment, the mutations can, alternatively, be introduced randomly over all or part of the sequence encoding the  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase or  $\Delta$ 6-elongase, for example by saturation mutagenesis, and the resulting mutants can be screened by recombinant expression for the hereindescribed  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase or  $\Delta$ 6-elongase activity in order to identify mutants which have retained the  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 5-elongase or  $\Delta$ 6-elongase activity.

The polyunsaturated fatty acids produced in the process according to the invention advantageously comprise at least two, preferably three, four, five or six, double bonds. The fatty acids especially preferably comprise four, five or six double bonds. Fatty acids produced in the process preferably have a length of 20 C or 22 C atoms.

Saturated fatty acids are preferably reacted to a minor degree with the nucleic acids used in the process, or not at all. "A minor degree" is understood as meaning that, in comparison with polyunsaturated fatty acids, the saturated fatty acids are reacted with less than 5%, preferably with less than 3%, especially preferably with less than 2%, most preferably with less than 1, 0.5, 0.25 or 0.125% of the activity. The fatty acids produced may constitute the only product of the process or else may be present in a fatty acid mixture.

The polyunsaturated fatty acids produced in the process are advantageously bound in membrane lipids and/or triacylglycerides, but may also occur in the organisms as free fatty acids or else bound in the form of other fatty acid esters. In this context, they may be present as "pure products" or else advantageously in the form of mixtures of various fatty acids or mixtures of different glycerides. The various fatty acids which are bound in the triacylglycerides can be derived from short-chain fatty acids with 4 to 6 C atoms, medium-chain fatty acids with 8 to 12 C atoms or long-chain fatty acids with 14 to 24 C atoms, preferred are the long-chain fatty acids, especially preferred are the long-chain fatty acids LCPUFAs of C<sub>18</sub>-, C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids, very especially preferred are the long-chain fatty acids LCPUFAs of C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids such as ARA, EPA, DHA or their combination.

The process according to the invention advantageously yields fatty acid esters with polyunsaturated C<sub>18</sub>-, C<sub>20</sub>- and/or C<sub>22</sub>-fatty acid molecules with at least two double bonds in the fatty acid ester, advantageously with at least three, four, five or six double bonds in the fatty acid ester, especially advantageously four, five or six double bonds in the fatty acid ester, very especially advantageously at least five or six double bonds in the fatty acid ester. This advantageously leads to the synthesis of linoleic acid (=LA, C18:2 <sup>$\Delta$ 9,12</sup>),  $\gamma$ -linolenic acid (=GLA, C18:3 <sup>$\Delta$ 6,9,12</sup>), stearidonic acid (=SDA, C18:4 <sup>$\Delta$ 6,9,12,15</sup>), dihomo- $\gamma$ -linolenic acid (=DGLA, 20:3 <sup>$\Delta$ 8,11,14</sup>),  $\omega$ 3-eicosatetraenoic acid (=ETA, C20:4 <sup>$\Delta$ 5,8,11,14</sup>), arachidonic acid (ARA, C20:4 <sup>$\Delta$ 5,8,11,14</sup>), eicosapentaenoic acid (EPA, C20:4 <sup>$\Delta$ 5,8,11,14</sup>) or mixtures of

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these,  $\omega$ 3-eicosapentaenoic acid (=ETA, C20:4<sup>A5,8,11,14,17</sup>), arachidonic acid (ARA, C20:4<sup>A5,8,11,14</sup>), eicosapentaenoic acid (EPA, C20:5<sup>A5,8,11,14,17</sup>)  $\omega$ 6-docosapentaenoic acid (C22:5<sup>A4,7,10,13,16</sup>),  $\omega$ 6-docosapentaenoic acid (C22:4<sup>A7,10,13,16</sup>),  $\omega$ 3-docosapentaenoic acid (=DPA, C22:5<sup>A7,10,13,16,19</sup>), docosahexaenoic acid (=DHA, C22:6<sup>A4,7,10,13,16,19</sup>) or their mixtures are preferably produced, and ARA, EPA and/or DHA are very especially produced.  $\omega$ 3-Fatty acids such as EPA and/or DHA, preferably DHA, are advantageously produced.

The fatty acid esters with polyunsaturated C<sub>18</sub>-, C<sub>20</sub>- and/or C<sub>22</sub>-fatty acid molecules, advantageously with polyunsaturated-C<sub>20</sub>- and/or C<sub>22</sub>-fatty acid molecules, can be isolated in the form of an oil or lipid, for example in the form of compounds such as sphingolipids, phosphoglycerides, lipids, glycolipids such as glycosphingolipids, phospholipids such as phosphatidylethanolamine, phosphatidylcholine, phosphatidylserine, phosphatidylglycerol, phosphatidylinositol or diphosphatidylglycerol, monoacylglycerides, diacylglycerides, triacylglycerides or other fatty acid esters such as the acetyl-coenzyme A esters which comprise the polyunsaturated fatty acids with at least two, three, four, five or six, preferably four, five or six, especially preferably five or six, double bonds, from the plants which were used for the preparation of the fatty acid esters. Preferably, they are isolated in the form of their diacylglycerides, triacylglycerides and/or in the form of phosphatidylcholine, especially preferably in the form of the triacylglycerides. In addition to these esters, the polyunsaturated fatty acids are also present in the plants as free fatty acids or bound in other compounds. As a rule, the various abovementioned compounds (fatty acid esters and free fatty acids) are present in the organisms with an approximate distribution of 80 to 90% by weight of triglycerides, 2 to 5% by weight of diglycerides, 5 to 10% by weight of monoglycerides, 1 to 5% by weight of free fatty acids, 2 to 8% by weight of phospholipids, the total of the various compounds amounting to 100% by weight.

In the method(s) according to the invention (for the purposes of the invention and the disclosure shown herein, the singular is to comprise the plural and vice versa), the LCPUFAs produced are produced in a content of at least 3, 5, 6, 7 or 8% by weight, advantageously at least 9, 10, 11, 12, 13, 14 or 15% by weight, preferably at least 16, 17, 18, 19 or 20% by weight, especially preferably at least 21, 22, 23, 24 or 25% by weight, very especially preferably at least 26, 27, 28, 29 or 30% by weight based on the total fatty acids in the transgenic organisms, advantageously in the seeds of the transgenic plants. Here, C<sub>18</sub>- and/or C<sub>20</sub>-fatty acids which are present in the host organisms are advantageously converted into the corresponding products such as ARA, EPA, DPA or DHA, to mention but a few by way of example, at the rate of at least 10%, advantageously at least 20%, especially advantageously at least 30%, very especially advantageously at least 40%. The fatty acids are advantageously produced in bound form.

Polyunsaturated C<sub>20</sub>-fatty acids with four or five double bonds in the molecule are advantageously produced in the process in a content of all such fatty acids together of at least 15, 16, 17, 18, 19, or 20% by weight, advantageously at least 21, 22, 23, 24 or 25% by weight, especially advantageously at least 26, 27, 28, 29 or 30% by weight based on the total fatty acids, in the seeds of the transgenic plants.

Polyunsaturated C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids with four, five or six double bonds in the molecule are advantageously produced in the process in a content of all such fatty acids together of at least 15, 16, 17, 18, 19, or 20% by weight, advantageously at least 21, 22, 23, 24 or 25% by weight,

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especially advantageously at least 26, 27; 28, 29 or 30% by weight, very especially advantageously at least 31, 32, 33, 34 or 35% by weight based on the total fatty acids in the seeds of the transgenic plants.

ARA is produced in the process according to the invention in a content of at least 3, 5, 6, 7, 8, 9 or 10% by weight, advantageously at least 11, 12, 13, 14 or 15% by weight, preferably at least 16, 17, 18, 19 or 20% by weight, especially preferably at least 21, 22, 23, 24 or 25% by weight, most preferably at least 26% by weight, based on the total lipid content in the seeds of the transgenic plants.

EPA is produced in the process according to the invention in a content of at least 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 or 1% by weight, advantageously at least 2, 3, 4 or 5% by weight, preferably at least 6, 7, 8, 9 or 10% by weight, especially preferably at least 11, 12, 13, 14 or 15% by weight and most preferably at least 16% by weight, based on the total lipid content in the seeds of transgenic plants.

DHA is produced in the process according to the invention in a content of at least 0.01 or 0.02% by weight, advantageously at least 0.03 or 0.05% by weight, advantageously at least 0.09 or 0.1% by weight, especially preferably at least 0.2 or 0.3% by weight and most preferably at least 0.35% by weight, based on the total lipid content in the seeds of the transgenic plants.

It is possible, with the aid of the nucleic acids used in the process according to the invention, for these unsaturated fatty acids to be positioned at the sn1, sn2 and/or sn3 position of the triglycerides which have advantageously been produced. Since in the process according to the invention the starting compounds linoleic acid (C18:2) and linolenic acid (C18:3) pass through a plurality of reaction steps, the end product of the process, such as, for example, arachidonic acid (ARA), eicosapentaenoic acid (EPA),  $\omega$ 6-docosapentaenoic acid or DHA, are not obtained as absolutely pure products, small traces of the precursors are also always present in the end product. If, for example, both linoleic acid and linolenic acid are present in the starting organism, or the starting plants, the end product, such as ARA, EPA or DHA, are present as mixtures. It is advantageous that, in the end product ARA or DHA, only minor amounts of the in each case other end product should be present. This is why, in a DHA-comprising lipid and/or oil, less than 15, 14, 13, 12 or 11% by weight, advantageously less than 10, 9, 8, 7, 6 or 5% by weight, especially advantageously less than 4, 3, 2 or 1% by weight, of EPA and/or ARA should be present. This is why, in a EPA-comprising lipid and/or oil, less than 15, 14, 13, 12 or 11% by weight, advantageously less than 10, 9, 8, 7, 6 or 5% by weight, especially advantageously less than 4, 3, 2 or 1% by weight, of ARA should be present. This is also why less than 15, 14, 13, 12 or 11% by weight, advantageously less than 10, 9, 8, 7, 6 or 5% by weight, especially advantageously less than 4, 3, 2 or 1% by weight of EPA and/or DHA should be present in an ARA-comprising lipid and/or oil.

However, mixtures of different polyunsaturated C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids in one product may also be desirable. In such cases, DHA-comprising lipids and/or oils may comprise at least 1, 2, 3, 4 or 5% by weight of ARA and/or EPA, advantageously at least 6, 7 or 8% by weight, especially advantageously at least 9, 10, 11, 12, 13, 14 or 15% by weight, very especially advantageously at least 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25% by weight, based on the total lipid content in the seeds of the transgenic plants.

The precursors should advantageously not amount to more than 20% by weight, preferably not to more than 15% by weight, especially preferably not to more than 10% by

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weight, very especially preferably not to more than 5% by weight, based on the amount of the end product in question. Advantageously, only ARA, EPA or only DHA, bound or as free acids, are produced as end products in the process of the invention in a transgenic plant. If the compounds ARA, EPA and DHA are produced simultaneously, they are advantageously produced in a ratio of at least 1:1:2 (EPA:ARA:DHA), advantageously at least 1:1:3, preferably 1:1:4, especially preferably 1:1:5. If the compounds ARA and EPA are produced simultaneously, they are advantageously produced, in the plant, in a ratio of at least 1:6 (EPA:ARA), advantageously of at least 1:8, preferably of at least 1:10, especially preferably of at least 1:12.

Fatty acid esters or fatty acid mixtures produced by the process according to the invention advantageously comprise 6 to 15% of palmitic acid, 1 to 6% of stearic acid, 7-85% of oleic acid, 0.5 to 8% of vaccenic acid, 0.1 to 1% of arachic acid, 7 to 25% of saturated fatty acids, 8 to 85% of monounsaturated fatty acids and 60 to 85% of polyunsaturated fatty acids, in each case based on 100% and on the total fatty acid content of the organisms.

Moreover, the fatty acid esters or fatty acid mixtures which have been produced by the process of the invention advantageously comprise fatty acids selected from the group of the fatty acids erucic acid (13-docosaenoic acid), stercularic acid (9,10-methyleneoctadec-9-enoic acid), malvalic acid (8,9-methyleneheptadec-8-enoic acid), chaulmoogric acid (cyclopentenedodecanoic acid), furan fatty acid (9,12-epoxyoctadeca-9,11-dienoic acid), vernolic acid (9,10-epoxyoctadec-12-enoic acid), tariric acid (6-octadecynoic acid), 6-nonadecynoic acid, santalbic acid (11-octadecen-9-ynoic acid), 6,9-octadecenynoic acid, pyrulic acid (10-heptadecen-8-ynoic acid), crepenynic acid (9-octadecen-12-ynoic acid), 13,14-dihydrooropheic acid, octadecen-13-ene-9,11-diyenoic acid, petroselenic acid (cis-6-octadecenoic acid), 9c,12t-octadecadienoic acid, calendulic acid (8t10t12c-octadecatrienoic acid), catalpic acid (9t11t13c-octadecatrienoic acid), eleostearic acid (9c11t13t-octadecatrienoic acid), jacaric acid (8c10t12c-octadecatrienoic acid), punnic acid (9c11t13c-octadecatrienoic acid), parinaric acid (9c11t13t15c-octadecatetraenoic acid), pinolenic acid (all-cis-5,9,12-octadecatrienoic acid), laballenic acid (5,6-octadecadienallenic acid), ricinoleic acid (12-hydroxyoleic acid) and/or coriolic acid (13-hydroxy-9c,11t-octadecadienoic acid). The abovementioned fatty acids are, as a rule, advantageously only found in traces in the fatty acid esters or fatty acid mixtures produced by the process according to the invention, that is to say that, based on the total fatty acids, they occur to less than 30%, preferably to less than 25%, 24%, 23%, 22% or 21%, especially preferably to less than 20%, 15%, 10%, 9%, 8%, 7%, 6% or 5%, very especially preferably to less than 4%, 3%, 2% or 1%. In a further preferred form of the invention, these abovementioned fatty acids occur to less than 0.9%, 0.8%, 0.7%, 0.6% or 0.5%, especially preferably to less than 0.4%, 0.3%, 0.2%, 0.1%, based on the total fatty acids. The fatty acid esters or fatty acid mixtures produced by the process according to the invention advantageously comprise less than 0.1%, based on the total fatty acids, or no butyric acid, no cholesterol, no clupanodonic acid (=docosapentaenoic acid, C22:5<sup>Δ4,8,12,15,21</sup>) and no nisinic acid (tetracosahexaenoic acid, C23:6<sup>Δ3,8,12,15,18,21</sup>).

Owing to the nucleic acid sequences according to the invention or nucleic acid sequences used in the process according to the invention, an increase in the yield of polyunsaturated fatty acids, mainly ARA and EPA, but also DHA, of at least 50, 80 or 100%, advantageously at least

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150, 200 or 250%, especially advantageously at least 300, 400, 500, 600, 700, 800 or 900%, very especially advantageously at least 1000, 1100, 1200, 1300, 1400 or 1500% in comparison with the nontransgenic starting plant, for example a plant such as *Brassica juncea*, *Brassica napus*, *Camelina sativa*, *Arabidopsis thaliana* or *Linum usitatissimum* when compared by means of GC analysis; see Examples.

Advantageously, as described above, the polyunsaturated C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids with four, five or six double bonds in the molecule, which are produced in the process, will comprise in the seeds of plants which comprise only very small amounts of C12:0- or C14:0-fatty acids, or none at all. Even shorter saturated fatty acids, such as the fatty acids C4:0, C6:0, C8:0 or C10:0 should not be present in the lipid and/or oil or only in very small amounts. Only very small amounts are advantageously understood as amounts which, in GC analysis, are advantageously under 5, 4, 3, 2 or 1%, advantageously under 0.9, 0.8, 0.7, 0.6 or 0.5%, especially advantageously under 0.4, 0.3, 0.2 or 0.1%, very especially preferably under 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 or 0.01 units area in the GC. The fatty acid C16:0 should advantageously be in a range of from 1 to 28% GC units area. The fatty acid C16:0 should advantageously be present in GC units area in amounts of less than 25%, 20%, 15% or 10%, advantageously less than 9%, 8%, 7%, 6% or 5%, especially advantageously less than 4%, 3%, 2% or 1% or not at all, in the lipids, oils and/or free fatty acids. The fatty acid C16:1 should advantageously amount to less than 1, 0.5, 0.4, 0.3, 0.2 or 0.1%, especially advantageously 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 or 0.01 units area in the GC. Very especially preferably, the fatty acid C16:1 should not be present in the oils and/or lipids produced by the process. The same applies to the fatty acids C15:0, C17:0, C16:1<sup>Δ3</sup>trans, C16:4<sup>Δ4,7,10,13</sup> and C18:5<sup>Δ3,6,9,12,15</sup>. Besides oleic acid (C18:1<sup>Δ9</sup>), the isomers (C18:1<sup>Δ7</sup>, 18:1<sup>Δ11</sup>) may also be present in the lipids, oils or free fatty acids. Advantageously in amounts of less than 5%, 4%, 3%, 2% or 1%, measured as units GC area. The fatty acids C20:0, C20:1, C24:0 and C24:1 should in each case be in the range of from 0 to 1%, 0 to 3% and 0 to 5%, respectively, units GC area. Furthermore, little dihomo-γ-linolenic acid (=DGLA) should be detectable in the GC analysis in units GC area in the seed oil and/or seed lipid. Little is understood as meaning less than 2, 1.9, 1.8, 1.7, 1.6 or 1.5%, advantageously less than 1.4, 1.3, 1.2, 1.1 or 1%, especially advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5 or 0.4% in units GC area.

In a preferred embodiment of the process, DGLA and ARA should be produced in a ratio of from 1:1 up to 1:100, advantageously from 1:2 up to 1:80, especially advantageously from 1:3 up to 1:70, very especially from 1:5 up to 1:60.

In a further preferred embodiment, DGLA and EPA should be produced in a ratio of from 1:1 up to 1:100, advantageously from 1:2 up to 1:80, especially advantageously from 1:3 up to 1:70, very especially from 1:5 up to 1:60.

The lipids and/or oils produced in the process according to the invention should advantageously have a high unsaturated, advantageously polyunsaturated, fatty acid content of at least 30, 40 or 50% by weight, advantageously at least 60, 70 or 80% by weight, based on the total fatty acid content in the seeds of the transgenic plants.

All saturated fatty acids together should advantageously only amount to a small quantity in the plants preferably used in the process according to the invention. In this context, a small amount is understood as meaning an amount of less



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than 15%, 14%, 13%, 12%, 11% or 10%, preferably less than 9%, 8%, 7% or 6%, in units GC area.

Furthermore, the genes for the synthesis of the polyunsaturated fatty acids, which are used in the process and which have been introduced, in the process, via different processes, advantageously as host plant, should advantageously have a higher oil content than protein content in the seed, advantageously plants have an oil/protein content ratio of from 5:1, 4:1, 3:1, 2:1 or 1:1. In this context, the oil content based on the total weight of the seed should be in a range of 15-55%, advantageously between 25-50%, especially advantageously between 35-50%. Advantageous host plants used in the process should have a distribution of the unsaturated fatty acids such as oleic acid, linoleic acid and linolenic acid, which are the starting compounds in the process according to the invention for the synthesis of polyunsaturated fatty acids, in the sn1, sn2 and sn3 position of the triglyceride, as shown in Table 5 hereinbelow, where rows No. 1-7 represent different advantageous alternatives of such distributions, n.p. means not present.

TABLE 5

Plants with advantageous fatty acid distribution in the sn1, sn2 and sn3 position on the triglyceride									
No.	Oleic acid			Linoleic acid			$\alpha$ -Linolenic acid		
	sn1	sn2	sn3	sn1	sn2	sn3	sn1	sn2	sn3
1.	1	1	1	2	4	1	n.p.	n.p.	n.p.
2.	1.4	2.2	1	2.8	9	1	2	6.7	1
3.	0.8	0.8	1	1.1	1.6	1	1	0.8	1
4.	0.9	0.9	1	1.2	1.6	1	0.9	1	1
5.	0.9	0.9	1	1	1.3	1	1	1	1
6.	1	1.1	1	2	2.8	1	1	1	n.p.
7.	1.3	9.7	1	1	9	traces	1	n.p.	n.p.

The rows show the ratios of the following plants: row 1=*Arachis hypogaea*, row 2=*Brassica napus*, row 3=*Glycine max*, row 4=*Linum usitatissimum*, row 5=*Zea mays*, row 6=*Olea europaea* and row 7=*Theobroma cacao*.

Host plants which are advantageous for the process are those which have a high oleic acid content, that means at least 40, 50, 60 or 70% by weight based on the total fatty acid content of the plant, in comparison with linoleic acid and/or linolenic acid in the lipids and/or oils, especially in the triglyceride, such as, for example, *Anacardium occidentale*, *Argania spinosa*, *Bombax malabaricum*, *Brassica napus*, *Butyrospermum parkii*, high-oleic safflower (*Carthamus tinctorius*), *Citrullus colocythis*, *Corylus avellana*, *Cucurbita foetidissima*, *Cucurbita pepo*, *Guizotia abyssinica*, high-oleic sunflower (*Helianthus annuus*), *Macadamia integrifolia*, *Nigella sativa*, *Olea europaea*, *Papaver somniferum*, *Passiflora edulis*, *Persea americana*, *Prunus amygdalis*, *Prunus armeniaca*, *Prunus dulcis*, *Prunus communis*, *Sesamum indicum*, *Simarouba glauca*, *Thea sasungua*, or *Theobroma cacao*. Further advantageous plants have a higher content of the unsaturated fatty acids oleic acid, linoleic acid and  $\alpha$ -linolenic acid in the sn2 position in comparison with the other positions sn1 and sn3. A higher content is understood as meaning ratios of (sn1:sn2:sn3) 1:1.1:1, 1:1.5:1 to 1:3:1. Advantageous plants such as *Actinidia chinensis*, *Aleurites moluccana*, *Arnebia griffithii*, *Brassica alba*, *Brassica hirta*, *Brassica nigra*, *Brassica juncea*, *Brassica carinata*, *Camelina sativa*, *Cannabis sativa*, *Echium rubrum*, *Echium vulgare*, *Humulus lupulus*, *Juglans regia*, *Linum usitatissimum*, *Ocimum* spp., *Perilla frutescens*, *Portulaca oleracea*, *Prunus cerasus*, *Salicornia*

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*bigelovii*, *Salvia hispanica* are also those which have a high  $\alpha$ -linolenic acid content in the lipid and/or oil of the plant, that is to say an  $\alpha$ -linolenic acid content of at least 10, 15 or 20% by weight, advantageously at least 25, 30, 35, 40, 45 or 50% by weight, based on the total fatty acid content of the plant. Very especially advantageous plants likewise show an advantageous preference for the sn2 position over the positions sn1 and sn3 in the triglyceride of from 1:1.1:1, 1:1.5:1 to 1:3:1 for the arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid produced in the process.

Plants used for the process should advantageously have an erucic acid content of less than 2% by weight based on the total fatty acid content of the plant. Also, the content of saturated fatty acids C16:0 and/or C18:0 should advantageously be less than 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10% by weight; advantageously less than 9, 8, 7, 6 or 5% by weight, based on the total fatty acid content of the plant. Also, longer fatty acids such as C20:0 or C22:1 should advantageously not be present, or only in small amounts, advantageously in amounts of less than 4, 3, 2 or 1% by weight, advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 or 0.1% by weight based on the total fatty acid content of the plant in the plants used in the process. Typically, C16:1 is not present as fatty acid, or only present in small amounts, in the plants used for the process according to the invention. Small amounts are advantageously understood as meaning fatty acid contents which are less than 4, 3, 2 or 1% by weight, advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 or 0.1% by weight based on the total fatty acid content of the plant.

For economic reasons, that is to say because of the area under cultivation and the oil yield, plants which are grown on a large scale, such as soybean, oilseed rape, mustard, *Camelina*, linseed, sunflower, oil palm, cotton, sesame, maize, olive, are preferred, preferably oilseed rape, *Camelina*, linseed, sunflower are used frequently as host plant in the process.

Chemically pure polyunsaturated fatty acids or fatty acid compositions can also be synthesized by the processes described above. To this end, the fatty acids or the fatty acid compositions are isolated from the plants, advantageously the seeds of the plants, in the known manner, for example via crushing the seeds, such as grinding, followed by extraction, distillation, crystallization, chromatography or a combination of these methods. These chemically pure fatty acids or fatty acid compositions are advantageous for applications in the food industry sector, the cosmetic sector and especially the pharmacological industry sector.

Plants which are suitable for the process according to the invention 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 Adolotheciaceae, Anacardiaceae, Asteraceae, Apiaceae, Betulaceae, Boraginaceae, Brassicaceae, Bromeliaceae, Caricaceae, Cannabaceae, Compositae, Convolvulaceae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Ericaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Juglandaceae, Lauraceae, Leguminosae, Linaceae, Malvaceae, Moringaceae, Marchantiaceae, Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae, Pedaliaceae, Poaceae, Rosaceae or Solanaceae, vorteilhaft Anacardiaceae, Asteraceae, Boraginaceae, Brassicaceae, Cannabaceae, Compositae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Leguminosae; Linaceae, Malvaceae, Moringaceae, Marchantiaceae, Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae,

Pedaliaceae, Poaceae or Solanaceae, but other plants which are suitable for the process are vegetable plants or ornamentals such as *Tagetes*.

Examples which may be mentioned are the following plants selected from the group consisting of: Anacardiaceae such as the genera *Pistacia*, *Mangifera*, *Anacardium*, for example the genus and species *Pistacia vera* [pistachio], *Mangifer 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 *Artemisia sphaerocephala*, *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 *Adelocaryum*, *Alkanna*, *Anchusa*, *Borago*, *Brunnera*, *Cerinth*, *Cynoglossum*, *Echium*, *Gastrocayle*, *Lithospermum*, *Moltkia*, *Nonea*, *Onosma*, *Onosmodium*, *Paracaryum*, *Pectocarya*, *Symphytum* for example the genus and species *Adelocaryum coelestinum*, *Alkanna orientalis*, *Anchusa anzurea*, *Anchusa capensis*, *Anchusa hybrida*, *Borago officinalis* [borage], *Brunnera orientalis*, *Cerinth minor*, *Cynoglossum amabile*, *Cynoglossum lanceolatum*, *Echium rubrum*, *Echium vulgare*, *Gastrocayle hispida*, *Lithospermum arvense*, *Lithospermum purpureocaeruleum*, *Moltkia aurea*, *Moltkia coerules*, *Nonea macrosperma*, *Onosma sericeum*, *Onosmodium molle*, *Onosmodium occidentale*, *Paracaryum caelestinum*, *Pectocarya platycarpa*, *Symphytum officinale*, Brassicaceae, such as the genera *Brassica*, *Camelina*, *Melanosinapis*, *Sinapis*, *Arabadopsis*, for example the genera and species *Brassica alba*, *Brassica carinata*, *Brassica hirta*, *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*, for example 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 *Ipomea batatas*, *Ipomea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomea fastigiata*, *Ipomea tiliacea*, *Ipomea 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], Cryptocodiniaceae, such as the genus *Cryptocodium*, for example the genus and species *Cryptocodium cohni*, Cucurbitaceae, such as the genus *Cucurbita*, for example the genera and species *Cucurbita maxima*, *Cucurbita mixta*, *Cucurbita pepo* or *Cucurbita moschata* [pumpkin/squash],

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 occidentals*, *Cistus chamaerhondendros* or *Kalmia lucida* [mountain laurel], 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 lebbeck*, *Acacia berteriana*, *Acacia littoralis*, *Albizia berteriana*, *Albizia berteriana*, *Cathormion berteriana*, *Feuillea berteriana*, *Inga fragrans*, *Pithecolobium berterianum*, *Pithecolobium fragrans*, *Pithecolobium berterianum*, *Pseudalbizia berteriana*, *Acacia julibrissin*, *Acacia nemu*, *Albizia nemu*, *Feuillea julibrissin*, *Mimosa julibrissin*, *Mimosa speciosa*, *Sericandra julibrissin*, *Acacia lebbeck*, *Acacia macrophylla*, *Albizia lebbeck*, *Feuillea lebbeck*, *Mimosa lebbeck*, *Mimosa speciosa* [silk tree], *Medicago sativa*, *Medicago falcata*, *Medicago varia* [alfalfa] *Glycine max*, *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida* or *Soja max* [soybean], 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 ailanthifolia*, *Juglans sieboldiana*, *Juglans cinerea*, *Wallia cinerea*, *Juglans bixbyi*, *Juglans californica*, *Juglans hindsii*, *Juglans 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*, *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 berteriana*, *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 orientate*, *Papaver rhoeas*, *Papaver dubium*

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[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*, *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 saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum caffrorum*, *Sorghum cernuum*, *Sorghum dochna*, *Sorghum drummondii*, *Sorghum durra*, *Sorghum guineense*, *Sorghum lanceolatum*, *Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum miliaceum*, *Panicum militaceum* [millet], *Oryza sativa*, *Oryza iatifolia* [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 *Chrodthece*, *Flintiella*, *Petrovanella*, *Porphyridium*, *Rhodella*, *Rhodorus*, *Vanhoeffenia*, for example the genus and species *Porphyridium cruentum*, Proteaceae, such as the genus *Macadamia*, for example the genus and species *Macadamia intergrifolia* [macadamia], Rosaceae, such as the genus *Prunus*, for example the genus and species *Prunus armeriaca*, *Prunus amygdalus*, *Prunus avilum*, 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 *Scrophularia*, *Verbascum*, for example the genera and species *Scrophularia marilandica*, *Verbascum blattaria*, *Verbascum chaixii*, *Verbascum densiflorum*, *Verbascum lagurus*, *Verbascum longifolium*, *Verbascum lychnitis*, *Verbascum nigrum*, *Verbascum olympicum*, *Verbascum phlomooides*, *Verbascum phoenicum*, *Verbascum pulverulentum* or *Verbascum thapsus* [mullein], 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 glauca*, *Nicotiana glauca*, *Nicotiana glauca*, *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]. Further plants which may be mentioned are the genus and species *Argania spinosa*, *Arnebia griffithii*, *Adansonia digitata*, *Orbignya martiana*, *Carum carvi*, *Bertholletia excelsa*, *Aleurites moluccana*, *Hydnocarpus kursii*, *Salvia hispanica*, *Vitis vinifera*, *Corvlus avellana*, *Humulus lupulus*, *Hyptis spicigera* and *Shorea stenoptera*.

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Plants which are advantageously used in the process according to the invention are transgenic plants such as dicotyledonous or monocotyledonous plants. Plants which are especially advantageously used in the process according to the invention are transgenic plants which belong to the oil-producing plants, that is to say which are used for the production of oils, such as, preferably, oil fruit crops 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, mullein; thistle, wild roses, hazelnut; almond, *macadamia*, avocado, bay, pumpkin/squash, linseed, soybean, pistachios, borage, trees (oil palm, coconut, walnut) or 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 oilseed and oil crop plants such as peanut, oilseed rape, canola, sunflower, safflower, poppy, Indian mustard, mustard, hemp, castor-oil plant, olive, *Calendula*, *Punica*, evening primrose, pumpkin/squash, linseed, soybean, borage, trees (oil palm, coconut). Especially preferred are plants which are high in C18:2- and/or C18:3-fatty acids, such as sunflower, safflower, tobacco, mullein, sesame, cotton, pumpkin/squash, poppy, evening primrose, walnut, linseed, hemp, thistle or safflower. Very especially preferred plants are plants such as safflower, sunflower, poppy, evening primrose, walnut, linseed, Indian mustard, *Camelina* or hemp.

It is advantageous for the above-described processes according to the invention to additionally introduce, into the plant, further nucleic acids which encode enzymes of the fatty acid or lipid metabolism, in addition to the nucleic acids introduced in steps (a) to (e) or (a) to (c) of the process, and the optionally introduced nucleic acid sequences which encode the  $\omega$ 3-desaturases and/or the  $\Delta$ 12-desaturases.

In principle, all genes of the fatty acid or lipid metabolism can be used in the process for the production of polyunsaturated fatty acids, advantageously in combination with the  $\Delta$ 5-elongase(s),  $\Delta$ 6-elongase(s) and/or  $\omega$ 3-desaturases [for the purposes of the present invention, the plural is understood as encompassing the singular and vice versa]. Genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [=acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), acyl-CoA:lysophospholipid acyl-transferases, 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, lipoxygenases, triacylglycerol lipases, alle-noxide synthases, hydroperoxide lyases or fatty acid elongase(s) are advantageously used in combination with the  $\Delta$ 5-elongase,  $\Delta$ 6-elongase and/or  $\omega$ 3-desaturase. Genes selected from the group of the  $\Delta$ 4-desaturases,  $\Delta$ 5-desaturases,  $\Delta$ 6-desaturases,  $\Delta$ 8-desaturases,  $\Delta$ 9-desaturases,  $\Delta$ 12-desaturases,  $\Delta$ 6-elongases or  $\Delta$ 9-elongases are especially preferably used in combination with the above genes for the  $\Delta$ 5-elongase,  $\Delta$ 6-elongase and/or  $\omega$ 3-desaturase, it being possible to use individual genes or a plurality of genes in combination. The abovementioned genes are advantageously used in combination with the  $\Delta$ 6-elongase,  $\Delta$ 5-elongase,  $\Delta$ 5-desaturase,  $\Delta$ 6-desaturase and/or  $\Delta$ 12-desaturase used in accordance with the invention.

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Genes selected from the group of the  $\Delta 8$ -desaturases,  $\Delta 9$ -desaturases,  $\Delta 5$ -elongase or  $\Delta 9$ -elongases are especially preferably used in combination with the abovementioned genes.

Owing to the enzymatic activity of the nucleic acids used in the process according to the invention which encode polypeptides with  $\Delta 6$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 5$ -desaturase and/or  $\Delta 12$ -desaturase activity, advantageously in combination with nucleic acid sequences which encode polypeptides of the fatty acid or lipid metabolism, such as polypeptides with  $\Delta 8$ -desaturase, or  $\Delta 5$ - or  $\Delta 9$ -elongase activity, a wide range of polyunsaturated fatty acids can be produced in the process according to the invention. Depending on the choice of plants used for the process according to the invention, mixtures of the various polyunsaturated fatty acids or individual polyunsaturated fatty acids, such as EPA or ARA, can be produced in free or bound form. Depending on the prevailing fatty acid composition in the starting plant (C18:2- or C18:3-fatty acids), fatty acids which are derived from C18:2-fatty acids, such as GLA, DGLA or ARA, or fatty acids which are derived from C18:3-fatty acids, such as SDA, ETA or EPA, are thus obtained. If only linoleic acid (=LA, C18:2<sup>A9,12</sup>) is present as unsaturated fatty acid in the plant used for the process, the process can only afford GLA, DGLA and ARA as products, all of which can be present as free fatty acids or in bound form. If only  $\alpha$ -linolenic acid (=ALA, C18:3<sup>A9,12,15</sup>) is present as unsaturated fatty acid in the plant used for the process, as is the case, for example, in linseed, the process can only afford SDA, ETA or EPA as products, all of which can be present as free fatty acids or in bound form, as described above.

Owing to the activity of  $\Delta 6$ -desaturase and  $\Delta 6$ -elongase, products formed are, for example, GLA and DGLA, or SDA and ETA, respectively, depending on the starting plant and the unsaturated fatty acid present therein. DGLA or ETA or mixtures of these are preferentially formed. If  $\Delta 5$ -desaturase is additionally introduced into the plant, ARA and/or EPA are also formed. If, moreover, genes which encode a  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase activity are additionally introduced, the fatty acids DPA and/or DHA can be produced in the process according to the invention. Advantageously, only ARA, EPA and/or DHA or mixtures of these are synthesized, depending on the fatty acid present in the plant, which acts as starting substance for the synthesis. Since biosynthetic cascades are involved, the end-products in question are not present in pure form in the organisms. Small amounts of the precursor compounds are always additionally present in the end product. These small amounts amount to less than 20% by weight, advantageously less than 1.5% by weight, especially advantageously less than 10% by weight, most advantageously less than 5, 4, 3, 2 or 1% by weight, based on the end products DGLA, ETA or their mixtures, or ARA, EPA or their mixtures, or ARA, EPA, DHA or their mixtures.

In addition to the production directly in the plant, of the starting fatty acids for the enzymes used in the process of the invention, the fatty acids can also be fed externally. The production in the plant is preferred for reasons of economy. Substrates which are preferred for the production of ARA are linoleic acid (C18:2<sup>A9,12</sup>),  $\gamma$ -linolenic acid (C18:3<sup>A8,9,12</sup>) and dihomo- $\gamma$ -linolenic acid (20:3<sup>A8,11,14</sup>). Substrates which are preferred for the production of EPA are linolenic acid (C18:3<sup>A9,12,15</sup>), stearidonic acid (C18:4<sup>A6,9,12,15</sup>) and eicosatetraenoic acid (C20:4<sup>A8,11,14,17</sup>). Substrates which are preferred for the production of DHA are linolenic acid (C18:3<sup>A9,12,15</sup>), stearidonic acid (C18:4<sup>A6,9,12,15</sup>), eicosatetraenoic acid (C20:4<sup>A8,11,14,17</sup>), EPA and DPA.

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In comparison with the human elongases or elongases from non-human animals, such as those from *Oncorhynchus*, *Xenopus* or *Ciona*, the  $\Delta 5$ -elongases according to the invention have the advantageous characteristic that they do not elongate C<sub>22</sub>-fatty acids to the corresponding C<sub>24</sub>-fatty acids. Furthermore, they advantageously do not convert fatty acids with a double bond in the  $\Delta 6$ -position, as is the case with the human elongases or the elongases from non-human animals. Especially advantageously  $\Delta 5$ -elongases preferentially only convert unsaturated C<sub>20</sub>-fatty acids. These advantageous  $\Delta 5$ -elongases contain some putative transmembrane helices (5-7). Advantageously, only C<sub>20</sub>-fatty acids with one double bond in the  $\Delta 5$ -position are converted, with  $\omega 3$ -C<sub>20</sub>-fatty acids being preferred (EPA). Moreover, in a preferred embodiment of the invention, they have the characteristic that, besides the  $\Delta 5$ -elongase activity, they advantageously have no, or only relatively low,  $\Delta 6$ -elongase activity. In contrast, the human elongases or non-human animal elongases have approximately the same activity towards fatty acids with a  $\Delta 6$ - or  $\Delta 5$ -double bond. These advantageous elongases are referred to what are known as monofunctional elongases. In contrast, the human elongases or the non-human animal elongases are referred to as multifunctional elongases, which, besides the abovementioned substrates, also convert monounsaturated C<sub>16</sub>- and C<sub>18</sub>-fatty acids, for example with  $\Delta 9$ - or  $\Delta 11$ -double bonds. In a yeast feeding text, in which EPA was added to the yeast as the substrate, the monofunctional elongases convert at least 15% by weight of the added EPA into docosapentaenoic acid (DPA, C22:5<sup>A7,10,13,16,19</sup>), advantageously at least 20% by weight, especially, advantageously at least 25% by weight. If  $\nu$ -linolenic acid (=GLA, C18:3<sup>A6,9,12</sup>) is added as the substrate, this acid is advantageously not elongated at all. Likewise, C18:3<sup>A6,9,12</sup> is not elongated. In another advantageous embodiment, less than 60% by weight of the added GLA is converted into dihomo- $\gamma$ -linolenic acid (=C20:3<sup>A8,11,14</sup>), advantageously less than 55% by weight, preferably less than 50% by weight, especially advantageously less than 45% by weight, very especially advantageously less than 40% by weight. In a further, very preferred embodiment of the  $\Delta 5$ -elongase activity according to the invention, GLA is not converted.

FIGS. 27 and 28 show the measured substrate specificities of the various elongases. FIG. 27 shows the specificities of the multifunctional elongases from *Xenopus laevis* (FIG. 27 A), *Ciona intestinalis* (FIG. 27 B) and *Oncorhynchus mykiss* (FIG. 27 C). All these elongases convert a broad substrate spectrum. In the process according to the invention, this can lead to by-products, which must be converted by further enzymatic activities. This is why these enzymes are less preferred in the process according to the invention. The preferred monofunctional elongases and their substrate specificity are shown in FIG. 28. FIG. 28 A shows the specificity of the *Ostreococcus tauri*  $\Delta 5$ -elongase. This enzyme only converts fatty acids with a double bond in the  $\Delta 5$ -position. Advantageously, only C<sub>20</sub>-fatty acids are converted. A similarly high substrate specificity is shown by the *Thalassiosira pseudonana*  $\Delta 5$ -elongase (FIG. 28. C). Both the *Ostreococcus tauri*  $\Delta 6$ -elongase (FIG. 28 B) as that of *Thalassiosira pseudonana* (FIG. 28 D) advantageously only convert fatty acids with a double bond in the  $\Delta 6$ -position. Advantageously, only C<sup>18</sup>-fatty acids are converted. The  $\Delta 5$ -elongases from *Arabidopsis thaliana* and *Euglena gracilis* are also distinguished by their specificities.

Likewise, advantageous  $\Delta 6$ -elongases according to the invention are distinguished by a high specificity, that is to say that C<sub>18</sub>-fatty acids are preferentially elongated. They

advantageously convert fatty acids with a double bond in the  $\Delta 6$ -position. Especially advantageous  $\Delta 6$ -elongases advantageously convert  $C_{18}$ -fatty acids with three or four double bonds in the molecule, which fatty acids must comprise a double bond in the  $\Delta 6$ -position. Moreover, in a preferred embodiment of the invention, they have the characteristic that, besides the  $\Delta 6$ -elongase activity, they advantageously have no, or only relatively low,  $\Delta 5$ -elongase activity. In contrast, the human elongases or non-human animal elongases have approximately the same activity towards fatty acids with a  $\Delta 6$ - or  $\Delta 5$ -double bond. These advantageous elongases are referred to as what are known as monofunctional elongases. In contrast, the human elongases or the non-human animal elongases are referred to as multifunctional elongases, which, besides the abovementioned substrates, also convert monounsaturated  $C_{16}$ - and  $C_{18}$ -fatty acids, for example with  $\Delta 9$ - or  $\Delta 11$ -double bonds. In a yeast feeding test, in which EPA has been added to the yeasts as the substrate, the monofunctional elongases convert at least 10% by weight of the added  $\alpha$ -linolenic acid (=ALA,  $C_{18:3}^{\Delta 9,12,15}$ ) or at least 40% by weight of added  $\gamma$ -linolenic acid (=GLA,  $C_{18:3}^{\Delta 6,9,12}$ ), advantageously at least 20% by weight and 50% by weight, respectively, especially advantageously at least 25% by weight and 60% by weight, respectively. It is especially advantageous that  $C_{18:4}^{\Delta 6,9,12,15}$  (stearidonic acid) is also elongated. Here, SDA is converted to at least 40% by weight, advantageously to at least 50% by weight, especially advantageously to at least 60% by weight, very especially advantageously to at least 70% by weight. Especially advantageous  $\Delta 6$ -elongases show no, or only very low activity (less than 0.1% by weight conversion rate) toward the following substrates:  $C_{18:1}^{\Delta 6}$ ,  $C_{18:1}^{\Delta 9}$ ,  $C_{18:1}^{\Delta 11}$ ,  $C_{20:2}^{\Delta 11,14}$ ,  $C_{20:3}^{\Delta 11,14,17}$ ,  $C_{20:3}^{\Delta 8,11,14}$ ,  $C_{20:4}^{\Delta 5,8,11,14}$ ,  $C_{20:5}^{\Delta 5,8,11,14,17}$  or  $C_{22:4}^{\Delta 7,10,13,16}$ .

FIGS. 29 and 30 and Table 21 show the measured substrate specificities of the various elongases.

In comparison with the known  $\omega 3$ -desaturase, the  $\omega 3$ -desaturase used in the process according to the invention has the advantageous characteristic that it is capable of desaturating a broad spectrum of  $\omega 6$ -fatty acids, with  $C_{20}$ - and  $C_{22}$ -fatty acids such as  $C_{20:2}$ ,  $C_{20:3}$ ,  $C_{20:4}$ ,  $C_{22:4}$  or  $C_{22:5}$ -fatty acids being preferentially desaturated. However, the shorter  $C_{18}$ -fatty acids such as  $C_{18:2}$  or  $C_{18:3}$ -fatty acids are also advantageously desaturated. Owing to these characteristics of  $\omega 3$ -desaturase, it is advantageously possible to shift the fatty acid spectrum within an organism, advantageously within a plant or a fungus, from the  $\omega 6$ -fatty acids towards the  $\omega 3$ -fatty acids. The  $\omega 3$ -desaturase according to the invention preferentially desaturates  $C_{20}$ -fatty acids. Within the organism, these fatty acids are converted to at least 10%, 15%, 20%, 25% or 30% from the existing fatty acid pool to give the corresponding  $\omega 3$ -fatty acids. In comparison with the  $C_{18}$ -fatty acids, the activity of  $\omega 3$ -desaturase is lower by a factor of 10, that is to say only approximately 1.5 to 3% of the fatty acids present in the fatty acid pool are converted into the corresponding  $\omega 3$ -fatty acids. Preferred substrates of the  $\omega 3$ -desaturase according to the invention are the  $\omega 6$ -fatty acids bound in phospholipids. With reference to the desaturation of dihomogamma-linolenic acid [ $C_{20:4}^{\Delta 8,11,14}$ ], FIG. 19 shows clearly that  $\omega 3$ -desaturase advantageously does not differentiate between fatty acids bound at the sn1 or sn2 position when desaturation takes place. Both fatty acids bound at the sn1 position and fatty acids bound in the sn2 position in the phospholipids are desaturated. Another advantage is that  $\omega 3$ -desaturase converts a broad range of phospholipids such as phosphatidylcholine (=PC), phosphatidylinositol (=PIS) or phosphatidy-

lethanolamine (=PE). Finally, desaturation products are also found in the neutral lipids (=NL), i.e. in the triglycerides.

In comparison with the known  $\Delta 4$ -desaturases,  $\Delta 5$ -desaturases and  $\Delta 6$ -desaturases, the advantage of the  $\Delta 4$ -desaturases,  $\Delta 5$ -desaturases and  $\Delta 6$ -desaturases used in the process according to the invention is that they can convert fatty acids which are bound to phospholipids or CoA-fatty acid esters, advantageously CoA-fatty acid esters.

The  $\Delta 12$ -desaturases used in the process according to the invention advantageously convert oleic acid ( $C_{18:1}^{\Delta 9}$ ) into linoleic acid ( $C_{18:2}^{\Delta 9,12}$ ) or  $C_{18:2}^{\Delta 6,9}$  into  $C_{18:3}^{\Delta 6,9,12}$  (=GLA). The  $\Delta 12$ -desaturases used advantageously convert fatty acids which are bound to phospholipids or CoA-fatty acid esters, advantageously those which are bound to CoA-fatty acid esters.

Owing to the enzymatic activity of the nucleic acids used in the process according to the invention which encode polypeptides with  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or  $\omega 3$ -desaturase activity, advantageously in combination with nucleic acid sequences which encode polypeptides of the fatty acid or lipid metabolism, such as additionally polypeptides with  $\Delta 4$ -,  $\Delta 5$ -,  $\Delta 6$ -,  $\Delta 8$ -,  $\Delta 12$ -desaturase or  $\Delta 5$ -,  $\Delta 6$ - or  $\Delta 9$ -elongase activity, a very wide range of polyunsaturated fatty acids can be produced in the process according to the invention. Depending on the choice of the advantageous plants used for the process according to the invention, mixtures of the various polyunsaturated fatty acids or individual polyunsaturated fatty acids such as EPA, ARA or DHA, can be produced in free or bound form. Depending on the prevailing fatty acid composition in the starting plant ( $C_{18:2}$ - or  $C_{18:3}$ -fatty acids), fatty acids which are derived from  $C_{18:2}$ -fatty acids, such as GLA, DGLA or ARA, or which are derived from  $C_{18:3}$ -fatty acids, such as SDA, ETA, EPA or DHA, are thus obtained. If only linoleic acid (=LA,  $C_{18:2}^{\Delta 9,12}$ ) is present as unsaturated fatty acid in the plant used for the process, the process can only afford GLA, DGLA and ARA as products, all of which can be present as free fatty acids or in bound form. By expressing the additional  $\omega 3$ -desaturase in plants, the fatty acid spectrum can be shifted towards  $\alpha$ -linolenic acid, DPA and DHA. However, this shift in the fatty acid spectrum is only relatively limited. More advantageous is such a shift in plants which, as described hereinbelow, already have a high  $\alpha$ -linolenic acid content. If only  $\alpha$ -linolenic acid (=ALA,  $C_{18:3}^{\Delta 9,12,15}$ ) is present as unsaturated fatty acid in the plant, as is the case, for example, in linseed, the process can only afford SDA, ETA, EPA and/or DHA, which, as described above, may be present as free fatty acids or in bound form. Owing to the modification of the activity of the enzyme  $\Delta 5$ -elongase which plays a role in the synthesis, advantageously in combination with  $\Delta 4$ -,  $\Delta 5$ -,  $\Delta 6$ -,  $\Delta 12$ -desaturase and/or  $\Delta 6$ -elongase, or  $\Delta 4$ -,  $\Delta 5$ -,  $\Delta 8$ -,  $\Delta 12$ -desaturase, and/or  $\Delta 9$ -elongase, it is possible to produce; in a targeted fashion, only individual products in the abovementioned plants. Owing to the activity of  $\Delta 6$ -desaturase and  $\Delta 6$ -elongase, for example, GLA and DGLA, or SDA and ETA, are formed, depending on the starting plant and unsaturated fatty acids. DGLA or ETA or mixtures of these are preferentially formed. If  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and  $\Delta 4$ -desaturase are additionally introduced into the organisms, advantageously into the plant, ARA, EPA and/or DHA are additionally formed. This also applies to organisms into which  $\Delta 8$ -desaturase and  $\Delta 9$ -elongase have previously been introduced. Advantageously, only ARA, EPA or DHA or their mixtures are synthesized, depending on the fatty acid present in the plant, which acts as starting substance for the synthesis. Since biosynthetic cascades are involved, the end

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products in question are not present in pure form in the organisms. Small amounts of the precursor compounds are always additionally present in the end product. These small amounts amount to less than 20% by weight, advantageously less than 15% by weight, especially advantageously less than 10% by weight, very especially advantageously less than 5, 4, 3, 2, or 1% by weight, based on the end product DGLA, ETA or their mixtures, or ARA, EPA, DHA or their mixtures, advantageously EPA or DHA or their mixtures.

The nucleic acid with the SEQ ID NO: 53, which is derived from trout and which can be used in the process according to the invention, encodes a protein with high specificity for the two C18:4<sup>A6,9,12,15</sup>- and C20:5<sup>A5,8,11,14,17</sup>-fatty acids, which are precursors for the synthesis of DHA (precursors and synthesis of DHA, see FIG. 1). However, other fatty acids too are elongated by the enzyme. The protein encoded by SEQ ID NO: 53 thus has specificity for Δ6- and Δ5-fatty acids with additionally one ω3-double bond (FIG. 2). Δ5-elongase has a keto-acyl-CoA synthase activity which advantageously elongates fatty acid residues of acyl-CoA esters by 2 carbon atoms.

The synthesis of DHA in yeast (*Saccharomyces cerevisiae*) was detected by the gene product of the abovementioned fish Δ5-elongase gene and further Δ5-elongases, the Δ5-desaturase from *Phaeodactylum* and the Δ4-desaturase from *Euglena* (FIG. 3).

In addition to the production directly in the transgenic organism, advantageously in the transgenic plant, of the starting fatty acids for the Δ5-elongases, Δ6-elongases, Δ9-elongases, Δ4-desaturases, Δ5-desaturases, Δ6-desaturases, Δ12-desaturases and/or ω3-desaturases advantageously used in the process according to the invention, the fatty acids can also be shed externally. The production in the organism is preferred for reasons of economy. Preferred substrates of ω3-desaturase are linoleic acid (C18:2<sup>A9,12</sup>), γ-linolenic acid (C18:3<sup>A8,9,12</sup>), eicosadienoic acid (C20:2<sup>A11,14</sup>); dihomogamma-linolenic acid (C20:3<sup>A8,11,14</sup>), arachidonic acid; (C20:4<sup>A5,8,11,14</sup>), docosatetraenoic acid (C22:4<sup>A7,10,13,16</sup>) and docosapentaenoic acid (C22:5<sup>A4,7,10,13,15</sup>).

To increase the yield in the above-described process for the production of oils and/or triglycerides with an advantageously elevated content of polyunsaturated fatty acids, it is advantageous to increase the amount of starting product for the synthesis of fatty acids; this can be achieved for example by introducing, into the organism, a nucleic acid which encodes a polypeptide with Δ12-desaturase activity. This is particularly advantageous in oil-producing organisms such as those from the family of the Brassicaceae, such as the genus *Brassica*, for example oilseed rape; the family of the Elaeagnaceae, such as the genus *Elaeagnus*, for example the genus and species *Olea europaea*, or the family Fabaceae, such as the genus *Glycine*, for example the genus and species *Glycine max*, which are high in oleic acid. Since these organisms are only low in linoleic acid (Mikoklajczak et al., Journal of the American Oil Chemical Society, 38, 1961, 678-681), the use of the abovementioned Δ12-desaturases for producing the starting material linoleic acid is advantageous.

Nucleic acids used in the process according to the invention 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*, *Pseudoscourfielda*, *Pycnococcus*, *Pyramimonas*, *Scherffelia* or *Tetraselmis* such as the genera and

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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 desikacharyl*, *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 from 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 mixocylindrica*, *Euglena rostrifera* *Euglena viridis*, *Colacium stentorium*, *Trachelomonas cylindrica* or *Trachelomonas volvocina*. The nucleic acid sequences used in the process can also advantageously be derived from algae, such as the alga *Porphyridium cruentum*, *Isochrysis galbana* or *Chlorella minutissima*, *Chlorella vulgaris*, *Thraustochytrium aureum* or *Nannochloropsis oculata*. The nucleic acids used are advantageously derived from algae of the genera *Euglena*, *Mantoniella* or *Ostreococcus*.

Further advantageous plants as sources for the nucleic acid sequences used in the process according to the invention are algae such as *Isochrysis* or *Cryptocodinium*, 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*, *Eritomophthora*, *Mucor* or *Mortierella*, bacteria such as *Shewanella*, yeasts or animals such as nematodes such as *Caenorhabditis*, insects, frogs, sea cucumber or fish. The isolated nucleic acid sequences according to the invention 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 *Cryptocodinium*.

Advantageous nucleic acid used in the process according to the invention can also be derived from microorganisms such as fungi such as the genus *Mortierella*, *Phytium*, for example the genus and species *Mortierella alpina*, *Mortierella elongata*, *Phytium irregulare*, *Phytium ultimum* or bacteria such as the genus *Shewanella*, for example the genus and species *Shewanella hanedai*.

The process according to the invention advantageously employs the abovementioned nucleic acid sequences or their derivatives or homologs which encode polypeptides which retain the enzymatic activity of the proteins encoded by nucleic acid sequences. These sequences, individually or in combination with the nucleic acid sequences which encode  $\Delta 12$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or  $\omega$ -3-desaturase, are cloned into expression constructs and used for the introduction into, and expression in, organisms. Owing to their construction, these expression constructs make possible an advantageous optimal synthesis of the polyunsaturated fatty acids produced in the process according to the invention.

In a preferred embodiment, the process furthermore comprises the step of obtaining a transgenic plant which comprises the nucleic acid sequences used in the process, where the plant is transformed with a nucleic acid sequence according to the invention which encodes the  $\Delta 12$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or  $\omega$ 3-desaturase, a gene construct or a vector as described below, alone or in combination with further nucleic acid sequences which encode proteins of the fatty acid or lipid metabolism. In a further preferred embodiment, this process furthermore comprises the step of obtaining the oils, lipids or free fatty acids from the seed of the plant, such as, for example, the seed of an oil crop, such as, for example, peanut, oilseed rap, 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.

The invention furthermore relates to gene constructs which comprise the nucleic acid sequences according to the invention which encode a  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 6$ -elongase, the nucleic acid being linked functionally with one or more regulatory signals. In addition, the gene construct may comprise further biosynthesis genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [=acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), acyl-CoA:lysophospholipid acyltransferases, 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). Biosynthesis genes of the fatty acid or lipid metabolism selected from the group  $\Delta 8$ -desaturase,  $\Delta 9$ -desaturase,  $\Delta 9$ -elongase or  $\omega$ 3-desaturase are advantageously additionally present.

The nucleic acid sequences used in the process which encode proteins with  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 12$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 6$ -elongase activity are advantageously introduced into the plant alone or, preferably, in combination with an expression cassette (=nucleic acid construct) which makes possible the expression of the nucleic acids in the plant. The nucleic acid construct can comprise more than one nucleic acid sequence with an enzymatic activity, for example, of a  $\Delta 12$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 6$ -elongase.

To introduce the nucleic acids into the gene constructs, the nucleic acids used in the process 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 expediently 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.

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 preferably 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 genes. Owing to this fact, the last-mentioned vectors are relatively small, easy to manipulate and capable of replication both in 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 ligated 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 more than one codogenic gene segments. The codogenic gene segments in these constructs are preferably linked functionally with regulatory sequences. The regulatory sequences include, in particular, plant sequences such as promoters and terminator sequences. The constructs can advantageously be stably propagated in microorganisms, in particular in *E. coli* and *Agrobacterium tumefaciens*, under selection conditions and make possible a transfer of heterologous DNA into plants or microorganisms.

The nucleic acids used in the process can be introduced into plants, advantageously using cloning vectors, and thus be used in the transformation of plants such as those which are published and cited therein: Plant Molecular Biology and Biotechnology (CRC Press, Boca Raton, Fla.), 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, Eds.: Kung and R. Wu, Academic Press, 1993, 15-38; B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, Eds.:

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/or vectors used in the process can be used for the recombinant modification of a broad spectrum of plants so that the latter become better and/or more efficient PUFA producers.

A series of mechanisms by which a modification of the  $\Delta 12$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase and/or  $\Delta 6$ -desaturase protein is possible exists, so that the yield, production and/or production efficiency of the polyunsaturated fatty acids in a plant, preferably in an oilseed plant or oil crop, can be influenced directly owing to this modified protein. The number or activity of the  $\Delta 12$ -Desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase or  $\Delta 5$ -desaturase 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 a plant 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 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.

Owing to the introduction of a combination of  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or  $\Delta 5$ -desaturase genes into the plant, alone or in combination with other genes, 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 PUFAs is enhanced further. By optimizing the activity or increasing the number of one or more  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase or  $\Delta 5$ -desaturase genes which are involved in the biosynthesis of these compounds, or by destroying the activity of one or more genes which are involved in the degradation of these compounds, an enhanced yield, production and/or production efficiency of fatty acid and lipid molecules in plants is made possible.

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 plants.

In doing so, the nucleic acid sequences which encode  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase or  $\Delta 5$ -desaturase are linked functionally with one or more regulatory signals, 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 inductors 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. These, modified promoters can also be positioned on their own before the natural gene in the form of part-sequences (=promotor with parts of the nucleic acid sequences used in accordance with the invention) 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. Additional advantageous sequences, such as further regulatory elements or terminator sequences, may also be inserted at the 3' end of the DNA sequences.

The  $\Delta 12$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 6$ -elongase genes 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 plant. 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 host genome when the genes to be expressed are present together in one gene construct.

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.

In a further embodiment of the invention, one or more gene constructs comprising one or more sequences which are defined by SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201 or their derivatives and which encode polypeptides as shown in SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202 are present. The abovementioned  $\Delta 12$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase or  $\Delta 5$ -desaturase proteins advantageously lead to a desaturation or elongation of fatty acids, the substrate advantageously having one, two, three or four double bonds and advantageously 18, 20 or 22 carbon atoms in the fatty acid molecule. The same applies to their homologs, derivatives or analogs which are linked functionally with one or more regulatory signals, preferably for enhancing gene expression.

In principle, it is possible to use all natural promoters together with their regulatory sequences, such as those mentioned above, for the novel process. 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.

In order to achieve a particularly high PUFA content, especially in transgenic plants, the PUFA biosynthesis genes should advantageously be expressed in oilseeds 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) [U.S. Pat. No. 5,608,152], conlinin (linseed) [WO 02/102970], acyl carrier protein (oilseed rape) [U.S. Pat. No. 5,315,001 and WO 92/18634], oleosin (*Arabidopsis thaliana*) [WO 98/45461 and WO 93/20216], phaseolin (*Phaseolus vulgaris*) [U.S. Pat. No. 5,504,200], Bce4 [WO 91/13980], legumes 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 [U.S. Pat. No. 5,677,474], Bce4 (oilseed rape) [U.S. Pat. No. 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) [U.S. Pat. No. 5,689,040] or  $\alpha$ -amylase (barley) [EP 781 849].

Plant gene expression can also be facilitated via a chemically inducible promoter (see a 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 tetracyclin-inducible promoter (Gatz et al. (1992) Plant J. 2, 397-404) and an ethanol-inducible promoter.

To ensure the stable integration of the biosynthesis genes into the transgenic plant over a plurality of generations, each of the nucleic acids which encode  $\Delta$ 12-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 5-elongase,  $\Delta$ 6-elongase and/or  $\Delta$ 5-desaturase and which are used in the process should 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. 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, five, six or seven times, so that up to seven 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 four 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 shared promoter and, if appropriate, before a shared 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, which, however, may lead to undesired recombination events.

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 OCS1 terminator sequence. As is the case with the promoters, different terminator sequences should be used for each gene.

As described above, the gene construct can also comprise further genes to be introduced into the plants. It is possible and advantageous to introduce into the host plants, and to express, regulatory genes such as genes for inducitors, repressors or enzymes which, owing to their enzyme activity, engage in the regulation of one or more genes of a biosynthesis pathway. These genes can be of heterologous or of homologous origin.

Moreover, further biosynthesis genes of the fatty acid or lipid metabolism can advantageously be present in the nucleic acid construct, or gene construct; however, these genes can also be present on one or more further nucleic acid constructs. A biosynthesis gene of the fatty acid or lipid metabolism which is preferably chosen is a gene from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [=acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), acyl-CoA:lysophospholipid acyltransferases, 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, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) or combinations thereof.

Especially advantageous nucleic acid sequences are biosynthesis genes of the fatty acid or lipid metabolism selected from the group of the acyl-CoA:lysophospholipid acyltransferase,  $\omega$ 3-desaturase,  $\Delta$ 8-desaturase,  $\Delta$ 4-desaturase,  $\Delta$ 9-desaturase,  $\Delta$ 5-elongase and/or  $\Delta$ 9-elongase.

In this context, the abovementioned nucleic acids or genes can be cloned into expression cassettes, like those mentioned above, in combination with other elongases and desaturases and used for transforming plants with the aid of *Agrobacterium*.

Here, the regulatory sequences or factors can, as described above, preferably have a positive effect on, and thus enhance, the gene expression of the 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.

These advantageous vectors, preferably expression vectors, comprise the nucleic acids which encode the  $\Delta$ 12-desaturases,  $\Delta$ 6-desaturases,  $\Delta$ 5-elongases,  $\Delta$ 6-elongases or  $\Delta$ 5-desaturases and which are used in the process, or else a nucleic acid construct which comprises the nucleic acid used either alone or in combination with further biosynthesis genes of the fatty acid or lipid metabolism such as the acyl-CoA:lysophospholipid acyltransferases,  $\omega$ 3-desaturases,  $\Delta$ 8-desaturases,  $\Delta$ 9-desaturases,  $\omega$ 3-desaturases,  $\Delta$ 4-desaturases,  $\Delta$ 5-elongases and/or  $\Delta$ 9-elongases.

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. In the present description, "plasmid" and "vector" can be used interchangeably since the plasmid is the form of vector which is most frequently used. However, the invention is also intended to cover other forms of expression vectors, such as viral vectors, which exert similar functions. Furthermore, the term "vector" is also intended to encompass 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.

The recombinant expression vectors advantageously used in the process comprise the nucleic acids or the described gene construct used in accordance with the invention 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 functionally with the nucleic acid sequence to be expressed. In a recombinant expression vector, "linked functionally" or "in operable linkage" 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, Calif. (1990), or see: Gruber and Crosby, in: Methods in Plant Molecular Biology and Biotechnology, CRC Press, Boca Raton, Fla., Eds.: 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.

In a further embodiment of the process, the  $\Delta 12$ -desaturases,  $\Delta 6$ -desaturases,  $\Delta 5$ -elongases,  $\Delta 6$ -elongases and/or  $\Delta 5$ -desaturases can be expressed in single-celled plant cells (such as algae), see Falciorato 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, Eds.: Kung and R. Wu, Academic Press, 1993, p. 15-38.

A plant expression cassette preferably comprises regulatory sequences which are capable of governing the expression of genes in plant cells and which are linked functionally 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.

Since the regulation of plant gene expression is very often not limited to the transcriptional level, a plant expression cassette preferably comprises other sequences which are linked functionally, 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).

As described above, the gene to be expressed must be linked functionally with a suitable promoter which triggers gene expression with the correct planning 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 U.S. Pat. No. 5,352,605 and WO 84/02913), or constitutive plant promoters, such as the promoter of the Rubisco small subunit, which is described in U.S. Pat. No. 4,962,028.

As described above, plant gene expression can also be achieved via a chemically inducible promoter (see a 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.

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 (U.S. Pat. No. 5,187,267), the chill-inducible potato alpha-amylase promoter (WO 96/12814) or the wound-inducible pinII promoter (EP-A-0 375 091).

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 (U.S. Pat. No. 5,608,152), the linseed Conlinin promoter (WO 02/102970), 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 (U.S. Pat. No. 5,504, 200), the *Brassica* Bce4 promoter (WO 91/13980) or the legume 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 Ipt2 or Ipt1 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.

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

In particular, it may be desired to bring about the multi-parallel expression of the  $\Delta 12$ -desaturases,  $\Delta 6$ -desaturases,  $\Delta 5$ -elongases,  $\Delta 6$ -elongases and/or  $\Delta 5$ -desaturases used in the process. 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.

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

The process according to the invention employs the nucleic acid sequences with the SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201 or their derivatives or homologs which encode polypeptides which retain the enzymatic activity of the proteins encoded by nucleic acid sequences. These sequences, individually or in combination with the nucleic acid sequences which encode the other enzymes used, are cloned into expression constructs and used for the transformation into, and expression in, plants. Owing to their construction, these expression constructs make possible an advantageous optimal synthesis of the polyunsaturated fatty acids produced in the process according to the invention.

In a preferred embodiment, the process furthermore comprises the step of obtaining a cell or an intact plant which comprises the nucleic acid sequences used in the process, where the cell and/or the plant is transformed with a nucleic acid sequence encoding a polypeptide with a  $\Delta 12$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 6$ -elongase activity, 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. The resulting cell 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, mustard, sunflowers or borage.

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 according to the invention or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the

invention, all those constructions brought about by recombinant methods in which either

a) the nucleic acid sequence according to the invention, or  
b) a genetic control sequence which is operably linked with the nucleic acid sequence according to the invention, 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 used in the process according to the invention with the corresponding  $\Delta 12$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase, U)-3-desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -elongase and/or  $\Delta 5$ -elongase genes—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 U.S. Pat. No. 5,565,350 or WO 00/15815.

Transgenic plants for the purposes of the invention is therefore understood as meaning that the nucleic acids used in the process are not at their natural locus in the genome of the plant, it being possible for the nucleic acids to be expressed homologously or heterologously. However, transgenic also means that, while the nucleic acids according to the invention are at their natural position in the genome of the plant, however, the sequence having 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 according to the invention or the nucleic acid sequences used in the process according to the invention at an unnatural locus in the genome, i.e. homologous or, preferably, heterologous expression of the nucleic acids takes place. Preferred transgenic plants are oilseed or oil fruit crops.

Plants which are suitable for use in the process according to the invention are, in principle, advantageously all plants which are capable of synthesizing fatty acids, specifically unsaturated fatty acids such as ARA, EPA and/or DHA, and which are suitable for the expression of recombinant genes. Examples 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. Plants which are naturally capable of synthesizing large amounts of oils are preferred, such as soybean, oilseed rape, *Camelina*, Indian mustard, coconut, oil palm, safflower (*Carthamus tinctorius*), flax, hemp, castor-oil plant, *Calendula*, peanut, cacao bean or sunflower or yeast such as *Saccharomyces cerevisiae*, with soybean, flax, oilseed rape, safflower, sunflower, *Camelina*, indian mustard or *Calendula* being especially preferred.

Further host cells which can be used for cloning the nucleic acid sequences used in the process according to the

invention are detailed in: Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, Calif. (1990).

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, Calif. (1990) 119-128.

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 is derived from the actual transgenic plant and/or can be used for bringing about the transgenic plant.

Transgenic plants or advantageously the seeds thereof which comprise the polyunsaturated fatty acids in particular ARA, EPA and/or DHA, 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 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.

In principle, the process according to the invention is also suitable for the production of polyunsaturated fatty acids, in particular ARA, EPA and/or DHA, in plant cell cultures, followed by obtaining the fatty acids from the cultures. In particular, they may take the form of suspension or callus cultures.

However, the compound produced in the process according to the invention can also be isolated from the plants, advantageously the plant seeds, in the form of their oils, fat, lipids and/or free fatty acids. Polyunsaturated fatty acids produced by this process, in particular ARA, EPA and/or DHA, can be harvested by harvesting the plants or plant seeds either from the culture in which they grow, or from the field.

In a further preferred embodiment, this process furthermore comprises the step of obtaining the oils, lipids or free fatty acids from the plant or from the crop. The crop may, for example, take the form of a greenhouse- or field-grown plant crop.

The oils, lipids or free fatty acids can be isolated 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.

Thereafter, the resulting products which comprise the polyunsaturated fatty acids 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 fuller's earth or active charcoal. At the end, the product is deodorized, for example using steam.

The PUFAs or LCPUFAs produced by this process are preferably C<sub>18</sub>-, C<sub>20</sub>- or C<sub>22</sub>-fatty acid molecules, advantageously C<sub>20</sub>- or C<sub>22</sub>-fatty acid molecules, with at least two double bonds in the fatty acid molecule, preferably with three, four, five or six double bonds, especially preferably with four, five or six double bonds. These C<sub>18</sub>-, C<sub>20</sub>- or C<sub>22</sub>-fatty acid molecules can be isolated from the plant in the form of an oil, a lipid or a free fatty acid. Examples of suitable plants are those mentioned above. Suitable organisms are transgenic plants.

One embodiment of the invention are therefore oils, lipids or fatty acids or fractions thereof which have been prepared by the above-described process, especially preferably oils, lipids or a fatty acid composition which comprise PUFAs and originate from transgenic plants.

The fatty acids obtained in the process are also suitable as starting material for the chemical synthesis of products of value. For example, they can be used together or alone for the production of pharmaceuticals, foodstuffs, feedstuffs or cosmetics.

As described above, these oils, lipids or fatty acids advantageously comprise 6 to 15% of palmitic acid, 1 to 6% of stearic acid, 7-85% of oleic acid, 0.5 to 8% of vaccenic acid, 0.1 to 1% of arachic acid, 7 to 25% of saturated fatty acids, 8 to 85% of monounsaturated fatty acids and 60 to 85% of polyunsaturated fatty acids, in each case based on 100% and on the total fatty acid content of the organisms. Advantageous polyunsaturated fatty acids which are present in the fatty acid esters or fatty acid mixtures are preferably at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 or 1% of arachidonic acid, based on the total fatty acid content. Moreover, the fatty acid esters or fatty acid mixtures which have been produced by the process of the invention advantageously comprise fatty acids selected from the group of the fatty acids erucic acid (13-docosaenoic acid), steric acid (9,10-methyleneoctadec-9-enoic acid), malvalic acid (8,9-methyleneheptadec-8-enoic acid), chaulmoogric acid (cyclopentenedodecanoic acid), furan fatty acid (9,12-epoxyoctadeca-9,11-dienoic acid), vernolic acid (9,10-epoxyoctadec-12-enoic acid), tariric acid (6-octadecynoic acid), 6-nonadecynoic acid, santalbic acid (11-octadecen-9-ynoic acid), 6,9-octadecenynoic acid, pyrulic acid (10-heptadecen-8-ynoic acid), crepenynic acid (9-octadecen-12-ynoic acid), 13,14-dihydrooropheic acid, octadecen-13-ene-9,11-diyonic acid, petroselenic acid (cis-6-octadecenoic acid), 9c,12t-octadecadienoic acid, calendulic acid (8t10t12c-octadecatrienoic acid), catalpic acid (9t11t13c-octadecatrienoic acid), eleostearic acid (9c11t13t-octadecatrienoic acid), jacaric acid (8c10t12c-octadecatrienoic acid), punicic acid (9c11t13c-octadecatrienoic acid), parinaric acid (9c11t13t15c-octadecatetraenoic acid), pinolenic acid (all-cis-5,9,12-octadecatrienoic acid), laballic acid (5,6-octadecadienallenic acid), ricinoleic acid (12-hydroxyoleic acid) and/or coriolic acid (13-hydroxy-9c,11t-octadecadienoic acid). The abovementioned fatty acids are, as a rule, advantageously only found in traces in the fatty acid esters or fatty acid mixtures produced by the process according to the invention, that is to say that, based on the total fatty acids, they occur to less than 30%, preferably to less than 25%, 24%, 23%, 22% or 21%, especially preferably to less than 20%, 15%, 10%, 9%, 8%, 7%, 6% or 5%, very especially preferably to less than 4%, 3%, 2% or 1%. In a further preferred form of the invention, these abovementioned fatty

acids occur in amounts of less than 0.9%, 0.8%, 0.7%, 0.6% or 0.5%, especially preferably less than 0.4%, 0.3%, 0.2%, 0.1%, based on the total fatty acids. The fatty acid esters or fatty acid mixtures produced by the process according to the invention advantageously comprise less than 0.1%, based on the total fatty acids, and/or no butyric acid, no cholesterol, no clupanodonic acid (=docosapentaenoic acid, C22:5<sup>Δ4,8,12,15,21</sup>) and no nisinic acid (tetracosahexaenoic acid, C23:6<sup>Δ3,8,12,15,18,21</sup>).

As a rule, the abovementioned fatty acids are advantageously only found in traces in the fatty acid esters or fatty acid mixtures produced by the process according to the invention, that is to say that, based on the total fatty acids, they are found in amounts of less than 30%, preferably less than 25%, 24%, 23%, 22% or 21%, especially preferably less than 20%, 15%, 10%, 9%, 8%, 7%, 6% or 5%, very especially preferably less than 4%, 3%, 2% or 1%. In a further preferred embodiment of the invention, these abovementioned fatty acids are found relative to the total fatty acids in amounts of less than 0.9%, 0.8%, 0.7%, 0.6% or 0.5%, especially preferably less than 0.4%, 0.3%, 0.2%, 0.1%. The fatty acid esters or fatty acid mixtures produced by the process according to the invention advantageously comprise less than 0.1% based on the total fatty acids and/or no butyric acid, no cholesterol, no clupanodonic acid (=docosapentaenoic acid, C22:5<sup>Δ4,8,12,15,21</sup>) and no nisinic acid (tetracosahexaenoic acid, C23:6<sup>Δ3,8,12,15,18,21</sup>).

The oils, lipids or fatty acids according to the invention advantageously comprise at least 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or 10%, advantageously at least 11%, 12%, 13%, 14%, 15%, 16% or 17%, especially advantageously at least 18%, 19%, 20%; 21%, 22%, 23%, 24% or 25% of ARA or at least 0.5%; 1%, 2%, 3%, 4%, 5% or 6%, advantageously at least 7%, 8%, 9%, 10% or 11%, especially advantageously at least 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19% or 20% of EPA or at least 0.01%, 0.02%, 0.03%, 0.04% or 0.05% or 0.06%, advantageously at least 0.07%, 0.08%, 0.09% or 0.1%, especially advantageously at least 0.2%, 0.3% or 0.4% of DHA, based on the total fatty acid content of the production organism, advantageously of a plant, especially advantageously of an oil crop such as soybean, oilseed rape, coconut, oil palm, safflower, flax, hemp, castor-oil plant, *Calendula*, peanut, cacao bean, sunflower or the abovementioned other monocotyledonous or dicotyledonous oil crops. All percentages are by weight.

Owing to the nucleic acid sequences according to the invention, or the nucleic acid sequences used in the process according to the invention, it is possible to obtain an increase in the yield of polyunsaturated fatty acids, mainly ARA and EPA, but also DHA, of at least 50, 80 or 100%, advantageously at least 150, 200 or 250%, especially advantageously at least 300, 400, 500, 600, 700, 800 or 900%, very advantageously at least 1000, 1100, 1200, 1300, 1400 or 1500% in comparison with the non-transgenic starting plant, for example a plant such as *Brassica juncea*, *Brassica napus*, *Camelina sativa*, *Arabidopsis thaliana* or *Linum usitatissimum* when using a GC analysis for comparison purposes, see Examples.

The lipids and/or oils produced in the process according to the invention have a higher content of the unsaturated fatty acids oleic acid, linoleic acid and  $\alpha$ -linolenic acid in the sn2-position in comparison with the other positions sn1 and sn3. A higher content is understood as meaning ratios of (sn1:sn2:sn3) 1:1.1:1, 1:1.5:1 to 1:3:1. Also, the arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid produced in the process likewise show, in the lipids and/or oils, a preference for the sn2-position in the triglyceride in

comparison with the positions sn1 and sn3 of advantageously 1:1.1:1, 1:1.5:1 to 1:3:1.

As described above, the polyunsaturated C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids, produced in the process, with four, five or six double bonds in the molecule will in the seed of plants which comprise no, or only very small amounts, of C12:0- or C14:0-fatty acids. Even shorter saturated fatty acids such as the fatty acids C4:0, C6:0, C8:0 or C10:0, too, should not be present in the lipid and/or oil, or only in small amounts. Only small amounts are understood as meaning, advantageously, amounts which, when analyzed by GC, advantageously amount to less than 5, 4, 3, 2 or 1%, advantageously less than 0.9, 0.8, 0.7, 0.6 or 0.5%, especially advantageously less than 0.4, 0.3, 0.2 or 0.1%, very especially preferably less than 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 or 0.01 units GC peak area. The fatty acid C16:0 should advantageously be in the range of from 1 to 28% units GC peak area. Advantageously, the fatty acid C16:0 should be present in amounts of less than 25%, 20%, 15% or 10%, advantageously less than 9%, 8%, 7%, 6% or 5%, especially advantageously of less than 4%, 3%, 2% or 1% units GC peak area or not at all in the lipids, oils and/or free fatty acids. The fatty acid C16:1 should advantageously amount to less than 1, 0.5, 0.4, 0.3, 0.2 or 0.1%, especially advantageously 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02 or 0.01 units GC peak area. Very especially preferably, the fatty acid C16:1 should not be present in the oils and/or lipids produced in the process. The same applies to the fatty acids C15:0, C17:0, C16:1<sup>Δ3</sup>trans, C16:4<sup>Δ4,7,10,13</sup> and C18:5<sup>Δ3,6,9,12,15</sup>. Besides oleic acid (C18:1<sup>Δ9</sup>), the isomers (C18:1<sup>Δ7</sup>, C18:1<sup>Δ11</sup>) may also be present in the lipids, oils or free fatty acids. Advantageously in amounts of less than 5%, 4%, 3%, 2% or 1%, measured as units GC peak area. Each of the fatty acids C20:0, C20:1, C24:0 and C24:1 should be present in a range of from 0 to 1%, 0 to 3% and 0 to 5% units GC peak area, respectively. Moreover, little dihomo- $\gamma$ -linolenic acid (=DGLA) in terms of units GC peak area should be detectable in the seed oil and/or seed lipid in the GC analysis. Little is understood as meaning less than 2, 1.9, 1.8, 1.7, 1.6 and 1.5%, advantageously less than 1.4, 1.3, 1.2, 1.1 or 1%, especially advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5 or 0.4% in terms of units GC peak area.

In a preferred embodiment of the process, DGLA and ARA should be produced in a ratio of from 1:1 up to 1:100, advantageously 1:2 up to 1:80, especially advantageously 1:3 up to 1:70, very especially preferably 1:5 up to 1:60.

In a further preferred embodiment of the process, DGLA and EPA should be produced in a ratio of from 1:1 up to 1:100, advantageously 1:2 up to 1:80, especially advantageously 1:3 up to 1:70, very especially preferably 1:5 up to 1:60.

The lipids, oils and/or free fatty acids produced in the process according to the invention should advantageously have a high content of unsaturated fatty acids, advantageously of polyunsaturated acids, of at least 30, 40 or 50% by weight, advantageously of at least 60, 70 or 80% by weight, based on the total fatty acid content in the seeds of the transgenic plants.

All saturated fatty acids together should advantageously only account for a small amount in the lipids, oils and/or free fatty acids, preferably used plants. In this context, a small amount is understood as meaning an amount of less than 15%, 14%, 13%, 12%, 11% or 10%, preferably less than 9%, 8%, 7% or 6% in units GC peak area.

Lipids, oils and/or free fatty acids produced in the process should advantageously have an erucic acid content of less than 2% by weight based on the total fatty acid content of the

plant. Advantageously, no erucic acid should be present in the lipids and/or oils. Also, the content of saturated fatty acids C16:0 and/or C18:0 should advantageously be less than 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10% by weight, advantageously less than 9, 8, 7, 6 or 5% by weight, based on the total fatty acid content of the lipids and/or oils. Also, longer fatty acids such as C20:0 or C22:1 should not be present at all or only in small amounts of advantageously less than 4, 3, 2 or 1% by weight, advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 or 0.1% by weight, based on the total fatty acid content of the lipids and/or oils. Typically, no, or only small amounts, of C16:1 are present as fatty acid in the lipids and/or oils produced in the process according to the invention. Small amounts are advantageously understood as meaning fatty acid contents of less than 4, 3, 2 or 1% by weight, advantageously less than 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 or 0.1% by weight, based on the total fatty acid content of the lipids and/or oils.

The oils, lipids, fatty acids or fatty acid mixtures according to the invention which are obtained after pressing are referred to as what is known as crude oils. They still comprise all of the oil and/or lipid contents and also compounds which are soluble in these. Such compounds are the various tocopherols such as  $\alpha$ -tocopherol,  $\beta$ -tocopherol,  $\gamma$ -tocopherol and/or  $\delta$ -tocopherol or phytosterols such as brassicasterol, campesterol, stigmasterol,  $\beta$ -sitosterol, sitostanol,  $\Delta^5$ -avenasterol,  $\Delta^5,24$ -stigmastadienol,  $\Delta^7$ -stigmastanol or  $\Delta^7$ -avenasterol. These compounds are present in a range of from 1 to 1000 mg/100 g, advantageously 10 to 800 mg/100 g of lipid or oil. Triterpenes such as germaniol, amyirin, cycloartenol and others may also be present in these lipids and oils. These lipids and/or oils comprise the polyunsaturated fatty acids produced in the process, such as ARA, EPA and/or DHA, bound in polar and nonpolar lipids such as phospholipids, for example phosphatidylcholine, phosphatidylethanolamine, phosphatidylinositol, phosphatidylserine, phosphatidylglycerol, galactolipids, monoglycerides, diglycerides or triglycerides, to mention but a few. Lysophospholipids may also be present in the lipids and/or oils. These components of the lipids and/or oils can be separated from one another by suitable processes. Cholesterol is not present in these crude oils.

A further embodiment according to the invention is the use of the oil, lipid, fatty acids and/or the fatty acid composition in feedstuffs, foodstuffs, cosmetics or pharmaceuticals. The oils, lipids, fatty acids or fatty acid mixtures according to the invention 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. Typical of such fish oils short-chain fatty acids such as C12:0, C14:0, C14:1, branched C15:0, C15:1, C16:0 or C16:1. Polyunsaturated C16-fatty acids such as C16:2, C16:3 or C16:4, branched C17:0, C17:1, branched C18:0 and C19:0 and also C19:1 and C19:2 are also found in fish oil. Such fatty acids are typical of fish oils and are only found rarely, or not at all, in vegetable oils. Economically relevant fish oils are, for example, anchovy oil, menhaden oil, tuna oil, sardine oil, herring oil, mackerel oil, whale oil and salmon oil. These lipids and/or oils of animal origin can be used for mixing with the oils according to the invention in the form of crude oils, i.e. in the form of lipids and/or oils which have not yet been purified, or else various purified fractions may be used for mixing.

A further embodiment according to the invention is the use of the oil, lipid, fatty acids and/or fatty acid compositions in feedstuffs, foodstuffs, cosmetics or pharmaceuticals.

The oils, lipids, fatty acids or fatty acid mixtures according to the invention 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. Again, these oils, lipids, fatty acids or fatty acid mixtures, which are composed of vegetable and animal constituents, may be used for the preparation of foodstuffs, feedstuffs, cosmetics or pharmaceuticals.

The term "oil", "lipid" or "fat" is understood as meaning a fatty acid mixture comprising unsaturated or 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, dihomogamma-linolenic acid, arachidonic acid,  $\alpha$ -linolenic acid, stearidonic acid, eicosatetraenoic acid, eicosapentaenoic acid, docosapentaenoic acid or docosahexaenoic acid. 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%, 85% 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.

The polyunsaturated fatty acids with advantageously at least two double bonds which are produced in the process are, as described above, for example sphingolipids, phosphoglycerides, lipids, glycolipids, phospholipids, monoacylglycerol, diacylglycerol, triacylglycerol or other fatty acid esters.

Starting from the polyunsaturated fatty acids with advantageously at least five or six double bonds, which acids have been prepared in the process according to the invention, the 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,  $H_2SO_4$ . The fatty acids can also be liberated directly without the above-described processing step.

Mosses and algae are the only known plant systems which produce substantial amounts of polyunsaturated fatty acids such as arachidonic acid (ARA) and/or eicosapentaenoic acid (EPA) and/or docosahexaenoic acid (DHA). Mosses comprise PUFAs in membrane lipids, while algae, organisms which are related to algae and a few fungi also accumulate substantial amounts of PUFAs in the triacylglycerol fraction.

This is why nucleic acid molecules which are isolated from such strains which also accumulate PUFAs in the triacylglycerol fraction are particularly advantageous for the process according to the invention and thus for the modification of the lipid and PUFA production system in a host, in particular plants such as oil crops, for example oilseed rape, canola, linseed, hemp, soybeans, sunflowers and borage. They can therefore be used advantageously in the process according to the invention.

After their introduction into 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.

Naturally, the coexpression of a plurality of genes can be effected not only by introducing the genes on a shared recombinant nucleic acid construct. Rather, individual genes can also be introduced separately—simultaneously or in succession, on a variety of constructs. In this case, the simultaneous presence in the plant which coexpresses all of the genes is ensured by using different selection markers. This plant can be the product of one or more transformation procedures, or else be a hybridization product of plants comprising one or more of the genes.

Substrates which are advantageously suitable for the nucleic acids which are used in the process according to the invention and which encode polypeptides with  $\omega$ 3-desaturase,  $\Delta$ 4-desaturase,  $\Delta$ 5-desaturase,  $\Delta$ 6-desaturase,  $\Delta$ 8-desaturase,  $\Delta$ 12-desaturase,  $\Delta$ 5-elongase,  $\Delta$ 6-elongase and/or  $\Delta$ 9-elongase activity and/or the further nucleic acids used, such as the nucleic acids which encode polypeptides 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, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) are advantageously  $C_{16}$ -,  $C_{18}$ -,  $C_{20}$ - or  $C_{22}$ -fatty acids. The fatty acids converted as substrates in the process are preferably converted in the form of their acyl-CoA esters and/or their phospholipid esters. It is advantageous to use, in the process, desaturases with specificity for the acyl-CoA esters. The advantage here is that a substitution between the phospholipid esters, which are generally the substrate of the desaturation, and the acyl-CoA esters, can be dispensed with. Thus, a further enzyme step which, as has been shown, is limiting in some cases, can be dispensed with.

To produce the long-chain PUFAs according to the invention, the polyunsaturated  $C_{16}$ - or  $C_{18}$ -fatty acids must first be desaturated by the enzymatic activity of a desaturase and subsequently be elongated by at least two carbon atoms via an elongase. After one elongation cycle, this enzyme activity gives  $C_{18}$ - or  $C_{20}$ -fatty acids and after two elongation cycles  $C_{20}$ - or  $C_{22}$ -fatty acids. The activity of the desaturases and elongases used in the process according to the invention preferably leads to  $C_{18}$ -,  $C_{20}$ - and/or  $C_{22}$ -fatty acids, advantageously with at least two double bonds in the fatty acid molecule, preferably with three, four, five or six double bonds, especially preferably to give  $C_{20}$ - and/or  $C_{22}$ -fatty acids with, at least three double bonds in the fatty acid molecule, preferably with three, four, five or six double bonds, very specially preferably with four, five or six double bonds in the molecule/Products of the process according to the invention which are especially preferred are arachidonic acid, eicosapentaenoic acid and/or docosahexaenoic acid. The  $C_{18}$ -fatty acids with at least two double bonds in the

fatty acid can be elongated by the enzymatic activity according to the invention in the form of the free fatty acid or in the form of the esters, such as phospholipids, glycolipids, sphingolipids, phosphoglycerides, monoacylglycerol, diacylglycerol or triacylglycerol.

The preferred biosynthesis site of the fatty acids, oils, lipids or fats in the plants which are advantageously used is, for example, in general the seed or cell strata of the seed, so that seed-specific expression of the nucleic acids used in the process makes sense. However, it is obvious that the biosynthesis of fatty acids, oils or lipids need not be limited to the seed tissue, but can also take place in a tissue-specific manner in all the other parts of the plant, for example in epidermal cells or in the tubers.

Owing to the use of the nucleic acids according to the invention which encode a  $\Delta$ 5-elongase, the polyunsaturated fatty acids produced in the process can be increased by at least 5%, preferably by at least 10%, especially preferably by at least 20%, very especially preferably by at least 50% in comparison with the wild type of the organisms which do not comprise the nucleic acids recombinantly.

In principle, the polyunsaturated fatty acids produced by the process according to the invention in the plants used in the process can be increased in two different ways. Either the pool of free polyunsaturated fatty acids and/or the content of the esterified polyunsaturated fatty acids produced via the process can be enlarged. Advantageously, the pool of esterified polyunsaturated fatty acids in the transgenic organisms is enlarged by the process according to the invention.

A further subject matter according to the invention are isolated nucleic acid sequences which encode polypeptides with  $\Delta$ 5-elongase, the  $\Delta$ 5-elongases encoded by the nucleic acid sequences converting  $C_{20}$ -fatty acids having at least four double bonds in the fatty acid molecule; which are advantageously ultimately incorporated into diacylglycerides and/or triacylglycerides.

A further subject matter of the invention is thus an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 5-elongase and which has the sequence shown in SEQ ID NO: 197.

A further subject matter of the invention is an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 6-elongase activity and which has the sequence shown in SEQ ID NO: 199.

Yet a further subject matter of the invention is an isolated nucleic acid sequence which encodes polypeptides with  $\Delta$ 6-desaturase activity and which has the sequence shown in SEQ ID NO: 201.

The subject matters of the invention likewise extend to a recombinant nucleic acid molecule comprising:

- one or more copies of a promoter which is active in plant cells, preferably in seed cells,
- at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201 which encodes a  $\Delta$ 6-desaturase activity,
- at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 11 which encodes a  $\Delta$ 5-desaturase activity,
- at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199 which encodes a  $\Delta$ 6-elongase activity, and
- one or more copies of a terminator sequence.

Advantageously, an additional nucleic acid sequence with the sequence shown in SEQ ID NO: 195 and which encodes a  $\Delta$ 12-desaturase may also advantageously be present in the recombinant abovementioned nucleic acid molecule.

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In a further advantageous embodiment, an additional nucleic acid sequence with the sequence shown in SEQ ID NO: 197 and which encodes a  $\Delta 5$ -elongase may also be present in the recombinant nucleic acid molecule.

Besides these abovementioned sequences, further biosynthetic genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [=acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lyso-phospholipid 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) may also be introduced into the recombinant nucleic acid molecule.

These genes are by preference genes of the fatty acid or lipid metabolism selected from the group consisting of  $\Delta 4$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 9$ -desaturase or  $\Delta 9$ -elongase.

Yet a further subject matter of the invention are gene constructs which comprise the nucleic acid sequences SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 according to the invention, the nucleic acid being functionally linked to one or more regulatory signals.

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 such as an alga or an animal. By preference, the nucleic acid sequences are derived from the order *Salmoniformes*, *Xenopus* or *Ciona*, 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 nucleic acid sequences used in the process which encode proteins with  $\omega 3$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 9$ -desaturase,  $\Delta 12$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase or  $\Delta 9$ -elongase activity are advantageously introduced by themselves or by preference in combination with an expression cassette (=nucleic acid construct) which the expression of the nucleic acids in a plant. More than one nucleic acid sequence of an enzymatic activity such as, for example, a  $\Delta 12$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or to 3-desaturase may be present in the nucleic acid construct.

For introduction into the plant, the nucleic acids used in the process are advantageously subjected to amplification and ligation in the known manner as described above.

A series of mechanisms exist which enable a modification of the  $\Delta 12$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 6$ -desaturase and/or  $\omega 3$ -desaturase protein according to the invention and of the further proteins used in the process, such as the  $\Delta 12$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase or  $\Delta 4$ -desaturase proteins, so that the yield, production and/or production efficiency of the advantageously polyunsaturated fatty acids in a plant, preferably in an oil crop plant, can be influenced directly as the result of this modified protein: The number or activity of the  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase proteins or genes can be increased so that larger amounts of the gene products and thus ultimately larger amounts of the compounds of the general formula I are produced. A de-novo synthesis in a plant which had lacked

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the activity and ability to biosynthesize the compounds prior to the introduction of the gene(s) in question is also possible. The same also applies analogously to the combination with further desaturases or elongases or further enzymes from the fatty acid and lipid metabolism. Also, the use of different, divergent sequences, i.e. sequences which differ at the DNA sequence level, may be advantageous, or the use of promoters for gene expression which makes possible a different temporal gene expression, for example depending on the degree of maturity of a seed or oil-storing tissue.

By introducing a  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase gene into a plant alone or in combination with other genes into a cell may not only increase the biosynthetic flux towards the end product, but also increase the corresponding triacylglycerol composition or create it de novo. Likewise, the number or activity of other genes in the import of nutrients required for the biosynthesis of one or more fatty acids, oils, polar and/or neutral lipids may 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 PUFAs is increased further, as described hereinbelow. By optimizing the activity or increasing the number of one or more  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase genes which are involved in the biosynthesis of these compounds, or by destroying the activity of one or more genes which are involving in breaking down these compounds, it may be possible to increase the yield, production and/or production efficiency of fatty acid and lipid molecules from organisms and advantageously from plants.

The isolated nucleic acid molecules used in the process according to the invention encode proteins or parts of these, the proteins or the individual protein or parts thereof comprising an amino acid sequence with sufficient homology with an amino acid sequence which is shown in the sequences SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36; SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54; SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76; SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202 so that the proteins or parts thereof retain a  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase activity. The proteins or parts thereof, which is/are encoded by the nucleic acid molecule(s), preferably still retain(s) its/their essential enzymatic activity and the ability of participating in the metabolism of compounds required in the formation of cell membranes or lipid bodies in organisms, advantageously in plants, or in the transport of molecules across these membranes. Advantageously, the proteins encoded by the nucleic



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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 sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202. For the purposes of the invention, homology or homologous is understood as meaning identity or identical.

The homology was calculated over the entire amino acid or nucleic acid sequence region. A series of programs which are based on the various algorithms are available for comparing different sequences. In this context, the algorithms of Needleman and Wunsch or Smith and Waterman give especially reliable results. To carry out the sequence alignments, 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 Wis., USA 53711 (1991)], were used. The sequence homology values stated above as percentages were determined over the entire sequence region using the program GAP, with 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 sequence alignments.

Essential enzymatic activity of the  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase used in the process according to the invention is understood as meaning that, in comparison with the proteins/enzymes encoded by the sequence SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ

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ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 and their derivatives retain at least an enzymatic activity of at least 10%, preferably 20%, especially preferably 30% and very especially 40% and can thus participate in the metabolism of compounds required in the synthesis of fatty acids, fatty acid esters such as diacylglycerides and/or triacylglycerides in an organism, advantageously a plant or plant cell, or in the transport of molecules across membranes, meaning  $C_{18}$ -,  $C_{20}$ - or  $C_{22}$ -carbon chains in the fatty acid molecule with double bonds at least two, advantageously three, four, five or six positions.

The nucleic acids which can be used advantageously 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*, *Cryptocodium cohnii*, *Ceratodon purpureus*, *Isochrysis galbana*, *Aleurita farinosa*, *Thraustochytrium* sp., *Muscarioides vialii*, *Mortierella alpina*, *Borago officinalis*, *Phaeodactylum tricornutum*, *Caenorhabditis elegans* or especially advantageously from *Oncorhynchus mykiss*, *Euglena gracilis*, *Thalassiosira pseudonona* or *Cryptocodium cohnii*.

As an alternative, it is possible to use, in the process according to the invention, nucleotide sequences which encode a  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase and which hybridize, advantageously under stringent conditions, with a nucleotide sequence as shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201.

The nucleic acid sequences used in the process are advantageously introduced in an expression cassette which enables the expression of the nucleic acids in organisms such as microorganisms or plants.

In this context, the nucleic acid sequences which encode the  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase are advantageously linked functionally with one or more regulatory signals to increase gene expression. These regulatory sequences should enable the targeted expression of the genes and protein expression. For

example, this may mean, depending on the host plant, 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 inductors or repressors bind and thus regulate the expression of the nucleic acid. In addition to these new regulatory sequences, or instead of these sequences, the natural regulation 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 the natural regulation has been switched off and the expression of the genes enhanced. The expression cassette (=expression construct= gene construct) may, however, also be simpler in construction, that is to say no additional regulatory signals were 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 was mutated in such a way that regulation no longer takes place and/or gene expression is enhanced. These modified promoters can be placed before the natural gene in order to increase the activity either in the form of part-sequences (=promoter with parts of the nucleic acid sequences according to the invention) or else alone. Moreover, the gene construct can advantageously also comprise one or more what are known as "enhancer sequences" in functional linkage with the promoter, and these enable an increased expression of the nucleic acid sequence. Also, it is possible to insert additional advantageous sequences at the 3' end of the DNA sequences, such as further regulatory elements or terminators. The  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 4$ -desaturase,  $\Delta 5$ -desaturase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 5$ -elongase,  $\Delta 6$ -elongase and/or  $\Delta 9$ -elongase genes can be present in the expression cassette (=gene construct) as one or more copies. Advantageously, only in each case one copy of the genes is present in the 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 inserted in the genome. It is advantageous for the insertion of further genes in the host genome when the genes to be expressed are present together in one gene construct.

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

Advantageous regulatory sequences for the new process are present for example in promoters such as the plant promoters CaMV/35S [Franck et al., Cell 21 (1980) 285-294], PRP 1 [Ward et al., Plant Mol. Biol. 22 (1993)], SSU, OCS, lib4, usp, STLS1, B33, nos or in the ubiquitin or phaseolin promoter. Also advantageous in this context are inducible promoters, such as the promoters described in EP-A-0 388 186 (benzylsulfonamide-inducible), Plant J. 2, 1992:397-404 (Gatz et al., tetracyclin-inducible), EP-A-0 335 528 (abscisic-acid-inducible) or WO 93/21334 (ethanol- or cyclohexenol-inducible). Further suitable plant promoters are the promoter of cytosolic FBPase or the ST-LSI promoter from potato (Stockhaus et al., EMBO J. 8, 1989, 2445), the phosphoribosyl-pyrophosphate amidotransferase promoter from *Glycine max* (Genbank accession No.

U87999) or the node-specific promoter described in EP-A-0 249 676. Especially advantageous promoters are promoters which enable 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 in accordance with the practice, but also other promoters such as the LeB4, DC3, phaseolin or napin promoters. Further especially advantageous promoters are seed-specific promoters which can be used for monocotyledonous or dicotyledonous plants and which are described in U.S. Pat. No. 5,608,152 (napin promoter from oilseed rape), WO 98/45461 (oleosin promoter from *Arabidopsis*), U.S. Pat. No. 5,504,200 (phaseolin promoter from *Phaseolus vulgaris*), WO 91/13980 (Bce4 promoter from *Brassica*), by Baeumlein et al., Plant J., 2, 2, 1992:233-239 (LeB4 promoter from a legume), these promoters being suitable for dicots. The following promoters are suitable for example for monocots: Ipt-2 or Ipt-1 promoter from barley (WO 95/15389) and WO 95/23230), hordein promoter from barley and other promoters which are suitable and which are described in WO 99/16890.

In principle, it is possible to use all natural promoters together with their regulatory sequences, such as those mentioned above, for the novel process. Likewise, it is possible and advantageous to use synthetic promoters, either additionally or alone, especially when they mediate a seed-specific expression, such as, for example, as described in WO 99/16890.

To obtain a particularly high PUFA content especially in transgenic plants, the PUFA biosynthesis genes should advantageously be expressed in a seed-specific manner in oilseed crops. To this end, it is possible to use seed-specific promoters 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. Such advantageous promoters are detailed further above, for example the USP, Vicilin, Napin, Oleosin, Phaseolin, Bce4, LegB4, Lpt2, Ipt1, Amy32b, Amy 6-6, Aleurain or Bce4 promoter.

Moreover, chemically inducible promoters are also advantageously useful in the process according to the invention.

Further advantageous promoters which are advantageously suitable for expression in soybean are the promoters of the  $\beta$ -conglycinin  $\alpha$ -subunit, of the  $\beta$ -conglycinin  $\beta$ -subunit, of the Kunitz trypsin inhibitor, of annexin, of glycinin, of albumin 2S, of legumin A1, of legumin A2 and that of BD30.

Especially advantageous promoters are the USP, LegB4, Fad3, SBP, DC-3 or cruciferin 820 promoter.

Advantageous regulatory sequences which are used for the expression of the nucleic acid sequences used in the process according to the invention are terminators for the expression advantageously in soybean are Leg2A3', Kti3', Phas3', BD30 3' or A1S3'.

Especially advantageous terminators are the A7T, OCS, LeB3T or cat terminator.

To ensure a stable integration of the biosynthetic genes in the transgenic plant over several generations, each of the nucleic acids used in the process and which encodes  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase should, as described above, be under the control of its own promoter, preferably of a different promoter, since repeating sequence motifs can lead to instability of the T-DNA, or to recombination events. As

described above, the gene construct can also comprise further genes which are to be introduced into the plant.

In this context, the regulatory sequences or factors used advantageously for the expression of the nucleic acids used in the process according to the invention can, as described above, preferably have a positive effect on the gene expression of the genes introduced.

These advantageous vectors; preferably expression vectors, comprise the nucleic acids used in the process which encode the  $\Delta 12$ -desaturases,  $\omega 3$ -desaturases,  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases or  $\Delta 4$ -desaturases, or a nucleic acid construct which the used nucleic acid alone or in combination with further biosynthesis genes of the fatty acid or lipid metabolism such as the acyl-CoA:lysophospholipid acyl-transferases,  $\omega 3$ -desaturases,  $\Delta 4$ -desaturases,  $\Delta 5$ -desaturases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 9$ -desaturases,  $\Delta 12$ -desaturases,  $\omega 3$ -desaturases,  $\Delta 5$ -elongases,  $\Delta 6$ -elongases and/or  $\Delta 9$ -elongases.

As described and 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.

The recombinant expression vectors used can be designed for expressing  $\Delta 12$ -desaturases,  $\omega 3$ -desaturases,  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases and/or  $\Delta 4$ -desaturases in prokaryotic or eukaryotic cells. This is advantageous since, for the sake of simplicity, intermediate steps of the vector construction are frequently carried out in microorganisms. For example, the  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase genes can be expressed in bacterial cells, insect cells (using baculovirus expression vectors), yeast cells 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*, *Tetrahymana*, *Paramecium*, *Colpidium*, *Glaucoma*, *Platyophrya*, *Potomacus*, *Desaturaseudocohnlembus*, *Euplotes*, *Engelmanniella* and *Stylonychia*, in particular the genus *Stylonychia lemnae*, using vectors following a transformation process 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, Fla., chapter 6/7, pp. 71-119 (1993); F. F. White, B. Jené 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, Calif. (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.

In most cases, the expression of proteins in prokaryotes, advantageously for the simple detection of the enzyme activity for example for detecting the desaturase or elongase activity, is performed using vectors comprising constitutive or inducible promoters which control the expression of fusion or nonfusion proteins. Examples of typical fusion expression vectors are pGEX (Pharmacia Biotech Inc; Smith, D. B., and Johnson, K. S. (1988) *Gene* 67:31-40), pMAL (New England Labs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.), where glutathione S-transferase (GST), maltose-E-binding protein and protein A, respectively, are fused with the recombinant target protein.

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, Calif. (1990) 60-89). The target gene expression of the pTrc vector is based on the transcription from a hybrid trp-lac fusion promoter by host RNA polymerase. The target gene expression from the pET 11d vector is based on the transcription of a T7-gn10-lac fusion promoter, which is mediated by a coexpressed viral RNA polymerase (T7gn1). 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.

The skilled worker is familiar with other vectors which are suitable in prokaryotic organisms, these vectors are, for example *E. coli*, pLG338, pACYC184, the pBR series such as pBR322, the pUC series such as pUC18 or pUC19, the M113mp 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.

In a further embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in the yeast *S. cerevisiae* comprise pYeDesaturase1 (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, Calif.). 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. Bennett & 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, the  $\Delta 12$ -desaturases,  $\omega 3$ -desaturases,  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases and/or  $\Delta 4$ -desaturases can be expressed in insect cells using baculovirus expression vectors. Baculovirus 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 of possible suitable vectors. 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). Further suitable expression systems for prokaryotic and eukaryotic

cells, see the chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

To detect the enzyme activity,  $\Delta 12$ -desaturases,  $\omega$ -3-desaturases,  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases and/or  $\Delta 4$ -desaturases can be expressed in single-cell plant cells (such as algae), see Falciatore et al., 1999, *Marine Biotechnology* 1 (3):239-251 and the references cited therein, and 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.

A plant expression cassette preferably comprises regulatory sequences which are capable of controlling the gene expression in plant cells and which are functionally linked 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 the gene 3 of the Ti plasmid pTiACH5, which is known as octopine synthase (Gielen et al., *EMBO J.* 3 (1984) 835 et seq.) or functional equivalents of these, but all other terminators which are functionally active in plants are also suitable.

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

As described above, plant gene expression must be functionally linked to a suitable promoter which performs the expression of the gene in a timely, cell-specific or tissue-specific manner. Promoters which can be used 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 U.S. Pat. No. 5,352,605 and WO 84/02913) or plant promoters such as the promoter of the Rubisco small subunit, which is described in U.S. Pat. No. 4,962,028.

Other preferred sequences for the use in functional linkage in plant gene expression cassettes are targeting sequences which are required for targeting the gene product into its relevant cell compartment (for a review, see Ker-mode, *Crit. Rev. Plant Sci.* 15, 4 (1996) 285-423 and references cited therein), for example into the vacuole, the nucleus, all types of plastids, such as amyloplasts, chloroplasts, chromoplasts, the extracellular space, the mitochondria, the endoplasmic reticulum, oil bodies, peroxisomes and other compartments of plant cells.

As described above, plant gene expression can also be facilitated via a chemically inducible promoter (for a review, see Gatz 1997, *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, 48:89-108). Chemically inducible promoters are particularly suitable if it is desired that genes are expressed 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.

Promoters which respond to biotic or abiotic stress conditions are also suitable promoters, for example the pathogen-inducible PRP1-gene promoter (Ward et al., *Plant Mol. Biol.* 22 (1993) 361-366), the heat-inducible hsp80 promoter from tomato (U.S. Pat. No. 5,187,267), the cold-inducible alpha-amylase promoter from potato (WO 96/12814) or the wound-inducible pinII promoter (EP-A-0 375 091).

The promoters which are especially preferred are those which bring about the expression of genes in tissues and organs in which fatty acid, lipid and oil biosynthesis takes place, in seed cells such as the cells of endosperm and of the developing embryo. Suitable promoters are the napin gene promoters from oilseed rape (U.S. Pat. No. 5,608,152), the USP promoter from *Vicia faba* (Baeumlein et al., *Mol. Gen. Genet.* 1991, 225 (3):459-67), the oleosin promoter from *Arabidopsis* (WO 98/45461), the phaseolin promoter from *Phaseolus vulgaris* (U.S. Pat. No. 5,504,200), the Bce4 promoter from *Brassica* (WO 91/13980) or the legumin 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 promoters to be taken into consideration are the Ipt2 or Ipt1 gene promoter from barley (WO 95/15389 and WO 95/23230) or those which are described in WO 99/16890 (promoters from the barley hordein gene, the rice glutelin gene, the rice oryza gene, the rice prolamin gene, the wheat gliadin gene, wheat glutelin gene, the maize zein gene, the oat glutelin gene, the sorghum kasirin gene, the rye secalin gene).

In particular, the multiparallel expression of the  $\Delta 12$ -desaturases,  $\omega$ -3-desaturases,  $\Delta 9$ -elongases,  $\Delta 6$ -desaturases,  $\Delta 8$ -desaturases,  $\Delta 6$ -elongases,  $\Delta 5$ -desaturases,  $\Delta 5$ -elongases and/or  $\Delta 4$ -desaturases may be desired. Such expression cassettes can be introduced via a simultaneous transformation of a plurality of individual expression constructs or, preferably, by combining a plurality of expression cassettes on one construct. Also, it is possible to transform a plurality of vectors with in each case a plurality of expression cassettes and to transfer them to the host cell.

Likewise especially suitable are promoters which bring about the plastid-specific expression since plastids are 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.

Vector DNA can be introduced into prokaryotic or 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 prior-art processes for introducing 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*, 2<sup>nd</sup> ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) and other laboratory manuals,

such as Methods in Molecular Biology, 1995, Vol. 44, *Agrobacterium* protocols, Ed.: Gartland and Davey, Humana Press, Totowa, N.J.

The host organisms which are advantageously used are plant cells, preferably plants or parts thereof. Especially preferred plants are plants such as oilseed plants or oil crops, which comprise large amounts of lipid compounds, such as oilseed rape, evening primrose, hemp, thistle, peanut, canola, linseed, soybean, safflower, Indian mustard, sunflower, borage or plants 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, bushy plants (coffee, cacao, tea), *Salix* species, trees (oil palm, coconut) and perennial grasses and fodder crops. Especially preferred plants according to the invention are oil crops such as soybean, peanut, oilseed rape, canola, linseed, hemp, evening primrose, sunflower, safflower, trees (oil palm, coconut).

As described above, a further subject matter according to the invention is an isolated nucleic acid sequence which encodes polypeptides with  $\Delta 5$ -elongase activity and which has the sequence shown in SEQ ID NO: 197, where the elongase encoded by the nucleic acid sequence does not elongate  $C_{16}$ - and  $C_{18}$ -fatty acids with one double bond. Polyunsaturated  $C_{18}$ -fatty acids with one  $\Delta 6$ -double bond, or  $C_{22}$ -fatty acids, are not converted either. Advantageously, only polyunsaturated  $C_{20}$ -fatty acids with one  $\Delta 5$ -double bond are elongated by the enzymatic activity. Further subject matters of the invention are, as described above, a  $\Delta 6$ -elongase,  $\Delta 6$ -desaturase and a  $\Delta 12$ -desaturase.

In an advantageous embodiment, the term "nucleic acid (molecule)" as used in the present text additionally comprises the untranslated sequence at the 3' and at the 5' terminus of the coding gene region: at least 500, preferably 200, especially preferably 100 nucleotides of the sequence upstream of the 5' terminus of the coding region and at least 100, preferably 50, especially preferably 20 nucleotides of the sequence downstream of the 3' terminus of the coding gene region. An "isolated" nucleic acid molecule is separated 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' termini of the nucleic acid). In various embodiments, the isolated  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase molecule can, for example, comprise less 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 nucleic acid molecules used in the process, for example a nucleic acid molecule with a nucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89,

SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 or part thereof, can be isolated using standard techniques of molecular biology and the sequence information provided herein. Also, for example a homologous sequence or homologous, conserved sequence regions at the DNA or amino acid level can be identified with the aid of comparative algorithms. These sequence regions can be used as hybridization probe and standard hybridization techniques (such as, for example, described in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) for isolating further nucleic acid sequences which are useful in the process. Moreover, a nucleic acid molecule comprising a complete sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 or part thereof can be isolated by polymerase chain reaction, where oligonucleotide primers which on the basis of this sequence or parts thereof are used (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 on the basis of this very sequence). For example, mRNA can be isolated from cells (for example by the guanidinium thiocyanate extraction process by Chirgwin et al. (1979) Biochemistry 18:5294-5299) and cDNA can be generated by means of reverse transcriptase (for example Moloney-MLV reverse transcriptase, from Gibco/BRL, Bethesda, Md., or AMV reverse transcriptase, from Seikagaku America, Inc., St. Petersburg, Fla.). Synthetic oligonucleotide primers for the amplification by means of polymerase chain reaction can be generated on the basis of one of the sequences shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO:

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101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 or with the aid of the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202. One of the abovementioned nucleic acids can be amplified in accordance with standard PCR amplification techniques using cDNA or, alternatively, genomic DNA as template and suitable oligonucleotide primers. 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 nucleotide sequence can be generated by synthetic standard methods, for example using an automatic DNA synthesizer.

Homologs of the  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase nucleic acid sequences used, with the sequence SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, mean 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 one of the nucleotide sequences shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO:

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39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 or their homologs, derivatives or analogs or parts thereof. Furthermore, isolated nucleic acid molecules of a nucleotide sequence which hybridize, for example under stringent conditions, with one of the nucleotide sequences shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201 or a part thereof. A part in accordance with the invention is understood as meaning, in this context, 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. Advantageously, the entire sequence may also be used. Allelic variants comprise in particular functional variants which can be obtained by deletion, insertion or substitution of nucleotides from/into the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, the intention being, however, that the enzyme activity of the resulting protein synthesized advantageously being retained for the insertion of one or more genes. Proteins which still retain the enzymatic activity of  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,

$\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase or  $\Delta 4$ -desaturase, i.e. whose activity is essentially not reduced, mean proteins with at least 10%, preferably 20%, especially preferably 30%, very especially preferably 40% of the original enzyme activity in comparison with the protein encoded by SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201. The homology was calculated over the entire amino acid or nucleic acid sequence region. A series of programs based on a variety of algorithms is available to the skilled worker for comparing different sequences. In this context, the algorithms of Needleman and Wunsch or Smith and Waterman give particularly reliable results. To carry out the sequence alignments, 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 Wis., USA 53711 (1991)], were used. The sequence homology values detailed above in percent were determined using the program GAP over the entire sequence region with the following settings: Gap Weight: 50, Length Weight: 3, Average Match: 10.000 and Average Mismatch: 0.000, which, unless otherwise specified, were always used as standard settings for sequence alignments.

Homologs of the abovementioned nucleic acid sequences also mean for example bacterial, fungal and plant homologs, truncated sequences, single-stranded DNA or RNA of the coding and noncoding DNA sequence or else derivatives such as, for example, promoter variants. The promoters upstream of the nucleotide sequences stated can be modified by one or more nucleotide substitutions, by insertion(s) and/or deletion(s), without, however, the functionality or activity of the promoters being adversely affected. Furthermore, it is possible that the activity of the promoters is increased by modifying their sequence, or that they are replaced completely by more active promoters, including those from heterologous organisms.

The abovementioned nucleic acids and protein molecules with  $\Delta 12$ -desaturase,  $\omega 3$ -desaturase,  $\Delta 9$ -elongase,  $\Delta 6$ -desaturase,  $\Delta 8$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase,  $\Delta 5$ -elongase and/or  $\Delta 4$ -desaturase activity which are involved in the metabolism of lipids and fatty acids, PUFA cofactors and enzymes or in the transport of lipophilic compounds across membranes are used in the process according to the invention for modulating the production of PUFAs in transgenic plants such as maize, wheat, rye, oats, triticale, rice, barley, soybean, peanut, cotton, *Linum* species such as linseed or flax, *Brassica* species such as oilseed rape,

canola, Indian mustard and turnip rape, pepper, sunflower, borage, evening primrose and *Tagetes*. Solanaceae plants such as potato, tobacco, eggplant or tomato, *Vicia* species, pea, cassava, alfalfa, bushy plants (coffee, cacao, tea), *Salix* species, trees (oil palm, coconut) and perennial grasses and fodder crops either directly (for example when the overexpression or optimization of a fatty acid biosynthetic protein has a direct effect on the yield, production and/or production efficiency of the fatty acid from modified organisms) and/or can have an indirect effect which nevertheless entails an increase in the yield, production and/or production efficiency of the PUFAs or a decrease of undesired compounds (for example when the modulation of the metabolism of lipids and fatty acids, cofactors and enzymes results in changes in the yield, production and/or production efficiency or the composition of the desired compounds within the cells which, in turn, can have an effect on the production of one or more fatty acids).

Brassicaceae, Boraginaceae, Primulaceae or Linaceae are especially suitable for the production of PUFAs, preferably of arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. Especially suitable for the production of PUFAs with the nucleic acid sequences according to the invention, advantageously, as described, in combination with further desaturases and elongases are Indian mustard (*Brassica juncea*), oilseed rape and *Camelina sativa*.

The combination of a variety of precursor molecules and biosynthetic enzymes leads to the production of different fatty acid molecules, which has a major effect on the composition of the lipids since polyunsaturated fatty acids (=PUFAs) are incorporated not only into triacylglycerol but also into membrane lipids.

Brassicaceae, Boraginaceae, Primulaceae or Linaceae are especially suitable for the production of PUFAs, for example stearidonic acid, eicosapentaenoic acid or docosahexaenoic acid. Linseed (*Linum usitatissimum*) and *Brassica juncea* and *Camelina sativa* are especially advantageously suitable for the production of PUFAs with the nucleic acid sequences according to the invention, advantageously, as described, in combination with further desaturases and elongases.

Lipid synthesis can be divided into two sections: the synthesis of fatty acids and their binding to sn-glycerol-3-phosphate, and the addition or modification of a polar head group. Usual lipids which are used in membranes comprise phospholipids, glycolipids, sphingolipids and phosphoglycerides. Fatty acid synthesis starts with the conversion of acetyl-CoA into malonyl-CoA by acetyl-CoA carboxylase or into acetyl-ACP by acetyl transacylase. After condensation reaction, these two product molecules together form acetoacetyl-ACP, which is converted via a series of condensation, reduction and dehydration reactions so that a saturated fatty acid molecule with the desired chain length is obtained. The production of the unsaturated fatty acids from these molecules is catalyzed by specific desaturases, either aerobically by means of molecular oxygen or anaerobically (regarding the fatty acid synthesis in microorganisms, see F. C. Neidhardt et al. (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 612-636 and references cited therein; Lengeler et al. (Ed.) (1999) *Biology of Prokaryotes*. Thieme: Stuttgart, New York, and the references therein, and Magnuson, K., et al. (1993) *Microbiological Reviews* 57:522-542 and the references therein). To undergo the further elongation steps, the resulting phospholipid-bound fatty acids must be returned from the phospholipids to the fatty acid CoA ester pool. This is made possible by acyl-CoA:lysophospholipid acyltransferases. Moreover, these enzymes are capable of transferring the elongated fatty acids

from the CoA esters back to the phospholipids. If appropriate, this reaction sequence can be followed repeatedly.

Examples of precursors for PUFA biosynthesis are oleic acid, linoleic acid and linolenic acid. These C<sub>18</sub>-carbon fatty acids must be elongated to C<sub>20</sub> and C<sub>22</sub> to obtain fatty acids of the eicosa and docosa chain type. It is possible, with the aid of the desaturases used in the process, such as the Δ<sup>12</sup>-, ω<sup>3</sup>-, Δ<sup>4</sup>-, Δ<sup>5</sup>-, Δ<sup>6</sup>- and Δ<sup>8</sup>-desaturases and/or the Δ<sup>5</sup>-, Δ<sup>6</sup>-, Δ<sup>9</sup>-elongases to produce arachidonic acid, eicosapentaenoic acid, docosapentaenoic acid or docosahexaenoic acid, advantageously eicosapentaenoic acid and/or docosahexaenoic acid, and subsequently to use them for a variety of purposes in applications in the fields of foodstuffs, feedstuffs, cosmetics or pharmaceuticals. Using the abovementioned enzymes, C<sub>20</sub>- and/or C<sub>22</sub>-fatty acids with at least two, advantageously at least three, four, five or six double bonds in the fatty acid molecule, preferably C<sub>20</sub>- or C<sub>22</sub>-fatty acids with advantageously four, five or six double bonds in the fatty acid molecule can be produced. The desaturation can take place before or after elongation of the fatty acid in question. This is why the products of the desaturase activities and the further possible desaturation and elongation lead to preferred PUFAs with a higher degree of desaturation, including a further elongation of C<sub>20</sub>- to C<sub>22</sub>-fatty acids, to fatty acids such as γ-linolenic acid, dihomo-γ-linolenic acid, arachidonic acid, stearidonic acid, eicosatetraenoic acid or eicosapentaenoic acid. Substrates of the desaturases and elongases used in the process according to the invention are C<sub>16</sub>-, C<sub>18</sub>- or C<sub>20</sub>-fatty acids such as, for example, linoleic acid, γ-linolenic acid, α-linolenic acid, dihomo-γ-linolenic acid, eicosatetraenoic acid or stearidonic acid. Preferred substrates are linoleic acid, γ-linolenic acid and/or α-linolenic acid, dihomo-γ-linolenic acid or arachidonic acid, eicosatetraenoic acid or eicosapentaenoic acid. The synthesized C<sub>20</sub>- to C<sub>22</sub>-fatty acids with at least two, three, four, five or six, advantageously at least four, five or six double bonds in the fatty acid are obtained in the process according to the invention in the form of the free fatty acid or in the form of its esters, for example in the form of its glycerides.

The term "glyceride" is understood as meaning glycerol esterified with one, two or three carboxyl radicals (mono-, di- or triglyceride). "Glyceride" is also understood as meaning a mixture of various glycerides. The glyceride or glyceride mixture can comprise further additions, for example free fatty acids, antioxidants, proteins, carbohydrates, vitamins and/or other substances.

A "glyceride" for the purposes of the process according to the invention is furthermore understood as meaning derivatives which are derived from glycerol. In addition to the above-described fatty acid glycerides, these also include glycerophospholipids and glyceroglycolipids. Preferred examples which may be mentioned here are the glycerophospholipids such as lecithin (phosphatidylcholine), cardiolipin, phosphatidylglycerol, phosphatidylserine and alkylacylglycerophospholipids.

Furthermore, fatty acids must subsequently be transported to various sites of modification and incorporated into the triacylglycerol storage lipid. A further important step in lipid synthesis is the transfer of fatty acids onto the polar head groups, for example by glycerol-fatty-acid acyltransferase (see Frentzen, 1998, *Lipid*, 100(4-5):161-166).

Publications on plant fatty acid biosynthesis, desaturation, the lipid metabolism and the transmembrane transport of fatty compounds, beta-oxidation, fatty acid modification and cofactors, triacylglycerol storage and assembly, including the references therein, see the following articles: Kinney, 1997, *Genetic Engineering*, Ed., J K Setlow, 19:149-166;

Ohlrogge and Browse, 1995, *Plant Cell* 7:957-970; Shanklin and Cahoon, 1998, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:611-641; Voelker, 1996, *Genetic Engineering*, Ed.: J K Setlow, 18:111-13; Gerhardt, 1992, *Prog. Lipid R.* 31:397-417; Gühnemann-Schäfer & Kindl, 1995, *Biochim. Biophys Acta* 1256:181-186; Kunau et al., 1995, *Prog. Lipid Res.* 34:267-342; Stymme et al., 1993, in: *Biochemistry and Molecular Biology of Membrane and Storage Lipids of Plants*, Ed.: Murata and Somerville, Rockville, American Society of Plant Physiologists, 150-158, Murphy & Ross 1998, *Plant Journal*. 13(1):1-16.

The PUFAs produced in the process comprise a group of molecules which higher animals are no longer capable of synthesizing and must therefore take up, or which higher animals are no longer capable of synthesizing themselves in sufficient quantity and must therefore take up additionally, although they can be readily synthesized by other organisms such as bacteria; for example, cats are no longer capable of synthesizing arachidonic acid.

Phospholipids are to be understood as meaning, for the purposes of the invention, phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylglycerol and/or phosphatidylinositol, advantageously phosphatidylcholine.

The terms "production" or "productivity" are known in the art and refer to the concentration of the fermentation product (compounds of the formula I) formed within a certain period of time and a certain fermentation volume (for example kg of product per hour per liter). They also encompass the productivity within a plant cell or a plant, i.e. the content of the desired fatty acids produced in the process based on the content of all fatty acids in this cell or plant. The term production efficiency encompasses the time required for obtaining a certain amount of product (for example the time required by the cell for establishing a certain throughput rate of a fine chemical). The term "yield" or "product/carbon yield" is known in the art and comprises the efficiency of the conversion of the carbon source into the product (i.e. the fine chemical). This is usually expressed for example as kg of product per kg of carbon source. By increasing the yield or production of the compound, the amount of the obtained molecules or of the suitable obtained molecules of this compound in a certain amount of culture is increased over a specified period.

The terms "biosynthesis" or "biosynthetic pathway" are known in the art and comprise the synthesis of a compound, preferably of an organic compound, by a cell starting from intermediates, for example in a multistep process which is highly regulated. The terms "catabolism" or "catabolic pathway" are known in the art and comprise the cleavage of a compound, preferably of an organic compound, by a cell to give catabolytes (in more general terms, smaller or less complex molecules), for example in a multistep process which is highly regulated.

The term "metabolism" is known in the art and encompasses the totality of the biochemical reactions which take place in an organism. Thus, the metabolism of a certain compound (for example the metabolism of a fatty acid) comprises the totality of the biosynthetic, modification and catabolic pathways of this compound in the cell.

This invention is illustrated in greater detail by the examples which follow, which are not to be construed as limiting. The content of all of the references, patent applications, patents and published patent applications cited in the present patent application is herewith incorporated by reference.



## Example 1

## General Cloning Methods

The cloning methods such as, for example, restriction cleavages, agarose gel electrophoresis, purification of DNA

fragments, transfer of nucleic acids to nitrocellulose and nylon membranes, linkage of DNA fragments, transformation of *E. coli* cells, bacterial cultures and the sequence analysis of recombinant DNA were carried out as described by Sambrook et al. (1989) (Cold Spring Harbor Laboratory Press: ISBN 0-87969-309-6).

## Example 2

## Sequence Analysis of Recombinant DNA

Recombinant DNA molecules were, sequenced with an ABI laser fluorescence DNA sequencer by the process of Sanger (Sanger et al.: (1977) Proc. Natl. Acad. Sci. USA74, 5463-5467). Fragments resulting from a polymerase chain reaction were sequenced and verified to avoid polymerase errors in constructs to: be expressed.

## Example 3

Cloning Genes from *Oncorhynchus mykiss*

As the result of a search for conserved regions in the protein sequences corresponding to the elongase genes detailed in the application, two sequences with suitable motifs were identified in the Genbank sequence database.

Name of gene	Genbank No.	Amino acids
OmELO2	CA385234, CA364848, CA366480	264
OmELO3	CA360014, CA350786	295

Total RNA from *Oncorhynchus mykiss* was isolated with the aid of the RNAeasy Kit from Qiagen (Valencia, Calif., US). Poly-A+ RNA (mRNA) was isolated from the total RNA with the aid of oligo-dT cellulose (Sambrook et al., 1989). The RNA was subjected to reverse transcription using the reverse transcription system kit from Promega, and the cDNA synthesized was cloned into the lambda ZAP vector (lambda ZAP Gold, Stratagene). The cDNA was depackaged in accordance with the manufacturer's instructions to give the plasmid DNA. The cDNA plasmid library was then used for the PCR for cloning expression plasmids.

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To clone the two sequences for heterologous expression in yeasts, the following oligonucleotides were used for the PCR reaction:

Primer	Nucleotide sequence
5' f* OmELO2	5' aagcttacataaatggcttcaacatggcaa (SEQ ID NO: 179)
3' r* OmELO2	5' ggatccttatgtcttcttcttcttcttcttctt (SEQ ID NO: 180)
5' f OmELO3	5' aagcttacataaatggagacttttaaat (SEQ ID NO: 181)
3' r OmELO3	5' ggatccttcagtccccctcactttcc (SEQ ID NO: 182)

\*f: forward, r: reverse

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Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

25 5.00 µl of 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl of Advantage polymerase (Clontech)

PCR Reaction Conditions:

30 Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

35 The PCR product was first incubated for 2 hours at 37° C. with the restriction enzymes HindIII and BamHI. The yeast expression vector pYES3 (Invitrogen) was incubated in the same manner. Thereafter, the 812 bp PCR product and the 905 bp PCR product and the vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, the vector and the elongase cDNA were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pYES3-OmELO2 and pYES3-OmELO3 were verified by sequencing and transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by means of electroporation (1500 V). As a control, pYES3 was transformed in parallel. Thereafter, the yeasts were plated onto complete tryptophan dropout minimal medium supplement with 2% glucose. Cells which are capable of growing on without tryptophan in the medium thus comprise the corresponding plasmids pYES3, pYES3-OmELO2 (SEQ ID NO: 51) and pYES3-OmELO3 (SEQ ID NO: 53). After the selection, in each case two transformants were selected for the further functional expression.

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## Example 5

## Cloning Expression Plasmids for the Seed-Specific Expression in Plants

65 To transform plants, a further transformation vector based on pSUN-USP was generated. To this end, NotI cleavage sites were introduced at the 5' and 3' termini of the coding sequence using the following primer pair:

PSUN-OmELO2  
 (SEQ ID NO: 175)  
 Forward: 5'-GCGGCCGCATAATGGCTTCAACATGGCAA  
 (SEQ ID NO: 176)  
 Reverse: 3'-GCGGCCGCTTATGTCTTCTTGCTTCTCTGTT

PSUN-OmELO3  
 (SEQ ID NO: 177)  
 Forward: 5'-GCGGCCGCataatggagacttttaaat  
 (SEQ ID NO: 178)  
 Reverse: 3'-GCGGCCGctcagtcctccctcactttcc

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA  
 5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>  
 5.00 µl of 2 mM dNTP  
 1.25 µl of each primer (10 pmol/µl)  
 0.50 µl of Advantage polymerase (Clontech)  
 PCR Reaction Conditions:  
 Annealing temperature: 1 min 55° C.  
 Denaturation temperature: 1 min 94° C.  
 Elongation temperature: 2 min 72° C.  
 Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. Thereafter, the PCR products and the 7624 bp vector were separated by agarose gel electrophoresis, and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pSUN-OmELO2 and pSUN-OmELO3 were verified by sequencing.

pSUN300 is a derivative of the plasmid pPZP (Hajdukiewicz P., Svab, Z., Maliga P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. *Plant Mol. Biol.* 25:989-994). pSUN-USP originated from pSUN300 by inserting a USP promoter as EcoRI fragment into pSUN 300. The polyadenylation signal is that of the octopine synthase gene from the *A. tumefaciens* Ti plasmid (ocs terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene *J. Mol. Appl. Genet.* 1 (6), 499-511 (1982). The USP promoter corresponds to the nucleotides 1-684 (Genbank Accession X56240), part of the noncoding region of the USP gene being present in the promoter. The promoter fragment, which is 684 base pairs in size, was amplified via a PCR reaction by standard methods, by means of commercially available T7 standard primer (Stratagene) and with the aid of a synthesized primer (primer sequence: 5'-GTCGACCGGCGGACTAGTGGGC-CCTCTAGACCCGGGGGATCC GGATCTGCTTGGC-TATGAA-3', SEQ ID NO: 174). The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid named pSUN-USP. The construct was used for transforming *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

#### Example 6

##### Lipid Extraction from Yeasts and Seeds

The effect of the genetic modification in plants, fungi, algae, ciliates or on the production of a desired compound

(such as a fatty acid) can be determined by growing the modified microorganisms or the modified plant under suitable conditions (such as those described above) and analyzing the medium and/or the cellular components for the elevated production of the desired product (i.e. of the lipids or a fatty acid). These analytical techniques are known to the skilled worker and comprise spectroscopy, thin-layer chromatography, various types of staining methods, enzymatic and microbiological methods and analytical chromatography such as high-performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, Vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A., et al., (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 17; Rehm et al. (1993) Biotechnology, Vol. 3, Chapter III: "Product recovery and purification", p. 469-714, VCH: Weinheim; Belter, P. A., et al. (1988) Bioseparations: downstream processing for Biotechnology, John Wiley and Sons; Kennedy, J. F., and Cabral, J. M. S. (1992) Recovery processes for biological Materials, John Wiley and Sons; Shaeiwitz, J. A., and Henry, J. D. (1988) Biochemical Separations, in: Ullmann's Encyclopedia of Industrial Chemistry, Vol. B3; Chapter 11, p. 1-27, VCH: Weinheim; and Dechow, F. J. (1989) Separation and purification techniques in biotechnology, Noyes Publications).

In addition to the abovementioned methods, plant lipids are extracted from plant material as described by Cahoon et al. (1999) *Proc. Natl. Acad. Sci. USA* 96 (22): 12935-12940 and Browse et al: (1986) *Analytic Biochemistry* 152:141-145. The qualitative and quantitative analysis of lipids or fatty acids is described by Christie, William W., *Advances in Lipid Methodology*, Ayr/Scotland: Oily Press (Oily Press Lipid Library; 2); Christie, William W., *Gas Chromatography and Lipids. A Practical Guide—Ayr, Scotland: Oily Press, 1989, Repr. 1992, IX, 307 pp.* (Oily Press Lipid Library; 1); "Progress in Lipid Research, Oxford: Pergamon Press, 1 (1952)-16 (1977) under the title: Progress in the Chemistry of Fats and Other Lipids CODEN.

In addition to measuring the end product of the fermentation, it is also possible to analyze other components of the metabolic pathways which are used for the production of the desired compound, such as intermediates and by-products, in order to determine the overall production efficiency of the compound. The analytical methods comprise measuring the amount of nutrients in the medium (for example sugars, hydrocarbons, nitrogen sources, phosphate and other ions), measuring the biomass composition and the growth, analyzing the production of conventional metabolites of biosynthetic pathways and measuring gases which are generated during the fermentation. Standard methods for these measurements are described in *Applied Microbial Physiology; A Practical Approach*, P. M. Rhodes and P. F. Stanbury, Ed., IRL Press, p. 103-129; 131-163 and 165-192 (ISBN: 0199635773) and references cited therein.

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One example is the analysis of fatty acids (abbreviations: FAME, fatty acid methyl ester; GC-MS, gas liquid chromatography/mass spectrometry; TAG, triacylglycerol; TLC, thin-layer chromatography).

The unambiguous detection for the presence of fatty acid products can be obtained by analyzing recombinant organisms using analytical standard methods: GC, GC-MS or TLC, as described on several occasions by Christie and the references therein (1997, in: *Advances on Lipid Methodology*, Fourth Edition: Christie, Oily Press, Dundee, 119-169; 1998, *Gaschromatographie-Massenspektrometrie-Verfahren* [Gas chromatography/mass spectrometric methods], *Lipide* 33:343-353).

The material to be analyzed can be disrupted by sonication, grinding in a glass mill, liquid nitrogen and grinding or via other applicable methods. After disruption, the material must be centrifuged. The sediment is resuspended in distilled water, heated for 10 minutes at 100° C., cooled on ice and recentrifuged, followed by extraction for one hour at 90° C. in 0.5 M sulfuric acid in methanol with 2% dimethoxypropane, which leads to hydrolyzed oil and lipid compounds, which give transmethylated lipids. These fatty acid methyl esters are extracted in petroleum ether and finally subjected to a GC analysis using a capillary column (Chrompack, WCOT Fused Silica, CP-Wax-52 CB, 25 m, 0.32 mm) at a temperature gradient of between 170° C. and 240° C. for 20 minutes and 5 minutes at 240° C. The identity of the resulting fatty acid methyl esters must be defined using standards which are available from commercial sources (i.e. Sigma).

Plant material is initially homogenized mechanically by comminuting in a pestle and mortar to make it more amenable to extraction.

This is followed by heating at 100° C. for 10 minutes and, after cooling on ice, by resedimentation. The cell sediment is hydrolyzed for one hour at 90° C. with 1 M methanolic sulfuric acid and 2% dimethoxypropane, and the lipids are transmethylated. The resulting fatty acid methyl esters (FAMES) are extracted in petroleum ether. The extracted FAMES are analyzed by gas liquid chromatography using a capillary column (Chrompack, WCOT Fused Silica, CP-Wax-52 CB, 25 m, 0.32 mm) and a temperature gradient of from 170° C. to 240° C. in 20 minutes and 5 minutes at 240° C. The identity of the fatty acid methyl esters is confirmed by comparison with corresponding FAME standards (Sigma). The identity and position of the double bond can be analyzed further by suitable chemical derivatization of the FAME mixtures, for example to give 4,4-dimethoxyoxazolin derivatives (Christie, 1998) by means of GC-MS.

Yeasts which had been transformed with the plasmids pYES3, pYES3-OmELO2 and pYES3-OmELO3 as described in Example 4 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 10 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 in order to remove residual medium and fatty acids. Fatty acid methyl esters (FAMES) were prepared with the yeast cell sediments by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. with 2 ml of 1N methanolic sulfuric acid and 2% (v/v) dimethoxypropane. The FAMES were extracted by twice extracting with petroleum ether (PE). To remove non-derivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-

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Packard 6850 gas chromatograph with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 minutes at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma).

The methodology is described for example in Napier and Michaelson, 2001, *Lipids* 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*, 52(360):1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

#### Example 7

##### Functional Characterization of OmELO2 and OmELO3

OmELO2 shows no elongase activity, while a pronounced, activity was detected for OmELO3, using different substrates. The substrate specificity of OmELO3 was determined after expression and feeding with various fatty acids (FIG. 2). The fed substrates can be detected in large amounts in all transgenic yeasts. All transgenic yeasts show that new fatty acids have been synthesized, to the products of the OmELO3 reaction. This means that the gene OmELO3 was expressed functionally.

FIG. 2 demonstrates that OmELO3 has a substrate specificity which leads to the elongation of Δ5- and Δ6-fatty acids with one w-double bond with high specificity. Moreover, ω6-fatty acids (C18 and C20) were also elongated, with less specificity. The best substrates for OmELO3 were stearidonic acid (C18:4 ω3) and eicosapentaenoic acid (C20:5 ω3) (up to 66% elongation).

#### Example 8

##### Reconstitution of the Synthesis of DHA in Yeast

The reconstitution of the biosynthesis of DHA (22:6 ω3) was carried out starting from EPA (20:5 ω3) or stearidonic acid (18:4 ω3) by coexpressing OmELO3 together with the *Euglena gracilis* Δ4-desaturase or the *Phaeodactylum tri-cornutum* Δ5-desaturase and the *Euglena gracilis* Δ4-desaturase. To this end, the expression vectors pYes2-EgD4 and pESCLEu-PtD5 were additionally constructed. The abovementioned yeast strain which is already transformed with pYes3-OmELO3 (SEQ ID NO: 55), was then transformed further with pYes2-EgD4, or simultaneously with pYes2-EgD4 and pESCLEu-PtD5. The transformed yeasts were selected on complete minimal dropout tryptophan and uracil medium agar plates supplemented with 2% glucose in the case of the pYes3-pYes3-OmELO/pYes2-EgD4 strain and complete minimal dropout tryptophan, uracil and leucine medium in the case of the pYes3-OmELO/pYes2-EgD4+pESCLEu-PtD5 strain. Expression was then induced by addition of 2% (w/v) galactose. The cultures were subsequently incubated for a further 120 hours at 15° C.

FIG. 3 shows the fatty acid profiles of transgenic yeasts which have been fed 20:5 ω3. In the control yeast (A), which had been transformed with the vector pYes3-OmELO3 and the blank vector pYes2, 20:5 ω3 was elongated highly efficiently to give 22:5 ω3 (65% elongation). The additional introduction of the EEgΔ4-desaturase led to the conversion of 22:5 ω3 into 22:6 ω3 DHA. The fatty acid composition

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of the transgenic yeasts is shown in FIG. 5. After coexpression of OmElo3 and EgD4, up to 3% DHA was detected in yeasts.

In a further coexpression experiment, OmElo3, EgD4 and a  $\Delta 5$ -desaturase from *P. tricomutum* (PtD5) were expressed together. The transgenic yeasts were fed stearidonic acid (18:4  $\omega 3$ ) and analyzed (FIG. 4). The fatty acid composition of these yeasts is shown in FIG. 5. OmElo3 elongated the fed fatty acid 18:4  $\omega 3$  to give 20:4  $\omega 3$  (60% elongation). The latter was desaturated by PtD5 to give 20:5  $\omega 3$ . The PtD5 activity amounted to 15%. Furthermore, 20:5  $\omega 3$  was elongated by EmElo3 to give 22:5  $\omega 3$ . Thereafter, the newly synthesized 22:5  $\omega 3$  was desaturated to give 22:6  $\omega 3$  (DHA). Up to 0.7% of DHA was obtained in these experiments.

These experiments demonstrate that the sequences OmElo3, EgD4 and PtD5 which are used in the present invention are suitable for the production of DHA in eukaryotic cells.

#### Example 9

##### Generation of Transgenic Plants

a) Generation of Transgenic Oilseed Rape Plants (Modified Process of Moloney et al., 1992, Plant Cell Reports, 8:238-242)

The binary vectors in *Agrobacterium tumefaciens* C58C1: pGV2260 or *Escherichia coli* (Deblaere et al, 1984, Nucl. Acids. Res. 13, 4777-4788) can be used for generating transgenic oilseed rape plants. To transform oilseed rape plants (Var. Drakkar, NPZ Nordeutsche Pflanzenzucht, Hohenlieth, Germany), a 1:50 dilution of an overnight culture of a positively transformed agrobacterial colony in Murashige-Skoog medium (Murashige and Skoog 1962 Physiol. Plant. 15, 473) supplemented with 3% sucrose (3MS medium) is used. Petioles or hypocotyls of freshly germinated sterile oilseed rape plants (in each case approx. 1 cm<sup>2</sup>) are incubated with a 1:50 agrobacterial dilution for 5-10 minutes in a petri dish. This is followed by 3 days of coincubation in the dark at 25° C. on 3MS medium supplemented with 0.8% Bacto agar. The cultures are then grown for 3 days at 16 hours light/8 hours dark. The cultivation is then continued in a weekly rhythm on MS medium supplemented with 500 mg/l Claforan (cefotaxim sodium), 50 mg/l kanamycin, 20  $\mu$ M benzylaminopurine (BAP), now supplemented with 1.6 g/l of glucose. Growing shoots are transferred to MS medium supplemented with 2% sucrose, 250 mg/l Claforan and 0.8% Bacto agar. If no roots have developed after three weeks, 2-indolebutyric acid is added to the medium as growth hormone for rooting.

Regenerated shoots were obtained on 2MS medium supplemented with kanamycin and Claforan; after rooting, they were transferred to compost and, after growing on for

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two weeks in a controlled-environment cabinet or in the greenhouse, allowed to flower, and mature seeds were harvested and analyzed by lipid analysis for elongase expression, such as  $\Delta 5$ -elongase or  $\Delta 6$ -elongase activity. In this manner, lines with elevated contents of polyunsaturated C<sub>20</sub>- and C<sub>22</sub>-fatty acids can be identified.

b) Generation of Transgenic Linseed Plants

Transgenic linseed plants can be generated for example by the process of Bell et al., 1999, In Vitro Cell. Dev. Biol.-Plant. 35(6):456-465 by means of particle bombardment. Usually, an *agrobacteria*-mediated transformations was used for the transformation of linseed, for example by the process of Mlynarova et al. (1994), Plant Cell Report 13: 282-285.

#### Example 10

##### Cloning $\Delta 5$ -Elongase Genes from *Thraustochytrium aureum* ATCC34304 and *Thraustochytrium* ssp

Comparisons of the various elongase protein sequences found in the present application enabled the definition of conserved nucleic acid regions (histidin box: His-Val-X-His-His, tyrosin box: Met-Tyr-X-Tyr-Tyr). An EST database of *T. aureum* ATCC34304 and *Thraustochytrium* ssp. was screened for further  $\Delta 5$ -elongases with the aid of these sequences. The following new sequences were found:

Name of gene	Nucleotides	Amino acids
BioTaurELO1	828 bp	275
TL16y2	831	276

Total RNA from *T. aureum* ATCC34304 and *Thraustochytrium* ssp. was isolated with the aid of the RNAeasy Kits from Qiagen (Valencia, Calif., US). mRNA was isolated from the total RNA with the aid of the polyAtract isolation system (Promega). The mRNA was subjected to reverse transcription using the Marathon cDNA Amplification Kit (BD Biosciences) and adaptors were ligated in accordance with the manufacturer's instructions. The cDNA library was then employed for the PCR for cloning expression plasmids by means of 5'- and 3'-RACE (rapid amplification of cDNA ends).

#### Example 11

##### Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To clone the sequence for heterologous expression in yeasts, the following oligonucleotides were used for the PCR reaction:

Primer	Nucleotide sequence	
5' f* BioTaurELO1	5' gacataatgacgagcaacatgag	(SEQ ID NO: 170)
3' r* BioTaurELO1	5' eggcttaggcgacttgcccttggg	(SEQ ID NO: 171)
5' f* TL16y2	5' agacataatggacgctcgtcgagcagcaatg	(SEQ ID NO: 172)
3' r* TL16y2	5' ttagatggtctctctgcttcttgggccc	(SEQ ID NO: 173)

\*f: forward, r: reverse

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Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl of 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl of Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR products BioTaurELO1 (see (SEQ ID NO: 65) and TL16y2 (see SEQ ID NO: 83) were incubated for 30 minutes at 21° C. with the yeast expression vector pYES2.1-TOPO (Invitrogen) following the manufacturer's instructions. The PCR product is ligated into the vector by means of a T overhang and activity of a topoisomerase (Invitrogen). After incubation, *E. coli* DH5α cells were transformed. Suitable clones were identified by PCR, the plasmid DNA was isolated by means of Qiagen DNAeasy Kit and verified by sequencing. The correct sequence was then transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by electroporation (1500 V). As a control, the blank vector pYES2.1 was transformed in parallel. The yeasts were subsequently plated onto complete uracil dropout minimal medium supplemented with 2% glucose. Cells which were capable of growing in the medium without uracil thus comprise the corresponding plasmids pYES2.1, pYES2.1-BioTaurELO1 and pYES2.1-TL16y2. After the selection, in each case two transformants were selected for further functional expression.

## Example 12

## Cloning Expression Plasmids for the Seed Specific Expression in Plants

A further transformation vector based on pSUN-USP was generated for the transformation of plants. To this end, NotI cleavage sites were introduced at the 5' and 3' termini of the coding sequence, using the following primer pair:

PSUN-BioTaurELO1

Forward:

(SEQ ID NO: 166)

5' -GCGGCCGATAATGACGAGCAACATGAGC

Reverse:

(SEQ ID NO: 167)

3' -GCGGCCGCTTAGGCCGACTTGGCCTTGGG

PSUN-TL16y2 -

Forward:

(SEQ ID NO: 168)

5' -GCGGCCGACCATGGACGTCGTCGAGCAGCAATG

Reverse:

(SEQ ID NO: 169)

5' -GCGGCCGCTTAGATGGTCTTCTGCTTCTGGGCGCC

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase

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The Advantage polymerase from Clontech was employed.

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

5 Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. 10 Thereafter, the PCR products and the 7624 bp vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR 15 products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pSUN-BioTaurELO1 and pSUN-TL16y2 were verified by sequencing.

20 pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P; Svab, Z; Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 25 in the form of an EcoRI fragment. The polyadenylation signal is that of the octopine synthase gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide 30 sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP 35 gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene). (Primer sequence: 5'-GTTCGAC- 40 CCGCGGACTAGTGGGCCCTCTAGAC-CCGGGGGATCC GGATCTGCTGGCTATGAA-3', SEQ ID NO: 165). The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The 45 construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

Lipids were extracted from yeasts and seeds as described for Example 6.

## Example 13

## Functional Characterization of BioTaurELO1 and TL16y2

55 The substrate specificity of BioTaurELO1 was determined after expression and feeding of various fatty acids (FIG. 6). FIG. 6 shows the feeding experiments for determining the functionality and substrate specificity with yeast strains comprising either the vector pYes2.1 (control) or the 60 vector pYes2.1-BioTaurELO1 (=BioTaur) with the Δ5-elongase. In both approaches, 200 nm of γ-linolenic acid and eicosapentaenoic acid were added to the yeast incubation medium and incubated for 24 hours. After the fatty acids had been extracted from the yeasts, they were transmethylated 65 and separated by gas chromatography. The elongation products originating from the two fatty acids which had been fed are identified by arrows.

The substrates which had been fed can be detected in large amounts in all transgenic yeasts. All transgenic yeasts show that new fatty acids have been synthesized, the products of the BioTaurELO1 reaction; This means that the gene BioTaurELO1 has been expressed functionally.

FIG. 6 shows that BioTaurELO1 has a substrate specificity which leads with high specificity to the elongation of  $\Delta 5$ - and  $\Delta 6$ -fatty acids with one  $\omega$ -3-double bond. Moreover,  $\omega 6$ -fatty acids (C18 and C20) were also elongated.  $\gamma$ -Linolenic acid (C18:3  $\omega 6$ ) is converted with a conversion rate of 65.28%, stearidonic acid (C18:4  $\omega 3$ ) with a conversion rate of 65.66% and eicosapentaenoic acid (C20:5  $\omega 3$ ) with a conversion rate of 22.01%. The substrate specificities of the various feeding experiments are shown in Table 6 (see end of the description).

The conversion rate of GLA when feeding GLA and EPA was 65.28%. The conversion rate of EPA, again when feeding GLA and EPA, was 9.99%. When only EPA was fed, the EPA conversion rate was 22.01%. Arachidonic acid (=ARA) was also converted when fed. The conversion rate was 14.47%. Stearidonic acid (=SDA) was also converted. In this case, the conversion rate was 65.66%.

The functionality and substrate specificity of TL16y2 were determined after expression and feeding of various fatty acids. Table 7 shows the feeding experiments. The feeding experiments were carried out in the same manner as described for BioTaurELO1. The substrates which have been fed can be detected in large amounts in all transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the TL16y2 reaction (FIG. 11). This means that the gene TL16y2 has been expressed functionally.

TABLE 7

		Expression of TL16y2 in yeast. % areas in the gas-chromatographic analysis							
Plasmid	Fatty acid	C18:3 (n-6)	C18:4 (n-3)	C20:3 (n-6)	C20:4 (n-6)	C20:4 (n-3)	C20:5 (n-3)	C22:4 (n-6)	C22:5 (n-3)
pYES	250 $\mu$ m EPA						13.79		
TL16y2	250 $\mu$ m EPA						25.81		<b>2.25</b>
pYES	50 $\mu$ m EPA						5.07		
TL16y2	50 $\mu$ m EPA						2.48		<b>1.73</b>
pYES	250 $\mu$ m GLA	8.31							
TL16y2	250 $\mu$ m GLA	3.59		<b>10.71</b>					
pYES	250 $\mu$ m ARA					16.03			
TL16y2	250 $\mu$ m ARA				15.2		<b>3.87</b>		
pYES	250 $\mu$ m SDA		26.79			0.35			
TL16y2	250 $\mu$ m SDA		7.74			<b>29.17</b>			

The results with TL16y2, which are shown in Table 7, show the following conversion rates in % of the control: a) conversion rate of EPA in % (250  $\mu$ m): 8%, b) conversion rate of EPA in % (50  $\mu$ m): 41%, c) conversion rate of ARA in %: 20.3%, d) conversion rate of SDA in %: 79.4%, and e) conversion rate of GLA in %: 74.9%.

Thus, TL16y2 shows  $\Delta 5$ -,  $\Delta 6$ - and  $\Delta 8$ -elongase activity. The activity is highest for C18-fatty acids with  $\Delta 6$ -double

bond. Then, C20-fatty acids with a  $\Delta 5$ - or  $\Delta 8$ -double bond are elongated, depending on the concentration of fatty acids which are fed.

## Example 14

Cloning Genes from *Ostreococcus tauri*

The search for conserved regions in the protein sequences with the aid of the elongase genes with  $\Delta 5$ -elongase activity or  $\Delta 6$ -elongase activity which are shown in the application allowed the identification of sequences with suitable motifs in an *Ostreococcus tauri* sequence database (genomic sequences).

The sequences were the following:

Name of gene	SEQ ID	Amino acids
OtELO1, ( $\Delta 5$ -elongase)	SEQ ID NO: 67	300
OtELO2, ( $\Delta 6$ -elongase)	SEQ ID NO: 69	292

OtElo1 shows the highest similarity with an elongase from *Danio rerio* (GenBank AAN77156; identity approx. 26%), while OtElo2 shows the highest similarity with the *Physcomitrella* Elo (PSE) [approx. 36% identity] (alignments were carried out using the tBLASTn algorithm (Altschul et al., J. Mol. Biol. 1990, 215:403-410).

The cloning procedure was as follows:

40 ml of an *Ostreococcus tauri* culture in the stationary phase were spun down, resuspended in 100 of double-distilled water and stored at  $-20^{\circ}$  C. The respective genomic

DNAs were amplified on the basis of the PCR process. The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient translation (Kozak, Cell 1986, 44:283-292) next to the start codon. The amplification of the OtElo DNAs was carried out in each case using 1  $\mu$ l of defrosted cells, 200  $\mu$ m of dNTPs, 2.5 U Taq polymerase and 100 pmol of each primer in a total volume of 50  $\mu$ l. The PCR conditions were as follows: first denaturation for 5 minutes at  $95^{\circ}$  C., followed by 30 cycles

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of 30 seconds at 94° C., 1 minute at 55° C. and 2 minutes at 72° C., and a last elongation step of 10 minutes at 72° C.

## Example 15

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To characterize the function of the *Ostreococcus tauri* elongases, the open reading frames of the DNAs in question were cloned downstream of the galactose-inducible GAL1 promoter of pYES2.1/V5-His-TOPO (Invitrogen), giving rise to pOTE1 and pOTE2.

The *Saccharomyces cerevisiae* strain 334 was transformed by electroporation (1500 v) with the vector pOTE1 or pOTE2. A yeast which was transformed with the blank vector pYES2 was used as the control. The transformed yeasts were selected on complete minimal dropout uracil medium (CMDum) agar plates supplemented with 2% glucose. After the selection, in each case three transformants were selected for the further functional expression.

To express the Ot elongases, precultures of in each case 5 ml of dropout uracil CMDum liquid medium supplemented with 2% (w/v) raffinose were inoculated with the selected transformants and incubated for 2 days at 30° C., 200 rpm.

5 ml of CMDum liquid medium (without uracil) supplemented with 2% raffinose and 300 µm of various fatty acids were then inoculated with the precultures to an OD<sub>600</sub> of 0.05. The expression was induced by addition of 2% (w/v) galactose. The cultures were incubated for a further 96 hours at 20° C.

## Example 16

## Cloning of Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP was generated for the transformation of plants. To this end, NotI cleavage sites were introduced at the 5' and 3' termini of the coding sequences, using PCR. The corresponding primer sequences are derived from the 5' and 3' regions of OtElo1 and OtElo2.

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase

The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. Thereafter, the PCR products and the vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pSUN-OtELO1 and pSUN-OtELO2 were verified by sequencing.

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pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P, Svab, Z, Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the *Ostreococcus* gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene). (Primer sequence: 5'-GTTCGAC-CCGCGGACTAGTGGGCCCTCTAGAC-CCGGGGGATCC GGATCTGCTGGCTATGAA-3', SEQ ID NO: 164).

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

## Example 17

## Expression of OtELO1 and OtELO2 in Yeasts

Yeasts which had been transformed with the plasmids pYES3, pYES3-OtELO1 and pYES3-OtELO2 as described in Example 15 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 to remove residual medium and fatty acids. Starting with the yeast cell sediments, fatty acid methyl esters (FAMES) were prepared by acid methanolysis. To this end, the cell sediments were incubated for one hour at 80° C. together with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) of dimethoxypropane. The FAMES were extracted twice with petroleum ether (PE). To remove non-derivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph equipped with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 min at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, Lipids. 36(8):761-766; Sayanova et al., 2001, Journal of Experimental Botany. 52(360): 1581-1585, Sperling et al., 2001, Arch. Biochem. Biophys. 388(2):293-298 and Michaelson et al., 1998, FEBS Letters. 439(3):215-218.

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Example 18

Functional Characterization of OtELO1 and OtELO2

The substrate specificity of OtELO1 could be determined after expression and the feeding of different fatty acids (Tab. 8). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the OtELO1 reaction. This means that the gene OtELO1 has been expressed functionally.

It can be seen from Table 7 that OtELO1 has a narrow substrate specificity. OtELO1 was only capable of elongating the C20-fatty acids eicosapentaenoic acid (FIG. 7) and arachidonic acid (FIG. 8), but preferred the ω3-desaturated eicosapentaenoic acid.

TABLE 8

Fatty acid substrate	Conversion rate (in %)
16:0	—
16:1 <sup>Δ9</sup>	—
18:0	—
18:1 <sup>Δ9</sup>	—
18:1 <sup>Δ11</sup>	—
18:2 <sup>Δ9,12</sup>	—
18:3 <sup>Δ6,9,12</sup>	—
18:3 <sup>Δ5,9,12</sup>	—
20:3 <sup>Δ8,11,14</sup>	—
20:4 <sup>Δ5,8,11,14</sup>	10.8 ± 0.6
20:5 <sup>Δ5,8,11,14,17</sup>	46.8 ± 3.6
22:4 <sup>Δ7,10,13,16</sup>	—
22:6 <sup>Δ4,7,10,13,16,19</sup>	—

Table 8 shows the substrate specificity of the elongase OtELO1 for C20-polyunsaturated fatty acids with one double bond in Δ5-position in comparison with various fatty acids.

The yeasts which had been transformed with the vector pOTE1 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC. Each value represents the mean (n=3)±standard deviation.

The substrate specificity of OtELO2 (SEQ ID NO: 81) could be determined after expression and the feeding of different fatty acids (Tab. 9). The substrates fed could be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the OtELO2 reaction. This means that the gene OtELO2 has been expressed functionally.

TABLE 9

Fatty acid substrate	Conversion rate (in %)
16:0	—
16:1 <sup>Δ9</sup>	—
16:3 <sup>Δ7,10,13</sup>	—
18:0	—
18:1 <sup>Δ9</sup>	—
18:1 <sup>Δ11</sup>	—
18:2 <sup>Δ9,12</sup>	—
18:3 <sup>Δ6,9,12</sup>	15.3±
18:3 <sup>Δ5,9,12</sup>	—
18:4 <sup>Δ6,9,12,15</sup>	21.1±
20:2 <sup>Δ11,14</sup>	—
20:3 <sup>Δ8,11,14</sup>	—
20:4 <sup>Δ5,8,11,14</sup>	—
20:5 <sup>Δ5,8,11,14,17</sup>	—

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TABLE 9-continued

Fatty acid substrate	Conversion rate (in %)
22:4 <sup>Δ7,10,13,16</sup>	—
22:5 <sup>Δ7,10,13,16,19</sup>	—
22:6 <sup>Δ4,7,10,13,16,19</sup>	—

Table 9 shows the substrate specificity of the elongase OtELO2 for various fatty acids.

The yeasts which had been transformed with the vector pOTE2 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC. Each value represents the mean (n=3)±standard deviation.

The enzymatic activity shown in Table 9 clearly demonstrates that OTELO2 is a Δ6-elongase.

Example 19

Cloning Genes from *Thalassiosira pseudonana*

The search for conserved regions in the protein sequences with the aid of the elongase genes with Δ5-elongase activity or Δ6-elongase activity which are shown in the application allowed the identification of two sequences with suitable motifs in a *Thalassiosira pseudonana* sequence database (genomic sequences). The sequences were the following:

Name of gene	SEQ ID	Amino acids
TpELO1 (Δ5-elongase)	43	358
TpELO2 (Δ5-elongase)	59	358
TpELO3 (Δ6-elongase)	45	272

A 2 l culture of *T. pseudonana* was grown in f/2 medium (Guillard, R. R. L. 1975. Culture of phytoplankton for feeding marine invertebrates. In *Culture of Marine Invertebrate Animals* (Eds. Smith, W. L. and Chanley, M. H.), Plenum Press, New York, pp 29-60) for 14 d (=days) at a light intensity of 80 E/cm<sup>2</sup>. After the cells had been spun down, RNA was isolated with the aid of the RNAeasy Kit from Quiagen (Valencia, Calif., US) following the manufacturer's instructions. The mRNA was subjected to reverse transcription using the Marathon cDNA Amplification Kit (BD Biosciences) and adaptors were ligated in accordance with the manufacturer's instructions. Then, the cDNA library was used for the PCR for cloning expression plasmids by means of 5'- and 3'-RACE (rapid amplification of cDNA ends).

Example 20

Cloning Expression Plasmids for the Heterologous Expression in Yeasts

The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient translation (Kozak, Cell 1986, 44:283-292) next to the start codon. The amplification of the TpELO DNAs was carried out in each case using 1 μl of cDNA, 200 μm of dNTPs, 2.5 U of Advantage polymerase and 100 pmol of each primer in a total volume of 50 μl. The PCR conditions were as follows: first denaturation for 5 minutes at 95° C., followed by 30 cycles of 30 seconds at 94° C., 1 minute at 55° C. and 2 minutes at 72° C., and a last elongation step of 10 minutes at 72° C.



To clone the sequence for the heterologous expression in yeasts, the following oligonucleotides were used for the PCR reaction:

Name of gene and SEQ ID NO:	Primer sequence
TpELO1 (A5-elongase), SEQ ID NO: 59	F: 5'-accatgtgctcaccaccgcccgtc (SEQ ID NO: 158) R: 5'-ctacatggcaccagtaac (SEQ ID NO: 159)
TpELO2 (A5-elongase), SEQ ID NO: 85	F: 5'-accatgtgctcatcaccgcccgtc (SEQ ID NO: 160) R: 5'-ctacatggcaccagtaac (SEQ ID NO: 161)
TpELO3 (A6-elongase), SEQ ID NO: 45	F: 5'-accatggacgcctacaacgctgc (SEQ ID NO: 162) R: 5'-ctaagcactcttcttcttt (SEQ ID NO: 163)

\*F = forward primer, R = reverse primer

The PCR products were incubated for 30 minutes at 21° C. with the yeast expression vector pYES2.1-TOPO (Invitrogen) following the manufacturer's instructions. The PCR product is ligated into the vector by means of a T overhang and activity of a topoisomerase (Invitrogen). After incubation, *E. coli* DH5α cells were transformed. Suitable clones were identified by PCR, the plasmid DNA was isolated by means of Qiagen DNAeasy Kit and verified by sequencing. The correct sequence was then transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by electroporation (1500 V). As a control, the blank vector pYES2.1 was transformed in parallel. The yeasts were subsequently plated onto complete uracil dropout minimal medium supplemented with 2% glucose. Cells which were capable of growing in the medium without uracil thus comprise the corresponding plasmids pYES2.1, pYES2.1-TpELO1, pYES2.1-TpELO2 and pYES2.1-TpELO3. After the selection, in each case two transformants were selected for further functional expression.

Example 21

Cloning Expression Plasmids for the Seed Specific Expression in Plants

A further transformation vector based on pSUN-USP is generated for the transformation of plants. To this end, NotI cleavage sites are introduced at the 5' and 3' termini of the coding sequences, using the following primer pair:

PSUN-TPELO1	
Forward:	(SEQ ID NO: 152)
5' -GCGGCCGCACCATGTGCTCACCACCGCCGTC	
Reverse:	(SEQ ID NO: 153)
3' -GCGGCCGCCTACATGGCACCAGTAAC	
PSUN-TPELO2	
Forward:	(SEQ ID NO: 154)
5' -GCGGCCGCACCATGTGCTCATCACCACCGTC	
Reverse:	(SEQ ID NO: 155)
3' -GCGGCCGCCTACATGGCACCAGTAAC	

-continued

PSUN-TPELO3	
Forward:	(SEQ ID NO: 156)
5' -GCGGCCGCACCATGGACGCCTACAACGCTGC	
Reverse:	(SEQ ID NO: 157)
3' -GCGGCCGCCTAAGCACTCTTCTTCTTT	

- 10 Composition of the PCR Mix (50 μl):  
5.00 μl template cDNA  
5.00 μl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>  
5.00 μl 2 mM dNTP  
1.25 μl of each primer (10 pmol/μl)
- 15 0.50 μl Advantage polymerase  
The Advantage polymerase from Clontech was employed.  
PCR Reaction Conditions:  
Annealing temperature: 1 min 55° C.  
Denaturation temperature: 1 min 94° C.  
Elongation temperature: 2 min 72° C.
- 20 Number of cycles: 35

The PCR products are incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP is incubated in the same manner. Thereafter, the PCR products and the 7624 bp vector are separated by agarose gel electrophoresis and the corresponding DNA fragments are excised. The DNA is purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products are ligated. The Rapid Ligation Kit from Roche is used for this purpose. The resulting plasmids pSUN-TPELO1, pSUN-TPELO2 and pSUN-TPELO3 are verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P, Svab, Z, Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the octopine synthase gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene).

(Primer sequence: SEQ ID NO: 151  
5' -GTCGACCCCGGACTAGTGGGCCCTCTAGACCCGGGGATCCGGATC  
TGCTGGCTATGAA-3' ) ; .

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

Lipids were extracted from yeasts and seeds as described for Example 6.

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## Example 22

## Expression of TpELO1, TpELO2 and TpELO3 in Yeasts

Yeasts which had been transformed with the plasmids pYES2, pYES2-TpELO1, pYES2-TpELO2 and pYES2-TpELO3 as in Example 4 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 in order to remove residual medium and fatty acids. Fatty acid methyl esters (FAMES) were prepared from the yeast cell sediments by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) dimethoxypropane. The FAMES were extracted by twice extracting with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 minutes at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids* 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*, 52(360): 1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

## Example 23

## Functional Characterization of TpELO1 and TpELO3

The substrate specificity of TpELO1 could be determined after expression and the feeding of different fatty acids (FIG. 9). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the TpELO1 reaction. This means that the gene TpELO1 has been expressed functionally.

It can be seen from Table 10 that TpELO1 shows a narrow substrate specificity. TpELO1 was only capable of elongating the C<sub>20</sub>-fatty acids eicosapentaenoic acid and arachidonic acid, but preferred the ω3-desaturated eicosapentaenoic acid.

The yeasts which had been transformed with the vector pYES2-TpELO1 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

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## TABLE 10

Expression of TpELO1 in yeast. Columns 1 and 3 show the control reactions for columns 2 (fed: 250 µm 20:4 Δ5, 8, 11, 14) and 4 (fed: 250 µm 20:4 Δ5, 8, 11, 14, 17).

Fatty acids	Expression 1	Expression 2	Expression 3	Expression 4
16:0	18.8	17.8	25.4	25.2
16:1 <sup>Δ9</sup>	28.0	29.8	36.6	36.6
18:0	5.2	5.0	6.8	6.9
18:1 <sup>Δ9</sup>	25.5	23.6	24.6	23.9
20:4 <sup>Δ5,8,11,14</sup>	22.5	23.4	—	—
22:4 <sup>Δ7,10,13,16</sup>	—	0.4	—	—
20:5 <sup>Δ5,8,11,14,17</sup>	—	—	6.6	6.5
22:5 <sup>Δ7,10,13,16,19</sup>	—	—	—	0.9
% conversion	0	1.7	0	12.2

The substrate specificity of TpELO3 could be determined after expression and the feeding of different fatty acids (FIG. 10). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the TpELO3 reaction. This means that the gene TpELO3 has been expressed functionally.

It can be seen from Table 11 that TpELO3 shows a narrow substrate specificity. TpELO3 was only capable of elongating the C18-fatty acid γ-linolenic acid and stearidonic acid, but preferred the ω3-desaturated stearidonic acid.

The yeasts which had been transformed with the vector pYES2-TpELO3 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

## TABLE 11

Expression of TpELO3 in yeast. Column 1 shows the fatty acid profile of yeast without feeding. Column 2 shows the control reaction. In columns 3 to 6, the following were fed: γ-linolenic acid, stearidonic acid, arachidonic acid and eicosapentaenoic acid (250 µm of each fatty acid).

Fatty acids	1	2	3	4	5	6
16:0	17.9	20.6	17.8	16.7	18.8	18.8
16:1 <sup>Δ9</sup>	41.7	18.7	27.0	33.2	24.0	31.3
18:0	7.0	7.7	6.4	6.6	5.2	6.0
18:1 <sup>Δ9</sup>	33.3	16.8	24.2	31.8	25.5	26.4
18:2 <sup>Δ9,12</sup>	—	<b>36.1</b>	—	—	—	—
18:3 <sup>Δ6,9,12</sup>	—	—	<b>6.1</b>	—	—	—
18:4 <sup>Δ6,9,12,15</sup>	—	—	—	<b>1.7</b>	—	—
20:2 <sup>Δ11,14</sup>	—	<b>0</b>	—	—	—	—
20:3 <sup>Δ8,11,14</sup>	—	—	<b>18.5</b>	—	—	—
20:4 <sup>Δ8,11,14,17</sup>	—	—	—	<b>10.0</b>	—	—
20:4 <sup>Δ5,8,11,14</sup>	—	—	—	—	<b>22.5</b>	—
22:4 <sup>Δ7,10,13,16</sup>	—	—	—	—	<b>0</b>	—
20:5 <sup>Δ5,8,11,14,17</sup>	—	—	—	—	—	<b>17.4</b>
22:5 <sup>Δ7,10,13,16,19</sup>	—	—	—	—	—	<b>0</b>
% conversion	<b>0</b>	<b>0</b>	<b>75</b>	<b>85</b>	<b>0</b>	<b>0</b>

## Example 24

## Cloning and Expression Plasmid for the Heterologous Expression of the Pi-omega3Des in Yeasts

For the heterologous expression in yeasts, the Pi-omega3Des clone was cloned into the yeast expression vector pYES3 via PCR, using suitable Pi-omega3Des-specific primers. Here, exclusively the open reading frame, of

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the gene, which encodes the Pi-omega3Des protein was amplified and provided with two cleavage sites for cloning into the pYES3 expression vector:

(SEQ ID NO: 149)  
Forward Primer: 5'-TAAGCTTACATGGCGACGAAGGAGG

(SEQ ID NO: 150)  
Reverse Primer: 5'-TGGATCCACTTACGTGGACTTGGT

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl of the 5'ATG primer and the 3' Stopp primer)

0.50 µl Advantage polymerase

The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was incubated with the restriction enzymes HindIII and BamHI for 2 hours at 37° C. The yeast expression vector pYES3 (Invitrogen) was incubated in the same manner. Thereafter, the 1104 bp PCR product and the vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and desaturase cDNA were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pYES3-Pi-omega3Des was verified by sequencing and transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by means of electroporation (1500 V). pYES3 was transformed in parallel to act as a control. Thereafter, the yeasts were plated onto complete minimal dropout tryptophan medium supplemented with 2% glucose. Cells which were capable of growing in the medium without tryptophan thus comprise the relevant plasmids pYES3, pYES3-Pi-omega3Des. Following selection, in each case two transformants were selected for the further functional expression.

## Example 25

## Cloning Expression Plasmids for the Seed Specific Expression in Plants

A further transformation vector based on pSUN-USP was generated for the transformation of plants. To this end, NotI cleavage sites were introduced at the 5' and 3' termini of the coding sequence, using the following primer pair

PSUN-Pi-omega3Des  
(SEQ ID NO: 149)  
Reverse: 3'-GCGGCCGCTTACGTGGACTTGGTC

(SEQ ID NO: 149)  
Forward: 5'-GCGGCCGcAtGGCGACGAAGGAGG

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase

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The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 4 hours at 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. Thereafter, the PCR products and the 7624 bp vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pSUN-Piomega3Des was verified by sequencing.

## Example 26

## Expression of Pi-omega3Des in Yeasts

Yeasts which had been transformed with the plasmid pYES3 or pYES3-Pi-omega3Des, as described in Example 24, were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 in order to remove residual medium and fatty acids. Fatty acid methyl esters (FAMES) were prepared from the yeast cell sediments by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) dimethoxypropane. The FAMES were extracted by twice extracting with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 minutes at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids* 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*, 52(360): 1581-1585; Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

## Example 23

## Functional Characterization of Pi-omega3Des

The substrate specificity of Pi-omega3Des could be determined after expression and the feeding of different fatty acids (FIGS. 12 to 18). The substrates fed are present in large amounts in all of the transgenic yeasts, which proves that these fatty acids have been taken up into the yeasts. The transgenic yeasts demonstrate the synthesis of novel fatty acids, the products of the Pi-omega3Des reaction. This means that the gene Pi-omega3Des has been expressed functionally.

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FIG. 12 represents the desaturation of linoleic acid (18:2  $\omega$ 6-fatty acid) to give  $\alpha$ -linolenic acid (18:3  $\omega$ 3-fatty acid) by Pi-omega3Des. The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 12 A) or the vector pYES3-Pi-omega3Des (FIG. 12 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of 18:2<sup>A9,12</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

FIG. 13 represents the desaturation of  $\gamma$ -linolenic acid (18:3  $\omega$ 6-fatty acid) to give stearidonic acid (18:4  $\omega$ 3-fatty acid) by Pi-omega3Des. The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 13 A) or the vector pYes3-Pi-omega3Des (FIG. 13 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of  $\gamma$ C18:3<sup>A6,9,12</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

FIG. 14 represents the desaturation of C20:2- $\omega$ 6-fatty acid to give C20:3- $\omega$ 3-fatty acid by Pi-omega3Des. The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 14 A) or the vector pYes3-Pi-omega3Des (FIG. 14 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of C20:2<sup>A11,14</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

FIG. 15 represents the desaturation of C20:3- $\omega$ 6-fatty acid to give C20:4- $\omega$ 3-fatty acid by Pi-omega3Des. The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 15 A) or the vector pYes3-Pi-omega3Des (FIG. 15 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of C20:3<sup>A8,11,14</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

FIG. 16 shows the desaturation of arachidonic acid (C20:4-(A)-6-fatty acid) to give eicosapentaenoic acid (C20:5- $\omega$ 3-fatty acid) by Pi-omega3Des.

The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 16 A) or the vector pYes3-Pi-omega3Des (FIG. 16 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of C20:4<sup>A5,8,11,14</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

FIG. 17 represents the desaturation of docosatetraenoic acid (C22:4- $\omega$ 6-fatty acid) to give docosapentaenoic acid (C22:5- $\omega$ 3-fatty acid) by Pi-omega3Des. The fatty acid methyl esters were synthesized by subjecting intact cells which had been transformed with the blank vector pYES2 (FIG. 17 A) or the vector pYes3-Pi-omega3Des (FIG. 17 B) to acid methanolysis. The yeasts were cultured in minimal medium in the presence of C22:4<sup>A7,10,13,16</sup>-fatty acid (300  $\mu$ m). Thereafter, the FAMES were analyzed via GLC.

The substrate specificity of Pi-omega3Des with regard to different fatty acids can be seen from FIG. 18. The yeasts which had been transformed with the vector pYes3-Pi-omega3Des were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC. Each value represents a mean of three measurements. The conversion rates (% desaturation) were calculated using the formula:

$$\frac{[\text{product}]}{[\text{product}]+[\text{substrate}]} \times 100.$$

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As described in Example 9, Pi-omega3Des can also be used for generating transgenic plants. Then, the lipids can be extracted from the seeds of these plants as described under Example 6.

## Example 28

Cloning Desaturase Genes from *Ostreococcus tauri*

The search for conserved regions in the protein sequences with the aid of conserved motifs (H is boxes, Domergue et al. 2002, Eur. J. Biochem. 269; 4105-4113) allowed the identification of five sequences with corresponding motifs in an *Ostreococcus tauri* sequence database (genomic sequences). The sequences were the following:

Name of gene	SEQ ID	Amino acids	Homology
OtD4	SEQ ID NO: 95	536	$\Delta$ 4-desaturase
OtD5.1	SEQ ID NO: 91	201	$\Delta$ 5-desaturase
OtD5.2	SEQ ID NO: 93	237	$\Delta$ 5-desaturase
OtD6.1	SEQ ID NO: 89	456	$\Delta$ 6-desaturase
OtFad2	SEQ ID NO: 107	361	$\Delta$ 12-desaturase

The alignments for finding homologies of the individual genes were carried out using the tBLASTn algorithm (Altschul et al., J. Mol. Biol. 1990, 215:403-410).

The cloning procedure was as follows:

40 ml of an *Ostreococcus tauri* culture in the stationary phase were spun down, resuspended in 100  $\mu$ l of double-distilled water and stored at  $-20^{\circ}$  C. The respective genomic DNAs were amplified on the basis of the PCR process. The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient translation (Kozak, Cell 1986, 44:283-292) next to the start codon. The amplification of the OtDes DNAs was carried out in each case using 1  $\mu$ l of defrosted cells, 200  $\mu$ m of dNTPs, 2.5 U Taq polymerase and 100 pmol of each primer in a total volume of 50  $\mu$ l. The PCR conditions were as follows: first denaturation for 5 minutes at  $95^{\circ}$  C., followed by 30 cycles of 30 seconds at  $94^{\circ}$  C., 1 minute at  $55^{\circ}$  C. and 2 minutes at  $72^{\circ}$  C., and a last elongation step of 10 minutes at  $72^{\circ}$  C.

The following primers were employed in the PCR:

```
OtDes6.1 Forward:
                                     (SEQ ID NO: 145)
5'ggttaccacataaatgtgctggagacggaaaataacg3'

OtDes6.1 Reverse:
                                     (SEQ ID NO: 146)
5'ctcgagttacgcccgtcttccggagtggtggcc3'
```

## Example 29

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To characterize the function of the desaturase OtDes6.1 (=  $\Delta$ 6-desaturase) from *Ostreococcus tauri*, the open reading frame of the DNA was cloned downstream of the galactose-inducible GAL1 promoter of pYES2.1/V5-His-TOPO (Invitrogen), giving rise to the corresponding clone pYES2.1-OtDes6.1. Further desaturase genes from *Ostreococcus* can be cloned analogously.

The *Saccharomyces cerevisiae* strain 334 was transformed by electroporation (1500 v) with the vector

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pYES2.1-OtDes6.1. A yeast which was transformed with the blank vector pYES2 was used as the control. The transformed yeasts were selected on complete minimal dropout uracil medium (CMdum) agar plates supplemented with 2% glucose. After the selection, in each case three transformants were selected for the further functional expression.

To express the OtDes6.1 desaturase, precultures of in each case 5 ml of dropout uracil CMdum liquid medium supplemented with 2% (w/v) raffinose were inoculated with the selected transformants and incubated for 2 days at 30° C., 200 rpm. 5 ml of CMdum liquid medium (without uracil) supplemented with 2% raffinose and 300 µm of various fatty acids were then inoculated with the precultures to an OD<sub>600</sub> of 0.05. Expression was induced by addition of 2% (w/v) galactose. The cultures were incubated for a further 96 hours at 20° C.

#### Example 30

##### Cloning of Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP is generated for the transformation of plants. To this end, NotI cleavage sites are introduced at the 5' and 3' termini of the coding sequences, using PCR. The corresponding primer sequences are derived from the 5' and 3' regions of the desaturases.

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase

The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. Thereafter, the PCR products and the vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids were verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P., Svab, Z., Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. *Plant Mol Biol* 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the *Ostreococcus* gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene *J. Mol. Appl. Genet.* 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment

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which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene). (Primer sequence: 5'-GTTCGAC-CCGCGGACTAGTGGGCCCTCTAGAC-CCGGGGGATCC GGATCTGCTGGCTATGAA-3', SEQ ID NO: 144).

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

#### Example 31

##### Expression of OtDes6.1 in Yeasts

Yeasts which had been transformed with the plasmids pYES2, pYES2-OtDes6.2 as described in Example 4 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 to remove residual medium and fatty acids. Starting with the yeast cell sediments, fatty acid methyl esters (FAMES) were prepared by acid methanolysis. To this end, the cell sediments were incubated for one hour at 80° C. together with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) of dimethoxypropane. The FAMES were extracted twice with petroleum ether (PE). To remove non-derivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph equipped with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 min at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids*. 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*. 52(360): 1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

#### Example 32

##### Functional Characterization of Desaturases from *Ostreococcus*

The substrate specificity of desaturases can be determined after expression in yeast (see examples Cloning desaturase genes, Yeast expression) by feeding by means of different yeasts. Descriptions for determining the individual activities are found in WO 93/11245 for Δ15-desaturases, WO 94/11516 for Δ12-desaturases, WO 93/06712, U.S. Pat. No. 5,614,393, U.S. Pat. No. 5,614,393, WO 96/21022, WO 0021557 and WO 99/27111 for Δ6-desaturases, Qiu et al. 2001, *J. Biol. Chem.* 276, 31561-31566 for Δ4-desaturases, Hong et al. 2002, *Lipids* 37, 863-868 for Δ5-desaturases.

Table 12 represents the substrate specificity of the desaturase OtDes6.1 with regard to different fatty acids. The substrate specificity of OtDes6.1 was determined after

expression and feeding of various fatty acids. The substrates which have been fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the OtDes6.2 reaction (FIG. 20). This means that the gene OtDes6.1 has been expressed functionally.

The yeasts which had been transformed with the vector pYES2-OtDes6.1 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC. Each value represents the mean (n=3)±standard deviation. The activity corresponds to the conversion rate calculated using the formula [substrate/(substrate+product)\*100].

It can be seen from Table 12 that OtDes6.1 shows substrate specificity for linoleic and linolenic acid (18:2 and 18:3) since the highest activities are obtained with these

together with the *Physcomitrella patens* Δ6-elongase PSE1 (Zank et al. 2002, Plant J. 31:255-268) and the *Phaeodactylum tricornutum* Δ5-desaturase PtD5 (Domergue et al. 2002, Eur. J. Biochem. 269, 4105-4113) to give dihomo-γ-linolenic acid (=DHGLA) and arachidonic acid (=ARA, FIG. 21B) and dihomostearidonic acid (=DHSTA) and eicosapentaenoic acid (=EPA, FIG. 21D), respectively. FIG. 21 shows clearly that the reaction products GLA and STA of the Δ6-desaturase OtDes6.1 in the presence of the Δ6-elongase PSE1 is elongated virtually quantitatively to give DHGLA and DHSTA, respectively. The subsequent desaturation by the Δ5-desaturase PtD5 to give ARA and EPA, respectively, also proceeds smoothly. Approximately 25-30% of the elongase product is desaturated (FIGS. 21B and D).

TABLE 13

which follows gives an overview of the  
*Ostreococcus desaturases* which have been cloned:  
*Ostreococcus tauri desaturases*

Name	bp	aa	Homology	Cyt. B5	His box1	His box2	His box3
OtD4	1611	536	Δ4-desaturase	HPGG (SEQ ID NO: 227)	HCAH (SEQ ID NO: 228)	WRYHHQVSHHQQVEHHLFP (SEQ ID NO: 231)	QVHHHLFP (SEQ ID NO: 235)
OtD5.1	606	201	Δ5-desaturase	-	-	-	QVHHHLFP (SEQ ID NO: 236)
OtD5.2	714	237	Δ5-desaturase	-	-	WRYHHMVSHHQQIEHHLFP (SEQ ID NO: 232)	QVHHHLFP (SEQ ID NO: 237)
OtD6.1	1443	480	Δ6-desaturase	HPGG (SEQ ID NO: 227)	HEGGH (SEQ ID NO: 229)	WNSMHNKHH (SEQ ID NO: 233)	QVIHHLFP (SEQ ID NO: 238)
QtFAD2	1086	361	Δ12-desaturase	-	HECGH (SEQ ID NO: 230)	WQRSHAVHH (SEQ ID NO: 234)	HVAHH (SEQ ID NO: 239)

fatty acids. In contrast, the activity for oleic acid (18:1) and palmitoleic acid (16:1) is markedly lower. The preferred conversion of linoleic and linolenic acid demonstrates that this desaturase is suitable for the production of polyunsaturated fatty acids.

Substrates	Activity in %
16:1 <sup>Δ9</sup>	5.6
18:1 <sup>Δ9</sup>	13.1
18:2 <sup>Δ9,12</sup>	68.7
18:3 <sup>Δ9,12,15</sup>	64.6

FIG. 20 shows the conversion of linoleic acid by OtDes6.1. The FAMES were analyzed via gas chromatography. The substrate which has been fed (C18:2) is converted into γ-C18:3. Both the starting material and the resulting product are indicated by arrows.

FIG. 21 represents the conversion of linoleic acid (=LA) and α-linolenic acid (=ALA) in the presence of OtDes6.1 to give γ-linolenic acid (=GLA) and stearidonic acid (=STA), respectively (FIGS. 21A and C). Moreover, FIG. 21 shows the conversion of linoleic acid (=LA) and α-linolenic acid (=ALA) in the presence of the Δ6-desaturase OtDes6.1

Example 33

Cloning Desaturase Genes from *Thalassiosira pseudonana*

The search for conserved regions in the protein sequences with the aid of conserved motifs (His boxes, see motifs) allowed the identification of six sequences with corresponding motifs in an *Thalassiosira pseudonana* sequence database (genomic sequences). The sequences were the following:

Name of gene	SEQ ID	Amino acids	Homology
TpD4	SEQ ID NO: 103	503	Δ4-desaturase
TpD5-1	SEQ ID NO: 99	476	Δ5-desaturase
TpD5-2	SEQ ID NO: 101	482	Δ5-desaturase
TpD6	SEQ ID NO: 97	484	Δ6-desaturase
TpFAD2	SEQ ID NO: 109	434	Δ12-desaturase
TpO3	SEQ ID NO: 105	418	ω3-desaturase

The cloning procedure was as follows:  
40 ml of an *Thalassiosira pseudonana* culture in the stationary phase were spun down, resuspended in 100 of

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double-distilled water and stored at  $-20^{\circ}\text{C}$ . The respective genomic DNAs were amplified on the basis of the PCR method. The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient translation (Kozak, *Cell* 1986, 44:283-292) next to the start codon. The amplification of the TpDes DNAs was carried but in each case using 1  $\mu\text{l}$  of defrosted cells, 200  $\mu\text{m}$  of dNTPs, 2.5 U Taq polymerase and 100 pmol of each primer in a total volume of 50  $\mu\text{l}$ . The PCR conditions were as follows: first denaturation for 5 minutes at  $95^{\circ}\text{C}$ ., followed by 30 cycles of 30 seconds at  $94^{\circ}\text{C}$ ., 1 minute at  $55^{\circ}\text{C}$ . and 2 minutes at  $72^{\circ}\text{C}$ ., and a last elongation step of 10 minutes at  $72^{\circ}\text{C}$ .

## Example 34

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To characterize the function of the desaturases from *Thalassiosira pseudonana*, the open reading frame of the respective DNA was cloned downstream of the galactose-inducible GAL1 promoter of pYES2.1/V5-His-TOPO (Invitrogen), giving rise to the corresponding pYES2.1 clone.

The *Saccharomyces cerevisiae* strain 334 is transformed by electroporation (1500 v) with the vectors pYES2.1-TpDesaturasen. A yeast which is transformed with the blank vector pYES2 is used as the control. The transformed yeasts are selected on complete minimal dropout uracil medium (CMdum) agar plates supplemented with 2% glucose. After the selection, in each case three transformants are selected for the further functional expression.

To express the Tp desaturases, initially precultures of in each case 5 ml of dropout uracil CMdum liquid medium supplemented with 2% (w/v) raffinose are inoculated with the selected transformants and incubated for 2 days at  $30^{\circ}\text{C}$ ., 200 rpm. 5 ml of liquid CMdum medium (without uracil) supplemented with 2% raffinose and 300  $\mu\text{m}$  of various fatty acids are then inoculated with the precultures to an  $\text{OD}_{600}$  of 0.05. The expression is induced by addition of 2% (w/v) galactose. The cultures are incubated for a further 96 hours at  $20^{\circ}\text{C}$ .

## Example 35

## Cloning of Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP is generated for the transformation of plants. To this end, NotI cleavage sites are introduced at the 5' and 3' termini of the coding sequences, using PCR. The corresponding primer sequences are derived from the 5' and 3' regions of the desaturases.

Composition of the PCR Mix (50  $\mu\text{l}$ ):

5.00  $\mu\text{l}$  template cDNA

5.00  $\mu\text{l}$  10 $\times$  buffer (Advantage polymerase)+25 mM  $\text{MgCl}_2$

5.00  $\mu\text{l}$  2 mM dNTP

1.25  $\mu\text{l}$  of each primer (10 pmol/ $\mu\text{l}$ )

0.50  $\mu\text{l}$  Advantage polymerase

The Advantage polymerase from Clontech was employed.

PCR reaction conditions:

Annealing temperature: 1 min  $55^{\circ}\text{C}$ .

Denaturation temperature: 1 min  $94^{\circ}\text{C}$ .

Elongation temperature: 2 min  $72^{\circ}\text{C}$ .

Number of cycles: 35

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The PCR products are incubated with the restriction enzyme NotI for 16 hours at  $37^{\circ}\text{C}$ . The plant expression vector pSUN300-USP is incubated in the same manner. Thereafter, the PCR products and the vector are separated by agarose gel electrophoresis and the corresponding DNA fragments are excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products are ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids are verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P., Svab, Z., Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. *Plant Mol Biol* 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is the OCS gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene *J. Mol. Appl. Genet.* 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene).

(Primer sequence:

SEQ ID NO: 143  
GTCGACCCCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATCTGC  
TGGCTATGAA3', ) .

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

## Example 36

## Expression of Tp Desaturases in Yeasts

Yeasts which have been transformed with the plasmids pYES2 and pYES2-TpDesaturasen as described in Example 4 were analyzed as follows:

The yeast cells from the main cultures are harvested by centrifugation (100 $\times$ g, 5 min,  $20^{\circ}\text{C}$ .) and washed with 100 mM  $\text{NaHCO}_3$ , pH 8.0 to remove residual medium and fatty acids. Starting with the yeast cell sediments, fatty acid methyl esters (FAMES) are prepared by acid methanolysis. To this end, the cell sediments are incubated for one hour at  $80^{\circ}\text{C}$ . together with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) of dimethoxypropane. The FAMES were extracted twice with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases are washed in each case once with 2 ml of 100 mM  $\text{NaHCO}_3$ , pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases are dried with  $\text{Na}_2\text{SO}_4$ , evaporated under argon and taken up in 100  $\mu\text{l}$  of PE. The samples are separated on a DB-23 capillary column (30 m,

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0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph equipped with flame ionization detector. The conditions for the GLC analysis are as follows: the oven temperature is programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 min at 250° C. (holding).

The signals are identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids*, 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*, 52(360): 1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*, 439(3):215-218.

Example 37

Functional Characterization of Desaturases from *Thalassiosira pseudonana*

The substrate specificity of desaturases can be determined after expression in yeast (see examples Cloning desaturase genes, Yeast expression) by feeding by means of different yeasts. Descriptions for determining the individual activities are found in WO 93/11245 for Δ15-desaturases, WO 94/11516 for Δ12-desaturases, WO 93/06712, U.S. Pat. No. 5,614,393, U.S. Pat. No. 5,614,393, WO 96/21022, WO 0021557 and WO 99/27111 for Δ6-desaturases, Qiu et al. 2001, *J. Biol. Chem.* 276, 31561-31566 for Δ4-desaturases, Hong et al. 2002, *Lipids* 37, 863-868 for Δ5-desaturases.

The activity of the individual desaturases is calculated from the conversion rate using the formula [substrate/(substrate+product)\*100]

Tables 11 and 12 which follow give an overview of the cloned *Thalassiosira pseudonana* desaturases.

TABLE 14

Length and characteristic features of the cloned <i>Thalassiosira pseudonana</i> desaturases							
Desaturase	cdNA (bp)	Protein (aa)	His box				
			Cyt. B5	His box1	His box2	His box3	
TpD4	1512	503	HPGG (SEQ ID NO: 227)	HDGNH (SEQ ID NO: 240)	WELQHMLGHH (SEQ ID NO: 244)	QIEHHLFP (SEQ ID NO: 250)	
TpD5-1	1431	476	HPGG (SEQ ID NO: 227)	HDANH (SEQ ID NO: 241)	WMAQHWTHH (SEQ ID NO: 245)	QVEHHLFP (SEQ ID NO: 235)	
TpD5-2	1443	482	HPGG (SEQ ID NO: 227)	HDANH (SEQ ID NO: 241)	WLAQHWTHH (SEQ ID NO: 246)	QVEHHLFP (SEQ ID NO: 235)	
TpD6	1449	484	HPGG (SEQ ID NO: 227)	HDFLH (SEQ ID NO: 242)	WKNKHNGHH (SEQ ID NO: 247)	QVDHHLFP (SEQ ID NO: 251)	
TpFAD2 (d12)	1305	434	—	HECGH (SEQ ID NO: 230)	HAKHH (SEQ ID NO: 248)	HVAHHLFP (SEQ ID NO: 252)	
TpO3	1257	419	—	HDAGH (SEQ ID NO: 243)	WLFMVTYLQHH (SEQ ID NO: 249)	HWHHLF (SEQ ID NO: 253)	

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TABLE 15

Length, axons, homology and identities of the cloned desaturases.					
Des.	GDN A (bp)	Exon 1	Exon 2	First Blast Hit	Hom./
					Iden.
TpD4	2633	496-1314	1571-2260	<i>Thrautochitrium</i> D4-des	56%/43%
TpD5-1	2630	490-800	900-2019	<i>Phaeodactylum</i> D5-des	74%/62%
TpD5-2	2643	532-765	854-2068	<i>Phaeodactylum</i> D5-des	72%/61%
TpD6	2371	379-480	630-1982	<i>Phaeodactylum</i> D6-des	83%/69%
TpFAD2	2667	728-2032	—	<i>Phaeodactylum</i> FAD2	76%/61%
TpO3	2402	403-988	1073-1743	<i>Chaenorhabdidis</i> Fad2	49%/28%

The Δ12-desaturase genes from *Ostreococcus* and *Thalassiosira* can also be cloned analogously to the above examples.

Example 38

Cloning Elongase Genes from *Xenopus laevis* and *Ciona intestinalis*

The search for conserved regions (see consensus sequences, SEQ ID NO: 115 and SEQ ID NO: 116) in the protein sequences in gene databases (Genbank) with the aid of the elongase genes with Δ5-elongase activity or Δ6-elongase activity, which are detailed in the application, allowed the identification and isolation of further elongase sequences from other organisms. Further sequences were identified in each case from *X. laevis* and from *C. intestinalis*, using suitable motifs. The sequences were the following:



Name of gene	Organism	Genbank No.	SEQ ID NO:	Amino acids
ELO(XI)	<i>Xenopus laevis</i>	BC044967	117	303
ELO(Ci)	<i>Ciona intestinalis</i>	AK112719	119	290

The cDNA clone of *X. laevis* was obtained from the NIH (National Institute of Health) [Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus* initiative, Dev. Dyn. 225 (4), 384-391 (2002)].

The cDNA clone of *C. intestinalis* was obtained from the University of Kyoto [Satou, Y., Yamada, L., Mochizuki, Y., Takatori, N., Kawashima, T., Sasaki, A., Hamagu-chi, M., Awazu, S., Yagi, K., Sasakura, Y., Nakayama, A., Ishikawa, H., Inaba, K. and Satoh, N. "A cDNA resource from the basal chordate *Ciona intestinalis*" JOURNAL Genesis 33 (4), 153-154 (2002)].

### Example 39

#### Cloning Expression Plasmids for the Heterologous Expression in Yeasts

The elongase DNAs were amplified in each case using 1 µl of cDNA, 200 µM dNTPs, 2.5 U of Advantage polymerase and 100 pmol of each primer in a total volume of 50 µl. The PCR conditions were as follows: first denaturation for 5 minutes at 95° C., followed by 30 cycles of 30 seconds at 94° C., 1 minute at 55° C. and 2 minutes at 72° C., and a final elongation step of 10 minutes at 72° C.

To clone the sequence for heterologous expression in yeasts, the following oligonucleotides were used for the PCR reaction:

Name of gene and SEQ ID NO: Primer sequence
ELO(XI) SEQ ID NO: 121 F: 5' -AGGATCCATGGCCCTCAAGGAGCTCACATC SEQ ID NO: 122 R: 5' -CCTCGAGTCAATGGTTTTGCTTTTCAATGCACCG
ELO(Ci) SEQ ID NO: 123 F: 5' -TAAGCTTATGGACGTA <del>CT</del> TCATCGT SEQ ID NO: 124 R: 5' -TCAGATCTTAAATCGGTTTTACCATT

\*F = forward primer, R = reverse primer

The PCR products were incubated for 30 minutes at 21° C. with the yeast expression vector pYES2.1-TOPO (Invitrogen) following the manufacturer's instructions. The PCR product is ligated into the vector by means of a T overhang and activity of a topoisomerase (Invitrogen). After incubation, *E. coli* DH5α cells were transformed. Suitable clones were identified by PCR, the plasmid DNA was isolated by means of Qiagen DNAeasy Kit and verified by sequencing. The correct sequence was then transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by electroporation (1500 V). As a control, the blank vector pYES2.1 was transformed in parallel. The yeasts were subsequently plated onto complete uracil dropout minimal medium supplemented with 2% glucose. Cells which were capable of growing in the medium without uracil thus comprise the corresponding plasmids pYES2.1, pYES2.1-ELO(XI) and pYES2.1-ELO(Ci). After the selection, in each case two transformants were selected for further functional expression.

#### Cloning Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP is generated for the transformation of plants. To this end, NotI cleavage sites are introduced at the 5' and 3' ends of the coding sequence, using the following primer pair:

pSUN-ELO(XI) Forward:	(SEQ ID NO: 125)
5' -GCGGCCGCACCATGGCCCTCAAGGAGCTCACATC	
Reverse:	(SEQ ID NO: 126)
3' -GCGGCCGCCTTCAATGGTTTTGCTTTTCAATGCACCG	
pSUN-ELO(Ci) Forward:	(SEQ ID NO: 127)
5' -GCGGCCGCACCATGGACGTA <del>CT</del> TCATCGT	
Reverse:	(SEQ ID NO: 128)
3' -GCGGCCGCTTAAATCGGTTTTACCATT	

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA  
5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>  
5.00 µl 2 mM dNTP  
1.25 µl of each primer (10 pmol/µl)  
0.50 µl Advantage polymerase

The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:  
35 Annealing temperature: 1 min 55° C.  
Denaturation temperature: 1 min 94° C.  
Elongation temperature: 2 min 72° C.  
Number of cycles: 35

The PCR products were incubated with the restriction enzyme NotI for 16 hours at . . . 37° C. The plant expression vector pSUN300-USP was incubated in the same manner. Thereafter, the PCR products and the 7624 bp vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pSUN-ELO(XI) and pSUN-ELO(Ci) were verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P, Svab, Z, Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the Octopine synthase gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR

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reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene).

Primer sequence:

(SEQ ID NO: 129)  
5'-GTCGACCCCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATC  
TGCTGGCTATGAA-3'.

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

Lipids were extracted from yeasts and seeds as described for Example 6.

## Example 41

## Expression of ELO(XI) and ELO(Ci) in Yeasts

Yeasts which had been transformed with the plasmids pYES2, pYES2-ELO(XI) and pYES2-ELO(Ci) as in Example 4 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100xg, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 in order to remove residual medium and fatty acids. Fatty acid methyl esters (FAMES) were prepared from the yeast cell sediments by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. with 2 ml of 1N methanolic sulfuric acid and 2% (v/v) dimethoxypropane. The FAMES were extracted by twice extracting with petroleum ether (PE). To remove non-derivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 minutes at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids* 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*, 52(360): 1581-1585; Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

## Example 42

## Functional Characterization of ELO(XI) and ELO(Ci)

The substrate specificity of ELO(XI) can be determined after expression and the feeding of different fatty acids (FIG. 22). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the ELO(XI) reaction. This means that the gene ELO(XI) has been expressed functionally.

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It can be seen from Table 16 that ELO(XI) shows a broad substrate specificity. Both C18- and C<sub>20</sub>-fatty acids are elongated, but a preference for Δ5- and Δ6-desaturated fatty acids can be observed.

The yeasts which had been transformed with the vector pYES2-ELO(XI) were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

TABLE 16

Expression of ELO(XI) in yeast. The conversion rate of different starting materials (amounts fed: in each case 250 µM) is described.

Starting materials	Conversion of the starting materials by ELO(XI) in %
16:0	3
16:1 <sup>Δ9</sup>	0
18:0	2
18:1 <sup>Δ9</sup>	0
18:2 <sup>Δ9,12</sup>	3
18:3 <sup>Δ6,9,12</sup>	12
18:3 <sup>Δ5,9,12</sup>	13
18:3 <sup>Δ9,12,15</sup>	3
18:4 <sup>Δ6,9,12,15</sup>	20
20:3 <sup>Δ8,11,14</sup>	5
20:3 <sup>Δ11,14,17</sup>	13
20:4 <sup>Δ5,8,11,14</sup>	15
20:5 <sup>Δ5,8,11,14,17</sup>	10
22:4 <sup>Δ7,10,13,16</sup>	0
22:6 <sup>Δ4,7,10,13,16,19</sup>	0

The substrate specificity of ELO(Ci) can be determined after expression and the feeding of different fatty acids (FIG. 23). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the ELO(Ci) reaction. This means that the gene ELO(Ci) has been expressed functionally.

TABLE 17

Expression of ELO(Ci) in yeast. The conversion rate of different starting materials (amounts fed: in each case 250 µM) is described.

Starting materials	Conversion of the starting materials by ELO(Ci) in %
16:0	0
16:1 <sup>Δ9</sup>	0
18:0	0
18:1 <sup>Δ9</sup>	0
18:2 <sup>Δ9,12</sup>	23
18:3 <sup>Δ6,9,12</sup>	10
18:3 <sup>Δ5,9,12</sup>	38
18:3 <sup>Δ9,12,15</sup>	25
18:4 <sup>Δ6,9,12,15</sup>	3
20:3 <sup>Δ8,11,14</sup>	10
20:3 <sup>Δ11,14,17</sup>	8
20:4 <sup>Δ5,8,11,14</sup>	10
20:5 <sup>Δ5,8,11,14,17</sup>	15
22:4 <sup>Δ7,10,13,16</sup>	0
22:6 <sup>Δ4,7,10,13,16,19</sup>	0

It can be seen from Table 17 that ELO(Ci) shows a broad substrate specificity. Both C18- and C<sub>20</sub>-fatty acids are elongated, but a preference for Δ5- and Δ6-desaturated fatty acids can be observed.

The yeasts which had been transformed with the vector pYES2-ELO(Ci) were cultured in minimal medium in the

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presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

## Example 43

Cloning Genes from *Ostreococcus tauri*

The search for conserved regions in the protein sequences with the aid of the elongase genes with  $\Delta 5$ -elongase activity or  $\Delta 6$ -elongase activity, which have been described herein, allowed the identification of in each case two sequences with corresponding motifs in an *Ostreococcus tauri* sequence database (genomic sequences). The sequences were the following:

Name of gene	SEQ ID	Amino acids
OtELO1, ( $\Delta 5$ -elongase)	SEQ ID NO: 67	300
OtELO1.2, ( $\Delta 5$ -elongase)	SEQ ID NO: 113	300
OtELO2, ( $\Delta 6$ -elongase)	SEQ ID NO: 69	292
OtELO2.1, ( $\Delta 6$ -elongase)	SEQ ID NO: 111	292

OtElo1 and OtElo1.2 show the highest similarity with an elongase from *Danio rerio* (GenBank AAN77156; approximately 26% identity), while OtElo2 and OtElo2.1 show the highest similarity with *Physcomitrella* Elo (PSE) [approx. 36% identity] (alignments were carried out using the tBLASTn algorithm (Altschul et al., J. Mol. Biol. 1990, 215: 403-410)).

The elongases were cloned as follows:

40 ml of an *Ostreococcus tauri* culture in the stationary phase were spun down, resuspended in 100  $\mu$ l of double-distilled water and stored at  $-20^{\circ}$  C. The respective genomic DNAs were amplified on the basis of the PCR method. The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient translation (Kozak, Cell 1986, 44:283-292) next to the start codon. The amplification of the OtElo DNAs was carried out in each case using 1  $\mu$ l of defrosted cells, 200  $\mu$ M of dNTPs, 2.5 U Taq polymerase and 100 pmol of each primer in a total volume of 50  $\mu$ l. The PCR conditions were as follows: first denaturation for 5 minutes at  $95^{\circ}$  C., followed by 30 cycles of 30 seconds at  $94^{\circ}$  C., 1 minute at  $55^{\circ}$  C. and 2 minutes at  $72^{\circ}$  C., and a last elongation step of 10 minutes at  $72^{\circ}$  C.

## Example 44

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To characterize the function of the elongases from *Ostreococcus tauri*, the open reading frames of the respective DNAs were cloned downstream of the galactose-inducible GAL1 promoter of pYES2.1/V5-His-TOPO (Invitrogen), giving rise to pOTE1, pOTE1.2, pOTE2 and pOTE2.1.

The *Saccharomyces cerevisiae* strain 334 was transformed by electroporation (1500 V) with the vector pOTE1, pOTE1.2, pOTE2 and pOTE2.1, respectively. A yeast which was transformed with the blank vector pYES2 was used as the control. The transformed yeasts were selected on complete minimal dropout uracil medium (CMdum) agar plates supplemented with 2% glucose. After the selection, in each case three transformants were selected for the further functional expression.

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To express the Ot elongases, precultures of in each case 5 ml of liquid CMdum medium supplemented with 2% (w/v) raffinose, but without uracil, were inoculated with the selected transformants and incubated for 2 days at  $30^{\circ}$  C., 200 rpm. 5 ml of liquid CMdum medium (without uracil) supplemented with 2% raffinose and 300  $\mu$ M of various fatty acids were then inoculated with the precultures to an OD<sub>600</sub> of 0.05. The expression was induced by addition of 2% (w/v) galactose. The cultures were incubated for a further 96 hours at  $20^{\circ}$  C.

## Example 45

## Cloning of Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP was generated for the transformation of plants. To this end, NotI cleavage sites were introduced at the 5' and 3' ends of the coding sequences, using PCR. The corresponding primer sequences were derived from the 5' and 3' regions of OtElo1, OtElo1.2, OtElo2 and OtElo2.1.

Composition of the PCR Mix (50  $\mu$ l):

5.00  $\mu$ l template cDNA  
5.00  $\mu$ l 10 $\times$  buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>  
5.00  $\mu$ l 2 mM dNTP  
1.25  $\mu$ l of each primer (10 pmol/ $\mu$ l)  
0.50  $\mu$ l Advantage polymerase

The Advantage polymerase from Clontech was employed.

PCR Reaction Conditions:

Annealing temperature: 1 min  $55^{\circ}$  C.

Denaturation temperature: 1 min  $94^{\circ}$  C.

Elongation temperature: 2 min  $72^{\circ}$  C.

Number of cycles: 35

The PCR products are incubated with the restriction enzyme NotI for 16 hours at  $37^{\circ}$  C. The plant expression vector pSUN300-USP is incubated in the same manner. Thereafter, the PCR products and the vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmids pSUN-OtELO1, pSUN-OtELO1.2, pSUN-OtELO2 and pSUN-OtELO2.2 were verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P, Svab, Z, Maliga, P., (-1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the *Ostreococcus* gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene).

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Primer sequence:

(SEQ ID NO: 130)  
 5'-GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGATCCGGATC

TGCTGGCTATGAA-3', .

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

## Example 46

## Expression of OtElo1, OtElo1.2, OtElo2 and OtELO2.2 in Yeasts

Yeasts which had been transformed with the plasmids pYES3, pYES3-OtEIO1, pYES3-OtEIO1.2, pYES3-OtELO2 and pYES3-OtELO2.2 as described in Example 15 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 to remove residual medium and fatty acids. Starting with the yeast cell sediments, fatty acid methyl esters (FAMES) were prepared by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. together with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) of dimethoxypropane. The FAMES were extracted twice with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph equipped with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 min at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids*. 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*. 52(360): 1581-1585; Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

## Example 47

## Functional Characterization of OtElo1, OtElo1.2, OtElo2 and OtELO2.1

The substrate specificity of OtElo1 was determined after expression and feeding of different fatty acids (Table 18). The substrates which have been fed can be detected in large amounts in all transgenic yeasts. The transgenic yeasts showed the synthesis of novel fatty acids, the products of the OtElo1 reaction. This means that the gene OtElo1 was expressed functionally.

It can be seen from Table 18 that OtElo1 and OtElo1.2 have a narrow substrate specificity. OtElo1 and OtElo1.2 were only capable of elongating the C20-fatty acids eicosa-

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pentaenoic acid (FIG. 24A, 24B) and arachidonic acid (FIG. 25A, 25B), but preference was given to the ω3-desaturated eicosapentaenoic acid.

Table 18 shows the substrate specificity of the elongase OtElo1 and OtElo1.2 for C20-poly unsaturated fatty acids with a double bond in the Δ5-position in comparison with different fatty acids.

The yeasts which had been transformed with the vector pOTE1 or pOTE1.2 were cultured in minimal medium in the presence of the fatty acids stated. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

The substrate specificity of OtElo2 (SEQ ID NO: 81) OtElo2.1 (SEQ ID NO: 111) can be determined after expression and the feeding of different fatty acids (Table 19). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the OtElo2 reaction; This means that the genes OtElo2 and OtElo2.1 have been expressed functionally.

TABLE 18

Fatty acid substrate	Conversion rate of OtElo1 (in %)	Conversion rate of OtElo1.2 (in %)
16:0	—	—
16:1 <sup>Δ9</sup>	—	—
18:0	—	—
18:1 <sup>Δ9</sup>	—	—
18:1 <sup>Δ11</sup>	—	—
18:2 <sup>Δ9,12</sup>	—	—
18:3 <sup>Δ6,9,12</sup>	—	—
18:3 <sup>Δ5,9,12</sup>	—	—
20:3 <sup>Δ8,11,14</sup>	—	—
20:4 <sup>Δ5,8,11,14</sup>	10.8 ± 0.6	38.0
20:5 <sup>Δ5,8,11,14,17</sup>	46.8 ± 3.6	68.6
22:4 <sup>Δ7,10,13,16</sup>	—	—
22:6 <sup>Δ4,7,10,13,16,19</sup>	—	—

Table 19 shows the substrate specificity of the elongase OtElo2 and OtElo2.1 with regard to various fatty acids. OtElo2.1 shows a markedly higher activity.

The yeasts which had been transformed with the vector pOTE2 or pOTE2.1 were cultured in minimal medium in the presence of the fatty acids stated. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC.

The enzymatic activity shown in Table 19 clearly demonstrates that OtElo2 and OtElo2.1, respectively, are a Δ6-elongase.

TABLE 19

Fatty acid substrate	Conversion rate of OtElo2 (in %)	Conversion rate of OtElo2.2 (in %)
16:0	—	—
16:1 <sup>Δ9</sup>	—	—
16:3 <sup>Δ7,10,13</sup>	—	—
18:0	—	—
18:1 <sup>Δ6</sup>	—	—
18:1 <sup>Δ9</sup>	—	—
18:1 <sup>Δ11</sup>	—	—
18:2 <sup>Δ9,12</sup>	—	—
18:3 <sup>Δ6,9,12</sup>	15.3	55.7
18:3 <sup>Δ5,9,12</sup>	—	—
18:4 <sup>Δ6,9,12,15</sup>	21.1	70.4
20:2 <sup>Δ11,14</sup>	—	—
20:3 <sup>Δ8,11,14</sup>	—	—

TABLE 19-continued

Fatty acid substrate	Conversion rate of OtElo2 (in %)	Conversion rate of OtElo2.2 (in %)
20:4 <sup>Δ5,8,11,14</sup>	—	—
20:5 <sup>Δ5,8,11,14,17</sup>	—	—
22:4 <sup>Δ7,10,13,16</sup>	—	—
22:5 <sup>Δ7,10,13,16,19</sup>	—	—
22:6 <sup>Δ4,7,10,13,16,19</sup>	—	—

FIG. 24 A-D shows the elongation of eicosapentaenoic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:5 $\omega$ 3).

FIG. 25 A-D shows the elongation of arachidonic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:4 $\omega$ 6).

#### Example 48

##### Cloning Elongase Genes from *Euglena gracilis* and *Arabidopsis thaliana*

The search for conserved regions in the protein sequences with the aid of the elongase genes with  $\Delta$ 5-elongase activity or  $\Delta$ 6-elongase activity, which are detailed in the application, allowed the identification of sequences from *Arabidopsis thaliana* and *Euglena gracilis*, respectively, with corresponding motifs in sequence databases (Genbank, Euglena EST Bank). The sequences were the following:

Name of gene	SEQ ID	Amino acids
EGY1019 ( <i>E. gracilis</i> )	SEQ ID NO: 131	262
EGY2019 ( <i>E. gracilis</i> )	SEQ ID NO: 133	262
At3g06460 ( <i>A. thaliana</i> )	SEQ ID NO: 135	298
At3g06470 ( <i>A. thaliana</i> )	SEQ ID NO: 137	278

The *Euglena gracilis* elongases were cloned as follows:

The *Euglena gracilis* strain 1224-5/25 was obtained from the Sammlung für Algenkulturen Göttingen [Göttingen collection of algal cultures] (SAG). For the isolation, the strain was grown for 4 days at 23° C. in medium II (Calvayrac R and Douce R, FEBS Letters 7:259-262, 1970) with a photoperiod of 8 h/16 h (light intensity 35 mol s<sup>-1</sup>m<sup>-2</sup>).

Total RNA of a four-day-old *Euglena* culture was isolated with the aid of the RNeasy Kit from Qiagen (Valencia, Calif., US). poly-A+ RNA (mRNA) was isolated from the total RNA with the aid of oligo-dT-cellulose (Sambrook et al., 1989). The RNA was subjected to reverse transcription with the Reverse Transcription System Kit from Promega, and the cDNA synthesized was cloned into the lambda ZAP vector (lambda ZAP Gold, Stratagene). The cDNA was depackaged in accordance with the manufacturer's instructions to give the plasmid DNA, and clones were partially sequenced for random sequencing. mRNA was isolated from the total RNA with the aid of the PolyAtract isolation system (Promega). The mRNA was subjected to reverse transcription with the Marathon cDNA Amplification Kit (BD Biosciences) and the adaptors were ligated in accordance with the manufacturer's instructions. The cDNA library was then used for the PCR for cloning expression plasmids by means of 5'- and 3'-RACE (rapid amplification of cDNA ends).

The *Arabidopsis thaliana* elongases were cloned as follows:

Starting from the genomic DNA, primers for the two genes were derived at the 5' and the 3' end of the open reading frame.

The method of Chrigwin et al., (1979) was used for isolating total RNA from *A. thaliana*. Leaves from 21-day-old plants were crushed in liquid nitrogen, treated with disruption buffer and incubated for 15 minutes at 37° C. After centrifugation (10 min, 4° C., 12 000×g), the RNA in the supernatant was precipitated at -20° C. for 5 hours using 0.02 volume of 3 M sodium acetate pH 5.0 and 0.75 volume ethanol. After a further centrifugation step, the RNA was taken up in 1 ml of TES per g of starting material, extracted once with one volume of phenol/chloroform and: once with one volume of chloroform, and the RNA was precipitated with 2.5 M LiCl. Following subsequent centrifugation and washing with 80% ethanol, the RNA was resuspended in water. The cDNA was synthesized in accordance with the method of Sambrook et al. 1989, and an RT-PCR was carried out using the derived primers. The PCR products were cloned into the vector pYES2.1-TOPO (Invitrogen) in accordance with the manufacturer's instructions.

#### Example 49

##### Cloning Expression Plasmids for Heterologous Expression in Yeasts

To characterize the function of the *A. thaliana* elongases, the open reading frames of the DNAs in question were cloned downstream of the galactose-inducible GAL1 promoter of pYES2.1/V5-His-TOPO (Invitrogen), giving rise to pAt60 and pAt70.

The *Saccharomyces cerevisiae* strain 334 was transformed by electroporation (1500 V) with the vector pAt60 and pAt70, respectively. A yeast which was transformed with the blank vector pYES2.1 was used as the control. The transformed yeasts were selected on complete minimal dropout uracil medium (CMdum) agar plates supplemented with 2% glucose. After the selection, in each case three transformants were selected for the further functional expression.

To express the At elongases, precultures of in each case 5 ml of dropout uracil CMdum liquid medium supplemented with 2% (w/v) raffinose were inoculated with the selected transformants and incubated for 2 days at 30° C., 200 rpm.

5 ml of liquid CMdum medium (without uracil) supplemented with 2% raffinose and 300  $\mu$ M of various fatty acids were then inoculated with the precultures to an OD<sub>600</sub> of 0.05. The expression was induced by addition of 2% (w/v) galactose. The cultures were incubated for a further 96 hours at 20° C.

#### Example 50

##### Expression of pAt60 and pAt70 in Yeasts

Yeasts which had been transformed with the plasmids pYES2.1, pAt60 and pAt70 as described in Example 5 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 to remove residual medium and fatty acids. Starting with the yeast cell sediments, fatty acid methyl esters (FAMES) were prepared by add methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. together with 2 ml of 1 N methanolic sulfuric acid and 2% (v/v) of dimethoxypropane. The FAMES were extracted

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twice with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph equipped with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 min at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids*. 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*. 52(360): 1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

## Example 51

## Functional Characterization of pAt60 and pAt70

The substrate specificity of the elongases At3g06460 and At3g06470 was determined after expression and feeding of various fatty acids (Table 20, FIG. 26). The substrates which have been fed can be detected in all transgenic yeasts. The transgenic yeasts showed the synthesis of novel fatty acids, the products of the genes At3g06460 and At3g06470, respectively. This means that these genes have been expressed functionally.

TABLE 20

Elongation of EPA by the elongases At3g06460 and At3g06470, respectively. Measurement of the yeast extracts after feeding of 250 µM EPA			
Gene	Fatty acid fed	C20:5n-3 content	C22:5n-3 content
At3g06460	EPA (C20:5n-3)	20.8	0.6
At3g06470	EPA (C20:5n-3)	25.4	1.1
Conversion rate of EPA		At3g06460: 3.0%	At3g06470: 4.1%

FIG. 26 represents the elongation of 20:5n-3 by the elongases At3g06470.

## Example 52

Cloning an Elongase from *Phaeodactylum tricorutum*

Starting from conserved regions in the protein sequences, degenerate primers were constructed with the aid of the elongase genes with Δ6-elongase activity detailed in the application, and these primers were used for searching a *Phaeodactylum* cDNA library by means of PCR. The following primer sequences were employed:

Name of primer	Sequence 5'-3' orientation	Corresponding amino acids
Phaelo forward 1	AA (C/T) CTUCTUTGGCTUTT (C/T) T A (SEQ ID NO: 185)	NLLWLFY (SEQ ID NO: 254)

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-continued

Name of primer	Sequence 5'-3' orientation	Corresponding amino acids
Phaelo reverse 1	GA (C/T) TGUAC (A/G) AA (A/G) AA (C/T) TGUG (A/G) AA (SEQ ID NO: 186)	FAQPFVQS (SEQ ID NO: 255)

Nucleotide bases in brackets mean that a mixture of oligonucleotides with in each case one or the other nucleotide base are present.

Construction of the *Phaeodactylum* cDNA Library:

A 2 l culture of *P. tricorutum* UTEX 646 was grown in f/2 medium (Guillard, R. R. L. 1975. Culture of phytoplankton for feeding marine invertebrates. In *Culture of Marine Invertebrate Animals* (Eds. Smith, W. L. and Chanley, M. H.), Plenum Press, New York, pp 29-60) for 14 d (=days) at a light intensity of 35 E/cm<sup>2</sup>. After centrifugation, frozen cells were ground to a fine powder in the presence of liquid nitrogen and resuspended in 2 ml of homogenization buffer (0.33 M sorbitol, 0.3 M NaCl, 10 mM EDTA, 10 mM EGTA, 2% SDS, 2% mercaptoethanol in 0.2 M Tris-Cl pH 8.5). After 4 ml of phenol and 2 ml of chloroform had been added, the mixture was shaken vigorously for 15 minutes at 40-50° C. Thereafter, the mixture was centrifuged (10 min×10 000 g) and the aqueous phase was extracted stepwise with chloroform. Nucleic acids were then precipitated by addition of 1/20 volume 4 M sodium hydrogencarbonate solution and centrifuged. The pellet was taken up in 80 mM Tris-borate pH 7.0 and 1 mM EDTA, and the RNA was precipitated with 8 M lithium chloride. After centrifugation and washing with 70% strength ethanol, the RNA pellet was taken up in RNase-free water. Poly(A)-RNA was isolated using Dynabeads (Dyna, Oslo, Norway) following the manufacturer's instructions, and the first-strand cDNA synthesis was carried out using MLV-Rtase from Roche (Mannheim). Then, the second-strand synthesis was carried out using DNA polymerase I and Klenow fragment, followed by a digestion with RNaseH. The cDNA was then treated with T4 DNA polymerase, and EcoRI/XhoI adaptors (Pharmacia, Freiburg) were subsequently attached by means of T4 ligase. After digestion with XhoI, phosphorylation and gel separation, fragments greater than 300 bp were ligated into the phage lambda ZAP Express following the manufacturer's instructions (Stratagene, Amsterdam, the Netherlands). Following bulk excision of the cDNA library and plasmid recovery, the plasmid library was transformed into *E. coli* DH10B cells and employed for the PCR screening.

Using the abovementioned degenerate primers, it was possible to generate the PCR fragment with the sequence number SEQ ID NO: 187.

This fragment was labeled with digoxigenin (Roche, Mannheim) and used as probe for screening the phage library.

With the aid of the sequence SEQ ID NO: 187, it was possible to obtain the gene sequence SEQ ID NO: 183, which constitutes the full-RNA molecule of the *Phaeodactylum* Δ6-elongase:

## Example 53

## Cloning Expression Plasmids for the Heterologous Expression in Yeasts

The relevant primer pairs were selected in such a way that they bore the yeast consensus sequence for highly efficient

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translation (Kozak, Cell 1986, 44:283-292) next to the start codon. The amplification of the PtELO6 DNAs was carried out in each case using 1 µl of cDNA, 200 µM of dNTPs, 2.5 U Advantage polymerase and 100 pmol of each primer in a total volume of 50 µl. The PCR conditions were as follows: first denaturation for 5 minutes at 95° C., followed by 30 cycles of 30 seconds at 94° C., 1 minute at 55° C. and 2 minutes at 72° C., and a last elongation step of 10 minutes at 72° C.

To clone the sequence for the heterologous expression in yeasts, the following oligonucleotides were used for the PCR reaction:

Name of gene and SEQ ID NO:	Primer sequence
PtELO6 (SEQ ID NO: 183)	F: 5'-GCGGCCGCACATAATGATGGTACCTCAA G (SEQ ID NO: 188)
	R: 3'-GAAGACAGCTTAATAGACTAGT (SEQ ID NO: 189)

\*F = forward primer, R = reverse primer

The PCR products were incubated for 30 minutes at 21° C. with the yeast expression vector pYES2.1-TOPO (Invitrogen) following the manufacturer's instructions. The PCR product (see SEQ ID NO: 192) was ligated into the vector by means of a T overhang and activity of a topoisomerase (Invitrogen). After incubation, *E. coli* DH5α cells were transformed. Suitable clones were identified by PCR, the plasmid DNA was isolated by means of Qiagen DNAeasy Kit and verified by sequencing. The correct sequence was then transformed into the *Saccharomyces* strain INVSc1 (Invitrogen) by electroporation (1500 V). As a control, the blank vector pYES2.1 was transformed in parallel. The yeasts were subsequently plated onto complete uracil drop-out minimal medium supplemented with 2% glucose. Cells which were capable of growing in the medium without uracil thus comprise the corresponding plasmids pYES2.1 and pYES2.1-PtELO6. After the selection, in each case two transformants were selected for further functional expression.

#### Example 54

##### Cloning Expression Plasmids for the Seed-Specific Expression in Plants

A further transformation vector based on pSUN-USP is generated for the transformation of plants. To this end, NotI cleavage sites are introduced at the 5' and 3' ends of the coding sequence, using the following primer pair:

PSUN-PtELO6  
 Forward: (SEQ ID NO: 190)  
 5'-GCGGCCGCACCATGATGGTACCTCAAGTTA  
 Reverse: (SEQ ID NO: 191)  
 3'-GAAGACAGCTTAATAGGCGGCCGC

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA  
 5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>  
 5.00 µl 2 mM dNTP  
 1.25 µl of each primer (10 pmol/µl)  
 0.50 µl Advantage polymerase

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The Advantage polymerase from Clontech was employed. PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.  
 Denaturation temperature: 1 min 94° C.  
 Elongation temperature: 2 min 72° C.  
 Number of cycles: 35

The PCR products are incubated with the restriction enzyme NotI for 16 hours at 37° C. The plant expression vector pSUN300-USP is incubated in the same manner. Thereafter, the PCR products and the 7624 bp vector are separated by agarose gel electrophoresis and the corresponding DNA fragments are excised. The DNA is purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR products are ligated. The Rapid Ligation Kit from Roche is used for this purpose. The resulting plasmids pSUN-PtELO is verified by sequencing.

pSUN300 is a derivative of plasmid pPZP (Hajdukiewicz, P, Svab, Z, Maliga, P., (1994) The small versatile pPZP family of *Agrobacterium* binary vectors for plant transformation. Plant Mol Biol 25:989-994). pSUN-USP originated from pSUN300, by inserting a USP promoter into pSUN300 in the form of an EcoRI fragment. The polyadenylation signal is that of the Octopine synthase gene from the *A. tumefaciens* Ti plasmid (ocs-Terminator, Genbank Accession V00088) (De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)). The USP promoter corresponds to nucleotides 1 to 684 (Genbank Accession X56240), where part of the noncoding region of the USP gene is present in the promoter. The promoter fragment which is 684 base pairs in size was amplified by a PCR reaction and standard methods with the aid of a synthesized primer and by means of a commercially available T7 standard primer (Stratagene).

(Primer sequence: (SEQ ID NO: 151)  
 5'-GTCCGACCCCGGACTAGTGGGCCCTTAGACCCGGGGATCCGGATC  
 TGCTGGCTAGAA-3';).

The PCR fragment was recut with EcoRI/SalI and inserted into the vector pSUN300 with OCS terminator. This gave rise to the plasmid with the name pSUN-USP. The construct was used for the transformation of *Arabidopsis thaliana*, oilseed rape, tobacco and linseed.

Lipids were extracted from yeasts and seeds as described for Example 6.

#### Example 55

##### Expression of PtElo in Yeasts

Yeasts which had been transformed with the plasmids pYES2 and pYES2-PtELO6 as in Example 4 were analyzed as follows:

The yeast cells from the main cultures were harvested by centrifugation (100×g, 5 min, 20° C.) and washed with 100 mM NaHCO<sub>3</sub>, pH 8.0 in order to remove residual medium and fatty acids. Fatty acid methyl esters (FAMES) were prepared from the yeast cell sediments by acid methanolysis. To this end, the cell sediments were incubated for 1 hour at 80° C. with 2 ml of 1N methanolic sulfuric acid and 2% (v/v)

dimethoxypropane. The FAMES were extracted by twice extracting with petroleum ether (PE). To remove nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM NaHCO<sub>3</sub>, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na<sub>2</sub>SO<sub>4</sub>, evaporated under argon and taken up in 100 µl of PE. The samples were separated on a DB-23 capillary column (30 m, 0.25 mm, 0.25 µm, Agilent) in a Hewlett-Packard 6850 gas chromatograph with flame ionization detector. The conditions for the GLC analysis were as follows: the oven temperature was programmed from 50° C. to 250° C. with an increment of 5° C./min and finally 10 minutes at 250° C. (holding).

The signals were identified by comparing the retention times with corresponding fatty acid standards (Sigma). The methodology is described for example in Napier and Michaelson, 2001, *Lipids*. 36(8):761-766; Sayanova et al., 2001, *Journal of Experimental Botany*. 52(360): 1581-1585, Sperling et al., 2001, *Arch. Biochem. Biophys.* 388(2):293-298 and Michaelson et al., 1998, *FEBS Letters*. 439(3):215-218.

Example 56

Functional Characterization of PtELO6

FIG. 29 represents the conversion of C18:3<sup>Δ6,9,12</sup> and C18:4<sup>Δ6,9,12,15</sup>. The substrates are elongated by in each case two carbon atoms; this results in the fatty acids C20:3<sup>Δ8,11,14</sup> and C20:4<sup>Δ8,11,14,17</sup>, respectively. The substrate specificity of PtELO6 can be determined after expression and the feeding of different fatty acids (FIG. 30). The substrates fed can be detected in large amounts in all of the transgenic yeasts. The transgenic yeasts demonstrated the synthesis of novel fatty acids, the products of the PtELO6 reaction. This means that the gene PtELO6 has been expressed functionally.

It can be seen from Table 21 that PtELO6 shows a narrow substrate specificity. PtELO6 was only capable of elongating the C18-fatty acids linoleic acid, linolenic acid, γ-linolenic acid and stearidonic acid, but preferred the ω3-desaturated stearidonic acid (see also FIG. 30).

Feeding experiment: fatty acid's (in bold) were added in each case in amounts of 250 µM. The underlined fatty acids were formed de novo.

TABLE 21

	Substrate specificity of PtELO6				
	Fatty acid fed:				
	+18:2	+18:3	+18:3	+18:3	+18:4
16:0	16.2	18.2	15.2	20	04:48
16:1	50.6	20.5	22.8	33.5	34.2
18:0	5.4	6.3	6.2	5.2	12.4
18:1	27.7	14.6	19.6	19.3	16.7
18:2		40			
18:3			32.9		
18:3				12.3	
18:4					4.5
20:2		<u>0.4</u>			
20:3			<u>3.4</u>		
20:3				<u>9.7</u>	
20:4					<u>14.5</u>
% elongation	<b>0.0</b>	<b>0.99</b>	<b>9.37</b>	<b>44.09</b>	<b>76.32</b>

The following fatty acids were fed, but not converted:  
 18:1<sup>Δ6</sup>, 18:1<sup>Δ9</sup>, 18:1<sup>Δ11</sup>  
 20:2<sup>Δ11,14</sup>, 20:3<sup>Δ11,14,17</sup>, 20:3<sup>Δ8,11,14</sup>, 20:4<sup>Δ5,8,11,14</sup>,  
 20:5<sup>Δ5,8,11,14,17</sup>  
 22:4<sup>Δ7,10,13,16</sup>

The yeasts which had been transformed with the vector pYES2-PtELO6 were cultured in minimal medium in the presence of the fatty acids detailed. The fatty acid methyl esters were synthesized by subjecting intact cells to acid methanolysis. Thereafter, the FAMES were analyzed via GLC. The results shown in FIGS. 29 and 30 and in Table 19 were thus determined.

Example 57

Cloning Expression Plasmids for the Seed-Specific Expression in Plants

The general conditions described hereinbelow apply to all of the subsequent experiments, unless otherwise specified.

The following are preferably used in accordance with the invention for the examples which follow: Bin19, pBI101, pBinAR, pGPTV and pCAMBIA. An overview of binary vectors and their use is found in Hellens et al., *Trends in Plant Science* (2000) 5, 446-451. A pGPTV derivative as described in DE10205607 was used. This vector differs from pGPTV by an additionally inserted AscI restriction cleavage site.

Starting point of the cloning procedure was the cloning vector pUC19 (Maniatis et al.). In the first step, the Conlinin promoter fragment was amplified using the following primers:

Cn11 C (SEQ ID NO: 203)  
 5' : gaattcggcgccgagctcctcgagcaacgggtccggcggtataga  
 gttgggtaattcga

Cn11 C (SEQ ID NO: 204)  
 3' : cccgggatcgatgccggcagatctccaccatttttgggtggtgat

Composition of the PCR Mix (50 µl):

- 5.00 µl template cDNA
- 5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>
- 5.00 µl 2 mM dNTP

- 1.25 µl of each primer (10 pmol/µl)
- 0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

- Annealing temperature: 1 min 55° C.
- Denaturation temperature: 1 min 94° C.
- Elongation temperature: 2 min 72° C.
- Number of cycles: 35

The PCR product was first incubated with the restriction enzyme EcoRI for 2 hours at 37° C. and then for 12 hours at 25° C. with the restriction enzyme SmaI. The cloning vector pUC19 was incubated in the same manner. Thereafter, the PCR product and the cut, 2668 bp vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cn11-C was verified by sequencing.

In the next step, the OCS terminator (Genbank Accession V00088; De Greve, H., Dhaese, P., Seurinck, J., Lemmers, M., Van Montagu, M. and Schell, J. Nucleotide sequence and transcript map of the *Agrobacterium tumefaciens* Ti



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plasmid-encoded octopine synthase gene J. Mol. Appl. Genet. 1 (6), 499-511 (1982)) from the vector pGPVT-USP/OCS

(DE 102 05 607) was amplified using the following primers:

(SEQ ID NO: 205)  
OCS\_C 5': aggcctccatggcctgctttaatgagatatgagagagcc

(SEQ ID NO: 206)  
OCS\_C 3': cccgggcccggacaatcagtaaatggaacggag

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was first incubated with the restriction enzyme StuI for 2 hours at 37° C. and then for 12 hours at 25° C. with the restriction enzyme SmaI. The vector pUC19-Cnl1-C was incubated for 12 hours at 25° C. with the restriction enzyme SmaI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1-C\_OCS was verified by sequencing.

In the next step, the Cnl1-B promoter was amplified by PCR using the following primers:

Cnl1-B (SEQ ID NO: 207)  
5': aggcctcaacggttcggcggtatag

Cnl1-B (SEQ ID NO: 208)  
3': cccggggttaacgctagcgggcccgatatcggatccccatttttgggtggtagttggttct

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was first incubated with the restriction enzyme StuI for 2 hours at 37° C. and then for 12 hours at 25° C. with the restriction enzyme SmaI. The vector pUC19-Cnl1-C was incubated for 12 hours at 25° C. with the restriction enzyme SmaI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter,

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vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1C\_Cnl1B\_OCS was verified by sequencing.

In a further step, the OCS terminator for Cnl1B was inserted. To this end, the PCR was carried out with the following primers:

(SEQ ID NO: 209)  
OCS2 5': aggcctcctgctttaatgagatatgagagac

(SEQ ID NO: 210)  
OCS2 3': cccgggcccggacaatcagtaaatggaacggag

15 Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

20 0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

25 Number of cycles: 35

The PCR product was first incubated with the restriction enzyme StuI for 2 hours at 37° C. and then for 12 hours at 25° C. with the restriction enzyme SmaI. The vector pUC19-Cnl1C\_Cnl1B\_OCS was incubated for 12 hours at 25° C. with the restriction enzyme SmaI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1C\_Cnl1B\_OCS2 was verified by sequencing.

In the next step, the Cnl1-A promoter was amplified by PCR using the following primers:

Cnl1-B (SEQ ID NO: 211)  
5': aggcctcaacggttcggcggtatag

Cnl1-B (SEQ ID NO: 212)  
3': aggccttctagactgcaggcggcccgcatttttggtaggtgatt

gggt

55 Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

60 Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was incubated for 2 hours at 37° C. with the restriction enzyme StuI. The vector pUC19-Cnl1-C was incubated for 12 hours at 25° C. with the restriction enzyme SmaI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by

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means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS2 was verified by sequencing.

In a further step, the OCS terminator for Cnl1A was inserted. To this end, the PCR was carried out with the following primers:

OCS2 (SEQ ID NO: 213)  
5':ggcctcctgctttaatgagatatgcga

OCS2 (SEQ ID NO: 214)  
3':aagcttgggcgccgagctcgtcgacggacaatcagtaaatggaacg

gaga

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was first incubated with the restriction enzyme StuI for 2 hours at 37° C. and then for 2 hours at 37° C. with the restriction enzyme HindIII. The vector pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS2 was incubated for 2 hours at 37° C. with the restriction enzyme StuI and for 2 hours at 37° C. with the restriction enzyme HindIII. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS3 was verified by sequencing.

In the next step, the plasmid pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS3 was used for cloning the Δ6-, Δ5-desaturase and Δ6-elongase. To this end, the Δ6-desaturase from *Phytium irregulare* (WO02/26946) was amplified using the following PCR primers:

(SEQ ID NO: 215)  
D6Des(Pir) 5':agatctatggtggacctcaagcctggagtg

(SEQ ID NO: 216)  
D6Des(Pir) 3':ccatggcccggttacatcgctgggaactcggtgat

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

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The PCR product was first incubated with the restriction enzyme BglIII for 2 hours at 37° C. and then for 2 hours at 37° C. with the restriction enzyme A/col. The vector pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS3 was incubated for 2 hours at 37° C. with the restriction enzyme BglIII and for 2 hours at 37° C. with the restriction enzyme NcoI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_d6Des(Pir) was verified by sequencing.

In the next step, the plasmid pUC19-Cnl1\_d6Des(Pir) was used for cloning the Δ5-desaturase from *Thraustochytrium* ssp. (WO02/26946): To this end, the Δ5-desaturase from *Thraustochytrium* ssp. was amplified using the following PCR primers:

(SEQ ID NO: 217)  
D5Des(Tc) 5':gggatccatgggcaagggcagcgaggggccg

(SEQ ID NO: 218)  
D5Des(Tc) 3':ggcgccgacaccaagaagcaggactgagatatc

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was first incubated with the restriction enzyme BamHI for 2 hours at 37° C. and then for 2 hours at 37° C. with the restriction enzyme EcoRV. The vector pUC19-Cnl1\_d6Des(Pir) was incubated for 2 hours at 37° C. with the restriction enzyme BamHI and for 2 hours at 37° C. with the restriction enzyme EcoRV. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc) was verified by sequencing.

In the next step, the plasmid pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc) was used for cloning the Δ6-elongase from *Physcomitrella patens* (WO01/59128), to which end an amplification with the following PCR primers was carried out:

(SEQ ID NO: 219)  
D6Elo(Pp) 5':gctggccgatggaggtcgtggagagattctacggtg

(SEQ ID NO: 220)  
D6Elo(Pp) 3':gcaaaaggagctaaaactgagtgatctaga

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

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1.25 µl of each primer (10 pmol/µl)  
 0.50 µl Advantage polymerase (Clontech)  
 PCR Reaction Conditions:  
 Annealing temperature: 1 min 55° C.  
 Denaturation temperature: 1 min 94° C.  
 Elongation temperature: 2 min 72° C.  
 Number of cycles: 35

The PCR product was first incubated with the restriction enzyme NotI for 2 hours at 37° C. and then for 2 hours at 37° C. with the restriction enzyme XbaI. The vector pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc) was incubated for 2 hours at 37° C. with the restriction enzyme NotI and for 2 hours at 37° C. with the restriction enzyme XbaI. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit following the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp) was verified by sequencing.

The binary vector for the plant transformation was generated starting from pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp). To this end, pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp) was incubated for 2 hours at 37° C. with the restriction enzyme AscI. The vector pGPTV was treated in the same manner. Thereafter, the fragment from pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp) and the cut pGPTV vector were separated by agarose gel electrophoresis and the relevant DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp) was verified by sequencing.

A further construct, pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co), was used. To this end, an amplification was performed starting from pUC19-Cnl1C\_OCS, using the following primers:

(SEQ ID NO: 221)  
 Cnl1\_OCS 5': gtcgatcaacgggttcggcggtatagagttg

(SEQ ID NO: 222)  
 Cnl1\_OCS 3': gtcgatcggacaatcagtaaatgaaacggaga

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA  
 5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>  
 5.00 µl 2 mM dNTP  
 1.25 µl of each primer (10 pmol/µl)  
 0.50 µl Advantage polymerase (Clontech)  
 PCR Reaction Conditions:  
 Annealing temperature: 1 min 55° C.  
 Denaturation temperature: 1 min 94° C.  
 Elongation temperature: 2 min 72° C.  
 Number of cycles: 35

The PCR product was incubated for 2 hours at 37° C. with the restriction enzyme Sall. The vector pUC19 was incubated for 2 hours at 37° C. with the restriction enzyme Sall. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche

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was used for this purpose. The resulting plasmid pUC19-Cnl1\_OCS was verified by sequencing.

In a further step, the Δ12-desaturase gene from *Calendula officinalis* (WO01/85968) was cloned into pUC19-Cnl1\_OCS. To this end, d12Des(Co) was amplified using the following primers:

(SEQ ID NO: 223)  
 D12Des(Co) 5': agatctatgggtgcagggcggtcgaatgc

(SEQ ID NO: 224)  
 D12Des(Co) 3': ccatggttaaatcttattacgatacc

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA  
 5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>  
 5.00 µl 2 mM dNTP  
 1.25 µl of each primer (10 pmol/µl)  
 0.50 µl Advantage polymerase (Clontech)  
 PCR Reaction Conditions:  
 Annealing temperature: 1 min 55° C.  
 Denaturation temperature: 1 min 94° C.  
 Elongation temperature: 2 min 72° C.  
 Number of cycles: 35

The PCR product was incubated for 2 hours at 37° C. with the restriction enzyme BglII and subsequently for 2 hours at the same temperature with A/col. The vector pUC19-Cnl1\_OCS was incubated in the same manner. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the corresponding DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_D12Des(Co) was verified by sequencing. The plasmid pUC19-Cnl1\_D12Des(Co) and the plasmid pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp) were incubated for 2 hours at 37° C. with the restriction enzyme Sall. Thereafter, the vector fragment and the vector were separated by agarose gel electrophoresis and the relevant DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and vector fragment were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co) was verified by sequencing.

The binary vector for the plant transformation was generated starting from pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co). To this end, pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co) was incubated for 2 hours at 37° C. with the restriction enzyme AscI. The vector pGPTV was treated in the same manner. Thereafter, the fragment from pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co) and the cut pGPTV vector were separated by agarose gel electrophoresis and the relevant DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co) was verified by sequencing.

A further vector which is suitable for the transformation of plants is pSUN2. To increase the number of expression cassettes present in the vector to more than four, this vector

was used in combination with the Gateway System (Invitrogen, Karlsruhe). To this end, the Gateway cassette A was inserted into the vector pSUN2 in accordance with the manufacturer's instructions as described hereinbelow:

The pSUN2 vector (1 µg) was incubated for 1 hour with the restriction enzyme EcoRV at 37° C. Thereafter, the Gateway cassette A (Invitrogen, Karlsruhe) was ligated into the cut vector by means of the Rapid Ligation Kit from Roche, Mannheim. The resulting plasmid was transformed into *E. coli* DB3.1 cells (Invitrogen). The isolated plasmid pSUN-GW was subsequently verified by sequencing.

In the second step, the expression cassette was excised from pUC19-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co) by means of *AscI* and ligated into the vector pSUN-GW, which had been treated in the same manner. The resulting plasmid pSUN-4G was used for further gene constructs.

To this end, a pENTR clone was first modified in accordance with the manufacturer's instructions (Invitrogen). The plasmid pENTR1A (Invitrogen) was incubated for 1 hour at 37° C. with the restriction enzyme *EcoRI*, subsequently treated for 30 minutes with Klenow enzyme and with one 1 µM dNTP mix, and the *AscI* adaptor (5'-ggcgcgcc; phosphorylated at the 5' terminus, double-stranded) was then ligated into the vector pENTR1A. Into this modified, genes were stepwise inserted into the *Cnl* cassette as described above and transferred into the pENTR vector via *AscI*.

The gene TL16y2 from *Thraustochytrium* ssp. (SEQ ID NO: 83) was transferred into the pSUN-4G vector in the above described manner:

In the next step, the plasmid pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS3 was used for cloning the Δ5-elongase TL16y2. To this end, the Δ5-elongase from *Thraustochytrium* ssp. was amplified using the following PCR primers:

(SEQ ID NO: 225)  
TL16y2 5': agatct atggacgtcgtcgagcagca

(SEQ ID NO: 226)  
TL16y2 3': ccattggtccggg agaagcagaagaccatctaa

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+ 25 mM MgCl<sub>2</sub>

5.00 µl 2 mM dNTP

1.25 µl of each primer (10 pmol/µl)

0.50 µl Advantage polymerase (Clontech)

PCR Reaction Conditions:

Annealing temperature: 1 min 55° C.

Denaturation temperature: 1 min 94° C.

Elongation temperature: 2 min 72° C.

Number of cycles: 35

The PCR product was first incubated for 2 hours at 37° C. with the restriction enzyme *Bgl*III and then for 2 hours at 37° C. with the restriction enzyme *Nco*II. The vector pUC19-Cnl1C\_Cnl1B\_Cnl1A\_OCS3 was incubated for 2 hours at 37° C. with the restriction enzyme *Bgl*III and for 2 hours at 37° C. with the restriction enzyme *Nco*II. Thereafter, the PCR product and the cut vector were separated by agarose gel electrophoresis and the relevant DNA fragments were excised. The DNA was purified by means of the Qiagen Gel Purification Kit in accordance with the manufacturer's instructions. Thereafter, vector and PCR product were ligated. The Rapid Ligation Kit from Roche was used for this purpose. The resulting plasmid pUC19-Cnl1\_TL16y2 was verified by sequencing. Thereafter, the cassette was

excised using *AscI* and ligated into an *AscI*-pretreated pENTR vector. The resulting plasmid pENTR-Cnl1\_TL16y2 was then incubated with the vector pSUN-4G in a recombination reaction in accordance with the manufacturer's instructions (Invitrogen). The product gave the vector pSUN-5G, which was used for the transformation of plants.

In a further step, the construct pSUN-8G was generated using the above-described methodology. To this end, 5' and 3' primers for the genes SEQ ID 41, 53, 87 and 113 with the above-described restriction cleavage sites and the first and in each case last 20 nucleotides of the open reading frame were generated, amplified under the standard conditions (see above) and ligated into the vector pENTR-Cnl.

A recombination reaction with the vector pSUN-4G gave rise to the construct pSUN-8G. This vector too was employed for the transformation of plants.

### Example 58

#### Generation of Transgenic Plants

a) Generation of Transgenic Indian Mustard Plants. The Protocol for the Transformation of Oilseed Rape Plants was Used (Modification of the Method of Moloney et al., 1992, Plant Cell Reports, 8:238-242)

To generate transgenic plants, the binary vectors pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co), pSUN-5G and pSUN-8G which had been generated were transformed into *Agrobacterium tumefaciens* C58C1: pGV2260 (Deblaere et al., 1984, Nucl. Acids Res. 13, 4777-4788). To transform Indian mustard plants, a 1:50 dilution of an overnight culture of a positively transformed agrobacterial colony in Murashige-Skoog medium (Murashige and Skoog 1962 Physiol. Plant. 15, 473) supplemented with 3% sucrose (3MS medium) was used. Petioles or hypocotyls of freshly germinated sterile plants (in each case approx. 1 cm<sup>2</sup>) were incubated for 5-10 minutes with a 1:50 agrobacterial dilution in a Petri dish. This is followed by 3 days of coincubation in the dark at 25° C. on 3MS medium supplemented with 0.8% Bacto agar. Cultivation was subsequently continued at 16 hours light/8 hours dark and in a weekly rhythm on MS medium supplemented with 500 mg/l of Claforan (cefotaxime-sodium), 50 mg/l kanamycin, 20 µM benzylaminopurine (BAP) and 1.6 g/l glucose. Growing shoots were transferred to MS medium supplemented with 2% sucrose, 250 mg/l Claforan and 0.8% Bacto agar. If no roots had formed after three weeks, 2-indolebutyric acid was added to the medium for rooting, to act as growth hormone.

Regenerated shoots were maintained on 2MS medium supplemented with kanamycin and Claforan, after rooting, transferred into soil and, after cultivation, grown for two weeks in a controlled-environment cabinet or in a greenhouse, allowed to flower, mature seeds were harvested and studied for elongase expression such as Δ6-elongase activity or Δ5- or Δ6-desaturase activity by means of lipid analyses. In this manner, lines with elevated contents of C20- and C22-polyunsaturated fatty acids were identified.

Transgenic oilseed rape plants were also generated successfully using this protocol.

b) Generation of Transgenic Linseed Plants

The transgenic linseed plants can be generated for example by the method of Bell et al., 1999, In Vitro Cell. Dev. Biol.-Plant. 35(6): 456-465 by means of particle bombardment. *Agrobacteria*-mediated transformations can be

carried out for example by the method of Mlynarova et al. (1994), *Plant Cell Report* 13:282-285.

#### Example 59

##### Lipid Extraction from Seeds

The effect of the genetic modification in plants on the production of a desired compound (such as a fatty acid) can be determined by growing the modified plant under suitable conditions (such as those described above) and analyzing the medium and/or the cellular components for the elevated production of the desired product (i.e. of the lipids or a fatty acid). These analytical techniques are known to the skilled worker and comprise spectroscopy, thin-layer chromatography, various types of staining methods, enzymatic and microbiological methods and analytical chromatography such as high-performance liquid chromatography (see, for example, Ullman, *Encyclopedia of Industrial Chemistry*, Vol. A2, pp 89-90 and pp 443-613, VCH: Weinheim (1985); Fallon, A., et al., (1987) "Applications of HPLC in Biochemistry" in: *Laboratory Techniques in Biochemistry and Molecular Biology*, Vol. 17; Rehm et al. (1993) *Biotechnology*, Vol. 3, Chapter III: "Product recovery and purification", pp 469-714, VCH: Weinheim; Belter, P. A., et al. (1988) *Bioseparations: downstream processing for Biotechnology*, John Wiley and Sons; Kennedy, J. F., and Cabral, J. M. S. (1992) *Recovery processes for biological Materials*, John Wiley and Sons; Shaeiwitz, J. A., and Henry, J. D. (1988) *Biochemical Separations*, in: *Ullmann's Encyclopedia of Industrial Chemistry*, Vol. B3; Chapter 11, pp 1-27, VCH: Weinheim; and Dechow, F. J. (1989) *Separation and purification techniques in biotechnology*, Noyes Publications).

In addition to the abovementioned methods, plant lipids are extracted from plant material as described by Cahoon et al. (1999) *Proc. Natl. Acad. Sci. USA* 96 (22): 12935-12940 and Browse et al. (1986) *Analytic Biochemistry* 152:141-145. The qualitative and quantitative analysis of lipids or fatty acids is described by Christie, William W., *Advances in Lipid Methodology*, Ayr/Scotland: Oily Press (Oily Press Lipid Library; 2); Christie, William W., *Gas Chromatography and Lipids. A Practical Guide—Ayr, Scotland: Oily Press, 1989, Repr. 1992, IX, 307 pp* (Oily Press Lipid Library; 1); "Progress in Lipid Research, Oxford: Pergamon Press, 1 (1952)-16 (1977) under the title: Progress in the Chemistry of Fats and Other Lipids CODEN.

In addition to measuring the end product of the fermentation, it is also possible to analyze other-components of the metabolic pathways which are used for the production of the desired compound, such as intermediates and by-products, in order to determine the overall production efficiency of the compound. The analytical methods comprise measuring the amount of nutrients in the medium (for example sugars, hydrocarbons, nitrogen sources, phosphate and other ions), measuring the biomass composition and the growth, analyzing the production of conventional metabolites of biosynthetic pathways and measuring gases which are generated during the fermentation. Standard methods for these measurements are described in *Applied Microbial Physiology; A Practical Approach*, P. M. Rhodes and P. F. Stanbury, Ed., IRL Press, pp 103-129; 131-163 and 165-192 (ISBN: 0199635773) and references cited therein.

One example is the analysis of fatty acids (abbreviations: FAME, fatty acid methyl ester; GC-MS, gas liquid chromatography/mass spectrometry; TAG, triacylglycerol; TLC, thin-layer chromatography).

Unambiguous proof of the presence of fatty acid products can be obtained by analyzing recombinant organisms using standard analytical methods: GC, GC-MS or TLC, as described on several occasions by Christie and the references therein (1997, in: *Advances on Lipid Methodology*, Fourth Edition: Christie, Oily Press, Dundee, 119-169; 1998, *Gaschromatographie-Massenspektrometrie-Verfahren [Gas chromatography/mass spectrometry methods]*, *Lipide* 33:343-353).

The material to be analyzed can be disrupted by sonication, grinding in a glass mill, liquid nitrogen and grinding or via other applicable methods. After disruption, the material must be centrifuged. The sediment is resuspended in distilled water, heated for 10 minutes at 100° C., cooled on ice and recentrifuged, followed by extraction for 1 hour at 90° C. in 0.5 M sulfuric acid in methanol with 2% dimethoxypropane, which leads to hydrolyzed oil and lipid compounds, which give transmethylated lipids. These fatty acid methyl esters are extracted in petroleum ether and finally subjected to a GC analysis using a capillary column (Chrompack, WCOT Fused Silica, CP-Wax-52 CB, 25 µm, 0.32 mm) at a temperature gradient of between 170° C. and 240° C. for 20 minutes and 5 minutes at 240° C. The identity of the resulting fatty acid methyl esters must be defined using standards which are available from commercial sources (i.e. Sigma).

Plant material is initially homogenized mechanically by crushing in a pestle and mortar to make it more amenable, to extraction.

This is followed by heating at -100° C. for 10 minutes and, after cooling on ice, by resedimentation. The cell sediment is hydrolyzed for 1 hour at 90° C. with 1 M methanolic sulfuric acid and 2% dimethoxypropane, and the lipids are transmethylated. The resulting fatty acid methyl esters (FAMES) are extracted in petroleum ether. The extracted FAMES are analyzed by gas liquid chromatography using a capillary column (Chrompack, WCOT Fused Silica, CP-Wax-52 CB, 25 m, 0.32 mm) and a temperature gradient of from 170° C. to 240° C. in 20 minutes and 5 minutes at 240° C. The identity of the fatty acid methyl esters is confirmed by comparison with corresponding FAME standards (Sigma). The identity and position of the double bond can be analyzed further by suitable chemical derivatization of the FAME mixtures, for example to give 4,4-dimethoxyoxazolin derivatives (Christie, 1998) by means of GC-MS.

#### Example 60

##### Analysis of the Seeds from the Transgenic Plants which have been Generated

Analogously to Example 59, the seeds of the plants which had been transformed with the constructs pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co), pSUN-5G and pSUN-8G were analyzed. FIG. 32 shows the fatty acid spectrum of seeds with the construct pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co). In comparison with control plants which were not transformed (wild-type control, WT), a pronounced change in the fatty acid spectrum was observed. It was thus possible to demonstrate that the transformed genes are functional, Table 22 compiles the results of FIG. 32.

TABLE 22

Lines	Fatty acids								
	16:0	18:0	18:1	18:2	GLA	18:3	SDA	ARA	EPA
WT control	5.6	6.5	31.7	41.7	nd	12.1	nd	nd	nd
1424_Ko82_4	6.6	1.5	8.9	10.5	42.2	3.1	2.8	17.2	0.2
1424_Ko82_5	6.1	1.5	11.0	9.0	40.6	2.9	4.0	15.0	1.5
1424_Ko82_6	5.7	1.6	15.5	10.6	37.1	3.0	3.2	14.6	0.2
1424_Ko82_7	5.4	2.0	20.4	10.7	32.6	3.5	3.2	12.1	1.0
1424_Ko82_8	5.4	1.4	15.1	12.5	39.9	2.6	2.4	12.2	0.7
1424_Ko82_9	6.0	1.8	25.0	9.9	29.7	2.2	2.5	10.2	0.8
1424_Ko82_10	5.7	1.3	10.1	10.3	42.5	2.6	3.5	13.9	1.1
1424_Ko82_11	5.4	1.4	15.7	11.3	38.2	2.6	2.8	14.1	1.0

Here, the analysis of the seeds with the construct pSUN-5G reveals lines with a pronounced increase in the arachidonic acid content in comparison with the construct pGPTV-Cnl1\_d6Des(Pir)\_d5Des(Tc)\_D6Elo(Pp)\_D12Des(Co). In this context, lines with up to 25% ARA were obtained. The additional elongase (TL16y2) must be responsible for this effect (FIG. 31, pSUN-5G). The results from this line are compiled in Table 23.

TABLE 23

Fatty acid analysis of transgenic seeds which have been transformed with the construct pSUN-5G.											
Lines	Fatty acids										
	16:0	18:0	18:1	18:2 LA	18:3 GLA	18:3 ALA	18:4 SDA	20:3 HGLA	ARA	EPA	
WT	5.2	2.3	34.2	37.9	0.0	11.6	0.0	0.0	0.0	0.0	
16-1-2	4.2	1.6	20.1	21.5	25.9	4.1	1.8	1.7	8.9	0.8	
16-1-3	5.8	2.3	9.9	14.6	33.6	3.1	2.2	2.2	16.0	1.4	
16-1-8	5.0	2.8	11.1	12.6	34.9	2.2	1.8	2.6	16.3	1.2	
16-2-1	4.9	1.6	14.5	17.4	32.9	3.5	2.0	1.6	12.3	1.0	
16-2-5	5.5	3.3	12.9	13.8	32.9	2.9	2.2	1.4	15.4	1.4	
16-4-2	5.8	2.5	18.8	14.7	32.0	3.5	2.3	1.2	12.0	1.2	
16-4-3	5.9	2.0	19.7	15.0	32.0	3.8	2.4	1.1	11.4	1.2	
16-7-2	6.2	4.4	14.3	10.2	30.7	2.0	2.1	1.7	19.4	1.9	
16-7-3	5.0	2.5	21.6	13.6	30.7	2.1	1.8	1.5	12.6	1.1	
16-7-4	5.3	4.1	18.8	19.5	23.1	4.2	2.2	2.9	11.3	1.4	
16-7-5	7.4	1.8	4.2	6.8	33.7	1.8	2.7	2.6	25.8	2.6	

## Example 61

## Detection of DHA in Seeds of Transgenic Indian Mustard Plants

Seeds of plants which had been generated with the construct pSUN-8G as described in Example 58 were analyzed as described in Example 59. Besides the LCPUFAs arachidonic acid and eicosapentaenoic acid, docosahexaenoic acid, the product after conversion by the  $\Delta 4$ -desaturase from *Thraustochytrium* and  $\Delta 5$ -elongases from *Onchorynchis mykiss* and *Ostreococcus tauri*, was also detected in

these seeds. FIG. 32 shows the chromatogram with the modified fatty acid spectrum in comparison with an untransformed control plant. The results of several measurements are compiled in Table 24.

Table 24 shows the fatty acid analysis of transgenic seeds which have been transformed with the construct pSUN-8G.

In this experiment, the synthesis of docosahexaenoic acid in seeds was demonstrated for the first time. While the

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synthesis of DHA in higher plants has been described, for example in WO 2004/071467, the synthesis has not been demonstrated for seeds, only for an embryogenic cell culture.

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## EQUIVALENTS

Many equivalents of the specific embodiments according to the invention described herein can be seen or found by the skilled worker by simple routine experiments. These equivalents are intended to be included in the patent claims.

TABLE 2

Fatty acid distribution in the seeds of the three different transgenic <i>B. juncea</i> lines								
<i>B. juncea</i> lines	No.	18:1	18:2 (LA)	$\gamma$ 18:3 (GLA)	$\alpha$ 18:3 (ALA)	18:4 (SDA)	20:3 (HGLA)	20:4 (ARA)
WT	1	33.2	38.2	0	12.2	0	0	0
	2	31.3	41.2	0	11.7	0	0	0
8-1424-5	1	25.1	12.8	26.4	3.5	2.4	0.6	8.3
	2	26	12.7	26.3	3.8	2.6	0.6	8.2
	3	25	12.5	25.9	3.4	2.4	0.8	8.5
8-1424-8	1	28.1	13.1	25	5.8	3.7	0.2	6.2
	2	24.7	14.8	26.4	5.2	3	0.3	6.8
8-1424-10	1	25.2	14.2	29.8	5.2	3.4	0.5	5
	2	27.2	12.7	27.9	4.2	2.9	0.3	6.3

The amounts of fatty acids were stated in % by weight.

LA = linoleic acid,

GLA =  $\gamma$ -linolenic acid,

ALA =  $\alpha$ -linolenic acid,

SDA = stearidonic acid,

HGLA = dihomogamma-linolenic acid,

ARA = arachidonic acid,

ETA = eicosatetraenoic acid,

EPA = eicosapentaenoic acid

TABLE 3

Fatty acid distribution in the seeds of the three different transgenic <i>B. juncea</i> lines												
Sample	No.	18:1 $\Delta$ 9	18:2 $\Delta$ 6, 9	18:2 $\Delta$ 9, 12 (LA)	18:3 $\Delta$ 6, 9, 12 (GLA)	18:3 $\Delta$ 9, 12, 15 (ALA)	18:4 $\Delta$ 6, 9, 12, 15 (SDA)	20:3 $\Delta$ 8, 11, 14 (HGLA)	20:4 $\Delta$ 5, 8, 11, 14 (ARA)	20:4 $\Delta$ 8, 11, 14, 17 (ETA)	20:5 $\Delta$ 5, 8, 11, 14, 17 (EPA)	
WT	1	35.10	0.00	35.71	0.00	10.80	0.00	0.00	0.00	0.00	0.00	
	2	27.79	0.00	32.83	0.00	8.94	0.71	0.00	0.00	0.00	0.00	
9-1424-1	1	17.62	1.07	12.32	29.92	2.84	2.17	0.97	13.05	<0.01	1.21	
	2	23.68	2.17	10.57	23.70	2.39	1.80	0.98	11.60	<0.01	1.16	
	3	17.15	0.94	12.86	31.16	3.19	2.40	1.01	12.09	<0.01	1.16	
9-1424-5	1	16.48	1.47	11.09	30.49	3.06	2.56	0.75	11.84	<0.01	1.24	
	2	17.70	1.23	11.42	27.94	2.35	1.88	0.64	12.30	0.03	1.12	
	3	19.29	1.05	10.95	26.11	2.85	2.11	1.07	12.09	<0.01	1.21	
9-1424-6	1	24.71	0.00	41.87	0.00	12.32	0.00	0.00	0.00	0.00	0.00	
	2	28.84	0.00	40.65	0.00	10.94	0.00	0.00	0.00	0.00	0.00	
	3	29.28	0.00	41.34	0.00	10.76	0.00	0.00	0.00	0.00	0.00	
9-1424-7	1	32.41	0.00	37.26	0.00	10.05	0.00	0.00	0.00	0.00	0.00	
	2	27.76	0.00	36.66	0.00	11.43	0.00	0.00	0.00	0.00	0.00	
	3	32.03	0.00	36.27	0.00	9.27	0.00	0.00	0.00	0.00	0.00	
9-1424-8	1	19.08	0.61	11.26	23.31	3.73	2.14	1.11	10.93	0.08	1.11	
	2	20.34	3.78	10.07	19.59	2.36	1.72	0.68	8.21	<0.01	1.00	
	3	28.27	0.00	37.19	0.00	9.32	0.00	0.00	0.00	0.00	0.00	
9-1424-9	1	25.95	0.00	37.87	0.00	9.15	0.00	0.00	0.00	0.00	0.00	
	2	22.94	0.00	42.69	0.00	9.14	0.00	0.00	0.00	0.00	0.00	
	3	18.96	0.61	14.09	23.76	3.17	1.86	0.97	10.46	<0.01	0.94	

The amounts of fatty acids were stated in % by weight.

LA = linoleic acid,

GLA =  $\gamma$ -linolenic acid,

ALA =  $\alpha$ -linolenic acid,

SDA = stearidonic acid,

HGLA = dihomogamma-linolenic acid,

ARA = arachidonic acid,

ETA = eicosatetraenoic acid,

EPA = eicosapentaenoic acid

TABLE 4

Fatty acid analysis in seeds of <i>Brassica juncea</i>																
	16:0	18:0	18:1c9	18:1c11	18:2c6, 9	LA 18:2	GLA 18:3	ALA 18:3	SDA 18:4	20:0	20:1c5	20:2 c8, 11	HGLA 20:3 c8, 11, 14	ARA 20:4	ETA 20:4	EPA 20:5
WT	5.2	2.3	34.2	3.2	0.0	37.9	0.0	11.6	0.0	0.4	1.1	3.7	0.0	0.0	0.0	0.0
16-1-2	4.2	1.6	20.1	2.3	0.1	21.5	25.9	4.1	1.8	0.4	1.5	3.9	1.7	8.9	0.5	0.8

TABLE 4-continued

Fatty acid analysis in seeds of <i>Brassica juncea</i>																
	16:0	18:0	18:1c9	18:1c11	18:2c6, 9	LA 18:2	GLA 18:3	ALA 18:3	SDA 18:4	20:0	20:1c5	20:2 c8, 11	HGLA 20:3 c8, 11, 14	ARA 20:4	ETA 20:4	EPA 20:5
16-1-3	5.8	2.3	9.9	2.7	0.1	14.6	33.6	3.1	2.2	0.6	1.0	3.2	2.2	16.0	0.4	1.4
16-1-8	5.0	2.8	11.1	2.1	0.3	12.6	34.9	2.2	1.8	0.6	1.3	3.7	2.6	16.3	0.4	1.2
16-2-1	4.9	1.6	14.5	2.9	0.2	17.4	32.9	3.5	2.0	0.4	0.9	1.6	1.6	12.3	1.9	1.0
16-2-5	5.5	3.3	12.9	3.0	0.4	13.8	32.9	2.9	2.2	0.7	1.0	2.2	1.4	15.4	0.3	1.4
16-4-2	5.8	2.5	18.8	2.6	0.9	14.7	32.0	3.5	2.3	0.7	0.8	0.6	1.2	12.0	0.1	1.2
16-4-3	5.9	2.0	19.7	2.5	1.1	15.0	32.0	3.8	2.4	0.5	0.8	0.5	1.1	11.4	0.1	1.2
16-7-2	6.2	4.4	14.3	2.2	0.7	10.2	30.7	2.0	2.1	0.9	0.9	2.1	1.7	19.4	0.3	1.9
16-7-3	5.0	2.5	21.6	1.7	1.5	13.6	30.7	2.1	1.8	0.6	1.1	2.0	1.5	12.6	0.2	1.1
16-7-4	5.3	4.1	18.8	2.2	0.7	19.5	23.1	4.2	2.2	0.7	1.0	1.8	2.9	11.3	0.3	1.4
16-7-5	7.4	1.8	4.2	3.9	0.0	6.8	33.7	1.8	2.7	0.8	0.8	3.2	2.6	25.8	0.6	2.6

The amounts of fatty acids were stated in % by weight.

LA = linoleic acid,

GLA =  $\gamma$ -linolenic acid,

ALA =  $\alpha$ -linolenic acid,

SDA = stearidonic acid,

HGLA = dihomogamma-linolenic acid,

ARA = arachidonic acid,

ETA = eicosatetraenoic acid,

EPA = eicosapentaenoic acid

TABLE 6

Conversion rates of the fatty acids which have been fed. The conversion rates were calculated using the formula  
 $[\text{conversion rate}] = \frac{[\text{product}]}{([\text{substrate}] + [\text{product}])} * 100$   
 BioTaur clones area in % of the GC analysis

Clone	fatty acid	C16:0	C16:1 (n-7)	C18:0	C18:1 (n-9)	C18:3 (n-6)	C18:4 (n-3)	C20:3 (n-6)	C20:4 (n-6)	C20:4 (n-3)	C20:5 (n-3)	C22:4 (n-6)	C22:4 (n-3)	C22:5 (n-3)
Vector	none	21.261	41.576	4.670	25.330									
BioTaur	none	20.831	37.374	4.215	26.475									
Vector	GLA + EPA	22.053	23.632	5.487	17.289	<b>11.574</b>					<b>13.792</b>			
BioTaur	GLA + EPA	20.439	25.554	6.129	19.587	<b>3.521</b>		<b>6.620</b>			<b>10.149</b>			<b>1.127</b>
Vector	EPA	20.669	28.985	6.292	21.712						<b>16.225</b>			
BioTaur	EPA	20.472	26.913	6.570	23.131						<b>11.519</b>			<b>3.251</b>
Vector	ARA	23.169	23.332	6.587	12.735				<b>27.069</b>					
BioTaur	ARA	20.969	31.281	5.367	21.351				<b>9.648</b>			<b>1.632</b>		
Vector	SDA	18.519	12.626	6.642	6.344		<b>47.911</b>							
BioTaur	SDA	19.683	15.878	7.246	8.403		<b>13.569</b>			<b>25.946</b>				<b>0.876</b>

TABLE 24

Fatty acid analysis of transgenic seeds which have been transformed with the construct pSUN-8G

I	16:0	18:0	18:1 $\Delta 9$	LA	GLA	ALA	SDA	HGLA	ARA	EPA	22:5	DHA
				18:2 $\Delta 9, 12$	18:3 $\Delta 6, 9, 12$	18:3 $\Delta 9, 12, 15$	18:4 $\Delta 6, 9, 12, 15$	20:3 $\Delta 8, 11, 14$	20:4 $\Delta 5, 8, 11, 14$	20:5 $\Delta 5, 8, 11, 14, 17$	$\Delta 7, 10, 13, 16, 19$	$\Delta 4, 7, 10, 13, 16, 19$
WT	5.26	1.80	30.78	43.93	nd	12.47	nd	nd	nd	nd	nd	nd
Bj-17-1-3	4.73	2.28	19.30	14.04	31.48	3.09	2.40	1.70	3.37	8.65	0.19	0.25
Bj-17-2-1	4.34	2.17	17.60	15.56	29.97	3.37	2.44	2.14	4.05	9.14	0.23	0.40
Bj-17-4-3	4.31	1.70	14.45	16.94	35.54	3.43	2.39	0.10	5.09	9.43	0.24	0.23
II				% saturated fatty acids	% mono-unsaturated fatty acids			% poly-unsaturated fatty acids			% LCFAs	% VLCFAs
WT				7.96	35.43			56.62			97.71	2.29
Bj-17-1-3				9.18	24.95			65.87			79.64	20.36
Bj-17-2-1				9.83	25.44			64.73			80.44	19.56
Bj-17-4-3				14.05	20.36			65.60			75.27	24.73

LCFAs = all fatty acids up to a length of 18 carbon atoms in the fatty acid chain

VLCFAs = all fatty acids with a length of 20 or more carbon atoms in the fatty acid chain



## SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 255

<210> SEQ ID NO 1

<211> LENGTH: 1266

<212> TYPE: DNA

<213> ORGANISM: *Euglena gracilis*

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1266)

<223> OTHER INFORMATION: Delta-8 desaturase

<400> SEQUENCE: 1

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atg aag tca aag cgc caa cgc ctt ccc ctt aca att gat gga aca aca      48
Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1                    5                      10                    15

tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att      96
Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20                   25                   30

ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg     144
Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35                   40                   45

cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat     192
His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50                   55                   60

ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag     240
Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65                   70                   75                   80

gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat     288
Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85                   90                   95

gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt     336
Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
100                  105                  110

gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att     384
Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
115                  120                  125

ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct     432
Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
130                  135                  140

cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac     480
His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
145                  150                  155                  160

ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca     528
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
165                  170                  175

tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa     576
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
180                  185                  190

ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag     624
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
195                  200                  205

gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc     672
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
210                  215                  220

cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg     720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
225                  230                  235                  240

tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac     768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
245                  250                  255

caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg     816

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Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu		
		260						265					270				
cat	tgg	aca	ttg	aag	gcc	ctg	ttc	cac	tta	ttc	ttt	atg	ccc	agc	atc		864
His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile		
		275					280					285					
ctc	aca	tcg	ctg	ttg	gta	ttt	ttc	ggt	tcg	gag	ctg	gtt	ggc	ggc	ttc		912
Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe		
	290					295				300							
ggc	att	gcg	atc	gtg	gtg	ttc	atg	aac	cac	tac	cca	ctg	gag	aag	atc		960
Gly	Ile	Ala	Ile	Val	Val	Phe	Met	Asn	His	Tyr	Pro	Leu	Glu	Lys	Ile		
	305				310					315					320		
ggg	gac	tcg	gtc	tgg	gat	ggc	cat	gga	ttc	tcg	ggt	ggc	cag	atc	cat		1008
Gly	Asp	Ser	Val	Trp	Asp	Gly	His	Gly	Phe	Ser	Val	Gly	Gln	Ile	His		
			325					330					335				
gag	acc	atg	aac	att	cgg	cga	ggg	att	atc	aca	gat	tgg	ttt	ttc	gga		1056
Glu	Thr	Met	Asn	Ile	Arg	Arg	Gly	Ile	Ile	Thr	Asp	Trp	Phe	Phe	Gly		
		340					345						350				
ggc	ttg	aac	tac	cag	atc	gag	cac	cat	ttg	tgg	ccg	acc	ctc	cct	cgc		1104
Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Trp	Pro	Thr	Leu	Pro	Arg		
		355					360					365					
cac	aac	ctg	aca	gcg	ggt	agc	tac	cag	gtg	gaa	cag	ctg	tgc	cag	aag		1152
His	Asn	Leu	Thr	Ala	Val	Ser	Tyr	Gln	Val	Glu	Gln	Leu	Cys	Gln	Lys		
	370					375					380						
cac	aac	ctg	ccg	tat	cgg	aac	ccg	ctg	ccc	cat	gaa	ggg	ttg	gtc	atc		1200
His	Asn	Leu	Pro	Tyr	Arg	Asn	Pro	Leu	Pro	His	Glu	Gly	Leu	Val	Ile		
	385				390					395					400		
ctg	ctg	cgc	tat	ctg	gcg	gtg	ttc	gcc	cgg	atg	gcg	gag	aag	caa	ccc		1248
Leu	Leu	Arg	Tyr	Leu	Ala	Val	Phe	Ala	Arg	Met	Ala	Glu	Lys	Gln	Pro		
			405					410						415			
gcg	ggg	aag	gct	cta	taa												1266
Ala	Gly	Lys	Ala	Leu													
			420														

&lt;210&gt; SEQ ID NO 2

&lt;211&gt; LENGTH: 421

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Euglena gracilis*

&lt;400&gt; SEQUENCE: 2

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

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145	150	155	160
Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr	165	170	175
Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln	180	185	190
Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu	195	200	205
Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe	210	215	220
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp	225	230	235
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn	245	250	255
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu	260	265	270
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile	275	280	285
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe	290	295	300
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile	305	310	315
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His	325	330	335
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly	340	345	350
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg	355	360	365
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys	370	375	380
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile	385	390	395
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro	405	410	415
Ala Gly Lys Ala Leu	420		

<210> SEQ ID NO 3  
 <211> LENGTH: 777  
 <212> TYPE: DNA  
 <213> ORGANISM: Isochrysis galbana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(777)  
 <223> OTHER INFORMATION: Delta-9 elongase

<400> SEQUENCE: 3

atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc	48
Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr	
1 5 10 15	
gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg	96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro	
20 25 30	
ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg	144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg	
35 40 45	
acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg	192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu	

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50	55	60	
agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly 65 70 75 80			240
gcg tgg ctg cgc agg caa acc gcc gac aca ccg cag ccg ctc ttc cag Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln 85 90 95			288
tgc ccg tcc ccg gtt tgg gac tgc aag ctc ttc aca tgg acc gcc aag Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys 100 105 110			336
gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu 115 120 125			384
agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp 130 135 140			432
gtg tac ctc gcc att cgg ctg cac aac gag gcc gta tgg atc ttc atg Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met 145 150 155 160			480
ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac gcc ctc Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu 165 170 175			528
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met 180 185 190			576
cag atc tgc cag ttc gtg gcc gcc ttc ctg ttg gtc tgg gac tac atc Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile 195 200 205			624
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala 210 215 220			672
ttc aac tat gca tac gtc gcc tcg gtc ttc ttg ctc ttc tgc cac ttt Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe 225 230 235 240			720
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg gcc aag Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys 245 250 255			768
cag ctc tag Gln Leu			777

&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 258

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Isochrysis galbana

&lt;400&gt; SEQUENCE: 4

Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr  
1 5 10 15

Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro  
20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg  
35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu  
50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly  
65 70 75 80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln  
85 90 95

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Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
 100 105 110  
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
 115 120 125  
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
 130 135 140  
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
 145 150 155 160  
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu  
 165 170 175  
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met  
 180 185 190  
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile  
 195 200 205  
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala  
 210 215 220  
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe  
 225 230 235 240  
 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys  
 245 250 255  
 Gln Leu

<210> SEQ ID NO 5  
 <211> LENGTH: 1410  
 <212> TYPE: DNA  
 <213> ORGANISM: Phaeodactylum tricornutum  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1410)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 5

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Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val	
1 5 10 15	
gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt	96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser	
20 25 30	
ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat	144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr	
35 40 45	
gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt	192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe	
50 55 60	
ggg ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat	240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His	
65 70 75 80	
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat	288
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp	
85 90 95	
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa	336
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys	
100 105 110	
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg	384
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu	
115 120 125	
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg	432
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu	
130 135 140	

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cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc	480
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala	
145 150 155 160	
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc	528
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala	
165 170 175	
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc	576
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly	
180 185 190	
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa	624
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln	
195 200 205	
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat	672
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp	
210 215 220	
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat	720
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp	
225 230 235 240	
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg	768
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met	
245 250 255	
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att	816
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile	
260 265 270	
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac	864
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp	
275 280 285	
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct	912
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala	
290 295 300	
gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc	960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly	
305 310 315 320	
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg	1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val	
325 330 335	
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc	1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe	
340 345 350	
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa	1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu	
355 360 365	
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt	1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly	
370 375 380	
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa	1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu	
385 390 395 400	
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc	1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala	
405 410 415	
ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac	1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr	
420 425 430	
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac	1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His	
435 440 445	
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc	1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro	

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450          455          460
ttg acc gga cgg gcg taa
Leu Thr Gly Arg Ala
465

<210> SEQ ID NO 6
<211> LENGTH: 469
<212> TYPE: PRT
<213> ORGANISM: Phaeodactylum tricornutum

<400> SEQUENCE: 6

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

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Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
           355                                  360                                  365  
 Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
           370                                  375                                  380  
 Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
           385                                  390                                  395                                  400  
 His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
                                   405                                  410                                  415  
 Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
                                   420                                  425                                  430  
 Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
           435                                  440                                  445  
 Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
           450                                  455                                  460  
 Leu Thr Gly Arg Ala  
           465

<210> SEQ ID NO 7  
 <211> LENGTH: 1344  
 <212> TYPE: DNA  
 <213> ORGANISM: Ceratodon purpureus  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1344)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 7

atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat           48  
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
   1                  5                                  10                                  15  
 gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt           96  
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
                   20                                  25                                  30  
 ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc       144  
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
           35                                  40                                  45  
 cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa       192  
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
   50                                  55                                  60  
 ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag       240  
 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
   65                                  70                                  75                                  80  
 gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat       288  
 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
           85                                  90                                  95  
 att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta       336  
 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
           100                                  105                                  110  
 cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc       384  
 Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
           115                                  120                                  125  
 tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc       432  
 Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
           130                                  135                                  140  
 tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga       480  
 Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
   145                                  150                                  155                                  160  
 gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat       528  
 Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His



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165				170				175								
cag	ttg	ttc	aaa	aac	aga	tac	tac	aat	gat	ttg	gcc	agc	tat	ttc	gtt	576
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	
			180							185				190		
gga	aac	ttt	tta	caa	gga	ttc	tca	tct	ggt	ggt	tgg	aaa	gag	cag	cac	624
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	
		195					200					205				
aat	gtg	cat	cac	gca	gcc	aca	aat	ggt	ggt	gga	cga	gac	gga	gat	ctt	672
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	
	210				215						220					
gat	tta	gtc	cca	ttc	tat	gct	aca	gtg	gca	gaa	cat	ctc	aac	aat	tat	720
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	
	225				230					235				240		
tct	cag	gat	tca	tgg	ggt	atg	act	cta	ttc	aga	tgg	caa	cat	ggt	cat	768
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	
			245							250				255		
tgg	aca	ttc	atg	tta	cca	ttc	ctc	cgt	ctc	tcg	tgg	ctt	ctt	cag	tca	816
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	
		260					265							270		
atc	att	ttt	ggt	agt	cag	atg	cca	act	cat	tat	tat	gac	tat	tac	aga	864
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	
		275					280					285				
aat	act	gcg	att	tat	gaa	cag	ggt	ggt	ctc	tct	ttg	cac	tgg	gct	tgg	912
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	
	290				295					300						
tca	ttg	ggt	caa	ttg	tat	ttc	cta	ccc	gat	tgg	tca	act	aga	ata	atg	960
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	
	305				310					315				320		
ttc	ttc	ctt	ggt	tct	cat	ctt	ggt	gga	ggt	ttc	ctg	ctc	tct	cat	gta	1008
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	
			325						330					335		
ggt	act	ttc	aat	cat	tat	tca	gtg	gag	aag	ttt	gca	ttg	agc	tcg	aac	1056
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	
			340						345					350		
atc	atg	tca	aat	tac	gct	tgt	ctt	caa	atc	atg	acc	aca	aga	aat	atg	1104
Ile	Met	Ser	Asn	Tyr	Ala	Cys	Leu	Gln	Ile	Met	Thr	Thr	Arg	Asn	Met	
		355				360							365			
aga	cct	gga	aga	ttc	att	gac	tgg	ctt	tgg	gga	ggt	ctt	aac	tat	cag	1152
Arg	Pro	Gly	Arg	Phe	Ile	Asp	Trp	Leu	Trp	Gly	Gly	Leu	Asn	Tyr	Gln	
	370				375					380						
att	gag	cac	cat	ctt	ttc	cca	acg	atg	cca	cga	cac	aac	ttg	aac	act	1200
Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Thr	
	385				390					395				400		
ggt	atg	cca	ctt	ggt	aag	gag	ttt	gca	gca	gca	aat	ggt	tta	cca	tac	1248
Val	Met	Pro	Leu	Val	Lys	Glu	Phe	Ala	Ala	Ala	Asn	Gly	Leu	Pro	Tyr	
			405						410					415		
atg	gtc	gac	gat	tat	ttc	aca	gga	ttc	tgg	ctt	gaa	att	gag	caa	ttc	1296
Met	Val	Asp	Asp	Tyr	Phe	Thr	Gly	Phe	Trp	Leu	Glu	Ile	Glu	Gln	Phe	
			420						425				430			
cga	aat	att	gca	aat	ggt	gct	gct	aaa	ttg	act	aaa	aag	att	gcc	tag	1344
Arg	Asn	Ile	Ala	Asn	Val	Ala	Ala	Lys	Leu	Thr	Lys	Lys	Ile	Ala		
		435				440						445				

&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 447

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Ceratodon purpureus

&lt;400&gt; SEQUENCE: 8

Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp

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1	5	10	15
Gly	Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly	20	25 30
Gly	Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe	35	40 45
His	Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu	50	55 60
Leu	Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys	65	70 75 80
Asp	Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn	85	90 95
Ile	Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu	100	105 110
Arg	Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe	115	120 125
Tyr	Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe	130	135 140
Tyr	Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly	145	150 155 160
Val	Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His	165	170 175
Gln	Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val	180	185 190
Gly	Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His	195	200 205
Asn	Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu	210	215 220
Asp	Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr	225	230 235 240
Ser	Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His	245	250 255
Trp	Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser	260	265 270
Ile	Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg	275	280 285
Asn	Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp	290	295 300
Ser	Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met	305	310 315 320
Phe	Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val	325	330 335
Val	Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn	340	345 350
Ile	Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met	355	360 365
Arg	Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln	370	375 380
Ile	Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr	385	390 395 400
Val	Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr	405	410 415
Met	Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe	420	425 430

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Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

<210> SEQ ID NO 9  
 <211> LENGTH: 1443  
 <212> TYPE: DNA  
 <213> ORGANISM: Physcomitrella patens  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1443)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 9

atg gcg ccc cac tct gcg gat act gct ggg ctc gtg cct tct gac gaa 48  
 Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu  
 1 5 10 15

ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96  
 Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr  
 20 25 30

ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144  
 Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala  
 35 40 45

gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192  
 Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp  
 50 55 60

att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag 240  
 Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln  
 65 70 75 80

gat tcc act cag ctt ttc gat tcc tat cac ccc ctt tat gtc agg aaa 288  
 Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys  
 85 90 95

atg ctc gcg aag tac tgt att ggg gaa tta gta ccg tct gct ggt gat 336  
 Met Leu Ala Lys Tyr Cys Ile Gly Glu Leu Val Pro Ser Ala Gly Asp  
 100 105 110

gac aag ttt aag aaa gca act ctg gag tat gca gat gcc gaa aat gaa 384  
 Asp Lys Phe Lys Lys Ala Thr Leu Glu Tyr Ala Asp Ala Glu Asn Glu  
 115 120 125

gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt 432  
 Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser  
 130 135 140

aac aag ata aac ccc caa att cat cca cat atg atc ctg aag tca ttg 480  
 Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu  
 145 150 155 160

ttc att ctt ggg gga tat ttc gcc agt tac tat tta gcg ttc ttc tgg 528  
 Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp  
 165 170 175

tct tca agt gtc ctt gtt tct ttg ttt ttc gca ttg tgg atg ggg ttc 576  
 Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe  
 180 185 190

ttc gca gcg gaa gtc ggc gtg tcg att caa cat gat gga aat cat ggt 624  
 Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly  
 195 200 205

tca tac act aaa tgg cgt ggc ttt gga tat atc atg gga gcc tcc cta 672  
 Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu  
 210 215 220

gat cta gtc gga gcc agt agc ttc atg tgg aga cag caa cac gtt gtg 720  
 Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val  
 225 230 235 240

gga cat cac tcg ttt aca aat gtg gac aac tac gat cct gat att cgt 768  
 Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg  
 245 250 255

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gtg aaa gat cca gat gtc agg agg gtt gcg acc aca caa cca aga caa	816
Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln	
260 265 270	
tgg tat cat gcg tat cag cat atc tac ctg gca gta tta tat gga act	864
Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr	
275 280 285	
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca	912
Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr	
290 295 300	
gga tca att ggc cct gtc aag gtg gcg aaa atg acc ccc ctg gag ttc	960
Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe	
305 310 315 320	
aac atc ttc ttt cag gga aag ctg cta tat gcg ttc tac atg ttc gtg	1008
Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val	
325 330 335	
ttg cca tct gtg tac ggt gtt cac tcc gga gga act ttc ttg gca cta	1056
Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu	
340 345 350	
tat gtg gct tct cag ctc att aca ggt tgg atg tta gct ttt ctt ttt	1104
Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe	
355 360 365	
caa gta gca cat gtc gtg gat gat gtt gca ttt cct aca cca gaa ggt	1152
Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly	
370 375 380	
ggg aag gtg aag gga gga tgg gct gca atg cag gtt gca aca act acg	1200
Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr	
385 390 395 400	
gat ttc agt cca cgc tca tgg ttc tgg ggt cat gtc tct gga gga tta	1248
Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu	
405 410 415	
aac aac caa att gag cat cat ctg ttt cca gga gtg tgc cat gtt cat	1296
Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His	
420 425 430	
tat cca gcc att cag cct att gtc gag aag acg tgc aag gaa ttc gat	1344
Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp	
435 440 445	
gtg cct tat gta gcc tac cca act ttt tgg act gcg ttg aga gcc cac	1392
Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His	
450 455 460	
ttt gcg cat ttg aaa aag gtt gga ttg aca gag ttt cgg ctc gat ggc	1440
Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly	
465 470 475 480	
tga	1443

&lt;210&gt; SEQ ID NO 10

&lt;211&gt; LENGTH: 480

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Physcomitrella patens

&lt;400&gt; SEQUENCE: 10

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

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Ile	Pro	Asn	His	Pro	Gly	Gly	Ser	Leu	Ile	His	Val	Lys	Ala	Gly	Gln	65	70	75	80
Asp	Ser	Thr	Gln	Leu	Phe	Asp	Ser	Tyr	His	Pro	Leu	Tyr	Val	Arg	Lys	85	90	95	
Met	Leu	Ala	Lys	Tyr	Cys	Ile	Gly	Glu	Leu	Val	Pro	Ser	Ala	Gly	Asp	100	105	110	
Asp	Lys	Phe	Lys	Lys	Ala	Thr	Leu	Glu	Tyr	Ala	Asp	Ala	Glu	Asn	Glu	115	120	125	
Asp	Phe	Tyr	Leu	Val	Val	Lys	Gln	Arg	Val	Glu	Ser	Tyr	Phe	Lys	Ser	130	135	140	
Asn	Lys	Ile	Asn	Pro	Gln	Ile	His	Pro	His	Met	Ile	Leu	Lys	Ser	Leu	145	150	155	160
Phe	Ile	Leu	Gly	Gly	Tyr	Phe	Ala	Ser	Tyr	Tyr	Leu	Ala	Phe	Phe	Trp	165	170	175	
Ser	Ser	Ser	Val	Leu	Val	Ser	Leu	Phe	Phe	Ala	Leu	Trp	Met	Gly	Phe	180	185	190	
Phe	Ala	Ala	Glu	Val	Gly	Val	Ser	Ile	Gln	His	Asp	Gly	Asn	His	Gly	195	200	205	
Ser	Tyr	Thr	Lys	Trp	Arg	Gly	Phe	Gly	Tyr	Ile	Met	Gly	Ala	Ser	Leu	210	215	220	
Asp	Leu	Val	Gly	Ala	Ser	Ser	Phe	Met	Trp	Arg	Gln	Gln	His	Val	Val	225	230	235	240
Gly	His	His	Ser	Phe	Thr	Asn	Val	Asp	Asn	Tyr	Asp	Pro	Asp	Ile	Arg	245	250	255	
Val	Lys	Asp	Pro	Asp	Val	Arg	Arg	Val	Ala	Thr	Thr	Gln	Pro	Arg	Gln	260	265	270	
Trp	Tyr	His	Ala	Tyr	Gln	His	Ile	Tyr	Leu	Ala	Val	Leu	Tyr	Gly	Thr	275	280	285	
Leu	Ala	Leu	Lys	Ser	Ile	Phe	Leu	Asp	Asp	Phe	Leu	Ala	Tyr	Phe	Thr	290	295	300	
Gly	Ser	Ile	Gly	Pro	Val	Lys	Val	Ala	Lys	Met	Thr	Pro	Leu	Glu	Phe	305	310	315	320
Asn	Ile	Phe	Phe	Gln	Gly	Lys	Leu	Leu	Tyr	Ala	Phe	Tyr	Met	Phe	Val	325	330	335	
Leu	Pro	Ser	Val	Tyr	Gly	Val	His	Ser	Gly	Gly	Thr	Phe	Leu	Ala	Leu	340	345	350	
Tyr	Val	Ala	Ser	Gln	Leu	Ile	Thr	Gly	Trp	Met	Leu	Ala	Phe	Leu	Phe	355	360	365	
Gln	Val	Ala	His	Val	Val	Asp	Asp	Val	Ala	Phe	Pro	Thr	Pro	Glu	Gly	370	375	380	
Gly	Lys	Val	Lys	Gly	Gly	Trp	Ala	Ala	Met	Gln	Val	Ala	Thr	Thr	Thr	385	390	395	400
Asp	Phe	Ser	Pro	Arg	Ser	Trp	Phe	Trp	Gly	His	Val	Ser	Gly	Gly	Leu	405	410	415	
Asn	Asn	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Gly	Val	Cys	His	Val	His	420	425	430	
Tyr	Pro	Ala	Ile	Gln	Pro	Ile	Val	Glu	Lys	Thr	Cys	Lys	Glu	Phe	Asp	435	440	445	
Val	Pro	Tyr	Val	Ala	Tyr	Pro	Thr	Phe	Trp	Thr	Ala	Leu	Arg	Ala	His	450	455	460	
Phe	Ala	His	Leu	Lys	Lys	Val	Gly	Leu	Thr	Glu	Phe	Arg	Leu	Asp	Gly	465	470	475	480

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<210> SEQ ID NO 11
<211> LENGTH: 1320
<212> TYPE: DNA
<213> ORGANISM: Thraustrochytrium
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1320)
<223> OTHER INFORMATION: Delta-5-Desaturase

<400> SEQUENCE: 11
atg ggc aag ggc agc gag ggc cgc agc gcg gcg cgc gag atg acg gcc      48
Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
1                               5                               10                               15

gag cgc aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg      96
Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
20                               25                               30

tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc     144
Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
35                               40                               45

ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag     192
Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
50                               55                               60

ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg     240
Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
65                               70                               75                               80

aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag     288
Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
85                               90                               95

gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag     336
Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
100                              105                              110

ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac     384
Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
115                              120                              125

cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg     432
Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
130                              135                              140

tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc     480
Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly
145                              150                              155                              160

att gcg cag ggc cgc tgc ggc tgg gtc atg cac gag atg ggc cac ggg     528
Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly
165                              170                              175

tcg ttc acg ggc gtc atc tgg ctc gac gac cgg atg tgc gag ttc ttc     576
Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe
180                              185                              190

tac ggc gtc ggc tgc ggc atg agc ggg cac tac tgg aag aac cag cac     624
Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His
195                              200                              205

agc aag cac cac gcc gcg ccc aac cgc ctc gag cac gat gtc gat ctc     672
Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu
210                              215                              220

aac acg ctg ccc ctg gtc gcc ttt aac gag cgc gtc gtg cgc aag gtc     720
Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val
225                              230                              235                              240

aag ccg gga tcg ctg ctg gcg ctc tgg ctg cgc gtg cag gcg tac ctc     768
Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu
245                              250                              255

ttt gcg ccc gtc tcg tgc ctg ctc atc gcc ctt ggc tgg acg ctc tac     816
Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr
260                              265                              270

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ctg cac ccg cgc tac atg ctg cgc acc aag cgg cac atg gag ttc gtc	864
Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val	
275 280 285	
tgg atc ttc gcg cgc tac att ggc tgg ttc tcg ctc atg ggc gct ctc	912
Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu	
290 295 300	
ggc tac tcg ccg ggc acc tcg gtc ggg atg tac ctg tgc tcg ttc ggc	960
Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly	
305 310 315 320	
ctc ggc tgc att tac att ttc ctg cag ttc gcc gtc agc cac acg cac	1008
Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His	
325 330 335	
ctg ccg gtg acc aac ccg gag gac cag ctg cac tgg ctc gag tac gcg	1056
Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala	
340 345 350	
gcc gac cac acg gtg aac att agc acc aag tcc tgg ctc gtc acg tgg	1104
Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp	
355 360 365	
tgg atg tcg aac ctg aac ttt cag atc gag cac cac ctc ttc ccc acg	1152
Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr	
370 375 380	
gcg ccg cag ttc cgc ttc aag gaa atc agt cct cgc gtc gag gcc ctc	1200
Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu	
385 390 395 400	
ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg	1248
Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala	
405 410 415	
gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc	1296
Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly	
420 425 430	
gcc gac acc aag aag cag gac tga	1320
Ala Asp Thr Lys Lys Gln Asp	
435	

&lt;210&gt; SEQ ID NO 12

&lt;211&gt; LENGTH: 439

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Thraustrochytrium

&lt;400&gt; SEQUENCE: 12

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

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Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly  
 145 150 155 160

Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly  
 165 170 175

Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe  
 180 185 190

Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His  
 195 200 205

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

Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val  
 225 230 235 240

Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu  
 245 250 255

Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr  
 260 265 270

Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val  
 275 280 285

Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu  
 290 295 300

Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly  
 305 310 315 320

Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His  
 325 330 335

Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala  
 340 345 350

Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp  
 355 360 365

Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr  
 370 375 380

Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu  
 385 390 395 400

Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala  
 405 410 415

Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly  
 420 425 430

Ala Asp Thr Lys Lys Gln Asp  
 435

<210> SEQ ID NO 13  
 <211> LENGTH: 1341  
 <212> TYPE: DNA  
 <213> ORGANISM: Mortierella alpina  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1341)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 13

atg gga acg gac caa gga aaa acc ttc acc tgg gaa gag ctg gcg gcc	48
Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala	
1 5 10 15	
cat aac acc aag gac gac cta ctc ttg gcc atc cgc ggc agg gtg tac	96
His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr	
20 25 30	
gat gtc aca aag ttc ttg agc cgc cat cct ggt gga gtg gac act etc	144
Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu	



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35		40		45												
ctg	ctc	gga	gct	ggc	cga	gat	gtt	act	ccg	gtc	ttt	gag	atg	tat	cac	192
Leu	Leu	Gly	Ala	Gly	Arg	Asp	Val	Thr	Pro	Val	Phe	Glu	Met	Tyr	His	
	50						55				60					
gcg	ttt	ggg	gct	gca	gat	gcc	att	atg	aag	aag	tac	tat	gtc	ggt	aca	240
Ala	Phe	Gly	Ala	Ala	Asp	Ala	Ile	Met	Lys	Lys	Tyr	Tyr	Val	Gly	Thr	
	65					70					75				80	
ctg	gtc	tcg	aat	gag	ctg	ccc	atc	ttc	ccg	gag	cca	acg	gtg	ttc	cac	288
Leu	Val	Ser	Asn	Glu	Leu	Pro	Ile	Phe	Pro	Glu	Pro	Thr	Val	Phe	His	
				85						90				95		
aaa	acc	atc	aag	acg	aga	gtc	gag	ggc	tac	ttt	acg	gat	cgg	aac	att	336
Lys	Thr	Ile	Lys	Thr	Arg	Val	Glu	Gly	Tyr	Phe	Thr	Asp	Arg	Asn	Ile	
			100						105					110		
gat	ccc	aag	aat	aga	cca	gag	atc	tgg	gga	cga	tac	gct	ctt	atc	ttt	384
Asp	Pro	Lys	Asn	Arg	Pro	Glu	Ile	Trp	Gly	Arg	Tyr	Ala	Leu	Ile	Phe	
		115					120							125		
gga	tcc	ttg	atc	gct	tcc	tac	tac	gcg	cag	ctc	ttt	gtg	cct	ttc	gtt	432
Gly	Ser	Leu	Ile	Ala	Ser	Tyr	Tyr	Ala	Gln	Leu	Phe	Val	Pro	Phe	Val	
	130					135					140					
gtc	gaa	cgc	aca	tgg	ctt	cag	gtg	gtg	ttt	gca	atc	atc	atg	gga	ttt	480
Val	Glu	Arg	Thr	Trp	Leu	Gln	Val	Val	Phe	Ala	Ile	Ile	Met	Gly	Phe	
	145				150					155					160	
gcg	tgc	gca	caa	gtc	gga	ctc	aac	cct	ctt	cat	gat	gcg	tct	cac	ttt	528
Ala	Cys	Ala	Gln	Val	Gly	Leu	Asn	Pro	Leu	His	Asp	Ala	Ser	His	Phe	
				165						170					175	
tca	gtg	acc	cac	aac	ccc	act	gtc	tgg	aag	att	ctg	gga	gcc	acg	cac	576
Ser	Val	Thr	His	Asn	Pro	Thr	Val	Trp	Lys	Ile	Leu	Gly	Ala	Thr	His	
			180						185					190		
gac	ttt	ttc	aac	gga	gca	tcg	tac	ctg	gtg	tgg	atg	tac	caa	cat	atg	624
Asp	Phe	Phe	Asn	Gly	Ala	Ser	Tyr	Leu	Val	Trp	Met	Tyr	Gln	His	Met	
		195					200					205				
ctc	ggc	cat	cac	ccc	tac	acc	aac	att	gct	gga	gca	gat	ccc	gac	gtg	672
Leu	Gly	His	His	Pro	Tyr	Thr	Asn	Ile	Ala	Gly	Ala	Asp	Pro	Asp	Val	
	210					215					220					
tcg	acg	tct	gag	ccc	gat	gtt	cgt	cgt	atc	aag	ccc	aac	caa	aag	tgg	720
Ser	Thr	Ser	Glu	Pro	Asp	Val	Arg	Arg	Ile	Lys	Pro	Asn	Gln	Lys	Trp	
	225				230						235				240	
ttt	gtc	aac	cac	atc	aac	cag	cac	atg	ttt	ggt	cct	ttc	ctg	tac	gga	768
Phe	Val	Asn	His	Ile	Asn	Gln	His	Met	Phe	Val	Pro	Phe	Leu	Tyr	Gly	
				245					250						255	
ctg	ctg	gcg	ttc	aag	gtg	cgc	att	cag	gac	atc	aac	att	ttg	tac	ttt	816
Leu	Leu	Ala	Phe	Lys	Val	Arg	Ile	Gln	Asp	Ile	Asn	Ile	Leu	Tyr	Phe	
			260					265						270		
gtc	aag	acc	aat	gac	gct	att	cgt	gtc	aat	ccc	atc	tcg	aca	tgg	cac	864
Val	Lys	Thr	Asn	Asp	Ala	Ile	Arg	Val	Asn	Pro	Ile	Ser	Thr	Trp	His	
		275					280							285		
act	gtg	atg	ttc	tgg	ggc	ggc	aag	gct	ttc	ttt	gtc	tgg	tat	cgc	ctg	912
Thr	Val	Met	Phe	Trp	Gly	Gly	Lys	Ala	Phe	Phe	Val	Trp	Tyr	Arg	Leu	
	290					295					300					
att	ggt	ccc	ctg	cag	tat	ctg	ccc	ctg	ggc	aag	gtg	ctg	ctc	ttg	ttc	960
Ile	Val	Pro	Leu	Gln	Tyr	Leu	Pro	Leu	Gly	Lys	Val	Leu	Leu	Leu	Phe	
	305				310						315				320	
acg	gtc	gcg	gac	atg	gtg	tcg	tct	tac	tgg	ctg	gcg	ctg	acc	ttc	cag	1008
Thr	Val	Ala	Asp	Met	Val	Ser	Ser	Tyr	Trp	Leu	Ala	Leu	Thr	Phe	Gln	
				325						330				335		
gcg	aac	cac	ggt	ggt	gag	gaa	ggt	cag	tgg	ccg	ttg	cct	gac	gag	aac	1056
Ala	Asn	His	Val	Val	Glu	Glu	Val	Gln	Trp	Pro	Leu	Pro	Asp	Glu	Asn	
			340					345						350		
ggg	atc	atc	caa	aag	gac	tgg	gca	gct	atg	cag	gtc	gag	act	acg	cag	1104

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Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln
    355                               360                               365
gat tac gca cac gat tcg cac ctc tgg acc agc atc act ggc agc ttg      1152
Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu
    370                               375                               380
aac tac cag gct gtg cac cat ctg ttc ccc aac gtg tcg cag cac cat      1200
Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His
    385                               390                               395                               400
tat ccc gat att ctg gcc atc atc aag aac acc tgc agc gag tac aag      1248
Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys
    405                               410                               415
gtt cca tac ctt gtc aag gat acg ttt tgg caa gca ttt gct tca cat      1296
Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His
    420                               425                               430
ttg gag cac ttg cgt gtt ctt gga ctc cgt ccc aag gaa gag tag      1341
Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu
    435                               440                               445

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<210> SEQ ID NO 14
<211> LENGTH: 446
<212> TYPE: PRT
<213> ORGANISM: Mortierella alpina

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<400> SEQUENCE: 14

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

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Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe
      260                265                270
Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His
      275                280                285
Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu
      290                295                300
Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe
      305                310                315
Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln
      325                330                335
Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn
      340                345                350
Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln
      355                360                365
Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu
      370                375                380
Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His
      385                390                395
Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys
      405                410                415
Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His
      420                425                430
Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu
      435                440                445

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<210> SEQ ID NO 15
<211> LENGTH: 1344
<212> TYPE: DNA
<213> ORGANISM: Caenorhabditis elegans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1344)
<223> OTHER INFORMATION: Delta-5 desaturase

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<400> SEQUENCE: 15

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atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat      48
Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
1          5          10          15
gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt      96
Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
20         25         30
ggg agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc      144
Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
35         40         45
cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa      192
His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
50         55         60
ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag      240
Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
65         70         75         80
gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat      288
Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
85         90         95
att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta      336
Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
100        105        110
cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc      384
Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
115        120        125

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tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe 130 135 140	432
tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly 145 150 155 160	480
ggt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His 165 170 175	528
cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val 180 185 190	576
gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His 195 200 205	624
aat gtg cat cac gca gcc aca aat gtt gtt gga cga gac gga gat ctt Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu 210 215 220	672
gat tta gtc cca ttc tat gct aca gtg gca gaa cat ctc aac aat tat Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr 225 230 235 240	720
tct cag gat tca tgg gtt atg act cta ttc aga tgg caa cat gtt cat Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His 245 250 255	768
tgg aca ttc atg tta cca ttc ctc cgt ctc tcg tgg ctt ctt cag tca Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser 260 265 270	816
atc att ttt gtt agt cag atg cca act cat tat tat gac tat tac aga Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg 275 280 285	864
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp 290 295 300	912
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met 305 310 315 320	960
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val 325 330 335	1008
ggt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn 340 345 350	1056
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met 355 360 365	1104
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln 370 375 380	1152
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr 385 390 395 400	1200
ggt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr 405 410 415	1248
atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe 420 425 430	1296
cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala	1344

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435                      440                      445

<210> SEQ ID NO 16  
 <211> LENGTH: 447  
 <212> TYPE: PRT  
 <213> ORGANISM: *Caenorhabditis elegans*

<400> SEQUENCE: 16

Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
 1                      5                      10                      15

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
                     20                      25                      30

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
                     35                      40                      45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
                     50                      55                      60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys  
 65                      70                      75                      80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn  
                     85                      90                      95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu  
                     100                      105                      110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe  
                     115                      120                      125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe  
                     130                      135                      140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly  
 145                      150                      155                      160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His  
                     165                      170                      175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val  
                     180                      185                      190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His  
                     195                      200                      205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu  
                     210                      215                      220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr  
 225                      230                      235                      240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His  
                     245                      250                      255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser  
                     260                      265                      270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg  
                     275                      280                      285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp  
                     290                      295                      300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met  
 305                      310                      315                      320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val  
                     325                      330                      335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn  
                     340                      345                      350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met  
                     355                      360                      365

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Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

<210> SEQ ID NO 17  
 <211> LENGTH: 1683  
 <212> TYPE: DNA  
 <213> ORGANISM: Borago officinalis  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (42)..(1388)  
 <223> OTHER INFORMATION: Delta-6 desaturase

<400> SEQUENCE: 17

tatctgccta ccctcccaaa gagagtagtc atttttcatc a atg gct gct caa atc 56  
 Met Ala Ala Gln Ile  
 1 5

aag aaa tac att acc tca gat gaa ctc aag aac cac gat aaa ccc gga 104  
 Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn His Asp Lys Pro Gly  
 10 15 20

gat cta tgg atc tcg att caa ggg aaa gcc tat gat gtt tcg gat tgg 152  
 Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr Asp Val Ser Asp Trp  
 25 30 35

gtg aaa gac cat cca ggt ggc agc ttt ccc ttg aag agt ctt gct ggt 200  
 Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu Lys Ser Leu Ala Gly  
 40 45 50

caa gag gta act gat gca ttt gtt gca ttc cat cct gcc tct aca tgg 248  
 Gln Glu Val Thr Asp Ala Phe Val Ala Phe His Pro Ala Ser Thr Trp  
 55 60 65

aag aat ctt gat aag ttt ttc act ggg tat tat ctt aaa gat tac tct 296  
 Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr Leu Lys Asp Tyr Ser  
 70 75 80 85

gtt tct gag gtt tct aaa gat tat agg aag ctt gtg ttt gag ttt tct 344  
 Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu Val Phe Glu Phe Ser  
 90 95 100

aaa atg ggt ttg tat gac aaa aaa ggt cat att atg ttt gca act ttg 392  
 Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile Met Phe Ala Thr Leu  
 105 110 115

tgc ttt ata gca atg ctg ttt gct atg agt gtt tat ggg gtt ttg ttt 440  
 Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val Tyr Gly Val Leu Phe  
 120 125 130

tgt gag ggt gtt ttg gta cat ttg ttt tct ggg tgt ttg atg ggg ttt 488  
 Cys Glu Gly Val Leu Val His Leu Phe Ser Gly Cys Leu Met Gly Phe  
 135 140 145

ctt tgg att cag agt ggt tgg att gga cat gat gct ggg cat tat atg 536  
 Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp Ala Gly His Tyr Met  
 150 155 160 165

gta gtg tct gat tca agg ctt aat aag ttt atg ggt att ttt gct gca 584  
 Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met Gly Ile Phe Ala Ala  
 170 175 180

aat tgt ctt tca gga ata agt att ggt tgg tgg aaa tgg aac cat aat 632  
 Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp Lys Trp Asn His Asn  
 185 190 195

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gca cat cac att gcc tgt aat agc ctt gaa tat gac cct gat tta caa	680
Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr Asp Pro Asp Leu Gln	
200 205 210	
tat ata cca ttc ctt gtt gtg tct tcc aag ttt ttt ggt tca ctc acc	728
Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe Phe Gly Ser Leu Thr	
215 220 225	
tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc	776
Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe	
230 235 240 245	
ttt gta agt tat caa cat tgg aca ttt tac cct att atg tgt gct gct	824
Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Cys Ala Ala	
250 255 260	
agg ctc aat atg tat gta caa tct ctc ata atg ttg ttg acc aag aga	872
Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met Leu Leu Thr Lys Arg	
265 270 275	
aat gtg tcc tat cga gct cag gaa ctc ttg gga tgc cta gtg ttc tcg	920
Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly Cys Leu Val Phe Ser	
280 285 290	
att tgg tac ccg ttg ctt gtt tct tgt ttg cct aat tgg ggt gaa aga	968
Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro Asn Trp Gly Glu Arg	
295 300 305	
att atg ttt gtt att gca agt tta tca gtg act gga atg caa caa gtt	1016
Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr Gly Met Gln Gln Val	
310 315 320 325	
cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct	1064
Gln Phe Ser Leu Asn His Phe Ser Ser Val Tyr Val Gly Lys Pro	
330 335 340	
aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att	1112
Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile	
345 350 355	
tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa	1160
Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln	
360 365 370	
att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa	1208
Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys	
375 380 385	
atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac	1256
Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr	
390 395 400 405	
aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg	1304
Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu	
410 415 420	
agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag	1352
Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys	
425 430 435	
aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt	1398
Asn Leu Val Trp Glu Ala Leu His Thr His Gly	
440 445	
agttcatgta ataatttgag attatgtatc tcctatgttt gtgtcttgc ttggttctac	1458
ttgttgaggt cattgcaact tgccttttat ggtttattag atgtttttta atatatttta	1518
gaggttttgc tttcatctcc attattgatg aataaggagt tgcatttgt caattgttgt	1578
gctcaatata tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagetcat	1638
gtgtacttct atagactttg tttaaatggt tatgtcatgt tatatt	1683

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 448

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Borago officinalis

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&lt;400&gt; SEQUENCE: 18

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



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405				410				415								
Thr	Leu	Arg	Thr	Leu	Arg	Asn	Thr	Ala	Leu	Gln	Ala	Arg	Asp	Ile	Thr	
			420					425					430			
Lys	Pro	Leu	Pro	Lys	Asn	Leu	Val	Trp	Glu	Ala	Leu	His	Thr	His	Gly	
		435					440						445			
<210> SEQ ID NO 19																
<211> LENGTH: 1563																
<212> TYPE: DNA																
<213> ORGANISM: Ceratodon purpureus																
<220> FEATURE:																
<221> NAME/KEY: CDS																
<222> LOCATION: (1)..(1563)																
<223> OTHER INFORMATION: Delta-6 desaturase																
<400> SEQUENCE: 19																
atg	gtg	tcc	cag	ggc	ggc	ggt	ctc	tcg	cag	ggt	tcc	att	gaa	gaa	aac	48
Met	Val	Ser	Gln	Gly	Gly	Leu	Ser	Gln	Gly	Ser	Ile	Glu	Glu	Asn		
1			5					10					15			
att	gac	ggt	gag	cac	ttg	gca	acg	atg	ccc	ctc	gtc	agt	gac	ttc	cta	96
Ile	Asp	Val	Glu	His	Leu	Ala	Thr	Met	Pro	Leu	Val	Ser	Asp	Phe	Leu	
		20					25						30			
aat	gtc	ctg	gga	acg	act	ttg	ggc	cag	tgg	agt	ctt	tcc	act	aca	ttc	144
Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe	
		35				40						45				
gct	ttc	aag	agg	ctc	acg	act	aag	aaa	cac	agt	tcg	gac	atc	tcg	gtg	192
Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val	
	50					55					60					
gag	gca	caa	aaa	gaa	tcg	gtt	gcg	cgg	ggg	cca	gtt	gag	aat	att	tct	240
Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser	
65				70						75				80		
caa	tcg	ggt	gcg	cag	ccc	atc	agg	cgg	agg	tgg	gtg	cag	gat	aaa	aag	288
Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys	
			85						90					95		
ccg	ggt	act	tac	agc	ctg	aag	gat	gta	gct	tcg	cac	gat	atg	ccc	cag	336
Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln	
			100				105						110			
gac	tgc	tgg	att	ata	atc	aaa	gag	aag	gtg	tat	gat	gtg	agc	acc	ttc	384
Asp	Cys	Trp	Ile	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe	
		115					120					125				
gct	gag	cag	cac	cct	gga	ggc	acg	ggt	atc	aac	acc	tac	ttc	gga	cga	432
Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg	
	130				135						140					
gac	gcc	aca	gat	ggt	ttc	tct	act	ttc	cac	gca	tcc	acc	tca	tgg	aag	480
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys	
	145			150						155				160		
att	ctt	cag	aat	ttc	tac	atc	ggg	aac	ctt	ggt	agg	gag	gag	ccg	act	528
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr	
			165						170					175		
ttg	gag	ctg	ctg	aag	gag	tac	aga	gag	ttg	aga	gcc	ctt	ttc	ttg	aga	576
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	
			180						185				190			
gaa	cag	ctt	ttc	aag	agt	tcc	aaa	tcc	tac	tac	ctt	ttc	aag	act	ctc	624
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu	
		195				200						205				
ata	aat	ggt	tcc	att	ggt	gcc	aca	agc	att	gcg	ata	atc	agt	ctg	tac	672
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr	
		210				215					220					
aag	tct	tac	cgg	gcg	ggt	ctg	tta	tca	gcc	agt	ttg	atg	ggc	ttg	ttt	720
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	
					230					235				240		

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att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val 245 250 255	768
ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn 260 265 270	816
gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu 275 280 285	864
cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp 290 295 300	912
gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu 305 310 315 320	960
gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His 325 330 335	1008
cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe 340 345 350	1056
tgg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys 355 360 365	1104
ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser 370 375 380	1152
gtt gcg ttt tat ctg ctc ccc gga tgg aaa cca gtt gta tgg atg gtg Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val 385 390 395 400	1200
gtc agc gag ctc atg tct ggt ttc ctg ctg gga tac gta ttt gta ctc Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu 405 410 415	1248
agt cac aat gga atg gag gtg tac aat acg tca aag gac ttc gtg aat Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn 420 425 430	1296
gcc cag att gca tcg act cgc gac atc aaa gca ggg gtg ttt aat gat Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp 435 440 445	1344
tgg ttc acc gga ggt ctc aac aga cag att gag cat cat cta ttt cca Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro 450 455 460	1392
acg atg ccc agg cac aac ctt aat aaa att tct cct cac gtg gag act Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr 465 470 475 480	1440
ttg tgc aag aag cat gga ctg gtc tac gaa gac gtg agc atg gct tcg Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser 485 490 495	1488
ggc act tac cgg gtt ttg aaa aca ctt aag gac gtt gcc gat gct gct Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala 500 505 510	1536
tca cac cag cag ctt gct gcg agt tga Ser His Gln Gln Leu Ala Ala Ser 515 520	1563

&lt;210&gt; SEQ ID NO 20

&lt;211&gt; LENGTH: 520

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Ceratodon purpureus

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&lt;400&gt; SEQUENCE: 20

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Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn
1           5           10           15

Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu
20           25           30

Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe
35           40           45

Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val
50           55           60

Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser
65           70           75           80

Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys
85           90           95

Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln
100          105          110

Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe
115          120          125

Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg
130          135          140

Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys
145          150          155          160

Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr
165          170          175

Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg
180          185          190

Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu
195          200          205

Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr
210          215          220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe
225          230          235          240

Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val
245          250          255

Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn
260          265          270

Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu
275          280          285

His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp
290          295          300

Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu
305          310          315          320

Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His
325          330          335

Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe
340          345          350

Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys
355          360          365

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
370          375          380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
385          390          395          400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
405          410          415

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Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
 420 425 430  
 Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
 435 440 445  
 Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
 450 455 460  
 Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
 465 470 475 480  
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
 485 490 495  
 Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
 500 505 510  
 Ser His Gln Gln Leu Ala Ala Ser  
 515 520

<210> SEQ ID NO 21  
 <211> LENGTH: 1434  
 <212> TYPE: DNA  
 <213> ORGANISM: Phaeodactylum tricornutum  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1434)  
 <223> OTHER INFORMATION: Delta-6 desaturase

<400> SEQUENCE: 21

atg ggc aaa gga ggg gac gct cgg gcc tcg aag ggc tca acg gcg gct 48  
 Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala  
 1 5 10 15  
 cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac 96  
 Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp  
 20 25 30  
 gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac 144  
 Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His  
 35 40 45  
 gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg 192  
 Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met  
 50 55 60  
 acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg 240  
 Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met  
 65 70 75 80  
 aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag 288  
 Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu  
 85 90 95  
 ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa 336  
 Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys  
 100 105 110  
 ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac 384  
 Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr  
 115 120 125  
 aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc 432  
 Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
 130 135 140  
 ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg 480  
 Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu  
 145 150 155 160  
 gga aca ttc ttt cag cag tcg gga tgg ttg gca cac gac ttt ctg cac 528  
 Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His  
 165 170 175  
 cac cag gtc ttc acc aag cgc aag cac ggg gat ctc gga gga ctc ttt 576

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His	Gln	Val	Phe	Thr	Lys	Arg	Lys	His	Gly	Asp	Leu	Gly	Gly	Leu	Phe	
			180					185						190		
tgg	ggg	aac	ctc	atg	cag	ggt	tac	tcc	gta	cag	tgg	tgg	aaa	aac	aag	624
Trp	Gly	Asn	Leu	Met	Gln	Gly	Tyr	Ser	Val	Gln	Trp	Trp	Lys	Asn	Lys	
		195					200						205			
cac	aac	gga	cac	cac	gcc	gtc	ccc	aac	ctc	cac	tgc	tcc	tcc	gca	gtc	672
His	Asn	Gly	His	His	Ala	Val	Pro	Asn	Leu	His	Cys	Ser	Ser	Ala	Val	
		210				215					220					
gcg	caa	gat	ggg	gac	ccg	gac	atc	gat	acc	atg	ccc	ctt	ctc	gcc	tgg	720
Ala	Gln	Asp	Gly	Asp	Pro	Asp	Ile	Asp	Thr	Met	Pro	Leu	Leu	Ala	Trp	
		225			230					235					240	
tcc	gtc	cag	caa	gcc	cag	tct	tac	cgg	gaa	ctc	caa	gcc	gac	gga	aag	768
Ser	Val	Gln	Gln	Ala	Gln	Ser	Tyr	Arg	Glu	Leu	Gln	Ala	Asp	Gly	Lys	
				245					250					255		
gat	tcg	ggt	ttg	gtc	aag	ttc	atg	atc	cgt	aac	caa	tcc	tac	ttt	tac	816
Asp	Ser	Gly	Leu	Val	Lys	Phe	Met	Ile	Arg	Asn	Gln	Ser	Tyr	Phe	Tyr	
			260					265						270		
ttt	ccc	atc	ttg	ttg	ctc	gcc	cgc	ctg	tcg	tgg	ttg	aac	gag	tcc	ttc	864
Phe	Pro	Ile	Leu	Leu	Leu	Ala	Arg	Leu	Ser	Trp	Leu	Asn	Glu	Ser	Phe	
		275					280						285			
aag	tgc	gcc	ttt	ggg	ctt	gga	gct	gcg	tcg	gag	aac	gct	gct	ctc	gaa	912
Lys	Cys	Ala	Phe	Gly	Leu	Gly	Ala	Ala	Ser	Glu	Asn	Ala	Ala	Leu	Glu	
		290				295					300					
ctc	aag	gcc	aag	ggt	ctt	cag	tac	ccc	ctt	ttg	gaa	aag	gct	ggc	atc	960
Leu	Lys	Ala	Lys	Gly	Leu	Gln	Tyr	Pro	Leu	Leu	Glu	Lys	Ala	Gly	Ile	
		305			310						315				320	
ctg	ctg	cac	tac	gct	tgg	atg	ctt	aca	ggt	tcg	tcc	ggc	ttt	gga	cgc	1008
Leu	Leu	His	Tyr	Ala	Trp	Met	Leu	Thr	Val	Ser	Ser	Gly	Phe	Gly	Arg	
				325					330					335		
ttc	tcg	ttc	gcg	tac	acc	gca	ttt	tac	ttt	cta	acc	gcg	acc	gcg	tcc	1056
Phe	Ser	Phe	Ala	Tyr	Thr	Ala	Phe	Tyr	Phe	Leu	Thr	Ala	Thr	Ala	Ser	
			340					345					350			
tgt	gga	ttc	ttg	ctc	gcc	att	gtc	ttt	ggc	ctc	ggc	cac	aac	ggc	atg	1104
Cys	Gly	Phe	Leu	Leu	Ala	Ile	Val	Phe	Gly	Leu	Gly	His	Asn	Gly	Met	
		355					360						365			
gcc	acc	tac	aat	gcc	gac	gcc	cgt	ccg	gac	ttc	tgg	aag	ctc	caa	gtc	1152
Ala	Thr	Tyr	Asn	Ala	Asp	Ala	Arg	Pro	Asp	Phe	Trp	Lys	Leu	Gln	Val	
		370				375						380				
acc	acg	act	cgc	aac	gtc	acg	ggc	gga	cac	ggt	ttc	ccc	caa	gcc	ttt	1200
Thr	Thr	Thr	Arg	Asn	Val	Thr	Gly	Gly	His	Gly	Phe	Pro	Gln	Ala	Phe	
					390						395				400	
gtc	gac	tgg	ttc	tgt	ggt	ggc	ctc	cag	tac	caa	gtc	gac	cac	cac	tta	1248
Val	Asp	Trp	Phe	Cys	Gly	Gly	Leu	Gln	Tyr	Gln	Val	Asp	His	His	Leu	
			405						410					415		
ttc	ccc	agc	ctg	ccc	cga	cac	aat	ctg	gcc	aag	aca	cac	gca	ctg	gtc	1296
Phe	Pro	Ser	Leu	Pro	Arg	His	Asn	Leu	Ala	Lys	Thr	His	Ala	Leu	Val	
			420					425					430			
gaa	tcg	ttc	tgc	aag	gag	tgg	ggt	gtc	cag	tac	cac	gaa	gcc	gac	ctt	1344
Glu	Ser	Phe	Cys	Lys	Glu	Trp	Gly	Val	Gln	Tyr	His	Glu	Ala	Asp	Leu	
			435				440						445			
gtg	gac	ggg	acc	atg	gaa	gtc	ttg	cac	cat	ttg	ggc	agc	gtg	gcc	ggc	1392
Val	Asp	Gly	Thr	Met	Glu	Val	Leu	His	His	Leu	Gly	Ser	Val	Ala	Gly	
			450			455					460					
gaa	ttc	gtc	gtg	gat	ttt	gta	cgc	gat	gga	ccc	gcc	atg	taa			1434
Glu	Phe	Val	Val	Asp	Phe	Val	Arg	Asp	Gly	Pro	Ala	Met				
			465		470					475						

&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 477

&lt;212&gt; TYPE: PRT

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&lt;213&gt; ORGANISM: Phaeodactylum tricornutum

&lt;400&gt; SEQUENCE: 22

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

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Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu  
 405 410 415  
 Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val  
 420 425 430  
 Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445  
 Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460  
 Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

<210> SEQ ID NO 23  
 <211> LENGTH: 1578  
 <212> TYPE: DNA  
 <213> ORGANISM: Physcomitrella patens  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1578)  
 <223> OTHER INFORMATION: Delta-6 desaturase

<400> SEQUENCE: 23

atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac	48
Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn	
1 5 10 15	
atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc	96
Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe	
20 25 30	
agt tat gtg tct tca act gtt ggt tcg tgg agc gta cac agt ata caa	144
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln	
35 40 45	
cct ttg aag cgc ctg acg agt aag aag cgt gtt tcg gaa agc gct gcc	192
Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala	
50 55 60	
gtg caa tgt ata tca gct gaa gtt cag aga aat tcg agt acc cag gga	240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly	
65 70 75 80	
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg	288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg	
85 90 95	
tca tct cag tgg aag aag tcg aca cac ccc cta tca gaa gta gca gta	336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val	
100 105 110	
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat	384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr	
115 120 125	
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt	432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser	
130 135 140	
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca	480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala	
145 150 155 160	
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag	528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu	
165 170 175	
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga	576
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg	
180 185 190	
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat	624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr	
195 200 205	

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gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala 210 215 220	672
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys 225 230 235 240	720
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe 245 250 255	768
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly 260 265 270	816
tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys 275 280 285	864
gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr 290 295 300	912
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp 305 310 315 320	960
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile 325 330 335	1008
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt Leu Gln Tyr His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg 340 345 350	1056
ggt agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu 355 360 365	1104
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr 370 375 380	1152
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro 385 390 395 400	1200
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly 405 410 415	1248
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser 420 425 430	1296
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly 435 440 445	1344
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu 450 455 460	1392
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala 465 470 475 480	1440
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp 485 490 495	1488
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu 500 505 510	1536
gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser 515 520 525	1578



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<210> SEQ ID NO 24  
 <211> LENGTH: 525  
 <212> TYPE: PRT  
 <213> ORGANISM: *Physcomitrella patens*  
 <400> SEQUENCE: 24

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

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370	375	380	
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro			
385	390	395	400
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly			
	405	410	415
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser			
	420	425	430
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly			
	435	440	445
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu			
	450	455	460
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala			
	465	470	475
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp			
	485	490	495
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu			
	500	505	510
Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser			
	515	520	525
<210> SEQ ID NO 25			
<211> LENGTH: 1332			
<212> TYPE: DNA			
<213> ORGANISM: Caenorhabditis elegans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(1332)			
<223> OTHER INFORMATION: Delta-6 desaturase			
<400> SEQUENCE: 25			
atg gtc gtc gac aag aat gcc tcc ggg ctt cga atg aag gtc gat ggc			48
Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly			
1	5	10	15
aaa tgg ctc tac ctt agc gag gaa ttg gtg aag aaa cat cca gga gga			96
Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly			
	20	25	30
gct gtt att gaa caa tat aga aat tcg gat gct act cat att ttc cac			144
Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His			
	35	40	45
gct ttc cac gaa gga tct tct cag gct tat aag caa ctt gac ctt ctg			192
Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu			
	50	55	60
aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa ttg gaa aag			240
Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys			
	65	70	75
aga ctt gac aaa gtt gat atc aat gta tca gca tat gat gtc agt gtt			288
Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val			
	85	90	95
gca caa gaa aag aaa atg gtt gaa tca ttc gaa aaa cta cga cag aag			336
Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys			
	100	105	110
ctt cat gat gat gga tta atg aaa gca aat gaa aca tat ttc ctg ttt			384
Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe			
	115	120	125
aaa gcg att tca aca ctt tca att atg gca ttt gca ttt tat ctt cag			432
Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln			
	130	135	140
tat ctt gga tgg tat att act tct gca tgt tta tta gca ctt gca tgg			480
Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp			

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145	150	155	160	
caa caa ttc gga tgg tta aca cat gag ttc tgc cat caa cag cca aca				528
Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr	165	170	175	
aag aac aga cct ttg aat gat act att tct ttg ttc ttt ggt aat ttc				576
Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe	180	185	190	
tta caa gga ttt tca aga gat tgg tgg aag gac aag cat aac act cat				624
Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His	195	200	205	
cac gct gcc aca aat gta att gat cat gac ggt gat atc gac ttg gca				672
His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala	210	215	220	
cca ctt ttc gca ttt att cca gga gat ttg tgc aag tat aag gcc agc				720
Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser	225	230	235	240
ttt gaa aaa gca att ctc aag att gta cca tat caa cat ctc tat ttc				768
Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe	245	250	255	
acc gca atg ctt cca atg ctc cgt ttc tca tgg act ggt cag tca gtt				816
Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val	260	265	270	
caa tgg gta ttc aaa gag aat caa atg gag tac aag gtc tat caa aga				864
Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg	275	280	285	
aat gca ttc tgg gag caa gca aca att gtt gga cat tgg gct tgg gta				912
Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val	290	295	300	
ttc tat caa ttg ttc tta tta cca aca tgg cca ctt cgg gtt gct tat				960
Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr	305	310	315	320
ttc att att tca caa atg gga gga ggc ctt ttg att gct cac gta gtc				1008
Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val	325	330	335	
act ttc aac cat aac tct gtt gat aag tat cca gcc aat tct cga att				1056
Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile	340	345	350	
tta aac aac ttc gcc gct ctt caa att ttg acc aca cgc aac atg act				1104
Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr	355	360	365	
cca tct cca ttc att gat tgg ctt tgg ggt gga ctc aat tat cag atc				1152
Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile	370	375	380	
gag cac cac ttg ttc cca aca atg cca cgt tgc aat ctg aat gct tgc				1200
Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys	385	390	395	400
gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt cct tac ctc				1248
Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu	405	410	415	
gtc gat gac tac ttt gac gga tat gca atg aat ttg caa caa ttg aaa				1296
Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys	420	425	430	
aat atg gct gag cac att caa gct aaa gct gcc taa				1332
Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala	435	440		

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 443

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Caenorhabditis elegans

-continued

&lt;400&gt; SEQUENCE: 26

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

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405	410	415	
Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys			
420	425	430	
Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala			
435	440		
<210> SEQ ID NO 27			
<211> LENGTH: 873			
<212> TYPE: DNA			
<213> ORGANISM: Physcomitrella patens			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(873)			
<223> OTHER INFORMATION: Delta-6 elongase			
<400> SEQUENCE: 27			
atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg			48
Met Glu Val Val Glu Arg Phe Tyr Gly Leu Asp Gly Lys Val Ser			
1	5	10	15
cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat			96
Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp			
	20	25	30
acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc			144
Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile			
	35	40	45
gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg			192
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu			
	50	55	60
tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg			240
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu			
65	70	75	80
ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt			288
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser			
	85	90	95
ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac			336
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr			
	100	105	110
tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att			384
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile			
	115	120	125
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc			432
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr			
	130	135	140
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac			480
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His			
145	150	155	160
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat			528
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His			
	165	170	175
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga			576
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly			
	180	185	190
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga			624
Val His Val Leu Met Tyr Ala Tyr Phe Leu Ala Ala Cys Leu Arg			
	195	200	205
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg			672
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu			
	210	215	220
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac			720
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr			
225	230	235	240

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tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att      768
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
                245                      250                      255

ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac      816
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
                260                      265                      270

gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa      864
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
                275                      280                      285

act gag tga                                                                873
Thr Glu
    290

<210> SEQ ID NO 28
<211> LENGTH: 290
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> SEQUENCE: 28
Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
 1          5          10          15
Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20          25          30
Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35          40          45
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50          55          60
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
 65          70          75          80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
 85          90          95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
 100         105         110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
 115        120        125
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
 130        135        140
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
 145        150        155        160
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
 165        170        175
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
 180        185        190
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
 195        200        205
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
 210        215        220
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
 225        230        235        240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
 245        250        255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
 260        265        270
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
 275        280        285

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Thr Glu
 290

<210> SEQ ID NO 29
<211> LENGTH: 1049
<212> TYPE: DNA
<213> ORGANISM: Thraustochytrium
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (43)..(858)
<223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 29

gaattcggca cgagagcgcg cggagcggag acctcggccg cg atg atg gag ccg      54
                                     Met Met Glu Pro
                                     1

ctc gac agg tac agg gcg ctg gcg gag ctc gcc gcg agg tac gcc agc      102
Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala Arg Tyr Ala Ser
 5                               10                               15                               20

tcg gcg gcc ttc aag tgg caa gtc acg tac gac gcc aag gac agc ttc      150
Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe
                25                               30                               35

gtc ggg ccc ctg gga atc cgg gag ccg ctc ggg ctc ctg gtg ggc tcc      198
Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser
                40                               45                               50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac      246
Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn
                55                               60                               65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc      294
Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His Asn Leu Gly Leu
 70                               75                               80

tgc ctc ttc tcg ggc gcc gtg tgg atc tac acg agc tac ctc atg atc      342
Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser Tyr Leu Met Ile
 85                               90                               95                               100

cag gat ggg cac ttt cgc agc ctc gag gcg gca acg tgc gag ccg ctc      390
Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr Cys Glu Pro Leu
                105                               110                               115

aag cat ccg cac ttc cag ctc atc agc ttg ctc ttt gcg ctg tcc aag      438
Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe Ala Leu Ser Lys
                120                               125                               130

atc tgg gag tgg ttc gac acg gtg ctc ctc atc gtc aag ggc aac aag      486
Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val Lys Gly Asn Lys
                135                               140                               145

ctc cgc ttc ctg cac gtc ttg cac cac gcc acg acc ttt tgg ctc tac      534
Leu Arg Phe Leu His Val Leu His His Ala Thr Thr Phe Trp Leu Tyr
                150                               155                               160

gcc atc gac cac atc ttt ctc tcg tcc atc aag tac ggc gtc gcg gtc      582
Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr Gly Val Ala Val
                165                               170                               175                               180

aat gct ttc atc cac acc gtc atg tac gcg cac tac ttc cgc cca ttc      630
Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr Phe Arg Pro Phe
                185                               190                               195

ccg aag ggc ttg cgc ccg ctt att acg cag ttg cag atc gtc cag ttc      678
Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln Ile Val Gln Phe
                200                               205                               210

att ttc agc atc ggc atc cat acc gcc att tac tgg cac tac gac tgc      726
Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp His Tyr Asp Cys
                215                               220                               225

gag ccg ctc gtg cat acc cac ttt tgg gaa tac gtc acg ccc tac ctt      774
Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu
                230                               235                               240

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ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag      822
Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln
245                250                255                260

```

```

tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca      868
Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala
                265                270

```

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gtagaccagc agcgccgagg acgcggtgccg cgttatcgcg aagcacgaaa taaagaagat      928

```

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catttgattc aacgaggcta cttgcggcca cgagaaaaaa aaaaaaaaaa aaaaaaaaaa      988

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1048

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c                                                                 1049

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<210> SEQ ID NO 30

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<211> LENGTH: 271

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<212> TYPE: PRT

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<213> ORGANISM: Thraustochytrium

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<400> SEQUENCE: 30

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Met Met Glu Pro Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala
 1                5                10                15

```

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Arg Tyr Ala Ser Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala
                20                25                30

```

```

Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu
 35                40                45

```

```

Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr
 50                55                60

```

```

Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His
 65                70                75                80

```

```

Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser
 85                90                95

```

```

Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr
 100               105               110

```

```

Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe
 115               120               125

```

```

Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val
 130               135               140

```

```

Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr
 145               150               155               160

```

```

Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr
 165               170               175

```

```

Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr
 180               185               190

```

```

Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln
 195               200               205

```

```

Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp
 210               215               220

```

```

His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val
 225               230               235               240

```

```

Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe
 245               250               255

```

```

Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala
 260               265               270

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<210> SEQ ID NO 31

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<211> LENGTH: 837

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<212> TYPE: DNA

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<213> ORGANISM: Phytophthora infestans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(837)
<223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 31
atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg      48
Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr
1                               5                               10                               15

gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg      96
Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val
20                               25                               30

cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc      144
His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala
35                               40                               45

atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg      192
Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met
50                               55                               60

aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac      240
Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr
65                               70                               75                               80

aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc      288
Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala
85                               90                               95

atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt      336
Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe
100                              105                              110

aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc      384
Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu
115                              120                              125

tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag      432
Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys
130                              135                              140

aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg      480
Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
145                              150                              155                              160

ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca      528
Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
165                              170                              175

tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act      576
Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
180                              185                              190

tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac      624
Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
195                              200                              205

ctc acg cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc      672
Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
210                              215                              220

tac ctg acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg      720
Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
225                              230                              235                              240

ctc atg tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat      768
Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
245                              250                              255

ttc tac att cgc cgc tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag      816
Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
260                              265                              270

gaa tcg aag aag aag ttg taa      837
Glu Ser Lys Lys Lys Leu
275

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<210> SEQ ID NO 32  
 <211> LENGTH: 278  
 <212> TYPE: PRT  
 <213> ORGANISM: *Phytophthora infestans*  
 <400> SEQUENCE: 32  
 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
 1 5 10 15  
 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
 20 25 30  
 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
 35 40 45  
 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
 50 55 60  
 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
 65 70 75 80  
 Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala  
 85 90 95  
 Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe  
 100 105 110  
 Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu  
 115 120 125  
 Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys  
 130 135 140  
 Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val  
 145 150 155 160  
 Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser  
 165 170 175  
 Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr  
 180 185 190  
 Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
 195 200 205  
 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
 210 215 220  
 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
 225 230 235 240  
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
 245 250 255  
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
 260 265 270  
 Glu Ser Lys Lys Lys Leu  
 275

<210> SEQ ID NO 33  
 <211> LENGTH: 954  
 <212> TYPE: DNA  
 <213> ORGANISM: *Mortierella alpina*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(954)  
 <223> OTHER INFORMATION: Delta-6 elongase  
 <400> SEQUENCE: 33

atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc  
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro  
 1 5 10 15

48

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ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc	96
Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val	
20 25 30	
acc gga aag tcc atc gac tcc ttc gtc ttc cag gag gcc gtc acg cct	144
Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro	
35 40 45	
ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc	192
Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val	
50 55 60	
gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag	240
Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys	
65 70 75 80	
ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc	288
Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser	
85 90 95	
gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc	336
Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala	
100 105 110	
aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag	384
Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln	
115 120 125	
cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag	432
Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu	
130 135 140	
ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc	480
Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe	
145 150 155 160	
ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag	528
Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln	
165 170 175	
ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg	576
Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu	
180 185 190	
act gtc cac gtc ttc atg tac tac tac tac atg cgc tcc gct gcc ggt	624
Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly	
195 200 205	
gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag	672
Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln	
210 215 220	
ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc	720
Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe	
225 230 235 240	
gcc ttc acc tac ttc ccc tgg gct ccc aac gtc gcc aag tgc gcc ggt	768
Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly	
245 250 255	
acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc	816
Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu	
260 265 270	
ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag	864
Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys	
275 280 285	
gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc	912
Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser	
290 295 300	
ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa	954
Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile	
305 310 315	

&lt;210&gt; SEQ ID NO 34

&lt;211&gt; LENGTH: 317

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<212> TYPE: PRT
<213> ORGANISM: Mortierella alpina

<400> SEQUENCE: 34

Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
1          5          10          15

Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val
20          25          30

Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro
35          40          45

Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val
50          55          60

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

Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser
85          90          95

Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala
100         105         110

Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln
115         120         125

Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu
130         135         140

Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe
145         150         155         160

Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln
165         170         175

Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu
180         185         190

Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly
195         200         205

Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln
210         215         220

Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe
225         230         235         240

Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly
245         250         255

Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu
260         265         270

Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys
275         280         285

Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser
290         295         300

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile
305         310         315

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<210> SEQ ID NO 35
<211> LENGTH: 957
<212> TYPE: DNA
<213> ORGANISM: Mortierella alpina
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(957)
<223> OTHER INFORMATION: Delta-6 elongase

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<400> SEQUENCE: 35

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atg gag tcg att gcg cca ttc ctc cca tca aag atg ccg caa gat ctg
Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu

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48

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1	5	10	15	
ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc				96
Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val	20	25	30	
gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc				144
Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro	35	40	45	
acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct				192
Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro	50	55	60	
ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc				240
Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile	65	70	75	80
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag				288
Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys	85	90	95	
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt				336
Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe	100	105	110	
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag				384
Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu	115	120	125	
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc				432
Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr	130	135	140	
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc				480
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser	145	150	155	160
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac				528
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn	165	170	175	
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc				576
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe	180	185	190	
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac				624
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr	195	200	205	
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac				672
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr	210	215	220	
tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc				720
Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe	225	230	235	240
tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag				768
Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln	245	250	255	
tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac				816
Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr	260	265	270	
ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc				864
Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu	275	280	285	
ggt ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag				912
Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln	290	295	300	
gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa				957
Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln	305	310	315	

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<210> SEQ ID NO 36  
 <211> LENGTH: 318  
 <212> TYPE: PRT  
 <213> ORGANISM: Mortierella alpina

<400> SEQUENCE: 36

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

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<210> SEQ ID NO 37  
 <211> LENGTH: 867  
 <212> TYPE: DNA  
 <213> ORGANISM: Caenorhabditis elegans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(867)  
 <223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 37

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atg gct cag cat ccg ctc gtt caa cgg ctt ctc gat gtc aaa ttc gac	48
Met Ala Gln His Pro Leu Val Gln Arg Leu Leu Asp Val Lys Phe Asp	
1 5 10 15	
acg aaa cga ttt gtg gct att gct act cat ggg cca aag aat ttc cct	96
Thr Lys Arg Phe Val Ala Ile Ala Thr His Gly Pro Lys Asn Phe Pro	
20 25 30	
gac gca gaa ggt cgc aag ttc ttt gct gat cac ttt gat gtt act att	144
Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile	
35 40 45	
cag gct tca atc ctg tac atg gtc gtt gtg ttc gga aca aaa tgg ttc	192
Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe	
50 55 60	
atg cgt aat cgt caa cca ttc caa ttg act att cca ctc aac atc tgg	240
Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp	
65 70 75 80	
aat ttc atc ctc gcc gca ttt tcc atc gca gga gct gtc aaa atg acc	288
Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr	
85 90 95	
cca gag ttc ttt gga acc att gcc aac aaa gga att gtc gca tcc tac	336
Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr	
100 105 110	
tgc aaa gtg ttt gat ttc acg aaa gga gag aat gga tac tgg gtg tgg	384
Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp	
115 120 125	
ctc ttc atg gct tcc aaa ctt ttc gaa ctt gtt gac acc atc ttc ttg	432
Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu	
130 135 140	
gtt ctc cgt aaa cgt cca ctc atg ttc ctt cac tgg tat cac cat att	480
Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile	
145 150 155 160	
ctc acc atg atc tac gcc tgg tac tct cat cca ttg acc cca gga ttc	528
Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe	
165 170 175	
aac aga tac gga att tat ctt aac ttt gtc gtc cac gcc ttc atg tac	576
Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr	
180 185 190	
tct tac tac ttc ctt cgc tcg atg aag att cgc gtg cca gga ttc atc	624
Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile	
195 200 205	
gcc caa gct atc aca tct ctt caa atc gtt caa ttc atc atc tct tgc	672
Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys	
210 215 220	
gcc gtt ctt gct cat ctt ggt tat ctc atg cac ttc acc aat gcc aac	720
Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn	
225 230 235 240	
tgt gat ttc gag cca tca gta ttc aag ctc gca gtt ttc atg gac aca	768
Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr	
245 250 255	
aca tac ttg gct ctt ttc gtc aac ttc ttc ctc caa tca tat gtt ctc	816
Thr Tyr Leu Ala Leu Phe Val Asn Phe Phe Leu Gln Ser Tyr Val Leu	
260 265 270	
cgc gga gga aaa gac aag tac aag gca gtg cca aag aag aag aac aac	864
Arg Gly Gly Lys Asp Lys Tyr Lys Ala Val Pro Lys Lys Lys Asn Asn	
275 280 285	
taa	867

&lt;210&gt; SEQ ID NO 38

&lt;211&gt; LENGTH: 288

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Caenorhabditis elegans

-continued

&lt;400&gt; SEQUENCE: 38

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

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 1626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Euglena gracilis

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(1626)

&lt;223&gt; OTHER INFORMATION: Delta-4 desaturase

&lt;400&gt; SEQUENCE: 39

atg ttg gtg ctg ttt ggc aat ttc tat gtc aag caa tac tcc caa aag 48  
 Met Leu Val Leu Phe Gly Asn Phe Tyr Val Lys Gln Tyr Ser Gln Lys  
 1 5 10 15  
 aac ggc aag ccg gag aac gga gcc acc cct gag aac gga gcg aag ccg 96  
 Asn Gly Lys Pro Glu Asn Gly Ala Thr Pro Glu Asn Gly Ala Lys Pro  
 20 25 30  
 caa cct tgc gag aac ggc acg gtg gaa aag cga gag aat gac acc gcc 144  
 Gln Pro Cys Glu Asn Gly Thr Val Glu Lys Arg Glu Asn Asp Thr Ala



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35	40	45	
aac gtt cgg ccc acc cgt	cca gct gga ccc cgg	cgg gcc acg tac tac	192
Asn Val Arg Pro Thr Arg	Pro Ala Gly Pro Pro	Pro Ala Thr Tyr Tyr	
50	55	60	
gac tcc ctg gca gtg tcg	ggg cag ggc aag gag	cgg ctg ttc acc acc	240
Asp Ser Leu Ala Val Ser	Gly Gln Gly Lys Glu	Arg Leu Phe Thr Thr	
65	70	75 80	
gat gag gtg agg cgg cac	atc ctc ccc acc gat	ggc tgg ctg acg tgc	288
Asp Glu Val Arg Arg His	Ile Leu Pro Thr Asp	Gly Trp Leu Thr Cys	
85	90	95	
cac gaa gga gtc tac gat	gtc act gat ttc ctt	gcc aag cac cct ggt	336
His Glu Gly Val Tyr Asp	Val Thr Asp Phe Leu	Ala Lys His Pro Gly	
100	105	110	
ggc ggt gtc atc acg ctg	ggc ctt gga agg gac	tgc aca atc ctc atc	384
Gly Gly Val Ile Thr Leu	Gly Leu Gly Arg Asp	Cys Thr Ile Leu Ile	
115	120	125	
gag tca tac cac cct gct	ggg cgc ccg gac aag	gtg atg gag aag tac	432
Glu Ser Tyr His Pro Ala	Gly Arg Pro Asp Lys	Val Met Glu Lys Tyr	
130	135	140	
cgc att ggt acg ctg cag	gac ccc aag acg ttc	tat gct tgg gga gag	480
Arg Ile Gly Thr Leu Gln	Asp Pro Lys Thr Phe	Tyr Ala Trp Gly Glu	
145	150	155 160	
tcc gat ttc tac cct gag	ttg aag cgc cgg gcc	ctt gca agg ctg aag	528
Ser Asp Phe Tyr Pro Glu	Leu Lys Arg Arg Ala	Leu Ala Arg Leu Lys	
165	170	175	
gag gct ggt cag gcg cgg	cgc ggc ggc ctt ggg	gtg aag gcc ctc ctg	576
Glu Ala Gly Gln Ala Arg	Arg Gly Gly Leu Gly	Val Lys Ala Leu Leu	
180	185	190	
gtg ctc acc ctc ttc ttc	gtg tcg tgg tac atg	tgg gtg gcc cac aag	624
Val Leu Thr Leu Phe Phe	Val Ser Trp Tyr Met	Trp Val Ala His Lys	
195	200	205	
tcc ttc ctc tgg gcc gcc	gtc tgg ggc ttc gcc	ggc tcc cac gtc ggg	672
Ser Phe Leu Trp Ala Ala	Val Trp Gly Phe Ala	Gly Ser His Val Gly	
210	215	220	
ctg agc atc cag cac gat	ggc aac cac ggc gcg	ttc agc cgc aac aca	720
Leu Ser Ile Gln His Asp	Gly Asn His Gly Ala	Phe Ser Arg Asn Thr	
225	230	235 240	
ctg gtg aac cgc ctg gcg	ggg tgg ggc atg gac	ttg atc ggc gcg tcg	768
Leu Val Asn Arg Leu Ala	Gly Trp Gly Met Asp	Leu Ile Gly Ala Ser	
245	250	255	
tcc acg gtg tgg gag tac	cag cac gtc atc ggc	cac cac cag tac acc	816
Ser Thr Val Trp Glu Tyr	Gln His Val Ile Gly	His His Gln Tyr Thr	
260	265	270	
aac ctc gtg tcg gac acg	cta ttc agt ctg cct	gag aac gat ccg gac	864
Asn Leu Val Ser Asp Thr	Leu Phe Ser Leu Pro	Glu Asn Asp Pro Asp	
275	280	285	
gtc ttc tcc agc tac ccg	ctg atg cgc atg cac	ccg gat acg gcg tgg	912
Val Phe Ser Ser Tyr Pro	Leu Met Arg Met His	Pro Asp Thr Ala Trp	
290	295	300	
cag ccg cac cac cgc ttc	cag cac ctg ttc gcg	ttc cca ctg ttc gcc	960
Gln Pro His His Arg Phe	Gln His Leu Phe Ala	Phe Pro Leu Phe Ala	
305	310	315 320	
ctg atg aca atc agc aag	gtg ctg acc agc gat	ttc gct gtc tgc ctc	1008
Leu Met Thr Ile Ser Lys	Val Leu Thr Ser Asp	Phe Ala Val Cys Leu	
325	330	335	
agc atg aag aag ggg tcc	atc gac tgc tcc tcc	agg ctc gtc cca ctg	1056
Ser Met Lys Lys Gly Ser	Ile Asp Cys Ser Ser	Arg Leu Val Pro Leu	
340	345	350	
gag ggg cag ctg ctg ttc	tgg ggg gcc aag ctg	gcg aac ttc ctg ttg	1104

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Glu	Gly	Gln	Leu	Leu	Phe	Trp	Gly	Ala	Lys	Leu	Ala	Asn	Phe	Leu	Leu	
		355					360					365				
cag	att	gtg	ttg	cca	tgc	tac	ctc	cac	ggg	aca	gct	atg	ggc	ctg	gcc	1152
Gln	Ile	Val	Leu	Pro	Cys	Tyr	Leu	His	Gly	Thr	Ala	Met	Gly	Leu	Ala	
	370					375					380					
ctc	ttc	tct	ggt	gct	cac	ctt	gtg	tcg	ggg	gag	tac	ctc	gcg	atc	tgc	1200
Leu	Phe	Ser	Val	Ala	His	Leu	Val	Ser	Gly	Glu	Tyr	Leu	Ala	Ile	Cys	
	385				390					395					400	
ttc	atc	atc	aac	cac	atc	agc	gag	tct	tgt	gag	ttt	atg	aat	aca	agc	1248
Phe	Ile	Ile	Asn	His	Ile	Ser	Glu	Ser	Cys	Glu	Phe	Met	Asn	Thr	Ser	
			405						410					415		
ttt	caa	acc	gcc	gcc	cgg	agg	aca	gag	atg	ctt	cag	gca	gca	cat	cag	1296
Phe	Gln	Thr	Ala	Ala	Arg	Arg	Thr	Glu	Met	Leu	Gln	Ala	Ala	His	Gln	
			420					425					430			
gca	gcg	gag	gcc	aag	aag	gtg	aag	ccc	acc	cct	cca	ccg	aac	gat	tgg	1344
Ala	Ala	Glu	Ala	Lys	Lys	Val	Lys	Pro	Thr	Pro	Pro	Pro	Asn	Asp	Trp	
		435				440							445			
gct	gtg	aca	cag	gtc	caa	tgc	tgc	gtg	aat	tgg	aga	tca	ggt	ggc	gtg	1392
Ala	Val	Thr	Gln	Val	Gln	Cys	Cys	Val	Asn	Trp	Arg	Ser	Gly	Gly	Val	
	450					455					460					
ttg	gcc	aat	cac	ctc	tct	gga	ggc	ttg	aac	cac	cag	atc	gag	cat	cat	1440
Leu	Ala	Asn	His	Leu	Ser	Gly	Gly	Leu	Asn	His	Gln	Ile	Glu	His	His	
	465				470					475					480	
ctg	ttc	ccc	agc	atc	tcg	cat	gcc	aac	tac	ccc	acc	atc	gcc	cct	gtt	1488
Leu	Phe	Pro	Ser	Ile	Ser	His	Ala	Asn	Tyr	Pro	Thr	Ile	Ala	Pro	Val	
			485						490					495		
gtg	aag	gag	gtg	tgc	gag	gag	tac	ggg	ttg	ccg	tac	aag	aat	tac	gtc	1536
Val	Lys	Glu	Val	Cys	Glu	Glu	Tyr	Gly	Leu	Pro	Tyr	Lys	Asn	Tyr	Val	
			500					505					510			
acg	ttc	tgg	gat	gca	gtc	tgt	ggc	atg	ggt	cag	cac	ctc	cgg	ttg	atg	1584
Thr	Phe	Trp	Asp	Ala	Val	Cys	Gly	Met	Val	Gln	His	Leu	Arg	Leu	Met	
		515				520						525				
ggt	gct	cca	ccg	gtg	cca	acg	aac	ggg	gac	aaa	aag	tca	taa			1626
Gly	Ala	Pro	Pro	Val	Pro	Thr	Asn	Gly	Asp	Lys	Lys	Ser				
	530					535					540					

&lt;210&gt; SEQ ID NO 40

&lt;211&gt; LENGTH: 541

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Euglena gracilis

&lt;400&gt; SEQUENCE: 40

Met	Leu	Val	Leu	Phe	Gly	Asn	Phe	Tyr	Val	Lys	Gln	Tyr	Ser	Gln	Lys	
1				5					10					15		
Asn	Gly	Lys	Pro	Glu	Asn	Gly	Ala	Thr	Pro	Glu	Asn	Gly	Ala	Lys	Pro	
		20						25					30			
Gln	Pro	Cys	Glu	Asn	Gly	Thr	Val	Glu	Lys	Arg	Glu	Asn	Asp	Thr	Ala	
		35				40							45			
Asn	Val	Arg	Pro	Thr	Arg	Pro	Ala	Gly	Pro	Pro	Pro	Ala	Thr	Tyr	Tyr	
	50					55						60				
Asp	Ser	Leu	Ala	Val	Ser	Gly	Gln	Gly	Lys	Glu	Arg	Leu	Phe	Thr	Thr	
	65				70					75					80	
Asp	Glu	Val	Arg	Arg	His	Ile	Leu	Pro	Thr	Asp	Gly	Trp	Leu	Thr	Cys	
				85					90					95		
His	Glu	Gly	Val	Tyr	Asp	Val	Thr	Asp	Phe	Leu	Ala	Lys	His	Pro	Gly	
			100					105						110		
Gly	Gly	Val	Ile	Thr	Leu	Gly	Leu	Gly	Arg	Asp	Cys	Thr	Ile	Leu	Ile	
		115					120							125		

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Glu Ser Tyr His Pro Ala Gly Arg Pro Asp Lys Val Met Glu Lys Tyr  
 130 135 140  
 Arg Ile Gly Thr Leu Gln Asp Pro Lys Thr Phe Tyr Ala Trp Gly Glu  
 145 150 155 160  
 Ser Asp Phe Tyr Pro Glu Leu Lys Arg Arg Ala Leu Ala Arg Leu Lys  
 165 170 175  
 Glu Ala Gly Gln Ala Arg Arg Gly Gly Leu Gly Val Lys Ala Leu Leu  
 180 185 190  
 Val Leu Thr Leu Phe Phe Val Ser Trp Tyr Met Trp Val Ala His Lys  
 195 200 205  
 Ser Phe Leu Trp Ala Ala Val Trp Gly Phe Ala Gly Ser His Val Gly  
 210 215 220  
 Leu Ser Ile Gln His Asp Gly Asn His Gly Ala Phe Ser Arg Asn Thr  
 225 230 235 240  
 Leu Val Asn Arg Leu Ala Gly Trp Gly Met Asp Leu Ile Gly Ala Ser  
 245 250 255  
 Ser Thr Val Trp Glu Tyr Gln His Val Ile Gly His His Gln Tyr Thr  
 260 265 270  
 Asn Leu Val Ser Asp Thr Leu Phe Ser Leu Pro Glu Asn Asp Pro Asp  
 275 280 285  
 Val Phe Ser Ser Tyr Pro Leu Met Arg Met His Pro Asp Thr Ala Trp  
 290 295 300  
 Gln Pro His His Arg Phe Gln His Leu Phe Ala Phe Pro Leu Phe Ala  
 305 310 315 320  
 Leu Met Thr Ile Ser Lys Val Leu Thr Ser Asp Phe Ala Val Cys Leu  
 325 330 335  
 Ser Met Lys Lys Gly Ser Ile Asp Cys Ser Ser Arg Leu Val Pro Leu  
 340 345 350  
 Glu Gly Gln Leu Leu Phe Trp Gly Ala Lys Leu Ala Asn Phe Leu Leu  
 355 360 365  
 Gln Ile Val Leu Pro Cys Tyr Leu His Gly Thr Ala Met Gly Leu Ala  
 370 375 380  
 Leu Phe Ser Val Ala His Leu Val Ser Gly Glu Tyr Leu Ala Ile Cys  
 385 390 395 400  
 Phe Ile Ile Asn His Ile Ser Glu Ser Cys Glu Phe Met Asn Thr Ser  
 405 410 415  
 Phe Gln Thr Ala Ala Arg Arg Thr Glu Met Leu Gln Ala Ala His Gln  
 420 425 430  
 Ala Ala Glu Ala Lys Lys Val Lys Pro Thr Pro Pro Pro Asn Asp Trp  
 435 440 445  
 Ala Val Thr Gln Val Gln Cys Cys Val Asn Trp Arg Ser Gly Gly Val  
 450 455 460  
 Leu Ala Asn His Leu Ser Gly Gly Leu Asn His Gln Ile Glu His His  
 465 470 475 480  
 Leu Phe Pro Ser Ile Ser His Ala Asn Tyr Pro Thr Ile Ala Pro Val  
 485 490 495  
 Val Lys Glu Val Cys Glu Glu Tyr Gly Leu Pro Tyr Lys Asn Tyr Val  
 500 505 510  
 Thr Phe Trp Asp Ala Val Cys Gly Met Val Gln His Leu Arg Leu Met  
 515 520 525  
 Gly Ala Pro Pro Val Pro Thr Asn Gly Asp Lys Lys Ser  
 530 535 540

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<210> SEQ ID NO 41
<211> LENGTH: 1548
<212> TYPE: DNA
<213> ORGANISM: Thraustochytrium
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1548)
<223> OTHER INFORMATION: Delta-4 desaturase

<400> SEQUENCE: 41
atg acg gtc ggg ttt gac gaa acg gtg act atg gac acg gtc cgc aac      48
Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
1                               5                               10                               15

cac aac atg ccg gac gac gcc tgg tgc gcg atc cac ggc acc gtg tac      96
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
20                               25                               30

gac atc acc aag ttc agc aag gtg cac ccc ggc ggg gac atc atc atg     144
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
35                               40                               45

ctg gcc gct ggc aag gag gcc acc atc ctg ttc gag acc tac cac atc     192
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
50                               55                               60

aag ggc gtc ccg gac gcg gtg ctg cgc aag tac aag gtc ggc aag ctc     240
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
65                               70                               75                               80

ccc cag ggc aag aag ggc gaa acg agc cac atg ccc acc ggc ctc gac     288
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp
85                               90                               95

tcg gcc tcc tac tac tcg tgg gac agc gag ttt tac agg gtg ctc cgc     336
Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
100                              105                              110

gag cgc gtc gcc aag aag ctg gcc gag ccc ggc ctc atg cag cgc gcg     384
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
115                              120                              125

cgc atg gag ctc tgg gcc aag gcg atc ttc ctc ctg gca ggt ttc tgg     432
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
130                              135                              140

ggc tcc ctt tac gcc atg tgc gtg cta gac ccg cac ggc ggt gcc atg     480
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
145                              150                              155                              160

gta gcc gcc gtt acg ctc ggc gtg ttc gct gcc ttt gtc gga act tgc     528
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys
165                              170                              175

atc cag cac gac ggc agc cac ggc gcc ttc tcc aag tcg cga ttc atg     576
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met
180                              185                              190

aac aag gcg gcg gcc tgg acc ctc gac atg atc ggc gcg agt gcg atg     624
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met
195                              200                              205

acc tgg gag atg cag cac gtt ctt ggc cac cac ccg tac acc aac ctc     672
Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu
210                              215                              220

atc gag atg gag aac ggt ttg gcc aag gtc aag ggc gcc gac gtc gac     720
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp
225                              230                              235                              240

ccg aag aag gtc gac cag gag agc gac ccg gac gtc ttc agt acg tac     768
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr
245                              250                              255

ccg atg ctt cgc ctg cac ccg tgg cac cgc cag cgg ttt tac cac aag     816
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys
260                              265                              270

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ttc cag cac ctg tac gcc ccg ttt atc ttt ggg tct atg acg att aac	864
Phe Gln His Leu Tyr Ala Pro Phe Ile Phe Gly Ser Met Thr Ile Asn	
275 280 285	
aag gtg att tcc cag gat gtc ggg gtt gtg ctg cgc aag cgc ctg ttc	912
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe	
290 295 300	
cag atc gac gcc aac tgc cgg tat ggc agc ccc tgg tac gtg gcc cgc	960
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Tyr Val Ala Arg	
305 310 315 320	
ttc tgg atc atg aag ctc ctc acc acg ctc tac atg gtg gcg ctt ccc	1008
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro	
325 330 335	
atg tac atg cag ggg cct gct cag ggc ttg aag ctt ttc ttc atg gcc	1056
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala	
340 345 350	
cac ttc acc tgc gga gag gtc ctc gcc acc atg ttt att gtc aac cac	1104
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His	
355 360 365	
atc atc gag ggc gtc agc tac gct tcc aag gac gcg gtc aag ggc gtc	1152
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val	
370 375 380	
atg gct ccg ccg cgc act gtg cac ggt gtc acc ccg atg cag gtg acg	1200
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr	
385 390 395 400	
caa aag gcg ctc agt gcg gcc gag tcg gcc aag tcg gac gcc gac aag	1248
Gln Lys Ala Leu Ser Ala Ala Glu Ser Ala Lys Ser Asp Ala Asp Lys	
405 410 415	
acg acc atg atc ccc ctc aac gac tgg gcc gct gtg cag tgc cag acc	1296
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr	
420 425 430	
tct gtg aac tgg gct gtc ggg tcg tgg ttt tgg aac cac ttt tcg ggc	1344
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly	
435 440 445	
ggc ctc aac cac cag att gag cac cac tgc ttc ccc caa aac ccc cac	1392
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His	
450 455 460	
acg gtc aac gtc tac atc tcg ggc atc gtc aag gag acc tgc gaa gaa	1440
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu	
465 470 475 480	
tac ggc gtg ccg tac cag gct gag atc agc ctc ttc tct gcc tat ttc	1488
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe	
485 490 495	
aag atg ctg tcg cac ctc cgc acg ctc ggc aac gag gac ctc acg gcc	1536
Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala	
500 505 510	
tgg tcc acg tga	1548
Trp Ser Thr	
515	
<210> SEQ ID NO 42	
<211> LENGTH: 515	
<212> TYPE: PRT	
<213> ORGANISM: Thraustochytrium	
<400> SEQUENCE: 42	
Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn	
1 5 10 15	
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr	
20 25 30	
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met	

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35					40					45					
Leu	Ala	Ala	Gly	Lys	Glu	Ala	Thr	Ile	Leu	Phe	Glu	Thr	Tyr	His	Ile
50						55					60				
Lys	Gly	Val	Pro	Asp	Ala	Val	Leu	Arg	Lys	Tyr	Lys	Val	Gly	Lys	Leu
65					70					75					80
Pro	Gln	Gly	Lys	Lys	Gly	Glu	Thr	Ser	His	Met	Pro	Thr	Gly	Leu	Asp
				85					90					95	
Ser	Ala	Ser	Tyr	Tyr	Ser	Trp	Asp	Ser	Glu	Phe	Tyr	Arg	Val	Leu	Arg
			100					105					110		
Glu	Arg	Val	Ala	Lys	Lys	Leu	Ala	Glu	Pro	Gly	Leu	Met	Gln	Arg	Ala
		115					120					125			
Arg	Met	Glu	Leu	Trp	Ala	Lys	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Phe	Trp
130						135					140				
Gly	Ser	Leu	Tyr	Ala	Met	Cys	Val	Leu	Asp	Pro	His	Gly	Gly	Ala	Met
145					150					155					160
Val	Ala	Ala	Val	Thr	Leu	Gly	Val	Phe	Ala	Ala	Phe	Val	Gly	Thr	Cys
				165					170						175
Ile	Gln	His	Asp	Gly	Ser	His	Gly	Ala	Phe	Ser	Lys	Ser	Arg	Phe	Met
			180					185						190	
Asn	Lys	Ala	Ala	Gly	Trp	Thr	Leu	Asp	Met	Ile	Gly	Ala	Ser	Ala	Met
		195					200					205			
Thr	Trp	Glu	Met	Gln	His	Val	Leu	Gly	His	His	Pro	Tyr	Thr	Asn	Leu
210						215					220				
Ile	Glu	Met	Glu	Asn	Gly	Leu	Ala	Lys	Val	Lys	Gly	Ala	Asp	Val	Asp
225					230					235					240
Pro	Lys	Lys	Val	Asp	Gln	Glu	Ser	Asp	Pro	Asp	Val	Phe	Ser	Thr	Tyr
				245					250					255	
Pro	Met	Leu	Arg	Leu	His	Pro	Trp	His	Arg	Gln	Arg	Phe	Tyr	His	Lys
			260					265						270	
Phe	Gln	His	Leu	Tyr	Ala	Pro	Phe	Ile	Phe	Gly	Ser	Met	Thr	Ile	Asn
			275				280					285			
Lys	Val	Ile	Ser	Gln	Asp	Val	Gly	Val	Val	Leu	Arg	Lys	Arg	Leu	Phe
290					295						300				
Gln	Ile	Asp	Ala	Asn	Cys	Arg	Tyr	Gly	Ser	Pro	Trp	Tyr	Val	Ala	Arg
305					310					315					320
Phe	Trp	Ile	Met	Lys	Leu	Leu	Thr	Thr	Leu	Tyr	Met	Val	Ala	Leu	Pro
				325					330					335	
Met	Tyr	Met	Gln	Gly	Pro	Ala	Gln	Gly	Leu	Lys	Leu	Phe	Phe	Met	Ala
			340					345						350	
His	Phe	Thr	Cys	Gly	Glu	Val	Leu	Ala	Thr	Met	Phe	Ile	Val	Asn	His
			355				360					365			
Ile	Ile	Glu	Gly	Val	Ser	Tyr	Ala	Ser	Lys	Asp	Ala	Val	Lys	Gly	Val
370						375					380				
Met	Ala	Pro	Pro	Arg	Thr	Val	His	Gly	Val	Thr	Pro	Met	Gln	Val	Thr
385					390					395					400
Gln	Lys	Ala	Leu	Ser	Ala	Ala	Glu	Ser	Ala	Lys	Ser	Asp	Ala	Asp	Lys
				405					410					415	
Thr	Thr	Met	Ile	Pro	Leu	Asn	Asp	Trp	Ala	Ala	Val	Gln	Cys	Gln	Thr
			420					425					430		
Ser	Val	Asn	Trp	Ala	Val	Gly	Ser	Trp	Phe	Trp	Asn	His	Phe	Ser	Gly
			435				440					445			
Gly	Leu	Asn	His	Gln	Ile	Glu	His	His	Cys	Phe	Pro	Gln	Asn	Pro	His
450						455					460				

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Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu
465                               470                               475                               480

Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe
                               485                               490                               495

Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala
                               500                               505                               510

Trp Ser Thr
                               515

<210> SEQ ID NO 43
<211> LENGTH: 960
<212> TYPE: DNA
<213> ORGANISM: Thalassiosira pseudonana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(960)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 43

atg gtg ttg tac aat gtg gcg caa gtg ctg ctc aat ggg tgg acg gtg      48
Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val
1                               5                               10                               15

tat gcg att gtg gat gcg gtg atg aat aga gac cat ccg ttt att gga      96
Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly
                               20                               25                               30

agt aga agt ttg gtt ggg gcg gcg ttg cat agt ggg agc tcg tat gcg     144
Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala
                               35                               40                               45

gtg tgg gtt cat tat tgt gat aag tat ttg gag ttc ttt gat acg tat     192
Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr
50                               55                               60

ttt atg gtg ttg agg ggg aaa atg gac cag atg gta ctt ggt gaa gtt     240
Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val
65                               70                               75                               80

ggg ggc agt gtg tgg tgt ggc gtt gga tat atg gat atg gag aag atg     288
Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met
85                               90                               95

ata cta ctc agc ttt gga gtg cat cgg tct gct cag gga acg ggg aag     336
Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys
100                              105                              110

gct ttc acc aac aac gtt acc aat cca cat ctc acg ctt cca cct cat     384
Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His
115                              120                              125

tct aca aaa aca aaa aaa cag gtc tcc ttc ctc cac atc tac cac cac     432
Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His
130                              135                              140

acg acc ata gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt     480
Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly
145                              150                              155                              160

gga gac att tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc     528
Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu
165                              170                              175

atg tat tcc tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg     576
Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Lys Val Ser Cys Pro Trp
180                              185                              190

aaa cga tac ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg     624
Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val
195                              200                              205

gtt tat acg ggg tgt acg ggt tat act cat tac tat cat acg aag cat     672
Val Tyr Thr Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His

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210	215	220	
gga gcg gat gag aca cag cct agt tta gga acg tat tat ttc tgt tgt			720
Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys			
225	230	235	240
gga gtg cag gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc			768
Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile			
	245	250	255
ttt tat aaa cga tcc tat tcg aag aag aac aag tca gga gga aag gat			816
Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp			
	260	265	270
agc aag aag aat gat gat ggg aat aat gag gat caa tgt cac aag gct			864
Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala			
	275	280	285
atg aag gat ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg			912
Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala			
	290	295	300
aag gat gct gga aag ttg gtg gct acg aga gta agg tgt aag gtg taa			960
Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val			
305	310	315	
 <210> SEQ ID NO 44			
<211> LENGTH: 319			
<212> TYPE: PRT			
<213> ORGANISM: Thalassiosira pseudonana			
 <400> SEQUENCE: 44			
Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val			
1	5	10	15
Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly			
	20	25	30
Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala			
	35	40	45
Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr			
	50	55	60
Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val			
65	70	75	80
Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met			
	85	90	95
Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys			
	100	105	110
Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His			
	115	120	125
Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His			
	130	135	140
Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly			
145	150	155	160
Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu			
	165	170	175
Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp			
	180	185	190
Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val			
	195	200	205
Val Tyr Thr Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His			
	210	215	220
Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys			
225	230	235	240



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Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile  
 245 250 255  
 Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp  
 260 265 270  
 Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala  
 275 280 285  
 Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala  
 290 295 300  
 Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val  
 305 310 315

<210> SEQ ID NO 45  
 <211> LENGTH: 819  
 <212> TYPE: DNA  
 <213> ORGANISM: *Thalassiosira pseudonana*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(819)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 45

atg gac gcc tac aac gct gca atg gat aag atc ggt gcc gcc atc atc	48
Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile	
1 5 10 15	
gat tgg tct gat ccc gat gga aag ttc cgt gcc gat aga gag gac tgg	96
Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp	
20 25 30	
tgg ctc tgc gac ttc cgt agc gcc atc acc atc gcc ctc atc tac atc	144
Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile	
35 40 45	
gcc ttc gtc atc ctc ggt tcc gcc gtc atg caa tcc ctc ccc gca atg	192
Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met	
50 55 60	
gat ccc tac ccc atc aaa ttc ctc tac aac gtc tcc caa atc ttc ctt	240
Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu	
65 70 75 80	
tgt gcc tac atg act gtc gag gcg gga ttt ttg gcc tac cgc aat gga	288
Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly	
85 90 95	
tat acc gtc atg cct tgc aat cat ttc aat gtg aat gat cct ccc gtg	336
Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val	
100 105 110	
gcg aat ctt ctt tgg ttg ttt tat att tcc aag gtg tgg gac ttt tgg	384
Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp	
115 120 125	
gat acc att ttc att gtg ttg ggg aag aag tgg cgt caa tta tct ttc	432
Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe	
130 135 140	
ttg cat gta tac cat cac acc acc atc ttt cta ttc tat tgg ctg aat	480
Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn	
145 150 155 160	
gcc aat gtc ttg tac gat ggt gac atc ttc ctt acc atc ttg ctc aat	528
Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn	
165 170 175	
gga ttc atc cac acg gtg atg tac acg tat tac ttc atc tgt atg cat	576
Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His	
180 185 190	
acc aaa gat tcc aag acg ggc aag agt ctt cct ata tgg tgg aag tcg	624
Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser	
195 200 205	

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agt ttg acg gcg ttt cag ttg ttg caa ttc act atc atg atg agt cag      672
Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln
    210                      215                      220

gct acc tac ctt gtc ttc cac ggg tgt gat aag gtg tcg ctt cgt atc      720
Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile
    225                      230                      235                      240

acg att gtg tac ttt gtg tcc ctt ttg agt ttg ttc ttc ctt ttt gct      768
Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala
    245                      250                      255

cag ttc ttt gtg caa tca tac atg gca ccc aaa aag aag aag agt gct      816
Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala
    260                      265                      270

tag                                                                    819

<210> SEQ ID NO 46
<211> LENGTH: 272
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> SEQUENCE: 46
Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile
 1          5          10          15
Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp
 20          25          30
Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile
 35          40          45
Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met
 50          55          60
Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu
 65          70          75          80
Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly
 85          90          95
Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val
100          105          110
Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp
115          120          125
Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe
130          135          140
Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn
145          150          155          160
Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn
165          170          175
Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His
180          185          190
Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser
195          200          205
Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln
210          215          220
Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile
225          230          235          240
Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala
245          250          255
Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala
260          265          270

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&lt;210&gt; SEQ ID NO 47

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<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Crypthecodinium cohnii
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(936)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 47

atg tct gcc ttc atg act ctc cca cag gct ctc tcc gat gtg acc tcg      48
Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser
1          5          10          15

gcc ttg gtc acg ctg gga aag gat gtc tcc agc cct tca gct ttt caa      96
Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln
          20          25          30

gct gtc act ggc ttc tgc agg gag cag tgg ggg att ccg aca gta ttc     144
Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe
          35          40          45

tgc ctg ggc tac ttg gcc atg gtc tac gcg gcc aga aga ccc ctc ccg     192
Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro
          50          55          60

cag cac ggc tac atg gtt cgg gtg gac cgt tgc ttc gct gct tgg aac     240
Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn
          65          70          75          80

ttg gct ctc tct gtc ttc agc act tgg ggc ttc tac cac atg gct gtc     288
Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val
          85          90          95

ggg ctc tac aac atg aca gag acg agg ggc ttg caa ttc acc atc tgc     336
Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys
          100          105          110

ggt tcg act ggy gag ctc gtg cag aac ctt cag act ggc cca acc gct     384
Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala
          115          120          125

ctg gcg ctc tgc ctc ttc tgc ttc agc aag atc ccc gag ttg atg gac     432
Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp
          130          135          140

acg gtg ttt ctc atc ctg aag gcc aag aag gtc cgc ttc ttg cag tgg     480
Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp
          145          150          155          160

tac cac cat gcc aca gtc atg ctc ttc tgt tgg ctc gcc ctc gcg acg     528
Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr
          165          170          175

gag tac act cct ggc ttg tgg ttt gcg gcg acg aac tac ttc gtg cac     576
Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His
          180          185          190

tcc atc atg tac atg tac ttc ttc ctc atg acc ttc aag tcg gcc gcg     624
Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala
          195          200          205

aag gtg gtg aag ccc atc gcc cct ctc atc aca gtt atc cag att gct     672
Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala
          210          215          220

cag atg gtc tgg ggc ctc atc gtc aac ggc atc gcc atc acc acc ttc     720
Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe
          225          230          235          240

ttc acg act ggt gcc tgc cag atc cag tct gtg act gtg tat tcg gcc     768
Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala
          245          250          255

atc atc atg tac gct tcg tac ttc tac ctg ttc tcc cag ctc ttc ttc     816
Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe
          260          265          270

gag gcc cat ggt gcc gct ggc aag aac aag aag ttg acc cgc gag     864

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Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu  
                   275                                  280                                  285

ctc tct cga aaa atc tcg gag gct ctc ctg aac acc ggt gac gag gtt           912  
 Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val  
                   290                                  295                                  300

tcc aag cac ctg aag gtg aat tga   936  
 Ser Lys His Leu Lys Val Asn  
 305                                  310

<210> SEQ ID NO 48  
 <211> LENGTH: 311  
 <212> TYPE: PRT  
 <213> ORGANISM: Crypthecodinium cohnii

<400> SEQUENCE: 48

Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser  
 1                  5                                  10                                  15

Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln  
                   20                                  25                                  30

Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe  
                   35                                  40                                  45

Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro  
                   50                                  55                                  60

Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn  
 65                                  70                                  75                                  80

Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val  
                   85                                  90                                  95

Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys  
                   100                                  105                                  110

Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala  
                   115                                  120                                  125

Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp  
                   130                                  135                                  140

Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp  
 145                                  150                                  155                                  160

Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr  
                   165                                  170                                  175

Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His  
                   180                                  185                                  190

Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala  
                   195                                  200                                  205

Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala  
                   210                                  215                                  220

Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe  
 225                                  230                                  235                                  240

Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala  
                   245                                  250                                  255

Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe  
                   260                                  265                                  270

Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu  
                   275                                  280                                  285

Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val  
                   290                                  295                                  300

Ser Lys His Leu Lys Val Asn  
 305                                  310

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<210> SEQ ID NO 49
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Crypthecodinium cohnii
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(927)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 49

atg gct tcc tac caa caa gca ttc tcc gaa ttg gct aga gct ttg tcc      48
Met Ala Ser Tyr Gln Gln Ala Phe Ser Glu Leu Ala Arg Ala Leu Ser
1          5          10          15

act ttg aac cac gac ttc tcc agc gtc gag cca ttc aaa gtc gtg acg      96
Thr Leu Asn His Asp Phe Ser Ser Val Glu Pro Phe Lys Val Val Thr
20         25         30

cag ttc tgc agg gac cag tgg gcg atc ccg aca gtc ttt tgc atc ggt      144
Gln Phe Cys Arg Asp Gln Trp Ala Ile Pro Thr Val Phe Cys Ile Gly
35         40         45

tac ttg gca atg gtc tac gcc acg cga aga cct atc gcg aag cac ccc      192
Tyr Leu Ala Met Val Tyr Ala Thr Arg Arg Pro Ile Ala Lys His Pro
50         55         60

tac atg tct ctc gtg gat cgc tgc ttt gcg gcc tgg aac ttg ggc ctc      240
Tyr Met Ser Leu Val Asp Arg Cys Phe Ala Ala Trp Asn Leu Gly Leu
65         70         75         80

tcg ctc ttc agt tgc tgg ggc ttc tac cac atg gca gtg gga ctc tcc      288
Ser Leu Phe Ser Cys Trp Gly Phe Tyr His Met Ala Val Gly Leu Ser
85         90         95

cac acc act tgg aat ttc ggg ctc cag ttc acc atc tgc ggc agc acc      336
His Thr Thr Trp Asn Phe Gly Leu Gln Phe Thr Ile Cys Gly Ser Thr
100        105        110

acg gag ctt gtg aat ggc ttc cag aag ggc ccg gcg gcc ctc gcc ctc      384
Thr Glu Leu Val Asn Gly Phe Gln Lys Gly Pro Ala Ala Leu Ala Leu
115        120        125

atc ctg ttc tgc ttc tcc aag atc ccg gag ttg ggc gac acc gtc ttc      432
Ile Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Gly Asp Thr Val Phe
130        135        140

ttg atc ttg aag gga aag aag gtc cgc ttc ttg cag tgg tac cac cac      480
Leu Ile Leu Lys Gly Lys Lys Val Arg Phe Leu Gln Trp Tyr His His
145        150        155        160

acg acc gtg atg ctc ttc tgt tgg atg gcc ttg gcg act gag tac act      528
Thr Thr Val Met Leu Phe Cys Trp Met Ala Leu Ala Thr Glu Tyr Thr
165        170        175

cct gga ttg tgg ttc gcg gcc acg aac tac ttc gtg cac tcc atc atg      576
Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His Ser Ile Met
180        185        190

tac atg tac ttc ttc ctc atg acc ttc aag acg gcc gcc ggc atc atc      624
Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Thr Ala Ala Gly Ile Ile
195        200        205

aag ccc atc gcg cct ctc atc acc atc atc cag atc tcc cag atg gtc      672
Lys Pro Ile Ala Pro Leu Ile Thr Ile Ile Gln Ile Ser Gln Met Val
210        215        220

tgg ggc ttg gtc gtg aac gcc atc gcc gtc ggc acc ttc ttc acc aca      720
Trp Gly Leu Val Val Asn Ala Ile Ala Val Gly Thr Phe Phe Thr Thr
225        230        235        240

ggc aac tgc cag atc cag gca gtg aca gtc tac tcc gcc atc gtg atg      768
Gly Asn Cys Gln Ile Gln Ala Val Thr Val Tyr Ser Ala Ile Val Met
245        250        255

tac gcc tcc tac ttc tac ctc ttc ggc cag ctc ttc ttc gag gcc cag      816
Tyr Ala Ser Tyr Phe Tyr Leu Phe Gly Gln Leu Phe Phe Glu Ala Gln
260        265        270

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ggt tcg gct gga aag gac aag aag aag ttg gcc cga gag ctg agc cga 864  
 Gly Ser Ala Gly Lys Asp Lys Lys Lys Leu Ala Arg Glu Leu Ser Arg  
 275 280 285

aag gtc tcg cgg gct ctc aca gca acg ggc gaa gag gtg tcg aag cac 912  
 Lys Val Ser Arg Ala Leu Thr Ala Thr Gly Glu Glu Val Ser Lys His  
 290 295 300

atg aag gtg aat tga 927  
 Met Lys Val Asn  
 305

<210> SEQ ID NO 50  
 <211> LENGTH: 308  
 <212> TYPE: PRT  
 <213> ORGANISM: Crypthecodinium cohnii

<400> SEQUENCE: 50

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

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305

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<210> SEQ ID NO 51
<211> LENGTH: 795
<212> TYPE: DNA
<213> ORGANISM: Oncorhynchus mykiss
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(795)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 51
atg gct tca aca tgg caa agc gtt cag tcc atg cgc cag tgg att tta      48
Met Ala Ser Thr Trp Gln Ser Val Gln Ser Met Arg Gln Trp Ile Leu
1          5          10
gag aat gga gat aaa agg aca gac cca tgg cta ctg gtc tac tcc cct      96
Glu Asn Gly Asp Lys Arg Thr Asp Pro Trp Leu Leu Val Tyr Ser Pro
          20          25          30
atg cca gtg gcc att ata ttc ctc ctc tat ctt ggt gtg gtc tgg gct     144
Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala
          35          40          45
ggg ccc aag ctg atg aaa cgc agg gaa cca gtt gat ctc aag gct gta     192
Gly Pro Lys Leu Met Lys Arg Glu Pro Val Asp Leu Lys Ala Val
          50          55          60
ctc att gtc tac aac ttc gcc atg gtc tgc ctg tct gtc tac atg ttc     240
Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe
          65          70          75          80
cat gag ttc ttg gtc acg tcc ttg ctg tct aac tac agt tac ctg tgt     288
His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys
          85          90          95
caa cct gtg gat tac agc act agt cca ctg gcg atg agg atg gcc aaa     336
Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys
          100          105          110
gta tgc tgg tgg ttt ttc ttc tcc aag gtc ata gaa ttg gct gac acg     384
Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr
          115          120          125
gtg ttc ttc atc ctg agg aag aag aac agt cag ctg act ttc ctg cat     432
Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His
          130          135          140
gtc tat cac cat ggc acc atg atc ttc aac tgg tgg gca ggg gtc aag     480
Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys
          145          150          155          160
tat ctg gct gga ggc caa tcg ttc ttc atc ggc ctg ctc aat acc ttt     528
Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe
          165          170          175
gtg cac atc gtg atg tac tct tac tac gga ctg gct gcc ctg ggg cct     576
Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro
          180          185          190
cac acg cag aag tac tta tgg tgg aag cgc tat ctg acc tca ctg cag     624
His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln
          195          200          205
ctg ctc cag ttt gtc ctg ttg acc act cac act ggc tac aac ctc ttc     672
Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe
          210          215          220
act gag tgt gac ttc ccg gac tcc atg aac gct gtg gtg ttt gcc tac     720
Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr
          225          230          235          240
tgt gtc agt ctc att gct ctc ttc agc aac ttc tac tat cag agc tac     768
Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr
          245          250          255
ctc aac agg aag agc aag aag aca taa      795

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Leu Asn Arg Lys Ser Lys Lys Thr  
260

<210> SEQ ID NO 52  
<211> LENGTH: 264  
<212> TYPE: PRT  
<213> ORGANISM: Oncorhynchus mykiss

<400> SEQUENCE: 52

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

<210> SEQ ID NO 53  
<211> LENGTH: 885  
<212> TYPE: DNA  
<213> ORGANISM: Oncorhynchus mykiss  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(885)  
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 53

atg gag act ttt aat tat aaa cta aac atg tac ata gac tca tgg atg 48  
Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met  
1 5 10 15  
ggg ccc aga gat gag cgg gta cag gga tgg ctg ctt ctg gac aac tac 96



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Gly	Pro	Arg	Asp	Glu	Arg	Val	Gln	Gly	Trp	Leu	Leu	Leu	Asp	Asn	Tyr	
			20					25					30			
cct	cca	acc	ttt	gca	cta	aca	gtc	atg	tac	ctg	ctg	atc	gta	tgg	atg	144
Pro	Pro	Thr	Phe	Ala	Leu	Thr	Val	Met	Tyr	Leu	Leu	Ile	Val	Trp	Met	
		35					40					45				
ggg	ccc	aag	tac	atg	aga	cac	aga	cag	ccg	gtg	tct	tgc	cgg	ggt	ctc	192
Gly	Pro	Lys	Tyr	Met	Arg	His	Arg	Gln	Pro	Val	Ser	Cys	Arg	Gly	Leu	
	50					55				60						
ctc	ttg	gtc	tac	aat	ctg	ggc	ctc	acg	atc	ttg	tcc	ttc	tat	atg	ttc	240
Leu	Leu	Val	Tyr	Asn	Leu	Gly	Leu	Thr	Ile	Leu	Ser	Phe	Tyr	Met	Phe	
	65				70					75					80	
tat	gag	atg	gtg	tct	gct	gtg	tgg	cac	ggg	gat	tat	aac	ttc	ttt	tgc	288
Tyr	Glu	Met	Val	Ser	Ala	Val	Trp	His	Gly	Asp	Tyr	Asn	Phe	Phe	Cys	
				85					90					95		
caa	gac	aca	cac	agt	gca	gga	gaa	acc	gat	acc	aag	atc	ata	aat	gtg	336
Gln	Asp	Thr	His	Ser	Ala	Gly	Glu	Thr	Asp	Thr	Lys	Ile	Ile	Asn	Val	
			100					105						110		
ctg	tgg	tgg	tac	tac	ttc	tcc	aag	ctc	ata	gag	ttt	atg	gat	acc	ttc	384
Leu	Trp	Trp	Tyr	Tyr	Phe	Ser	Lys	Leu	Ile	Glu	Phe	Met	Asp	Thr	Phe	
		115					120						125			
ttc	ttc	atc	ctg	cgg	aag	aac	aac	cat	caa	atc	acg	ttt	ctg	cac	atc	432
Phe	Phe	Ile	Leu	Arg	Lys	Asn	Asn	His	Gln	Ile	Thr	Phe	Leu	His	Ile	
		130				135					140					
tac	cac	cat	gct	agc	atg	ctc	aac	atc	tgg	tgg	ttc	gtc	atg	aac	tgg	480
Tyr	His	His	Ala	Ser	Met	Leu	Asn	Ile	Trp	Trp	Phe	Val	Met	Asn	Trp	
					145		150			155					160	
gtg	ccc	tgt	ggt	cac	tcc	tac	ttt	ggt	gcc	tcc	ctg	aac	agc	ttc	atc	528
Val	Pro	Cys	Gly	His	Ser	Tyr	Phe	Gly	Ala	Ser	Leu	Asn	Ser	Phe	Ile	
				165					170					175		
cat	gtc	ctg	atg	tac	tct	tac	tat	ggg	ctc	tct	gct	gtc	ccg	gcc	ttg	576
His	Val	Leu	Met	Tyr	Ser	Tyr	Tyr	Gly	Leu	Ser	Ala	Val	Pro	Ala	Leu	
				180				185					190			
cgg	ccc	tat	cta	tgg	tgg	aag	aaa	tac	atc	aca	caa	gta	cag	ctg	att	624
Arg	Pro	Tyr	Leu	Trp	Trp	Lys	Lys	Tyr	Ile	Thr	Gln	Val	Gln	Leu	Ile	
		195					200						205			
cag	ttc	ttt	ttg	acc	atg	tcc	cag	acg	ata	tgt	gca	gtc	att	tgg	cca	672
Gln	Phe	Phe	Leu	Thr	Met	Ser	Gln	Thr	Ile	Cys	Ala	Val	Ile	Trp	Pro	
		210				215					220					
tgt	gat	ttc	ccc	aga	ggg	tgg	ctg	tat	ttc	cag	ata	ttc	tat	gtc	atc	720
Cys	Asp	Phe	Pro	Arg	Gly	Trp	Leu	Tyr	Phe	Gln	Ile	Phe	Tyr	Val	Ile	
					225		230			235					240	
aca	ctt	att	gcc	ctt	ttc	tca	aac	ttc	tac	att	cag	act	tac	aag	aaa	768
Thr	Leu	Ile	Ala	Leu	Phe	Ser	Asn	Phe	Tyr	Ile	Gln	Thr	Tyr	Lys	Lys	
				245					250					255		
cac	ctt	ggt	tca	caa	aag	aag	gag	tat	cat	cag	aat	ggc	tct	ggt	gct	816
His	Leu	Val	Ser	Gln	Lys	Lys	Glu	Tyr	His	Gln	Asn	Gly	Ser	Val	Ala	
				260				265					270			
tca	ttg	aat	ggc	cat	gtg	aat	ggg	gtg	aca	ccc	acg	gaa	acc	att	aca	864
Ser	Leu	Asn	Gly	His	Val	Asn	Gly	Val	Thr	Pro	Thr	Glu	Thr	Ile	Thr	
			275				280					285				
cac	agg	aaa	gtg	agg	ggg	gac										885
His	Arg	Lys	Val	Arg	Gly	Asp										
		290				295										

&lt;210&gt; SEQ ID NO 54

&lt;211&gt; LENGTH: 295

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Oncorhynchus mykiss

&lt;400&gt; SEQUENCE: 54

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Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met  
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Gly Pro Arg Asp Glu Arg Val Gln Gly Trp Leu Leu Leu Asp Asn Tyr  
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Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met  
 35 40 45

Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu  
 50 55 60

Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe  
 65 70 75 80

Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys  
 85 90 95

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

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe  
 115 120 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile  
 130 135 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp  
 145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile  
 165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu  
 180 185 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile  
 195 200 205

Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro  
 210 215 220

Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile  
 225 230 235 240

Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys  
 245 250 255

His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala  
 260 265 270

Ser Leu Asn Gly His Val Asn Gly Val Thr Pro Thr Glu Thr Ile Thr  
 275 280 285

His Arg Lys Val Arg Gly Asp  
 290 295

<210> SEQ ID NO 55  
 <211> LENGTH: 6753  
 <212> TYPE: DNA  
 <213> ORGANISM: Oncorhynchus mykiss  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (513)..(1397)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 55

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 ctggcccccac aaaccttcaa atgaacgaat caaattaaca accataggat gataatgcga 240  
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cggtttgtat tacttcttat tcaaatgtaa taaaagtatc aacaaaaaat tgttaatata	420
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cgactcacta tagggaatat taagcttaca ta atg gag act ttt aat tat aaa	533
Met Glu Thr Phe Asn Tyr Lys	
1 5	
cta aac atg tac ata gac tca tgg atg ggt ccc aga gat gag cgg gta	581
Leu Asn Met Tyr Ile Asp Ser Trp Met Gly Pro Arg Asp Glu Arg Val	
10 15 20	
cag gga tgg ctg ctt ctg gac aac tac cct cca acc ttt gca cta aca	629
Gln Gly Trp Leu Leu Leu Asp Asn Tyr Pro Pro Thr Phe Ala Leu Thr	
25 30 35	
gtc atg tac ctg ctg atc gta tgg atg ggg ccc aag tac atg aga cac	677
Val Met Tyr Leu Leu Ile Val Trp Met Gly Pro Lys Tyr Met Arg His	
40 45 50 55	
aga cag ccg gtg tct tgc cgg ggt ctc ctc ttg gtc tac aat ctg ggc	725
Arg Gln Pro Val Ser Cys Arg Gly Leu Leu Leu Val Tyr Asn Leu Gly	
60 65 70	
ctc acg atc ttg tcc ttc tat atg ttc tat gag atg gtg tct gct gtg	773
Leu Thr Ile Leu Ser Phe Tyr Met Phe Tyr Glu Met Val Ser Ala Val	
75 80 85	
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Trp His Gly Asp Tyr Asn Phe Phe Cys Gln Asp Thr His Ser Ala Gly	
90 95 100	
gaa acc gat acc aag atc ata aat gtg ctg tgg tgg tac tac ttc tcc	869
Glu Thr Asp Thr Lys Ile Ile Asn Val Leu Trp Trp Tyr Tyr Phe Ser	
105 110 115	
aag ctc ata gag ttt atg gat acc ttc ttc ttc atc ctg cgg aag aac	917
Lys Leu Ile Glu Phe Met Asp Thr Phe Phe Ile Leu Arg Lys Asn	
120 125 130 135	
aac cat caa atc acg ttt ctg cac atc tac cac cat gct agc atg ctc	965
Asn His Gln Ile Thr Phe Leu His Ile Tyr His His Ala Ser Met Leu	
140 145 150	
aac atc tgg tgg ttc gtc atg aac tgg gtg ccc tgt ggt cac tcc tac	1013
Asn Ile Trp Trp Phe Val Met Asn Trp Val Pro Cys Gly His Ser Tyr	
155 160 165	
ttt ggt gcc tcc ctg aac agc ttc atc cat gtc ctg atg tac tct tac	1061
Phe Gly Ala Ser Leu Asn Ser Phe Ile His Val Leu Met Tyr Ser Tyr	
170 175 180	
tat ggg ctc tct gct gtc ccg gcc ttg cgg ccc tat cta tgg tgg aag	1109
Tyr Gly Leu Ser Ala Val Pro Ala Leu Arg Pro Tyr Leu Trp Trp Lys	
185 190 195	
aaa tac atc aca caa gta cag ctg att cag ttc ttt ttg acc atg tcc	1157
Lys Tyr Ile Thr Gln Val Gln Leu Ile Gln Phe Phe Leu Thr Met Ser	
200 205 210 215	
cag acg ata tgt gca gtc att tgg cca tgt gat ttc ccc aga ggg tgg	1205
Gln Thr Ile Cys Ala Val Ile Trp Pro Cys Asp Phe Pro Arg Gly Trp	
220 225 230	
ctg tat ttc cag ata ttc tat gtc atc aca ctt att gcc ctt ttc tca	1253
Leu Tyr Phe Gln Ile Phe Tyr Val Ile Thr Leu Ile Ala Leu Phe Ser	
235 240 245	
aac ttc tac att cag act tac aag aaa cac ctt gtt tca caa aag aag	1301
Asn Phe Tyr Ile Gln Thr Tyr Lys Lys His Leu Val Ser Gln Lys Lys	
250 255 260	
gag tat cat cag aat ggc tct gtt gct tca ttg aat ggc cat gtg aat	1349
Glu Tyr His Gln Asn Gly Ser Val Ala Ser Leu Asn Gly His Val Asn	
265 270 275	
ggg gtg aca ccc acg gaa acc att aca cac agg aaa gtg agg ggg gac	1397

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gtctcgattc	tacgcgtacc	ggcatcacc	accatcacca	ttgagtttaa	accgctgat											1577
cctagagggc	cgcatcatgt	aattagttat	gtcacgctta	cattcacgcc	ctccccccac											1637
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&lt;210&gt; SEQ ID NO 56

&lt;211&gt; LENGTH: 295

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oncorhynchus mykiss*

&lt;400&gt; SEQUENCE: 56

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

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245			250			255										
His	Leu	Val	Ser	Gln	Lys	Lys	Glu	Tyr	His	Gln	Asn	Gly	Ser	Val	Ala	
			260					265						270		
Ser	Leu	Asn	Gly	His	Val	Asn	Gly	Val	Thr	Pro	Thr	Glu	Thr	Ile	Thr	
			275					280						285		
His	Arg	Lys	Val	Arg	Gly	Asp										
			290					295								
<p>&lt;210&gt; SEQ ID NO 57                  &lt;211&gt; LENGTH: 6645                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: <i>Oncorhynchus mykiss</i>                  &lt;220&gt; FEATURE:                  &lt;221&gt; NAME/KEY: CDS                  &lt;222&gt; LOCATION: (513)..(1304)                  &lt;223&gt; OTHER INFORMATION: Delta-5 elongase</p>																
<p>&lt;400&gt; SEQUENCE: 57</p>																
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Val	Gln	Ser	Met	Arg	Gln	Trp	Ile	Leu	Glu	Asn	Gly	Asp	Lys	Arg	Thr	
	10					15						20				
gac	cca	tgg	cta	ctg	gtc	tac	tcc	cct	atg	cca	gtg	gcc	att	ata	ttc	629
Asp	Pro	Trp	Leu	Leu	Val	Tyr	Ser	Pro	Met	Pro	Val	Ala	Ile	Ile	Phe	
	25					30					35					
ctc	ctc	tat	ctt	ggc	gtg	gtc	tgg	gct	ggg	ccc	aag	ctg	atg	aaa	cgc	677
Leu	Leu	Tyr	Leu	Gly	Val	Val	Trp	Ala	Gly	Pro	Lys	Leu	Met	Lys	Arg	
	40				45					50					55	
agg	gaa	cca	ggt	gat	ctc	aag	gct	gta	ctc	att	gtc	tac	aac	ttc	gcc	725
Arg	Glu	Pro	Val	Asp	Leu	Lys	Ala	Val	Leu	Ile	Val	Tyr	Asn	Phe	Ala	
			60					65						70		
atg	gtc	tgc	ctg	tct	gtc	tac	atg	ttc	cat	gag	ttc	ttg	gtc	acg	tcc	773
Met	Val	Cys	Leu	Ser	Val	Tyr	Met	Phe	His	Glu	Phe	Leu	Val	Thr	Ser	
			75					80						85		
ttg	ctg	tct	aac	tac	agt	tac	ctg	tgt	caa	cct	gtg	gat	tac	agc	act	821
Leu	Leu	Ser	Asn	Tyr	Ser	Tyr	Leu	Cys	Gln	Pro	Val	Asp	Tyr	Ser	Thr	
			90					95						100		
agt	cca	ctg	gcg	atg	agg	atg	gcc	aaa	gta	tgc	tgg	tgg	ttt	ttc	ttc	869
Ser	Pro	Leu	Ala	Met	Arg	Met	Ala	Lys	Val	Cys	Trp	Trp	Phe	Phe	Phe	
			105					110						115		
tcc	aag	gtc	ata	gaa	ttg	gct	gac	acg	gtg	ttc	ttc	atc	ctg	agg	aag	917
Ser	Lys	Val	Ile	Glu	Leu	Ala	Asp	Thr	Val	Phe	Phe	Ile	Leu	Arg	Lys	
			120			125								130		135
aag	aac	agt	cag	ctg	act	ttc	ctg	cat	gtc	tat	cac	cat	ggc	acc	atg	965
Lys	Asn	Ser	Gln	Leu	Thr	Phe	Leu	His	Val	Tyr	His	His	Gly	Thr	Met	
				140						145					150	

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atc ttc aac tgg tgg gca ggg gtc aag tat ctg gct gga ggc caa tcg	1013
Ile Phe Asn Trp Trp Ala Gly Val Lys Tyr Leu Ala Gly Gly Gln Ser	
155 160 165	
ttc ttc atc ggc ctg ctc aat acc ttt gtg cac atc gtg atg tac tct	1061
Phe Phe Ile Gly Leu Leu Asn Thr Phe Val His Ile Val Met Tyr Ser	
170 175 180	
tac tac gga ctg gct gcc ctg ggg cct cac acg cag aag tac tta tgg	1109
Tyr Tyr Gly Leu Ala Ala Leu Gly Pro His Thr Gln Lys Tyr Leu Trp	
185 190 195	
tgg aag cgc tat ctg acc tca ctg cag ctg ctc cag ttt gtc ctg ttg	1157
Trp Lys Arg Tyr Leu Thr Ser Leu Gln Leu Leu Gln Phe Val Leu Leu	
200 205 210 215	
acc act cac act ggc tac aac ctc ttc act gag tgt gac ttc ccg gac	1205
Thr Thr His Thr Gly Tyr Asn Leu Phe Thr Glu Cys Asp Phe Pro Asp	
220 225 230	
tcc atg aac gct gtg gtg ttt gcc tac tgt gtc agt ctc att gct ctc	1253
Ser Met Asn Ala Val Val Phe Ala Tyr Cys Val Ser Leu Ile Ala Leu	
235 240 245	
ttc agc aac ttc tac tat cag agc tac ctc aac agg aag agc aag aag	1301
Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr Leu Asn Arg Lys Ser Lys Lys	
250 255 260	
aca taaggatcca ctagtaacgg ccgccagtgt gctggaattc tgcagatate	1354
Thr	
catcacactg gcgcccgctc gagcatgcat cttagagggcc gcatcatgta attagttatg	1414
tcacgcttac attcacgcc tccccccaca tccgctctaa ccgaaaagga aggagttaga	1474
caacctgaag tctaggtccc tattttatctt tttatagtta tgtagtatt aagaacgtta	1534
tttatatttc aaattttctc tttttttctg tacagacgcy tgtagcctg taacattata	1594
ctgaaaacct tgcttgagaa ggttttggga cgctcgaagg ctttaatttg cggccctgca	1654
ttaatgaatc ggccaacgcy cggggagagg cggtttgcgt attgggcgct cttccgcttc	1714
ctcgtcact gactcgtgc gctcggctgt tcggctgcgy cgagcggat cagctcactc	1774
aaaggcggta atacggttat ccacagaatc aggggataac gcaggaaaga acatgtgagc	1834
aaaaggccag caaaagccca ggaaccgtaa aaaggccgcy ttgctggcgt tttccatag	1894
gctccgcccc cctgacgagc atcacaaaaa tcgacgctca agtcagagggt ggcgaaaccc	1954
gacaggacta taaagatacc aggcgtttcc ccctggaagc tccctcgtgc gctctcctgt	2014
tccgaccctg ccgcttaccg gatacctgtc cgcctttctc ccttcgggaa gcgtggcgct	2074
ttctcatagc tcacgctgta ggtatctcag ttcggtgtag gtcttcgct ccaagctggg	2134
ctgtgtgcac gaaccccccg ttcagcccca ccgctgcgcc ttatccgta actatcgtct	2194
tgagtcacaac ccggaagac acgacttatc gccactgcca gcagccactg gtaacaggat	2254
tagcagagcy aggtatgtag gcggtgctac agagttcttg aagtgggtggc ctaactacgg	2314
ctacactaga aggacagtat ttggtatctg cgctctgctg aagccagtta ccttcggaaa	2374
aagagttggg agctcttgat ccggcaaaaa aaccaccgct ggtagcggty gttttttgt	2434
ttgcaagcag cagattacgc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc	2494
tacggggtct gacgctcagt ggaacgaaaa ctcacgttaa gggatttttg tcatgagatt	2554
atcaaaaagg atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta	2614
aagtatatat gagtaaaactt ggtctgacag ttaccaatgc ttaatcagty aggcacctat	2674
ctcagcgatc tgtctatttc gttcatocat agttgctgca ctccccgctc tgtagataac	2734
tacgatacgg gacgcttac catctggccc cagtgctgca atgataccgc gagaccacg	2794



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ctcaccggct ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag	2854
tggtcctgca actttatccg cctccattca gtctattaat tggtagccggg aagctagagt	2914
aagtagttcg ccagttaata gtttgcgcaa cgttggtggc attgctacag gcacgtgggt	2974
gtcactctcg tcgtttgga tggttcatt cagctccggg tcccacgat caaggcgagt	3034
tacatgatcc cccatgttgt gcaaaaaagc ggtagctcc tcgggcctc cgatcgttgt	3094
cagaagtaag ttggccgag tgttatcact catggttatg gcagcactgc ataattctct	3154
tactgtcatg ccatccgtaa gatgcttttc tgtgactggg gagtactcaa ccaagtcatt	3214
ctgagaatag tgtatgccc gaccgagttg ctcttgccc gcgtcaatac gggataatag	3274
tgtatcacat agcagaactt taaaagtgt catcattgga aaacgctctt cggggcgaaa	3334
actctcaagg atcttacgc tgttgagatc cagttcgatg taaccactc gtgcaccaa	3394
ctgatcttca gcactcttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca	3454
aaatgccgca aaaaaggaa taaggcgac acggaatgt tgaatactca tactcttct	3514
ttttcaatgg gtaataactg atataattaa attgaagctc taatttgga gtttagtata	3574
catgcattta cttataatac agtttttag ttttgctggc cgcactctct caaatatgct	3634
tcccagctg cttttctgta acgttcaccc tctaccttag catcccttc ctttgcaaat	3694
agtcctctc caacaataat aatgtcagat cctgtagaga ccacatcctc cacggttcta	3754
tactgttgac ccaatgcgtc tccttctgca tctaaccaca caccgggtgt cataatcaac	3814
caatcgtaac cttcatctct tccaccatg tctctttgag caataaagc gataacaaaa	3874
tctttgtgc tcttcgcaat gtcaacagta cccttagtat attctccagt agataggag	3934
cccttgcatg acaattctgc taacatcaaa aggctctag gttcctttgt tacttctct	3994
gccgctgct tcaaacgct aacaatacct gggcccaca caccgtgtgc attcgtaatg	4054
tctgcccatt ctgctattct gtatacacc gcagagtact gcaatttgac tgtattacca	4114
atgtcagcaa atttctgtc ttcgaagagt aaaaaattgt acttgccgga taatgccttt	4174
agcggcttaa ctgtgcctc catggaaaa tcagtcaaga tatccacatg tgtttttagt	4234
aaacaaattt tgggacctaa tgcttcaact aactccagta attccttggg ggtacgaaca	4294
tccaatgaag cacacaagtt tgtttgcttt tcgtgcatga tattaatag cttggcagca	4354
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cgtttcctgc aggtttttgt tctgtgcagt tgggtaaga atactgggca atttcatggt	4474
tcttcaacac tacatagcgt tatatatacc aatctaagtc tggctcctt ccttcgttct	4534
tccttctggt cggagattac cgaatcaaaa aaatttcaaa gaaaccgaaa tcaaaaaaaaa	4594
gaataaaaaa aaaatgatga attgaattga aaagctagct tctcgatgat aagctgtcaa	4654
agatgagaat taattccacg gactatagac tatactagat actccgtcta ctgtacgata	4714
cacttccgct caggtccttg tctttaaacy aggccttacc actcttttgt tactctattg	4774
atccagctca gcaaaggcag tgtgatctaa gattctatct tcgcatgta gtaaaactag	4834
ctagaccgag aaagagacta gaaatgcaaa aggcacttct caaatggctg ccatcattat	4894
tatccgatgt gacgctgcag cttctcaatg atattogaat acgctttgag gagatacagc	4954
ctaatactcg acaaaactgt ttacagattt acgatcgtac ttgtaacca tcattgaatt	5014
ttgaacatcc gaacctggga gttttccctg aaacagatag tatatttgaa cctgtataat	5074
aatatatagt ctagccttt acggaagaca atgtatgat ttcggttctt ggagaaacta	5134
ttgcatctat tgcataagga atcttgcaag tcgcatcccc gggtcatttt ctgogtttcc	5194

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atcttgcaact tcaatagcat atctttgtta acgaagcatc tgtgcttcat tttgtagaac 5254
aaaaatgcaa cgcgagagcg ctaatttttc aaacaaagaa tctgagctgc atttttacag 5314
aacagaaatg caacgcgaaa gcgctatttt accaacgaag aatctgtgct tcatttttgt 5374
aaaacaaaaa tgcaacgcga cgagagcgct aatttttcaa acaagaatc tgagctgcat 5434
ttttacagaa cagaaatgca acgcgagagc gctattttac caacaaagaa tctatacttc 5494
ttttttgttc tacaaaaatg catcccgaga gcgctatttt tctaacaaag catcttagat 5554
tacttttttt ctcccttgtg cgctctataa tgcagctctt tgataacttt ttgcactgta 5614
ggtccggttaa ggttagaaga aggctacttt ggtgtctatt ttctcttcca taaaaaagc 5674
ctgactccac ttcccgcggt tactgattac tagcgaagct gcgggtgcat tttttcaaga 5734
taaaggcatc cccgattata ttctataccg atgtggattg cgcatacttt gtgaacagaa 5794
agtgatagcg ttgatgattc ttcattggtc agaaaattat gaacggtttc ttctattttg 5854
tctctatata ctacgtatag gaaatgttta cattttcgta ttgttttcga ttcactctat 5914
gaatagttct tactacaatt tttttgtcta aagagtaata ctagagataa acataaaaaa 5974
tgtagaggtc gagtttagat gcaagttaa ggagcgaag gtggatgggt aggttatata 6034
gggatatagc acagagatat atagcaaga gatacttttg agcaatgttt gtggaagcgg 6094
tattcgcaat gggaaactcc accccggttg ataatcagaa aagcccaaa aacaggaaga 6154
ttgtataagc aaatatttaa attgtaaagc ttaatatttt gttaaaattc gcgttaaatt 6214
ttgtttaa atcagctcattt ttttaacgaat agcccgaat cggcaaaatc ccttataaat 6274
caaaagaata gaccgagata gggttgagtg ttgttcagtt tccaacaag agtccactat 6334
taaagaactg ggactccaac gtcaaagggc gaaaagggt ctatcagggc gatggcccac 6394
tacgtgaacc atcaccctaa tcaagttttt tggggtcgag gtgccgtaaa gcagtaaatc 6454
ggaagggtaa acggatgccc ccatttagag cttgacgggg aaagccggcg aacgtggcga 6514
gaaaggaagg gaagaaagcg aaaggagcgg gggctagggc ggtgggaagt gtaggggtca 6574
cgctgggcgt aaccaccaca cccgccgcgc ttaatggggc gctacagggc gcgtggggat 6634
gatccactag t 6645

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&lt;210&gt; SEQ ID NO 58

&lt;211&gt; LENGTH: 264

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Oncorhynchus mykiss*

&lt;400&gt; SEQUENCE: 58

```

Met Ala Ser Thr Trp Gln Ser Val Gln Ser Met Arg Gln Trp Ile Leu
1           5           10           15
Glu Asn Gly Asp Lys Arg Thr Asp Pro Trp Leu Leu Val Tyr Ser Pro
20          25          30
Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala
35          40          45
Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val
50          55          60
Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe
65          70          75          80
His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys
85          90          95
Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys
100         105         110

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Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr  
 115 120 125

Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His  
 130 135 140

Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys  
 145 150 155 160

Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe  
 165 170 175

Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro  
 180 185 190

His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln  
 195 200 205

Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe  
 210 215 220

Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr  
 225 230 235 240

Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr  
 245 250 255

Leu Asn Arg Lys Ser Lys Lys Thr  
 260

<210> SEQ ID NO 59  
 <211> LENGTH: 1077  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1077)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 59

atg tgc tca tca ccg ccg tca caa tcc aaa aca aca tcc ctc cta gca 48  
 Met Cys Ser Ser Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala  
 1 5 10 15

egg tac acc acc gcc gcc ctc ctc ctc ctc acc ctc aca aca tgg tgc 96  
 Arg Tyr Thr Thr Ala Ala Leu Leu Leu Thr Leu Thr Thr Trp Cys  
 20 25 30

cac ttc gcc ttc cca gcc gcc acc gcc aca ccc ggc ctc acc gcc gaa 144  
 His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu  
 35 40 45

atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 192  
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
 50 55 60

agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag 240  
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 65 70 75 80

tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg 288  
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 85 90 95

gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg 336  
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 100 105 110

gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 384  
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 115 120 125

gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt 432  
 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 130 135 140

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gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg	480
Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly	
145 150 155 160	
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata	528
Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile	
165 170 175	
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att	576
Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile	
180 185 190	
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc	624
Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser	
195 200 205	
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac	672
Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr	
210 215 220	
ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg	720
Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr	
225 230 235 240	
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat	768
Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp	
245 250 255	
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag	816
Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln	
260 265 270	
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa	864
Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys	
275 280 285	
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag	912
Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys	
290 295 300	
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat	960
Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp	
305 310 315 320	
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct	1008
Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala	
325 330 335	
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act	1056
Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr	
340 345 350	
cgt gtt act ggt gcc atg tag	1077
Arg Val Thr Gly Ala Met	
355	

&lt;210&gt; SEQ ID NO 60

&lt;211&gt; LENGTH: 358

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 60

Met Cys Ser Ser Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala	
1 5 10 15	
Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys	
20 25 30	
His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu	
35 40 45	
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu	
50 55 60	
Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys	
65 70 75 80	

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Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 85 90 95

Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 100 105 110

Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 115 120 125

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 130 135 140

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 145 150 155 160

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 165 170 175

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 180 185 190

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 195 200 205

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 210 215 220

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 225 230 235 240

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 245 250 255

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 260 265 270

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 275 280 285

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 290 295 300

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 305 310 315 320

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
 325 330 335

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 340 345 350

Arg Val Thr Gly Ala Met  
 355

<210> SEQ ID NO 61  
 <211> LENGTH: 933  
 <212> TYPE: DNA  
 <213> ORGANISM: *Thalassiosira pseudonana*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(933)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 61

atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg	48
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu	
1 5 10 15	
agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag	96
Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys	
20 25 30	
tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg	144
Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val	
35 40 45	
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg	192

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Ala 50	Gln	Val	Leu	Leu	Asn 55	Gly	Trp	Thr	Val	Tyr 60	Ala	Ile	Val	Asp	Ala		
gtg	atg	aat	aga	gac	cat	ccg	ttt	att	gga	agt	aga	agt	ttg	gtt	ggg		240
Val	Met	Asn	Arg	Asp	His	Pro	Phe	Ile	Gly	Ser	Arg	Ser	Leu	Val	Gly		
65				70					75					80			
gcg	gcg	ttg	cat	agt	ggg	agc	tcg	tat	gcg	gtg	tgg	gtt	cat	tat	tgt		288
Ala	Ala	Leu	His	Ser	Gly	Ser	Ser	Tyr	Ala	Val	Trp	Val	His	Tyr	Cys		
				85				90					95				
gat	aag	tat	ttg	gag	ttc	ttt	gat	acg	tat	ttt	atg	gtg	ttg	agg	ggg		336
Asp	Lys	Tyr	Leu	Glu	Phe	Phe	Asp	Thr	Tyr	Phe	Met	Val	Leu	Arg	Gly		
			100					105					110				
aaa	atg	gac	cag	gtc	tcc	ttc	ctc	cac	atc	tac	cac	cac	acg	acc	ata		384
Lys	Met	Asp	Gln	Val	Ser	Phe	Leu	His	Ile	Tyr	His	His	Thr	Thr	Ile		
			115					120					125				
gcg	tgg	gca	tgg	tgg	atc	gcc	ctc	cgc	ttc	tcc	ccc	ggg	gga	gac	att		432
Ala	Trp	Ala	Trp	Trp	Ile	Ala	Leu	Arg	Phe	Ser	Pro	Gly	Gly	Asp	Ile		
	130					135					140						
tac	ttc	ggg	gca	ctc	ctc	aac	tcc	atc	atc	cac	gtc	ctc	atg	tat	tcc		480
Tyr	Phe	Gly	Ala	Leu	Leu	Asn	Ser	Ile	Ile	His	Val	Leu	Met	Tyr	Ser		
	145					150				155					160		
tac	tac	gcc	ctt	gcc	cta	ctc	aag	gtc	agt	tgt	cca	tgg	aaa	cga	tac		528
Tyr	Tyr	Ala	Leu	Ala	Leu	Leu	Lys	Val	Ser	Cys	Pro	Trp	Lys	Arg	Tyr		
				165					170					175			
ctg	act	caa	gct	caa	tta	ttg	caa	ttc	aca	agt	gtg	gtg	ggt	tat	acg		576
Leu	Thr	Gln	Ala	Gln	Leu	Leu	Gln	Phe	Thr	Ser	Val	Val	Val	Tyr	Thr		
				180				185						190			
ggg	tgt	acg	ggt	tat	act	cat	tac	tat	cat	acg	aag	cat	gga	gcg	gat		624
Gly	Cys	Thr	Gly	Tyr	Thr	His	Tyr	Tyr	His	Thr	Lys	His	Gly	Ala	Asp		
		195						200					205				
gag	aca	cag	cct	agt	tta	gga	acg	tat	tat	ttc	tgt	tgt	gga	gtg	cag		672
Glu	Thr	Gln	Pro	Ser	Leu	Gly	Thr	Tyr	Tyr	Phe	Cys	Cys	Gly	Val	Gln		
		210				215							220				
gtg	ttt	gag	atg	ggt	agt	ttg	ttt	gta	ctc	ttt	tcc	atc	ttt	tat	aaa		720
Val	Phe	Glu	Met	Val	Ser	Leu	Phe	Val	Leu	Phe	Ser	Ile	Phe	Tyr	Lys		
				225		230					235				240		
cga	tcc	tat	tcg	aag	aag	aac	aag	tca	gga	gga	aag	gat	agc	aag	aag		768
Arg	Ser	Tyr	Ser	Lys	Lys	Asn	Lys	Ser	Gly	Gly	Lys	Asp	Ser	Lys	Lys		
				245					250					255			
aat	gat	gat	ggg	aat	aat	gag	gat	caa	tgt	cac	aag	gct	atg	aag	gat		816
Asn	Asp	Asp	Gly	Asn	Asn	Glu	Asp	Gln	Cys	His	Lys	Ala	Met	Lys	Asp		
			260					265					270				
ata	tcg	gag	ggt	gcg	aag	gag	ggt	gtg	ggg	cat	gca	gcg	aag	gat	gct		864
Ile	Ser	Glu	Gly	Ala	Lys	Glu	Val	Val	Gly	His	Ala	Ala	Lys	Asp	Ala		
			275					280					285				
gga	aag	ttg	gtg	gct	acg	gcg	agt	aag	gct	gta	aag	agg	aag	gga	act		912
Gly	Lys	Leu	Val	Ala	Thr	Ala	Ser	Lys	Ala	Val	Lys	Arg	Lys	Gly	Thr		
		290				295					300						
cgt	ggt	act	ggt	gcc	atg	tag											933
Arg	Val	Thr	Gly	Ala	Met												
				305		310											

&lt;210&gt; SEQ ID NO 62

&lt;211&gt; LENGTH: 310

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 62

Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
1 5 10 15

Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys

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20					25					30					
Tyr	Asp	Met	Lys	Ser	Leu	Leu	Thr	Glu	Ser	Met	Val	Leu	Tyr	Asn	Val
	35						40					45			
Ala	Gln	Val	Leu	Leu	Asn	Gly	Trp	Thr	Val	Tyr	Ala	Ile	Val	Asp	Ala
	50					55					60				
Val	Met	Asn	Arg	Asp	His	Pro	Phe	Ile	Gly	Ser	Arg	Ser	Leu	Val	Gly
	65					70					75				80
Ala	Ala	Leu	His	Ser	Gly	Ser	Ser	Tyr	Ala	Val	Trp	Val	His	Tyr	Cys
				85					90					95	
Asp	Lys	Tyr	Leu	Glu	Phe	Phe	Asp	Thr	Tyr	Phe	Met	Val	Leu	Arg	Gly
			100					105					110		
Lys	Met	Asp	Gln	Val	Ser	Phe	Leu	His	Ile	Tyr	His	His	Thr	Thr	Ile
		115					120					125			
Ala	Trp	Ala	Trp	Trp	Ile	Ala	Leu	Arg	Phe	Ser	Pro	Gly	Gly	Asp	Ile
	130					135					140				
Tyr	Phe	Gly	Ala	Leu	Leu	Asn	Ser	Ile	Ile	His	Val	Leu	Met	Tyr	Ser
	145					150					155				160
Tyr	Tyr	Ala	Leu	Ala	Leu	Leu	Lys	Val	Ser	Cys	Pro	Trp	Lys	Arg	Tyr
			165						170					175	
Leu	Thr	Gln	Ala	Gln	Leu	Leu	Gln	Phe	Thr	Ser	Val	Val	Val	Tyr	Thr
		180						185						190	
Gly	Cys	Thr	Gly	Tyr	Thr	His	Tyr	Tyr	His	Thr	Lys	His	Gly	Ala	Asp
		195					200					205			
Glu	Thr	Gln	Pro	Ser	Leu	Gly	Thr	Tyr	Tyr	Phe	Cys	Cys	Gly	Val	Gln
	210					215					220				
Val	Phe	Glu	Met	Val	Ser	Leu	Phe	Val	Leu	Phe	Ser	Ile	Phe	Tyr	Lys
	225					230					235				240
Arg	Ser	Tyr	Ser	Lys	Lys	Asn	Lys	Ser	Gly	Gly	Lys	Asp	Ser	Lys	Lys
				245					250					255	
Asn	Asp	Asp	Gly	Asn	Asn	Glu	Asp	Gln	Cys	His	Lys	Ala	Met	Lys	Asp
			260					265						270	
Ile	Ser	Glu	Gly	Ala	Lys	Glu	Val	Val	Gly	His	Ala	Ala	Lys	Asp	Ala
		275					280					285			
Gly	Lys	Leu	Val	Ala	Thr	Ala	Ser	Lys	Ala	Val	Lys	Arg	Lys	Gly	Thr
	290					295					300				
Arg	Val	Thr	Gly	Ala	Met										
	305					310									

<210> SEQ ID NO 63  
 <211> LENGTH: 933  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(933)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 63

atg	cac	tcc	tac	aaa	gtc	cca	ctc	ggt	ctc	acc	gta	ttc	tac	ctg	ctg	48
Met	His	Ser	Tyr	Lys	Val	Pro	Leu	Gly	Leu	Thr	Val	Phe	Tyr	Leu	Leu	
1				5				10						15		
agt	cta	ccg	tca	cta	aag	tac	ggt	acg	gac	aac	tac	ctt	gcc	aaa	aag	96
Ser	Leu	Pro	Ser	Leu	Lys	Tyr	Val	Thr	Asp	Asn	Tyr	Leu	Ala	Lys	Lys	
		20					25					30				
tat	gat	atg	aag	tca	ctc	cta	acg	gaa	tca	atg	gtg	ttg	tac	aat	gtg	144
Tyr	Asp	Met	Lys	Ser	Leu	Leu	Thr	Glu	Ser	Met	Val	Leu	Tyr	Asn	Val	
		35					40					45				

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gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala 50 55 60	192
gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly 65 70 75 80	240
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys 85 90 95	288
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly 100 105 110	336
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile 115 120 125	384
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile 130 135 140	432
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser 145 150 155 160	480
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr 165 170 175	528
ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr 180 185 190	576
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp 195 200 205	624
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln 210 215 220	672
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys 225 230 235 240	720
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys 245 250 255	768
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp 260 265 270	816
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala 275 280 285	864
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr 290 295 300	912
cggt gtt act ggt gcc atg tag Arg Val Thr Gly Ala Met 305 310	933

&lt;210&gt; SEQ ID NO 64

&lt;211&gt; LENGTH: 310

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 64

Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu  
1 5 10 15



-continued

Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys  
 20 25 30

Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val  
 35 40 45

Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala  
 50 55 60

Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly  
 65 70 75 80

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys  
 85 90 95

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly  
 100 105 110

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile  
 115 120 125

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile  
 130 135 140

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser  
 145 150 155 160

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr  
 165 170 175

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr  
 180 185 190

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp  
 195 200 205

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln  
 210 215 220

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys  
 225 230 235 240

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys  
 245 250 255

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp  
 260 265 270

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala  
 275 280 285

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr  
 290 295 300

Arg Val Thr Gly Ala Met  
 305 310

<210> SEQ ID NO 65  
 <211> LENGTH: 825  
 <212> TYPE: DNA  
 <213> ORGANISM: Thraustochytrium aureum  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(825)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 65

atg acg agc aac atg agc gcg tgg ggc gtc gcc gtc gac cag acg cag 48  
 Met Thr Ser Asn Met Ser Ala Trp Gly Val Ala Val Asp Gln Thr Gln  
 1 5 10 15

cag gtc gtc gac cag atc atg ggc ggc gcc gag ccg tac aag ctg aca 96  
 Gln Val Val Asp Gln Ile Met Gly Gly Ala Glu Pro Tyr Lys Leu Thr  
 20 25 30

gaa ggg cgc atg acg aac gtc gag acg atg ctg gcg atc gag tgc ggc 144

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Glu	Gly	Arg	Met	Thr	Asn	Val	Glu	Thr	Met	Leu	Ala	Ile	Glu	Cys	Gly	
		35					40						45			
tac	gcc	gcc	atg	ctg	ctg	ttc	ctg	acc	ccg	atc	atg	aag	cag	gcc	gag	192
Tyr	Ala	Ala	Met	Leu	Leu	Phe	Leu	Thr	Pro	Ile	Met	Lys	Gln	Ala	Glu	
	50					55				60						
aag	ccc	ttc	gag	ctc	aag	tcc	ttc	aag	ctc	gcc	cac	aac	ctg	ttc	ctg	240
Lys	Pro	Phe	Glu	Leu	Lys	Ser	Phe	Lys	Leu	Ala	His	Asn	Leu	Phe	Leu	
65					70					75					80	
ttc	gtc	ctg	tcc	gcc	tac	atg	tgc	ctc	gag	acc	gtc	cgc	cag	gcc	tac	288
Phe	Val	Leu	Ser	Ala	Tyr	Met	Cys	Leu	Glu	Thr	Val	Arg	Gln	Ala	Tyr	
				85					90					95		
ctt	gcg	ggc	tac	tcg	gtg	ttc	ggc	aac	gac	atg	gag	aag	ggc	agc	gag	336
Leu	Ala	Gly	Tyr	Ser	Val	Phe	Gly	Asn	Asp	Met	Glu	Lys	Gly	Ser	Glu	
			100					105					110			
ccg	cac	gcg	cac	ggc	atg	gcc	caa	atc	gtg	tgg	atc	ttt	tac	gtg	tcc	384
Pro	His	Ala	His	Gly	Met	Ala	Gln	Ile	Val	Trp	Ile	Phe	Tyr	Val	Ser	
		115				120						125				
aag	gcg	tac	gag	ttc	gtg	gac	acg	ctg	atc	atg	atc	ctg	tgc	aaa	aag	432
Lys	Ala	Tyr	Glu	Phe	Val	Asp	Thr	Leu	Ile	Met	Ile	Leu	Cys	Lys	Lys	
	130					135					140					
ttc	aac	cag	gtc	tcc	gtc	ctg	cac	gtg	tac	cac	cac	gcc	acc	atc	ttt	480
Phe	Asn	Gln	Val	Ser	Val	Leu	His	Val	Tyr	His	His	Ala	Thr	Ile	Phe	
	145				150					155					160	
gct	atc	tgg	ttt	atg	atc	gcc	aag	tac	gcc	ccg	ggc	ggc	gac	gca	tac	528
Ala	Ile	Trp	Phe	Met	Ile	Ala	Lys	Tyr	Ala	Pro	Gly	Gly	Asp	Ala	Tyr	
			165						170					175		
ttt	agc	gtc	atc	ctg	aac	tcg	ttc	gtg	cac	acc	gtc	atg	tac	gcg	tac	576
Phe	Ser	Val	Ile	Leu	Asn	Ser	Phe	Val	His	Thr	Val	Met	Tyr	Ala	Tyr	
		180						185					190			
tac	ttc	ttc	tcg	tcg	cag	ggc	ttc	ggg	ttc	gtc	aag	ccg	atc	aag	ccg	624
Tyr	Phe	Phe	Ser	Ser	Gln	Gly	Phe	Gly	Phe	Val	Lys	Pro	Ile	Lys	Pro	
		195				200						205				
tac	atc	acc	tcg	ctg	cag	atg	acg	cag	ttc	atg	gcg	atg	ctc	gtg	cag	672
Tyr	Ile	Thr	Ser	Leu	Gln	Met	Thr	Gln	Phe	Met	Ala	Met	Leu	Val	Gln	
	210					215					220					
tcg	ctg	tac	gac	tac	ctt	tac	ccg	tgc	gac	tac	ccg	cag	ggg	ctc	gtc	720
Ser	Leu	Tyr	Asp	Tyr	Leu	Tyr	Pro	Cys	Asp	Tyr	Pro	Gln	Gly	Leu	Val	
	225				230					235				240		
aag	ctc	ctc	ggc	gtg	tac	atg	ctc	acc	ctg	ctt	gcg	ctc	ttc	ggc	aac	768
Lys	Leu	Leu	Gly	Val	Tyr	Met	Leu	Thr	Leu	Leu	Ala	Leu	Phe	Gly	Asn	
			245						250					255		
ttt	ttc	gtg	cag	agc	tac	ctc	aag	aag	tcg	aac	aag	ccc	aag	gcc	aag	816
Phe	Phe	Val	Gln	Ser	Tyr	Leu	Lys	Lys	Ser	Asn	Lys	Pro	Lys	Ala	Lys	
		260						265					270			
tcg	gcc	taa														825
Ser	Ala															

&lt;210&gt; SEQ ID NO 66

&lt;211&gt; LENGTH: 274

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Thraustochytrium aureum

&lt;400&gt; SEQUENCE: 66

Met	Thr	Ser	Asn	Met	Ser	Ala	Trp	Gly	Val	Ala	Val	Asp	Gln	Thr	Gln	
1				5					10					15		

Gln	Val	Val	Asp	Gln	Ile	Met	Gly	Gly	Ala	Glu	Pro	Tyr	Lys	Leu	Thr	
			20					25					30			

Glu	Gly	Arg	Met	Thr	Asn	Val	Glu	Thr	Met	Leu	Ala	Ile	Glu	Cys	Gly	
		35					40					45				

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Tyr Ala Ala Met Leu Leu Phe Leu Thr Pro Ile Met Lys Gln Ala Glu  
 50 55 60

Lys Pro Phe Glu Leu Lys Ser Phe Lys Leu Ala His Asn Leu Phe Leu  
 65 70 75 80

Phe Val Leu Ser Ala Tyr Met Cys Leu Glu Thr Val Arg Gln Ala Tyr  
 85 90 95

Leu Ala Gly Tyr Ser Val Phe Gly Asn Asp Met Glu Lys Gly Ser Glu  
 100 105 110

Pro His Ala His Gly Met Ala Gln Ile Val Trp Ile Phe Tyr Val Ser  
 115 120 125

Lys Ala Tyr Glu Phe Val Asp Thr Leu Ile Met Ile Leu Cys Lys Lys  
 130 135 140

Phe Asn Gln Val Ser Val Leu His Val Tyr His His Ala Thr Ile Phe  
 145 150 155 160

Ala Ile Trp Phe Met Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr  
 165 170 175

Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr  
 180 185 190

Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro  
 195 200 205

Tyr Ile Thr Ser Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln  
 210 215 220

Ser Leu Tyr Asp Tyr Leu Tyr Pro Cys Asp Tyr Pro Gln Gly Leu Val  
 225 230 235 240

Lys Leu Leu Gly Val Tyr Met Leu Thr Leu Leu Ala Leu Phe Gly Asn  
 245 250 255

Phe Phe Val Gln Ser Tyr Leu Lys Lys Ser Asn Lys Pro Lys Ala Lys  
 260 265 270

Ser Ala

<210> SEQ ID NO 67  
 <211> LENGTH: 903  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(903)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 67

atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac	48
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr	
1 5 10 15	
gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc	96
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly	
20 25 30	
atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg	144
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg	
35 40 45	
ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga	192
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly	
50 55 60	
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg	240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met	
65 70 75 80	
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg	288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly	
85 90 95	

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atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca      336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
      100                      105                      110

acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg      384
Thr Met Ala Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
      115                      120                      125

tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc      432
Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe
      130                      135                      140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat      480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
      145                      150                      155                      160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg      528
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
      165                      170                      175

gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg      576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
      180                      185                      190

ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc      624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
      195                      200                      205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa      672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
      210                      215                      220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac      720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
      225                      230                      235                      240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg      768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
      245                      250                      255

ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg      816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
      260                      265                      270

cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg      864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
      275                      280                      285

ccc agc gtg cga cgc acg cga tct cga aaa att gac taa      903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
      290                      295                      300

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&lt;210&gt; SEQ ID NO 68

&lt;211&gt; LENGTH: 300

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 68

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Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
1      5      10      15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
      20      25      30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
      35      40      45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
      50      55      60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
      65      70      75      80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
      85      90      95

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Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
 100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
 115 120 125

Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe  
 130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
 145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
 165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
 180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
 195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
 210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
 225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met  
 245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser  
 260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala  
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp  
 290 295 300

<210> SEQ ID NO 69  
 <211> LENGTH: 879  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(879)  
 <223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 69

atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48  
 Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys  
 1 5 10 15

tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96  
 Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe  
 20 25 30

cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144  
 Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45

att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc 192  
 Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60

aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa 240  
 Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80

att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg 288  
 Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
 85 90 95

ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa 336  
 Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
 100 105 110

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gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg	384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr	
115 120 125	
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata	432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile	
130 135 140	
tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg	480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg	
145 150 155 160	
caa gta agt ttc cta cac att tat cac cac agc acg att tcc ttt att	528
Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile	
165 170 175	
tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc	576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser	
180 185 190	
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta	624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu	
195 200 205	
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt	672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu	
210 215 220	
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc	720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe	
225 230 235 240	
aac gta ctt caa cgg ttg tac tgc gct tcg ttc tct acg tat ccc aag	768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys	
245 250 255	
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg	816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu	
260 265 270	
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag	864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln	
275 280 285	
aaa aaa cag cag tga	879
Lys Lys Gln Gln	
290	

&lt;210&gt; SEQ ID NO 70

&lt;211&gt; LENGTH: 292

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 70

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys	
1 5 10 15	
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe	
20 25 30	
Gln Trp Asp Ile Gly Pro Val Ser Ser Thr Ala His Leu Pro Ala	
35 40 45	
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val	
50 55 60	
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys	
65 70 75 80	
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala	
85 90 95	
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln	
100 105 110	
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr	
115 120 125	

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Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
 130 135 140  
 Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
 145 150 155 160  
 Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile  
 165 170 175  
 Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser  
 180 185 190  
 Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu  
 195 200 205  
 Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu  
 210 215 220  
 Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe  
 225 230 235 240  
 Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys  
 245 250 255  
 Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu  
 260 265 270  
 Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln  
 275 280 285  
 Lys Lys Gln Gln  
 290

<210> SEQ ID NO 71  
 <211> LENGTH: 1362  
 <212> TYPE: DNA  
 <213> ORGANISM: Primula farinosa  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1362)  
 <223> OTHER INFORMATION: Delta-6 desaturase

<400> SEQUENCE: 71

atg gct aac aaa tct cca cca aac ccc aaa aca ggt tac ata acc agc	48
Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser	
1 5 10 15	
tca gac ctg aaa tcc cac aac aag gca ggt gac cta tgg ata tca atc	96
Ser Asp Leu Lys Ser His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile	
20 25 30	
cac ggc caa gtc tac gac gtg tcc tct tgg gcc gcc ctt cat ccg ggg	144
His Gly Gln Val Tyr Asp Val Ser Ser Trp Ala Ala Leu His Pro Gly	
35 40 45	
ggc act gcc cct ctc atg gcc ctt gca gga cac gac gtg acc gat gct	192
Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala	
50 55 60	
ttc ctc gcg tac cat ccc cct tcc act gcc cgt ctc ctc cct cct ctc	240
Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu	
65 70 75 80	
tct acc aac ctc ctt ctt caa aac cac tcc gtc tcc ccc acc tcc tca	288
Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser	
85 90 95	
gac tac cgc aaa ctc ctc gac aac ttc cat aaa cat ggc ctt ttc cgc	336
Asp Tyr Arg Lys Leu Leu Asp Asn Phe His Lys His Gly Leu Phe Arg	
100 105 110	
gcc agg ggc cac act gct tac gcc acc ttc gtc ttc atg ata gcg atg	384
Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Phe Met Ile Ala Met	
115 120 125	
ttt cta atg agc gtg act gga gtc ctt tgc agc gac agt gcg tgg gtc	432

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Phe	Leu	Met	Ser	Val	Thr	Gly	Val	Leu	Cys	Ser	Asp	Ser	Ala	Trp	Val	
130						135					140					
cat	ttg	gct	agc	ggc	gga	gca	atg	ggg	ttc	gcc	tgg	atc	caa	tgc	gga	480
His	Leu	Ala	Ser	Gly	Gly	Ala	Met	Gly	Phe	Ala	Trp	Ile	Gln	Cys	Gly	
145				150					155					160		
tgg	ata	ggg	cac	gac	tct	ggg	cat	tac	cgg	att	atg	tct	gac	agg	aaa	528
Trp	Ile	Gly	His	Asp	Ser	Gly	His	Tyr	Arg	Ile	Met	Ser	Asp	Arg	Lys	
			165					170					175			
tgg	aac	tgg	ttc	gcg	caa	atc	cta	agc	aca	aac	tgc	ctc	cag	ggg	att	576
Trp	Asn	Trp	Phe	Ala	Gln	Ile	Leu	Ser	Thr	Asn	Cys	Leu	Gln	Gly	Ile	
			180				185					190				
agt	atc	ggg	tgg	tgg	aag	tgg	aac	cat	aat	gcg	cac	cac	atc	gct	tgc	624
Ser	Ile	Gly	Trp	Trp	Lys	Trp	Asn	His	Asn	Ala	His	His	Ile	Ala	Cys	
		195					200					205				
aat	agc	ctg	gat	tac	gac	ccc	gac	ctc	cag	tat	atc	cct	ttg	ctc	gtc	672
Asn	Ser	Leu	Asp	Tyr	Asp	Pro	Asp	Leu	Gln	Tyr	Ile	Pro	Leu	Leu	Val	
		210			215						220					
gtc	tcc	ccc	aag	ttc	ttc	aac	tcc	ctt	act	tct	cgt	ttc	tac	gac	aag	720
Val	Ser	Pro	Lys	Phe	Phe	Asn	Ser	Leu	Thr	Ser	Arg	Phe	Tyr	Asp	Lys	
				230					235					240		
aag	ctg	aac	ttc	gac	ggc	gtg	tcg	agg	ttt	ctg	ggt	tgc	tac	cag	cac	768
Lys	Leu	Asn	Phe	Asp	Gly	Val	Ser	Arg	Phe	Leu	Val	Cys	Tyr	Gln	His	
			245					250					255			
tgg	acg	ttt	tat	ccg	gtc	atg	tgt	gtc	gct	agg	ctg	aac	atg	ctc	gcg	816
Trp	Thr	Phe	Tyr	Pro	Val	Met	Cys	Val	Ala	Arg	Leu	Asn	Met	Leu	Ala	
			260			265							270			
cag	tca	ttt	ata	acg	ctt	ttc	tcg	agt	agg	gag	gtg	tgc	cat	agg	gcg	864
Gln	Ser	Phe	Ile	Thr	Leu	Phe	Ser	Ser	Arg	Glu	Val	Cys	His	Arg	Ala	
		275				280						285				
caa	gag	ggt	ttc	gga	ctt	gcc	gtg	ttt	tgg	ggt	tgg	ttt	ccg	ctt	tta	912
Gln	Glu	Val	Phe	Gly	Leu	Ala	Val	Phe	Trp	Val	Trp	Phe	Pro	Leu	Leu	
		290				295				300						
ctt	tct	tgt	tta	cct	aat	tgg	ggc	gag	agg	att	atg	ttt	ttg	ctt	gcg	960
Leu	Ser	Cys	Leu	Pro	Asn	Trp	Gly	Glu	Arg	Ile	Met	Phe	Leu	Leu	Ala	
		305			310					315					320	
agc	tat	tcc	ggt	acg	ggg	ata	caa	cac	gtg	cag	ttc	agc	ttg	aac	cat	1008
Ser	Tyr	Ser	Val	Thr	Gly	Ile	Gln	His	Val	Gln	Phe	Ser	Leu	Asn	His	
			325					330					335			
ttt	tct	tcg	gac	gtc	tat	gtg	ggc	ccg	cca	gta	ggt	aat	gac	tgg	ttc	1056
Phe	Ser	Ser	Asp	Val	Tyr	Val	Gly	Pro	Pro	Val	Gly	Asn	Asp	Trp	Phe	
			340				345						350			
aag	aaa	cag	act	gcc	ggg	aca	ctt	aac	ata	tcg	tgc	ccg	gcg	tgg	atg	1104
Lys	Lys	Gln	Thr	Ala	Gly	Thr	Leu	Asn	Ile	Ser	Cys	Pro	Ala	Trp	Met	
		355				360						365				
gat	tgg	ttc	cat	ggc	ggg	tta	cag	ttt	cag	gtc	gag	cac	cac	ttg	ttt	1152
Asp	Trp	Phe	His	Gly	Gly	Leu	Gln	Phe	Gln	Val	Glu	His	His	Leu	Phe	
		370				375				380						
ccg	cgg	atg	cct	agg	ggt	cag	ttt	agg	aag	att	tct	cct	ttt	gtg	agg	1200
Pro	Arg	Met	Pro	Arg	Gly	Gln	Phe	Arg	Lys	Ile	Ser	Pro	Phe	Val	Arg	
				390					395					400		
gat	ttg	tgt	aag	aaa	cac	aac	ttg	cct	tac	aat	atc	gcg	tct	ttt	act	1248
Asp	Leu	Cys	Lys	Lys	His	Asn	Leu	Pro	Tyr	Asn	Ile	Ala	Ser	Phe	Thr	
			405						410					415		
aaa	gcg	aat	gtg	ttt	acg	ctt	aag	acg	ctg	aga	aat	acg	gcc	att	gag	1296
Lys	Ala	Asn	Val	Phe	Thr	Leu	Lys	Thr	Leu	Arg	Asn	Thr	Ala	Ile	Glu	
			420					425					430			
gct	cgg	gac	ctc	tct	aat	ccg	ctc	cca	aag	aat	atg	gtg	tgg	gaa	gct	1344
Ala	Arg	Asp	Leu	Ser	Asn	Pro	Leu	Pro	Lys	Asn	Met	Val	Trp	Glu	Ala	
		435					440						445			



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ctt aaa act ctc ggg tga  
 Leu Lys Thr Leu Gly  
 450

1362

<210> SEQ ID NO 72  
 <211> LENGTH: 453  
 <212> TYPE: PRT  
 <213> ORGANISM: *Primula farinosa*

<400> SEQUENCE: 72

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

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355	360	365	
Asp Trp Phe His Gly Gly	Leu Gln Phe Gln Val	Glu His His Leu Phe	
370	375	380	
Pro Arg Met Pro Arg Gly	Gln Phe Arg Lys Ile Ser	Pro Phe Val Arg	
385	390	395	400
Asp Leu Cys Lys Lys His	Asn Leu Pro Tyr Asn	Ile Ala Ser Phe Thr	
	405	410	415
Lys Ala Asn Val Phe Thr	Leu Lys Thr Leu Arg	Asn Thr Ala Ile Glu	
	420	425	430
Ala Arg Asp Leu Ser Asn	Pro Leu Pro Lys Asn Met	Val Trp Glu Ala	
	435	440	445
Leu Lys Thr Leu Gly			
450			
<210> SEQ ID NO 73			
<211> LENGTH: 1362			
<212> TYPE: DNA			
<213> ORGANISM: Primula vialii			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(1362)			
<223> OTHER INFORMATION: Delta-6 desaturase			
<400> SEQUENCE: 73			
atg gct aac aaa tct cca cca aac ccc aaa aca ggt tac att acc agc			48
Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser			
1 5 10 15			
tca gac ctg aaa ggg cac aac aaa gca gga gac cta tgg ata tca atc			96
Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile			
20 25 30			
cac ggg gag gta tac gac gtg tcc tcg tgg gcc ggc ctt cac ccg ggg			144
His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly			
35 40 45			
ggc agt gcc ccc ctc atg gcc ctc gca gga cac gac gta acc gac gct			192
Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala			
50 55 60			
ttt cta gcg tat cat cct cct tct acc gcc cgc ctc ctc cct ccc ctc			240
Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu			
65 70 75 80			
tcc acc aac ctc ctc ctt caa aac cac tcc gtc tcc ccc acc tcc tct			288
Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser			
85 90 95			
gac tac cgc aaa ctc ctc cac aac ttc cat aaa att ggt atg ttc cgc			336
Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg			
100 105 110			
gcc agg ggc cac act gct tac gcc acc ttc gtc atc atg ata gtg atg			384
Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met			
115 120 125			
ttt cta acg agc gtg acc gga gtc ctt tgc agc gac agt gcg tgg gtc			432
Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val			
130 135 140			
cat ctg gct agc ggc gca gca atg ggg ttc gcc tgg atc cag tgc gga			480
His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly			
145 150 155 160			
tgg ata ggt cac gac tct ggg cat tac cgg att atg tct gac agg aaa			528
Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys			
165 170 175			
tgg aac tgg ttc gcg cag gtc ctg agc aca aac tgc ctc cag ggg atc			576
Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile			
180 185 190			

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agt atc ggg tgg tgg aag tgg aac cat aac gcc cac cac att gct tgc      624
Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys
      195                      200                      205

aat agc ctg gac tac gac ccc gac ctc cag tat atc cct ttg ctc gtg      672
Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val
      210                      215                      220

gtc tcc ccc aag ttc ttc aac tcc ctt act tct cgt ttc tac gac aag      720
Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys
      225                      230                      235                      240

aag ctg aat ttc gac ggc gtg tca agg ttt ctg gtt tgc tac cag cac      768
Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His
      245                      250                      255

tgg acg ttt tat cca gtc atg tgt gtc gct agg cta aac atg atc gca      816
Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala
      260                      265                      270

cag tcg ttt ata acg ctt ttc tcg agc agg gag gtg ggt cat agg gcg      864
Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala
      275                      280                      285

caa gag att ttc gga ctt gct gtg ttt tgg gtt tgg ttt ccg ctc ctg      912
Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu
      290                      295                      300

ctc tct tgc tta cct aat tgg agc gag agg att atg ttt ctg cta gcg      960
Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala
      305                      310                      315                      320

agc tat tcc gtt acg ggg ata cag cac gtg cag ttc agc ttg aac cat      1008
Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His
      325                      330                      335

ttt tct tcg gac gtc tac gtg ggc ccg cca gta gct aac gac tgg ttc      1056
Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe
      340                      345                      350

aag aaa cag act gct ggg aca ctt aac ata tcg tgc ccg gcg tgg atg      1104
Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met
      355                      360                      365

gac tgg ttc cat ggc ggg ttg cag ttt cag gtc gag cac cac ttg ttt      1152
Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe
      370                      375                      380

ccg cgg atg cct agg ggt cag ttt agg aag att tct cct ttt gtg agg      1200
Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg
      385                      390                      395                      400

gat ttg tgt aag aaa cac aac ttg cct tac aat atc gcg tct ttt act      1248
Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr
      405                      410                      415

aaa gca aac gtg ttg acg ctt aag acg ctg aga aat acg gcc att gag      1296
Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu
      420                      425                      430

gct cgg gac ctc tct aat ccg acc cca aag aat atg gtg tgg gaa gcc      1344
Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala
      435                      440                      445

gtc cac aca cac ggc tag      1362
Val His Thr His Gly
      450

```

&lt;210&gt; SEQ ID NO 74

&lt;211&gt; LENGTH: 453

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Primula vialii

&lt;400&gt; SEQUENCE: 74

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

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Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile  
                   20  25  30  
 His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly  
                   35  40  45  
 Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala  
                   50  55  60  
 Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu  
                   65  70  75  80  
 Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser  
                                   85  90  
 Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg  
                                   100  105  110  
 Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met  
                                   115  120  125  
 Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val  
                                   130  135  140  
 His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly  
                                   145  150  155  160  
 Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys  
                                   165  170  175  
 Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile  
                                   180  185  190  
 Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys  
                                   195  200  205  
 Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val  
                                   210  215  220  
 Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys  
                                   225  230  235  240  
 Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His  
                                   245  250  255  
 Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala  
                                   260  265  270  
 Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala  
                                   275  280  285  
 Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu  
                                   290  295  300  
 Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala  
                                   305  310  315  320  
 Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His  
                                   325  330  335  
 Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe  
                                   340  345  350  
 Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met  
                                   355  360  365  
 Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe  
                                   370  375  380  
 Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg  
                                   385  390  395  400  
 Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr  
                                   405  410  415  
 Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu  
                                   420  425  430

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Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala  
435 440 445

Val His Thr His Gly  
450

<210> SEQ ID NO 75  
<211> LENGTH: 903  
<212> TYPE: DNA  
<213> ORGANISM: *Ostreococcus tauri*  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(903)  
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 75

atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac 48  
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr  
1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96  
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly  
20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144  
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg  
35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192  
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly  
50 55 60

ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240  
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met  
65 70 75 80

ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288  
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly  
85 90 95

atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca 336  
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser  
100 105 110

acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg 384  
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val  
115 120 125

tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc 432  
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe  
130 135 140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480  
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr  
145 150 155 160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528  
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met  
165 170 175

gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg 576  
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser  
180 185 190

ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc 624  
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly  
195 200 205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa 672  
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln  
210 215 220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac 720  
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His  
225 230 235 240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg 768

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Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
      245                               250                               255

ctc gtc ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg      816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
      260                               265                               270

cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg      864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
      275                               280                               285

ccc agc gtc cga cgc acg cga tct cga aaa att gac taa      903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
      290                               295                               300

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<210> SEQ ID NO 76
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

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<400> SEQUENCE: 76

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Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr
 1      5      10      15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
 20      25      30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
 35      40      45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
 50      55      60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
 65      70      75      80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
 85      90      95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
100      105      110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
115      120      125

Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
130      135      140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145      150      155      160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
165      170      175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180      185      190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
195      200      205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210      215      220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225      230      235      240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
      245                               250                               255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
      260                               265                               270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
      275                               280                               285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
      290                               295                               300

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<210> SEQ ID NO 77
<211> LENGTH: 903
<212> TYPE: DNA
<213> ORGANISM: Ostreococcus tauri
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(903)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 77

atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac      48
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
1          5          10          15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc      96
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
          20          25          30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg     144
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
          35          40          45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga     192
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
50          55          60

ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg     240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65          70          75          80

ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg     288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
          85          90          95

atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca     336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
          100          105          110

acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg     384
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
          115          120          125

tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc     432
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
130          135          140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat     480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145          150          155          160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg     528
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
          165          170          175

gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg     576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
          180          185          190

ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc     624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
          195          200          205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa     672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210          215          220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac     720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225          230          235          240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg     768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
          245          250          255

ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg     816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser

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260	265	270	
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
275	280	285	
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
290	295	300	

<210> SEQ ID NO 78  
 <211> LENGTH: 300  
 <212> TYPE: PRT  
 <213> ORGANISM: *Ostreococcus tauri*

<400> SEQUENCE: 78

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

<210> SEQ ID NO 79  
 <211> LENGTH: 903  
 <212> TYPE: DNA



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<213> ORGANISM: Ostreococcus tauri
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(903)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 79

atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac      48
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr
1          5          10          15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc      96
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
          20          25          30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg     144
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
          35          40          45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga     192
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
          50          55          60

ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg     240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
          65          70          75          80

ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg     288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
          85          90          95

atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca     336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
          100          105          110

acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg     384
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
          115          120          125

tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc     432
Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe
          130          135          140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat     480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
          145          150          155          160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg     528
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
          165          170          175

gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg     576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
          180          185          190

ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc     624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
          195          200          205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa     672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
          210          215          220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac     720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
          225          230          235          240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg     768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
          245          250          255

ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg     816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
          260          265          270

cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg     864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
          275          280          285

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ccc agc gtg cga cgc acg cga tct cga aaa att gac taa      903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
    290                295                300

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<210> SEQ ID NO 80
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

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<400> SEQUENCE: 80

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

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<210> SEQ ID NO 81
<211> LENGTH: 879
<212> TYPE: DNA
<213> ORGANISM: Ostreococcus tauri
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(879)
<223> OTHER INFORMATION: Delta-6 elongase

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&lt;400&gt; SEQUENCE: 81

atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag	48
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys	
1 5 10 15	
tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt	96
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe	
20 25 30	
cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc	144
Gln Trp Asp Ile Gly Pro Val Ser Ser Thr Ala His Leu Pro Ala	
35 40 45	
att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc	192
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val	
50 55 60	
aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa	240
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys	
65 70 75 80	
att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg	288
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala	
85 90 95	
ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa	336
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln	
100 105 110	
gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg	384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr	
115 120 125	
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata	432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile	
130 135 140	
tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg	480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg	
145 150 155 160	
caa gta aga ttc cta cac act tat cac cac agc acg att tcc ttt att	528
Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile	
165 170 175	
tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc	576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser	
180 185 190	
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta	624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu	
195 200 205	
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt	672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu	
210 215 220	
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc	720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe	
225 230 235 240	
aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag	768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys	
245 250 255	
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc gcc ttg	816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu	
260 265 270	
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag	864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln	
275 280 285	
aaa aaa cag cag tga	879
Lys Lys Gln Gln	
290	

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<210> SEQ ID NO 82
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 82

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
 1           5           10           15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
 20           25           30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
 35           40           45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
 50           55           60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
 65           70           75           80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
 85           90           95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
100           105           110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
115           120           125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
130           135           140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
145           150           155           160

Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile
165           170           175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
180           185           190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
195           200           205

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

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
225           230           235           240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
245           250           255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
260           265           270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
275           280           285

Lys Lys Gln Gln
290

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<210> SEQ ID NO 83
<211> LENGTH: 831
<212> TYPE: DNA
<213> ORGANISM: Thraustochytrium sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(831)
<223> OTHER INFORMATION: Delta-5 elongase

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<400> SEQUENCE: 83

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atg gac gtc gtc gag cag caa tgg cgc cgc ttc gtg gac gcc gtg gac
Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp

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48

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1	5	10	15	
aac gga atc gtg gag ttc atg gag cat gag aag ccc aac aag ctg aac				96
Asn Gly Ile Val Glu Phe Met Glu His Glu Lys Pro Asn Lys Leu Asn	20	25	30	
gag ggc aag ctc ttc acc tcg acc gag gag atg atg gcg ctt atc gtc				144
Glu Gly Lys Leu Phe Thr Ser Thr Glu Glu Met Met Ala Leu Ile Val	35	40	45	
ggc tac ctg gcg ttc gtg gtc ctc ggg tcc gcc ttc atg aag gcc ttt				192
Gly Tyr Leu Ala Phe Val Val Leu Gly Ser Ala Phe Met Lys Ala Phe	50	55	60	
gtc gat aag cct ttc gag ctc aag ttc ctc aag ctc gtg cac aac atc				240
Val Asp Lys Pro Phe Glu Leu Lys Phe Leu Lys Leu Val His Asn Ile	65	70	75	80
ttc ctc acc ggt ctg tcc atg tac atg gcc acc gag tgc gcg cgc cag				288
Phe Leu Thr Gly Leu Ser Met Tyr Met Ala Thr Glu Cys Ala Arg Gln	85	90	95	
gca tac ctc ggc ggc tac aag ctc ttt ggc aac ccg atg gag aag ggc				336
Ala Tyr Leu Gly Gly Tyr Lys Leu Phe Gly Asn Pro Met Glu Lys Gly	100	105	110	
acc gag tcg cac gcc ccg ggc atg gcc aac atc atc tac atc ttc tac				384
Thr Glu Ser His Ala Pro Gly Met Ala Asn Ile Ile Tyr Ile Phe Tyr	115	120	125	
gtg agc aag ttc ctc gaa ttc ctc gac acc gtc ttc atg atc ctc ggc				432
Val Ser Lys Phe Leu Glu Phe Leu Asp Thr Val Phe Met Ile Leu Gly	130	135	140	
aag aag tgg aag cag ctc agc ttt ctc cac gtc tac cac cac gcg agc				480
Lys Lys Trp Lys Gln Leu Ser Phe Leu His Val Tyr His His Ala Ser	145	150	155	160
atc agc ttc atc tgg ggc atc atc gcc cgc ttc gcg ccc ggt ggc gac				528
Ile Ser Phe Ile Trp Gly Ile Ile Ala Arg Phe Ala Pro Gly Gly Asp	165	170	175	
gcc tac ttc tct acc atc ctc aac agc agc gtg cat gtc gtg ctc tac				576
Ala Tyr Phe Ser Thr Ile Leu Asn Ser Ser Val His Val Val Leu Tyr	180	185	190	
ggc tac tac gcc tcg acc acc ctc ggc tac acc ttc atg cgc ccg ctg				624
Gly Tyr Tyr Ala Ser Thr Thr Leu Gly Tyr Thr Phe Met Arg Pro Leu	195	200	205	
cgc ccg tac att acc acc att cag ctc acg cag ttc atg gcc atg gtc				672
Arg Pro Tyr Ile Thr Thr Ile Gln Leu Thr Gln Phe Met Ala Met Val	210	215	220	
gtc cag tcc gtc tat gac tac tac aac ccc tgc gac tac ccg cag ccc				720
Val Gln Ser Val Tyr Asp Tyr Tyr Asn Pro Cys Asp Tyr Pro Gln Pro	225	230	235	240
ctc gtc aag ctg ctc ttc tgg tac atg ctc acc atg ctc ggc ctc ttc				768
Leu Val Lys Leu Leu Phe Trp Tyr Met Leu Thr Met Leu Gly Leu Phe	245	250	255	
ggc aac ttc ttc gtg cag cag tac ctc aag ccc aag gcg ccc aag aag				816
Gly Asn Phe Phe Val Gln Gln Tyr Leu Lys Pro Lys Ala Pro Lys Lys	260	265	270	
cag aag acc atc taa				831
Gln Lys Thr Ile	275			
<210> SEQ ID NO 84				
<211> LENGTH: 276				
<212> TYPE: PRT				
<213> ORGANISM: Thraustochytrium sp.				
<400> SEQUENCE: 84				
Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp				

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

<210> SEQ ID NO 85  
 <211> LENGTH: 1077  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1077)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 85

atg tgc tca cca ccg ccg tca caa tcc aaa aca aca tcc ctc cta gca	48
Met Cys Ser Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala	
1 5 10 15	
cgg tac acc acc gcc gcc ctc ctc ctc ctc acc ctc aca acg tgg tgc	96
Arg Tyr Thr Thr Ala Ala Leu Leu Thr Leu Thr Thr Trp Cys	
20 25 30	
cac ttc gcc ttc cca gcc gcc acc gcc aca ccc ggc ctc acc gcc gaa	144
His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu	
35 40 45	
atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg	192
Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu	

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50	55	60	
agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys 65 70 75 80			240
tat gat atg aag tca ctc ctg acg gaa tca atg gtg ttg tac aat gtg Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val 85 90 95			288
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala 100 105 110			336
gtg atg aat aga gac cat cct ttt att gga agt aga agt ttg gtt ggg Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly 115 120 125			384
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys 130 135 140			432
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly 145 150 155 160			480
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile 165 170 175			528
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggc gga gac att Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile 180 185 190			576
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser 195 200 205			624
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr 210 215 220			672
ttg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr 225 230 235 240			720
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp 245 250 255			768
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln 260 265 270			816
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys 275 280 285			864
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys 290 295 300			912
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp 305 310 315 320			960
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala 325 330 335			1008
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr 340 345 350			1056
cgt gtt act ggt gcc atg tag Arg Val Thr Gly Ala Met 355			1077

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<210> SEQ ID NO 86
<211> LENGTH: 358
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> SEQUENCE: 86

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

Arg Val Thr Gly Ala Met
          355

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<210> SEQ ID NO 87
<211> LENGTH: 1086

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<212> TYPE: DNA
<213> ORGANISM: Phytophthora infestans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1086)
<223> OTHER INFORMATION: Omega-3 desaturase

<400> SEQUENCE: 87

atg gcg acg aag gag gcg tat gtg ttc ccc act ctg acg gag atc aag      48
Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
1          5          10          15

cgg tcg cta cct aaa gac tgt ttc gag gct tcg gtg cct ctg tcg ctc      96
Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
          20          25          30

tac tac acc gtg cgt tgt ctg gtg atc gcg gtg gct cta acc ttc ggt      144
Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
          35          40          45

ctc aac tac gct cgc gct ctg ccc gag gtc gag agc ttc tgg gct ctg      192
Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
          50          55          60

gac gcc gca ctc tgc acg ggc tac atc ttg ctg cag ggc atc gtg ttc      240
Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
65          70          75          80

tgg ggc ttc ttc acg gtg ggc cac gat gcc ggc cac ggc gcc ttc tcg      288
Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
          85          90          95

cgc tac cac ctg ctt aac ttc gtg gtg ggc act ttc atg cac tcg ctc      336
Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu
          100          105          110

atc ctc acg ccc ttc gag tcg tgg aag ctc acg cac cgt cac cac cac      384
Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His
          115          120          125

aag aac acg ggc aac att gac cgt gac gag gtc ttc tac ccg caa cgc      432
Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg
          130          135          140

aag gcc gac gac cac ccg ctg tct cgc aac ctg att ctg gcg ctc ggg      480
Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly
          145          150          155          160

gca gcg tgg ctc gcc tat ttg gtc gag ggc ttc cct cct cgt aag gtc      528
Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val
          165          170          175

aac cac ttc aac ccg ttc gag cct ctg ttc gtg cgt cag gtg tca gct      576
Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala
          180          185          190

gtg gta atc tct ctt ctc gcc cac ttc ttc gtg gcc gga ctc tcc atc      624
Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile
          195          200          205

tat ctg agc ctc cag ctg ggc ctt aag acg atg gca atc tac tac tat      672
Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr
          210          215          220

gga cct gtt ttt gtg ttc ggc agc atg ctg gtc att acc acc ttc cta      720
Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu
          225          230          235          240

cac cac aat gat gag gag acc cca tgg tac gcc gac tcg gag tgg acg      768
His His Asn Asp Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr
          245          250          255

tac gtc aag ggc aac ctc tcg tcc gtg gac cga tcg tac ggc gcg ctc      816
Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu
          260          265          270

att gac aac ctg agc cac aac atc ggc acg cac cag atc cac cac ctt      864
Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu

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275	280	285	
ttc cct atc att ccg cac tac aaa ctc aag aaa gcc act gcg gcc ttc			912
Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe			
290	295	300	
cac cag gct ttc cct gag ctc gtg cgc aag agc gac gag cca att atc			960
His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile			
305	310	315	320
aag gct ttc ttc cgg gtt gga cgt ctc tac gca aac tac ggc gtt gtg			1008
Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val			
325	330	335	
gac cag gag gcg aag ctc ttc acg cta aag gaa gcc aag gcg gcg acc			1056
Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr			
340	345	350	
gag gcg gcg gcc aag acc aag tcc acg taa			1086
Glu Ala Ala Ala Lys Thr Lys Ser Thr			
355	360		

<210> SEQ ID NO 88  
 <211> LENGTH: 361  
 <212> TYPE: PRT  
 <213> ORGANISM: *Phytophthora infestans*

<400> SEQUENCE: 88

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

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260	265	270	
Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu			
275	280	285	
Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe			
290	295	300	
His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile			
305	310	315	320
Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val			
325	330	335	
Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr			
340	345	350	
Glu Ala Ala Ala Lys Thr Lys Ser Thr			
355	360		
<210> SEQ ID NO 89			
<211> LENGTH: 1371			
<212> TYPE: DNA			
<213> ORGANISM: <i>Ostreococcus tauri</i>			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(1371)			
<223> OTHER INFORMATION: Delta-6 desaturase			
<400> SEQUENCE: 89			
atg tgc gtg gag acg gaa aat aac gat ggg atc ccc acg gtg gag atc			48
Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile			
1	5	10	15
gcg ttc gac ggt gag cgc gag cgg gcg gag gca aac gtg aag ctg tcc			96
Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser			
20	25	30	
gcg gag aag atg gag ccg gcg gcg ctg gcg aag acg ttc gcg agg cgg			144
Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg			
35	40	45	
tac gtc gtg atc gag ggg gtg gag tac gat gtg acg gat ttt aag cac			192
Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His			
50	55	60	
ccg gga gga acg gtt att ttc tat gcg ttg tca aac acc ggg gcg gac			240
Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp			
65	70	75	80
gcg acg gaa gcg ttc aag gag ttt cat cat cgg tcg aga aag gcg agg			288
Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg			
85	90	95	
aaa gcc ttg gcg gcg ctc ccg tct cga ccg gcc aag acg gcc aag gtg			336
Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val			
100	105	110	
gac gac gcg gag atg ctc caa gat ttc gcc aag tgg gcg aaa gaa ttg			384
Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu			
115	120	125	
gag aga gat gga ttc ttc aag ccc tct ccg gcg cac gtg gcg tat cgc			432
Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg			
130	135	140	
ttc gcc gag ctc gcg gcg atg tac gct ctc ggg acg tac ctg atg tac			480
Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr			
145	150	155	160
gct cga tac gtc gtc tcc tcg gtg ctc gtg tac gct tgc ttt ttc ggc			528
Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly			
165	170	175	
gcc cga tgc ggt tgg gtg cag cac gag ggc gga cac agc tcg ctg acg			576
Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr			
180	185	190	

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ggc aac att tgg tgg gac aag cgc atc cag gcc ttc aca gcc ggg ttc      624
Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
      195                               200                               205

ggt ctc gcc ggt agc ggc gac atg tgg aac tcg atg cac aac aag cat      672
Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
      210                               215                               220

cac gcg acg cct caa aag gtt cgt cac gac atg gat ctg gac acc acc      720
His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
      225                               230                               235                               240

ccc gcg gtg gcg ttc ttc aac acc gcg gtg gaa gac aat cgt ccc cgt      768
Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
      245                               250                               255

ggc ttt agc aag tac tgg ttg cgc ctt cag gcg tgg acc ttc atc ccc      816
Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro
      260                               265                               270

gtg acg tcc gcc ttg gtg ctc ctt ttc tgg atg ttt ttc ctc cac ccc      864
Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro
      275                               280                               285

tcc aag gct ttg aag ggt ggc aag tac gaa gag ttg gtg tgg atg ctc      912
Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu
      290                               295                               300

gcc gcg cac gtc atc cgc acg tgg acg atc aag gcg gtg acc gga ttc      960
Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe
      305                               310                               315                               320

acc gcg atg cag tcc tac ggc tta ttt ttg gcg acg agc tgg gtg agc      1008
Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser
      325                               330                               335

ggc tgc tat ctg ttt gca cac ttc tcc acg tcg cac acg cac ctg gat      1056
Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp
      340                               345                               350

gtg gtg ccc gcg gac gag cat ctc tcc tgg gtt cga tac gcc gtc gat      1104
Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp
      355                               360                               365

cac acg atc gac atc gat ccg agt caa ggt tgg gtg aac tgg ttg atg      1152
His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met
      370                               375                               380

ggc tac ctc aac tgc caa gtc atc cac cac ctc ttt ccg agc atg ccg      1200
Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro
      385                               390                               395                               400

cag ttc cgc cag ccc gag gta tct cgc cgc ttc gtc gcc ttt gcg aaa      1248
Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys
      405                               410                               415

aag tgg aac ctc aac tac aag gtc atg acc tac gcc ggt gcg tgg aag      1296
Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys
      420                               425                               430

gca acg ctc gga aac ctc gac aac gtg ggt aag cac tac tac gtg cac      1344
Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His
      435                               440                               445

ggc caa cac tcc gga aag acg gcg taa      1371
Gly Gln His Ser Gly Lys Thr Ala
      450                               455

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&lt;210&gt; SEQ ID NO 90

&lt;211&gt; LENGTH: 456

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 90

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Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
1           5           10           15

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Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser  
20 25 30

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg  
35 40 45

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His  
50 55 60

Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp  
65 70 75 80

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg  
85 90 95

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val  
100 105 110

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu  
115 120 125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg  
130 135 140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr  
145 150 155 160

Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly  
165 170 175

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr  
180 185 190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe  
195 200 205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His  
210 215 220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr  
225 230 235 240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg  
245 250 255

Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro  
260 265 270

Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro  
275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu  
290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe  
305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser  
325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp  
340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp  
355 360 365

His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met  
370 375 380

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro  
385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys  
405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys  
420 425 430

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Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His  
 435 440 445

Gly Gln His Ser Gly Lys Thr Ala  
 450 455

<210> SEQ ID NO 91  
 <211> LENGTH: 606  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(606)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 91

atg tac ggt ttg cta tcg ctc aag tcg tgc ttc gtc gac gat ttc aac 48  
 Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn  
 1 5 10 15

gcc tac ttc tcc gga cgc atc ggc tgg gtc aag gtg atg aag ttc acc 96  
 Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys Phe Thr  
 20 25 30

cgc ggc gag gcg atc gca ttt tgg ggc acc aag ctc ttg tgg gcc gcg 144  
 Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp Ala Ala  
 35 40 45

tat tac ctc gcg ttg ccg cta aag atg tcg cat cgg ccg ctc gga gaa 192  
 Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu Gly Glu  
 50 55 60

ctc ctc gca ctc tgg gcc gtc acc gag ttc gtc acc gga tgg ctg ttg 240  
 Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp Leu Leu  
 65 70 75 80

gcg ttc atg ttc caa gtc gcc cac gtc gtc ggc gag gtt cac ttc ttc 288  
 Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His Phe Phe  
 85 90 95

acc ctc gac gcg aag aac cgc gtg aac ttg gga tgg gga gag gca cag 336  
 Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu Ala Gln  
 100 105 110

ctc atg tcg agc gcg gat ttc gcc cac gga tcc aag ttt tgg acg cac 384  
 Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp Thr His  
 115 120 125

ttc tcc gga ggc tta aac tac caa gtc gtc cac cat ctc ttc ccg ggc 432  
 Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe Pro Gly  
 130 135 140

gtc tgc cac gtg cac tat ccc gcg ctc gcg cca att att aag gcg gca 480  
 Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys Ala Ala  
 145 150 155 160

gct gag aag cac ggc ctc cac tac cag att tac ccc acg ttt tgg tcc 528  
 Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe Trp Ser  
 165 170 175

gcc ctg cgc gcg cac ttc cgg cac ctc gcc aac gtc ggc cgc gcc gcg 576  
 Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg Ala Ala  
 180 185 190

tac gta ccg tcc ctc caa acc gtc gga tga 606  
 Tyr Val Pro Ser Leu Gln Thr Val Gly  
 195 200

<210> SEQ ID NO 92  
 <211> LENGTH: 201  
 <212> TYPE: PRT  
 <213> ORGANISM: *Ostreococcus tauri*

<400> SEQUENCE: 92

Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn

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

<210> SEQ ID NO 93  
 <211> LENGTH: 714  
 <212> TYPE: DNA  
 <213> ORGANISM: Ostreococcus tauri  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(714)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 93

atg gtg agc cat cac tcg tac tgt aac gac gcg gat ttg gat cag gat	48
Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp	
1 5 10 15	
gtg tac acc gca ctg ccg ctc ctg cgc ctg gac ccg tct cag gag ttg	96
Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu	
20 25 30	
aag tgg ttt cat cga tac cag gcg ttt tac gcc ccg ctc atg tgg ccg	144
Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro	
35 40 45	
ttt ttg tgg ctc gcg gcg cag ttt ggc gac gcg cag aac atc ctg atc	192
Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile	
50 55 60	
gac cga gcg tcg ccg ggc gtc gcg tac aag gga ttg atg gcg aac gag	240
Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu	
65 70 75 80	
gtc gcg ctg tac gtt ctc ggt aag gtt tta cac ttt ggt ctt ctc ctc	288
Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu	
85 90 95	
ggc gtt cct gcg tac ttg cac gga ttg tcc aac gcg atc gtt cca ttc	336
Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe	
100 105 110	
ttg gcg tac ggc gca ttc ggc tcc ttc gtc ctg tgc tgg ttc ttc atc	384

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Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile  
 115 120 125

gtc agc cat aac ctc gaa gcg ctg aca ccc gtt aac ctt aac aag tcc 432  
 Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser  
 130 135 140

acg aag aac gac tgg ggg gcg tgg cag atc gag aca tcg gcg tct tgg 480  
 Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp  
 145 150 155 160

ggc aac gcg ttc tgg agc ttc ttc tct gga ggt ctg aac ctg caa atc 528  
 Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile  
 165 170 175

gag cac cac ctc ttc ccg ggc atg gcg cac aac ctg tac ccg aag atg 576  
 Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met  
 180 185 190

gtg ccg atc atc aag gac gag tgt gcg aaa gcg ggc gtt cgc tac acc 624  
 Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr  
 195 200 205

ggt tac ggt ggc tac acc ggc ctg ctc ccg atc acc cgc gac atg ttc 672  
 Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe  
 210 215 220

tcc tac ctc cat aag tgt ggc cga acg gcg aaa cta gcc taa 714  
 Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala  
 225 230 235

<210> SEQ ID NO 94  
 <211> LENGTH: 237  
 <212> TYPE: PRT  
 <213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 94

Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp  
 1 5 10 15

Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu  
 20 25 30

Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro  
 35 40 45

Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile  
 50 55 60

Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu  
 65 70 75 80

Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu  
 85 90 95

Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe  
 100 105 110

Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile  
 115 120 125

Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser  
 130 135 140

Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp  
 145 150 155 160

Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile  
 165 170 175

Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met  
 180 185 190

Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr  
 195 200 205

Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe



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210	215	220	
Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala			
225	230	235	
<210> SEQ ID NO 95 <211> LENGTH: 1611 <212> TYPE: DNA <213> ORGANISM: <i>Ostreococcus tauri</i> <220> FEATURE: <221> NAME/KEY: CDS <222> LOCATION: (1)..(1611) <223> OTHER INFORMATION: Delta-4 desaturase <400> SEQUENCE: 95			
atg tac ctc gga cgc ggc cgt ctc gag agc ggg acg acg cga ggg atg			48
Met Tyr Leu Gly Arg Gly Arg Leu Glu Ser Gly Thr Thr Arg Gly Met			
1	5	10	15
atg cgg acg cac gcg cgg cga ccg tcg acg acg tcg aat ccg tgc gcg			96
Met Arg Thr His Ala Arg Arg Pro Ser Thr Thr Ser Asn Pro Cys Ala			
	20	25	30
cgg tca cgc gtg cgt aag acg acg gag cga tcg ctc gcg cga gtg cga			144
Arg Ser Arg Val Arg Lys Thr Thr Glu Arg Ser Leu Ala Arg Val Arg			
	35	40	45
cga tcg acg agt gag aag gga agc gcg ctc gtg ctc gag cga gag agc			192
Arg Ser Thr Ser Glu Lys Gly Ser Ala Leu Val Leu Glu Arg Glu Ser			
	50	55	60
gaa cgg gag aag gag gag gga ggg aaa gcg cga gcg gag gga ttg cga			240
Glu Arg Glu Lys Glu Glu Gly Gly Lys Ala Arg Ala Glu Gly Leu Arg			
	65	70	75
ttc caa cgc ccg gac gtc gcc gcg ccg ggg gga gcg gat cct tgg aac			288
Phe Gln Arg Pro Asp Val Ala Ala Pro Gly Gly Ala Asp Pro Trp Asn			
	85	90	95
gac gag aag tgg aca aag acc aag tgg acg gta ttc aga gac gtc gcg			336
Asp Glu Lys Trp Thr Lys Thr Lys Trp Thr Val Phe Arg Asp Val Ala			
	100	105	110
tac gat ctc gat cct ttc ttc gct cga cac ccc gga gga gac tgg ctc			384
Tyr Asp Leu Asp Pro Phe Phe Ala Arg His Pro Gly Gly Asp Trp Leu			
	115	120	125
ctg aac ttg gcc gtg gga cga gac tgc acc gcg ctc atc gaa tcc tat			432
Leu Asn Leu Ala Val Gly Arg Asp Cys Thr Ala Leu Ile Glu Ser Tyr			
	130	135	140
cac ttg cga cca gag gtg gcg acg gct cgt ttc aga atg ctg ccc aaa			480
His Leu Arg Pro Glu Val Ala Thr Ala Arg Phe Arg Met Leu Pro Lys			
	145	150	155
ctc gag gat ttt ccc gtc gag gcc gtg ccc aag tcc ccg aga ccg aac			528
Leu Glu Asp Phe Pro Val Glu Ala Val Pro Lys Ser Pro Arg Pro Asn			
	165	170	175
gat tcg ccg tta tac aac aac att cgc aac cga gtc cgc gaa gag ctc			576
Asp Ser Pro Leu Tyr Asn Asn Ile Arg Asn Arg Val Arg Glu Glu Leu			
	180	185	190
ttc cca gag gag gga aag aat atg cac aga cag ggc ggc gac cac ggc			624
Phe Pro Glu Glu Gly Lys Asn Met His Arg Gln Gly Gly Asp His Gly			
	195	200	205
gac ggt gac gat tct ggg ttt cgc cgc ctt ttg ctt atg ccg tgt acc			672
Asp Gly Asp Asp Ser Gly Phe Arg Arg Leu Leu Leu Met Pro Cys Thr			
	210	215	220
tat tcc ctt ccg ggg gtt cct ttc ccg ctg cct cct ccg gtc tcg ccg			720
Tyr Ser Leu Pro Gly Val Pro Phe Arg Leu Pro Pro Arg Val Ser Arg			
	225	230	235
ggg cgt gga ttg gtc tca cga ttc agg cac tgc gcc aac cac ggc gcg			768
Gly Arg Gly Leu Val Ser Arg Phe Arg His Cys Ala Asn His Gly Ala			

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		245	250	255												
atg	tct	cct	tcg	ccg	gcc	gtt	aac	ggc	gtc	ctc	ggt	ttg	acg	aac	gat	816
Met	Ser	Pro	Ser	Pro	Ala	Val	Asn	Gly	Val	Leu	Gly	Leu	Thr	Asn	Asp	
		260					265					270				
ctc	atc	ggc	ggc	tcg	tcc	ttg	atg	tgg	aga	tat	cac	cac	caa	gtc	agc	864
Leu	Ile	Gly	Gly	Ser	Ser	Leu	Met	Trp	Arg	Tyr	His	His	Gln	Val	Ser	
		275				280					285					
cac	cac	att	cat	tgc	aac	gac	aac	gcc	atg	gat	caa	gac	gtg	tac	acg	912
His	His	Ile	His	Cys	Asn	Asp	Asn	Ala	Met	Asp	Gln	Asp	Val	Tyr	Thr	
		290			295					300						
gcg	atg	cca	tta	ttg	cgt	ttc	gac	gct	cgc	cgg	ccc	aag	tcc	tgg	tac	960
Ala	Met	Pro	Leu	Leu	Arg	Phe	Asp	Ala	Arg	Arg	Pro	Lys	Ser	Trp	Tyr	
		305			310					315				320		
cat	cgc	ttc	cag	cag	tgg	tac	atg	ttt	tta	gcg	ttc	ccg	ttg	ttg	cag	1008
His	Arg	Phe	Gln	Gln	Trp	Tyr	Met	Phe	Leu	Ala	Phe	Pro	Leu	Leu	Gln	
			325						330					335		
gtt	gcc	ttc	caa	gtc	gga	gac	att	gcc	gca	ctg	ttc	acg	cgt	gat	acc	1056
Val	Ala	Phe	Gln	Val	Gly	Asp	Ile	Ala	Ala	Leu	Phe	Thr	Arg	Asp	Thr	
			340					345						350		
gaa	ggc	gct	aag	ctt	cac	ggg	gcg	acg	acg	tgg	gag	ctt	acc	acg	gtt	1104
Glu	Gly	Ala	Lys	Leu	His	Gly	Ala	Thr	Thr	Trp	Glu	Leu	Thr	Thr	Val	
		355				360						365				
gtc	ctc	ggt	aag	att	gtg	cac	ttc	ggt	ctt	ttg	ttg	ggg	ccg	ttg	atg	1152
Val	Leu	Gly	Lys	Ile	Val	His	Phe	Gly	Leu	Leu	Leu	Gly	Pro	Leu	Met	
		370				375					380					
aac	cac	gcg	gtg	agt	tct	gtt	ttg	ctg	ggg	atc	gtc	ggt	ttc	atg	gcg	1200
Asn	His	Ala	Val	Ser	Ser	Val	Leu	Leu	Gly	Ile	Val	Gly	Phe	Met	Ala	
				390						395				400		
tgc	caa	ggt	ata	gtt	ctg	gcg	tgc	acg	ttt	gct	gtg	agt	cac	aat	gtc	1248
Cys	Gln	Gly	Ile	Val	Leu	Ala	Cys	Thr	Phe	Ala	Val	Ser	His	Asn	Val	
			405					410						415		
gcg	gag	gcg	aag	ata	cct	gag	gac	acc	gga	gga	gaa	gcc	tgg	gag	aga	1296
Ala	Glu	Ala	Lys	Ile	Pro	Glu	Asp	Thr	Gly	Gly	Glu	Ala	Trp	Glu	Arg	
			420					425					430			
gat	tgg	ggt	gtc	cag	cag	ttg	gtg	act	agc	gcc	gac	tgg	ggt	gga	aag	1344
Asp	Trp	Gly	Val	Gln	Gln	Leu	Val	Thr	Ser	Ala	Asp	Trp	Gly	Gly	Lys	
		435				440							445			
ata	ggt	aac	ttc	ttc	acg	ggt	ggc	ctc	aac	ttg	caa	ggt	gag	cac	cac	1392
Ile	Gly	Asn	Phe	Phe	Thr	Gly	Gly	Leu	Asn	Leu	Gln	Val	Glu	His	His	
		450				455					460					
ttg	ttt	ccg	gcg	att	tgc	ttc	gtc	cac	tac	ccg	gac	atc	gcg	aag	atc	1440
Leu	Phe	Pro	Ala	Ile	Cys	Phe	Val	His	Tyr	Pro	Asp	Ile	Ala	Lys	Ile	
		465			470					475				480		
gtg	aag	gaa	gaa	gcg	gcc	aag	ctc	aac	atc	cct	tac	gcg	tct	tac	agg	1488
Val	Lys	Glu	Glu	Ala	Ala	Lys	Leu	Asn	Ile	Pro	Tyr	Ala	Ser	Tyr	Arg	
			485					490						495		
act	ctt	cct	ggt	att	ttc	gtc	caa	ttc	tgg	aga	ttt	atg	aag	gac	atg	1536
Thr	Leu	Pro	Gly	Ile	Phe	Val	Gln	Phe	Trp	Arg	Phe	Met	Lys	Asp	Met	
			500					505						510		
ggc	acg	gct	gag	caa	att	ggt	gaa	ggt	cca	ttg	ccg	aag	att	ccc	aac	1584
Gly	Thr	Ala	Glu	Gln	Ile	Gly	Glu	Val	Pro	Leu	Pro	Lys	Ile	Pro	Asn	
			515					520						525		
ccg	cag	ctc	gcg	ccg	aag	ctc	gct	tag								1611
Pro	Gln	Leu	Ala	Pro	Lys	Leu	Ala									
		530				535										

&lt;210&gt; SEQ ID NO 96

&lt;211&gt; LENGTH: 536

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

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&lt;400&gt; SEQUENCE: 96

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

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405				410				415								
Ala	Glu	Ala	Lys	Ile	Pro	Glu	Asp	Thr	Gly	Gly	Glu	Ala	Trp	Glu	Arg	
			420								425				430	
Asp	Trp	Gly	Val	Gln	Gln	Leu	Val	Thr	Ser	Ala	Asp	Trp	Gly	Gly	Lys	
			435				440								445	
Ile	Gly	Asn	Phe	Phe	Thr	Gly	Gly	Leu	Asn	Leu	Gln	Val	Glu	His	His	
			450				455								460	
Leu	Phe	Pro	Ala	Ile	Cys	Phe	Val	His	Tyr	Pro	Asp	Ile	Ala	Lys	Ile	
			465				470				475				480	
Val	Lys	Glu	Glu	Ala	Ala	Lys	Leu	Asn	Ile	Pro	Tyr	Ala	Ser	Tyr	Arg	
			485								490				495	
Thr	Leu	Pro	Gly	Ile	Phe	Val	Gln	Phe	Trp	Arg	Phe	Met	Lys	Asp	Met	
			500												510	
Gly	Thr	Ala	Glu	Gln	Ile	Gly	Glu	Val	Pro	Leu	Pro	Lys	Ile	Pro	Asn	
			515				520								525	
Pro	Gln	Leu	Ala	Pro	Lys	Leu	Ala									
			530				535									
<210> SEQ ID NO 97																
<211> LENGTH: 1455																
<212> TYPE: DNA																
<213> ORGANISM: Thalassiosira pseudonana																
<220> FEATURE:																
<221> NAME/KEY: CDS																
<222> LOCATION: (1)..(1455)																
<223> OTHER INFORMATION: Delta-6 desaturase																
<400> SEQUENCE: 97																
atg	gga	aaa	gga	gga	gac	gca	gcc	gca	gct	acc	aag	cgt	agt	gga	gca	48
Met	Gly	Lys	Gly	Asp	Ala	Ala	Ala	Ala	Thr	Lys	Arg	Ser	Gly	Ala		
1			5						10					15		
ttg	aaa	ttg	gcg	gag	aag	ccg	cag	aag	tac	act	tgg	cag	gag	gtg	aag	96
Leu	Lys	Leu	Ala	Glu	Lys	Pro	Gln	Lys	Tyr	Thr	Trp	Gln	Glu	Val	Lys	
			20						25					30		
aag	cac	atc	acc	ccc	gac	gat	gcc	tgg	gta	gtc	cac	caa	aac	aaa	gtc	144
Lys	His	Ile	Thr	Pro	Asp	Asp	Ala	Trp	Val	Val	His	Gln	Asn	Lys	Val	
			35				40							45		
tac	gac	gtc	tcc	aac	tgg	tac	gac	cac	ccc	ggg	gga	gcc	gtg	gtg	ttc	192
Tyr	Asp	Val	Ser	Asn	Trp	Tyr	Asp	His	Pro	Gly	Gly	Ala	Val	Val	Phe	
			50				55				60					
acc	cac	gcc	gga	gac	gac	atg	acg	gac	atc	ttc	gcc	gcc	ttc	cac	gcc	240
Thr	His	Ala	Gly	Asp	Asp	Met	Thr	Asp	Ile	Phe	Ala	Ala	Phe	His	Ala	
			65				70				75				80	
caa	ggc	tct	cag	gcc	atg	atg	aag	aag	ttt	tac	att	gga	gat	ttg	att	288
Gln	Gly	Ser	Gln	Ala	Met	Met	Lys	Lys	Phe	Tyr	Ile	Gly	Asp	Leu	Ile	
			85						90						95	
ccg	gag	agt	gtg	gag	cat	aag	gat	caa	aga	cag	ttg	gat	ttc	gag	aag	336
Pro	Glu	Ser	Val	Glu	His	Lys	Asp	Gln	Arg	Gln	Leu	Asp	Phe	Glu	Lys	
			100						105					110		
gga	tat	cgt	gat	tta	cgg	gcc	aag	ctt	gtc	atg	atg	ggg	atg	ttc	aag	384
Gly	Tyr	Arg	Asp	Leu	Arg	Ala	Lys	Leu	Val	Met	Met	Gly	Met	Phe	Lys	
			115				120							125		
tcg	agt	aag	atg	tat	tat	gca	tac	aag	tgc	tcg	ttc	aat	atg	tgc	atg	432
Ser	Ser	Lys	Met	Tyr	Tyr	Ala	Tyr	Lys	Cys	Ser	Phe	Asn	Met	Cys	Met	
			130				135							140		
tgg	ttg	gtg	gcg	gtg	gcc	atg	gtg	tac	tac	tcg	gac	agt	ttg	gca	atg	480
Trp	Leu	Val	Ala	Val	Ala	Met	Val	Tyr	Tyr	Ser	Asp	Ser	Leu	Ala	Met	
			145			150					155				160	
cac	att	gga	tcg	gct	ctc	ttg	ttg	gga	ttg	ttc	tgg	cag	cag	tgt	gga	528

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His	Ile	Gly	Ser	Ala	Leu	Leu	Leu	Gly	Leu	Phe	Trp	Gln	Gln	Cys	Gly	
				165					170					175		
tgg	ctt	gcg	cac	gac	ttt	ctt	cac	cac	caa	gtc	ttt	aag	caa	cga	aag	576
Trp	Leu	Ala	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Lys	Gln	Arg	Lys	
			180					185					190			
tac	gga	gat	ctc	ggt	ggc	atc	ttt	tgg	gga	gat	ctc	atg	cag	ggg	ttc	624
Tyr	Gly	Asp	Leu	Val	Gly	Ile	Phe	Trp	Gly	Asp	Leu	Met	Gln	Gly	Phe	
		195				200					205					
tcg	atg	cag	tgg	tgg	aag	aac	aag	cac	aat	ggc	cac	cat	gct	gtt	ccc	672
Ser	Met	Gln	Trp	Trp	Lys	Asn	Lys	His	Asn	Gly	His	His	Ala	Val	Pro	
	210					215					220					
aac	ttg	cac	aac	tct	tcc	ttg	gac	agt	cag	gat	ggg	gat	ccc	gat	att	720
Asn	Leu	His	Asn	Ser	Ser	Leu	Asp	Ser	Gln	Asp	Gly	Asp	Pro	Asp	Ile	
	225				230					235					240	
gat	acc	atg	cca	ctc	ctt	gct	tgg	agt	ctc	aag	cag	gct	cag	agt	ttc	768
Asp	Thr	Met	Pro	Leu	Leu	Ala	Trp	Ser	Leu	Lys	Gln	Ala	Gln	Ser	Phe	
			245						250					255		
aga	gag	atc	aat	aag	gga	aag	gac	agt	acc	ttc	gtc	aag	tac	gct	atc	816
Arg	Glu	Ile	Asn	Lys	Gly	Lys	Asp	Ser	Thr	Phe	Val	Lys	Tyr	Ala	Ile	
			260					265					270			
aaa	ttc	cag	gca	ttc	aca	tac	ttc	ccc	atc	ctc	ctc	ttg	gct	cgc	atc	864
Lys	Phe	Gln	Ala	Phe	Thr	Tyr	Phe	Pro	Ile	Leu	Leu	Leu	Ala	Arg	Ile	
		275					280						285			
tct	tgg	ttg	aat	gaa	tcc	ttc	aaa	act	gca	ttc	gga	ctc	gga	gct	gcc	912
Ser	Trp	Leu	Asn	Glu	Ser	Phe	Lys	Thr	Ala	Phe	Gly	Leu	Gly	Ala	Ala	
	290					295					300					
tcg	gag	aat	gcc	aag	ttg	gag	ttg	gag	aag	cgt	gga	ctt	cag	tac	cca	960
Ser	Glu	Asn	Ala	Lys	Leu	Glu	Leu	Glu	Lys	Arg	Gly	Leu	Gln	Tyr	Pro	
	305				310					315					320	
ctt	ttg	gag	aag	ctt	gga	atc	acc	ctt	cat	tac	act	tgg	atg	ttc	gtc	1008
Leu	Leu	Glu	Lys	Leu	Gly	Ile	Thr	Leu	His	Tyr	Thr	Trp	Met	Phe	Val	
				325						330				335		
ctc	tct	tcc	gga	ttt	gga	agg	tgg	tct	ctt	cca	tat	tcc	atc	atg	tat	1056
Leu	Ser	Ser	Gly	Phe	Gly	Arg	Trp	Ser	Leu	Pro	Tyr	Ser	Ile	Met	Tyr	
			340					345						350		
ttc	ttc	act	gcc	aca	tgc	tcc	tcg	gga	ctt	ttc	ctc	gca	ttg	gtc	ttt	1104
Phe	Phe	Thr	Ala	Thr	Cys	Ser	Ser	Gly	Leu	Phe	Leu	Ala	Leu	Val	Phe	
			355				360						365			
gga	ttg	gga	cac	aac	ggt	atg	tca	gtg	tac	gat	gcc	acc	acc	cga	cct	1152
Gly	Leu	Gly	His	Asn	Gly	Met	Ser	Val	Tyr	Asp	Ala	Thr	Thr	Arg	Pro	
	370					375					380					
gac	ttc	tgg	caa	ctc	caa	gtc	acc	act	aca	cgt	aac	atc	att	ggt	gga	1200
Asp	Phe	Trp	Gln	Leu	Gln	Val	Thr	Thr	Thr	Arg	Asn	Ile	Ile	Gly	Gly	
	385				390					395					400	
cac	ggc	att	ccc	caa	ttc	ttt	gtg	gat	tgg	ttc	tgc	ggg	gga	ttg	caa	1248
His	Gly	Ile	Pro	Gln	Phe	Phe	Val	Asp	Trp	Phe	Cys	Gly	Gly	Leu	Gln	
			405						410					415		
tac	caa	gtg	gat	cac	cac	ctc	ttc	ccc	atg	atg	cct	aga	aac	aat	atc	1296
Tyr	Gln	Val	Asp	His	His	Leu	Phe	Pro	Met	Met	Pro	Arg	Asn	Asn	Ile	
			420					425					430			
gcg	aaa	tgc	cac	aag	ctt	gtg	gag	tca	ttc	tgt	aag	gag	tgg	ggg	gtg	1344
Ala	Lys	Cys	His	Lys	Leu	Val	Glu	Ser	Phe	Cys	Lys	Glu	Trp	Gly	Val	
		435					440						445			
aag	tac	cat	gag	gcc	gat	atg	tgg	gat	ggg	acc	gtg	gaa	gtg	ttg	caa	1392
Lys	Tyr	His	Glu	Ala	Asp	Met	Trp	Asp	Gly	Thr	Val	Glu	Val	Leu	Gln	
	450					455					460					
cat	ctc	tcc	aag	gtg	tcg	gat	gat	ttc	ctt	gtg	gag	atg	gtg	aag	gat	1440
His	Leu	Ser	Lys	Val	Ser	Asp	Asp	Phe	Leu	Val	Glu	Met	Val	Lys	Asp	
	465				470						475				480	

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ttc cct gcc atg taa  
Phe Pro Ala Met 1455

<210> SEQ ID NO 98  
<211> LENGTH: 484  
<212> TYPE: PRT  
<213> ORGANISM: *Thalassiosira pseudonana*

<400> SEQUENCE: 98

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

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Gly Leu Gly His Asn Gly Met Ser Val Tyr Asp Ala Thr Thr Arg Pro  
 370 375 380  
 Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Ile Gly Gly  
 385 390 395 400  
 His Gly Ile Pro Gln Phe Phe Val Asp Trp Phe Cys Gly Gly Leu Gln  
 405 410 415  
 Tyr Gln Val Asp His His Leu Phe Pro Met Met Pro Arg Asn Asn Ile  
 420 425 430  
 Ala Lys Cys His Lys Leu Val Glu Ser Phe Cys Lys Glu Trp Gly Val  
 435 440 445  
 Lys Tyr His Glu Ala Asp Met Trp Asp Gly Thr Val Glu Val Leu Gln  
 450 455 460  
 His Leu Ser Lys Val Ser Asp Asp Phe Leu Val Glu Met Val Lys Asp  
 465 470 475 480  
 Phe Pro Ala Met

<210> SEQ ID NO 99  
 <211> LENGTH: 1431  
 <212> TYPE: DNA  
 <213> ORGANISM: *Thalassiosira pseudonana*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1431)  
 <223> OTHER INFORMATION: Delta-5 desaturase

<400> SEQUENCE: 99

atg ccc ccc aac gcc gat atc tcc cgc atc cgc aac cgc atc ccc acc	48
Met Pro Pro Asn Ala Asp Ile Ser Arg Ile Arg Asn Arg Ile Pro Thr	
1 5 10 15	
aaa aca ggt acc gtt gcc tct gcc gac aac aac gac ccc gcc acc caa	96
Lys Thr Gly Thr Val Ala Ser Ala Asp Asn Asn Asp Pro Ala Thr Gln	
20 25 30	
tcc gtc cga acc ctc aaa tct ctc aag gcc aac gag gtc gtc atc aac	144
Ser Val Arg Thr Leu Lys Ser Leu Lys Gly Asn Glu Val Val Ile Asn	
35 40 45	
ggc aca att tat gac att gct gac ttt gtc cat cct gga gga gag gtt	192
Gly Thr Ile Tyr Asp Ile Ala Asp Phe Val His Pro Gly Gly Glu Val	
50 55 60	
gtc aag ttc ttt ggt ggg aat gat gtt act att cag tat aat atg att	240
Val Lys Phe Phe Gly Gly Asn Asp Val Thr Ile Gln Tyr Asn Met Ile	
65 70 75 80	
cat ccg tat cat acg ggg aaa cat ctg gag aag atg aag gct gtt gga	288
His Pro Tyr His Thr Gly Lys His Leu Glu Lys Met Lys Ala Val Gly	
85 90 95	
aag gtt gta gat tgg cag tcg gac tac aag ttc gac acc ccc ttt gaa	336
Lys Val Val Asp Trp Gln Ser Asp Tyr Lys Phe Asp Thr Pro Phe Glu	
100 105 110	
cga gag atc aaa tca gaa gtg ttc aag atc gta cgt cgc ggg cgt gag	384
Arg Glu Ile Lys Ser Glu Val Phe Lys Ile Val Arg Arg Gly Arg Glu	
115 120 125	
ttc ggc aca aca ggc tac ttc ctc cgt gcc ttt ttc tac atc gct ctc	432
Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala Phe Phe Tyr Ile Ala Leu	
130 135 140	
ttc ttc acc atg caa tac act ttc gcc aca tgc acc acc ttc acc acc	480
Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr Cys Thr Thr Phe Thr Thr	
145 150 155 160	
tac gat cac tgg tat cag agt ggt gta ttc atc gca att gtg ttt ggt	528
Tyr Asp His Trp Tyr Gln Ser Gly Val Phe Ile Ala Ile Val Phe Gly	
165 170 175	

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att tca cag gca ttc att ggg ttg aat gtc cag cac gat gcc aat cac Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His 180 185 190	576
gga gct gcc agt aag cgt ccc tgg gtg aat gac ttg ttg gga ttt gga Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly 195 200 205	624
acg gat ttg att gga tct aac aaa tgg aat tgg atg gca cag cat tgg Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp 210 215 220	672
act cat cac gct tac act aac cat agt gag aag gat ccc gat agc ttc Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe 225 230 235 240	720
agc tcg gaa cct atg ttt gca ttc aat gac tat ccc att gga cac ccg Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro 245 250 255	768
aag aga aag tgg tgg cat agg ttc cag gga ggg tac ttc ctc ttc atg Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met 260 265 270	816
ctt gga ctt tac tgg ctc tcg act gta ttc aat ccg caa ttc att gat Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp 275 280 285	864
ctt cgt caa cgt ggg gct cag tac gtc gga att caa atg gag aat gat Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp 290 295 300	912
ttc att gtc aag agg agg aag tac gcc gtt gca ttg agg atg atg tac Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr 305 310 315 320	960
att tac ttg aac att gtc agc ccc ttc atg aac aat ggt ttg agc tgg Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp 325 330 335	1008
tct acc ttt gga atc atc atg ttg atg gga atc agc gag agt ctc act Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr 340 345 350	1056
ctc agt gtg ctc ttc tcg ttg tct cac aac ttc atc aat tcg gat cgt Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg 355 360 365	1104
gat cct acg gct gac ttc aaa aag acc gga gaa caa gtg tgc tgg ttc Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe 370 375 380	1152
aag tcg cag gtg gag act tcg tct acc tat ggg ggt ttt att tcc gga Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly 385 390 395 400	1200
tgt ctt acg gga gga ctc aac ttt cag gtg gaa cat cat ctc ttt ccc Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro 405 410 415	1248
cgt atg agc agt gct tgg tat cct tac att gca cct acg gtt cgt gag Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu 420 425 430	1296
gtt tgc aag aag cac ggg gtg aac tac gct tat tat cct tgg att ggg Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly 435 440 445	1344
cag aat ttg gta tca aca ttc aaa tac atg cat cgc gct ggt agt gga Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly 450 455 460	1392
gcc aac tgg gag ctc aag ccg ttg tct gga agt gcc taa Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala 465 470 475	1431

&lt;210&gt; SEQ ID NO 100



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&lt;211&gt; LENGTH: 476

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 100

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

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385	390	395	400	
Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro	405	410	415	
Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu	420	425	430	
Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly	435	440	445	
Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly	450	455	460	
Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala	465	470	475	
<210> SEQ ID NO 101				
<211> LENGTH: 1449				
<212> TYPE: DNA				
<213> ORGANISM: Thalassiosira pseudonana				
<220> FEATURE:				
<221> NAME/KEY: CDS				
<222> LOCATION: (1)..(1449)				
<223> OTHER INFORMATION: Delta-5 desaturase				
<400> SEQUENCE: 101				
atg cca ccc aac gcc gag gtc aaa aac ctc cgt tca cgt tcc atc cca				48
Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro	5	10	15	
1				
acg aag aag tcc agt tca tcg tca tcc acc gcg aac gac gat ccg gct				96
Thr Lys Lys Ser Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala	20	25	30	
acc caa tcc acc tca cct gtg aac cga acc ctc aag tct ttg aat gga				144
Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly	35	40	45	
aac gaa ata gct att gac ggt gtc atc tat gat att gat ggc ttt gtc				192
Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val	50	55	60	
cat cct gga gga gag gtt att agc ttc ttt gga ggc aac gat gtg act				240
His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr	65	70	75	80
gta cag tac aaa atg att cat ccg tat cat aat agt aag cat ctc gag				288
Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu	85	90	95	
aag atg aga gcc gtt gga aag att gca gac tac tcc aca gag tac aag				336
Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys	100	105	110	
ttc gac aca ccc ttt gaa cga gag atc aaa tcc gaa gtg ttc aaa atc				384
Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile	115	120	125	
gtc cgt cga gga cgt gaa ttc ggt aca aca gga tat ttc ctc cgt gcc				432
Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala	130	135	140	
ttc ttc tac att gct ctc ttc ttc acc atg caa tac acc ttc gcc aca				480
Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr	145	150	155	160
tgc act acc ttc acc tac gat cat tgg tat caa agt ggt gta ttc				528
Cys Thr Thr Phe Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe	165	170	175	
atc gcc att gtg ttt ggt atc tca caa gct ttc att ggg ttg aat gta				576
Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val	180	185	190	
caa cat gat gcc aat cac gga gct gct agc aaa cga cct tgg gtg aat				624
Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn				

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195	200	205	
gat ctc ctt gga tct gga gct gat ctc atc ggt gga tgc aaa tgg aac Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn 210 215 220			672
tgg ttg gct cag cat tgg act cat cat gcg tat acc aat cac gct gat Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp 225 230 235 240			720
aaa gat cct gat agc ttt agt tcc gag ccg gtc ttc aac ttt aac gat Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp 245 250 255			768
tat ccc att ggt cac ccc aaa aga aag tgg tgg cat agg ttc caa ggg Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly 260 265 270			816
ctc tac ttc cta atc atg ctg agt ttc tat tgg gta tgc atg gta ttc Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe 275 280 285			864
aac cca caa gtt atc gac ctc cgt cat gct gga gct gcc tac gtt gga Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly 290 295 300			912
ttt cag atg gag aac gac ttt atc gtc aaa cgg aga aag tat gca atg Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met 305 310 315 320			960
gca ctt cgt gca atg tac ttc tat ttc aac atc tat tgt ccg att gtc Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val 325 330 335			1008
aac aat gga ttg act tgg tgc aca gtt gga atc atc ctc tta atg gga Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly 340 345 350			1056
gtt agc gaa agc ttc atg ctc tcc ggt cta ttc gta ctc tca cac aac Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn 355 360 365			1104
ttt gaa aat tcc gaa cgt gat cct acc tct gag tat cgc aag act ggt Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly 370 375 380			1152
gag caa gta tgt tgg ttc aag tct caa gtg gag act tct tct acc tac Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr 385 390 395 400			1200
gga ggt atc gtt gct ggg tgt ctc act ggt gga ctc aac ttt caa gtg Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val 405 410 415			1248
gag cat cat ttg ttc ccg agg atg agc agt gct tgg tat cct ttc atc Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile 420 425 430			1296
gcg ccg aag gtt aga gag att tgt aag aag cat gga gtt aga tac gct Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala 435 440 445			1344
tac tat ccg tac atc tgg cag aac ttg cat tct acc gtg agt tac atg Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met 450 455 460			1392
cat ggg acg gga acg gga gct aga tgg gag ctt cag ccg ttg tct gga His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly 465 470 475 480			1440
agg gcg tag Arg Ala			1449

&lt;210&gt; SEQ ID NO 102

&lt;211&gt; LENGTH: 482

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Thalassiosira pseudonana

-continued

&lt;400&gt; SEQUENCE: 102

Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro  
 1 5 10 15  
 Thr Lys Lys Ser Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala  
 20 25 30  
 Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly  
 35 40 45  
 Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val  
 50 55 60  
 His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr  
 65 70 75 80  
 Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu  
 85 90 95  
 Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys  
 100 105 110  
 Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile  
 115 120 125  
 Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala  
 130 135 140  
 Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr  
 145 150 155 160  
 Cys Thr Thr Phe Thr Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe  
 165 170 175  
 Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val  
 180 185 190  
 Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn  
 195 200 205  
 Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn  
 210 215 220  
 Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp  
 225 230 235 240  
 Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp  
 245 250 255  
 Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly  
 260 265 270  
 Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe  
 275 280 285  
 Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly  
 290 295 300  
 Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met  
 305 310 315 320  
 Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val  
 325 330 335  
 Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly  
 340 345 350  
 Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn  
 355 360 365  
 Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly  
 370 375 380  
 Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr  
 385 390 395 400  
 Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val  
 405 410 415

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Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile  
 420 425 430  
 Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala  
 435 440 445  
 Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met  
 450 455 460  
 His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly  
 465 470 475 480  
 Arg Ala

<210> SEQ ID NO 103  
 <211> LENGTH: 1512  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1512)  
 <223> OTHER INFORMATION: Delta-4 desaturase

<400> SEQUENCE: 103

atg tgc aac ggc aac ctc cca gca tcc acc gca cag ctc aag tcc acc 48  
 Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr  
 1 5 10 15  
 tcg aag ccc cag cag caa cat gag cat cgc acc atc tcc aag tcc gag 96  
 Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu  
 20 25 30  
 ctc gcc caa cac aac acg ccc aaa tca gca tgg tgt gcc gtc cac tcc 144  
 Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser  
 35 40 45  
 act ccc gcc acc gac cca tcc cac tcc aac aac aaa caa cac gca cac 192  
 Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His  
 50 55 60  
 cta gtc ctc gac att acc gac ttt gcg tcc cgc cat cca ggg gga gac 240  
 Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp  
 65 70 75 80  
 ctc atc ctc ctc gct tcc ggc aaa gac gcc tcg gtg ctg ttt gaa aca 288  
 Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr  
 85 90 95  
 tac cat cca cgt gga gtt ccg acg tct ctc att caa aag ctg cag att 336  
 Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile  
 100 105 110  
 gga gtg atg gag gag gag gcg ttt cgg gat tcg ttt tac agt tgg act 384  
 Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr  
 115 120 125  
 gat tct gac ttt tat act gtg ttg aag agg agg gtt gtg gag cgg ttg 432  
 Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu  
 130 135 140  
 gag gag agg ggg ttg gac agg agg gga tcg aaa gag att tgg atc aag 480  
 Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys  
 145 150 155 160  
 gct ttg ttc ttg ttg gtt gga ttt tgg tac tgt ttg tac aag atg tat 528  
 Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr  
 165 170 175  
 act acg tcg gat atc gat cag tac ggt att gcc att gcc tat tct att 576  
 Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile  
 180 185 190  
 gga atg gga acc ttt gcg gca ttc atc ggc acg tgt att caa cac gat 624  
 Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp  
 195 200 205

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gga aat cac ggt gca ttc gct cag aac aag tta ctc aac aag ttg gct Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala 210 215 220	672
ggg tgg acg ttg gat atg att ggt gcg agt gcg ttt acg tgg gag ctt Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu 225 230 235 240	720
cag cac atg ctg ggg cat cat cca tat acg aat gtg ttg gat ggg gtg Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val 245 250 255	768
gag gag gag agg aag gag agg ggg gag gat gtt gct ttg gaa gaa aag Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys 260 265 270	816
gat cag gat ttt gaa gtt gcc aca tcc gga cga tta tat cat att gat Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp 275 280 285	864
gcc aat gta cgt tat ggt tcg gta tgg aat gtc atg agg ttt tgg gct Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala 290 295 300	912
atg aag gtc att acg atg gga tat atg atg gga tta cca atc tac ttt Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe 305 310 315 320	960
cat gga gta ctg agg gga gtt gga ttg ttt gtt att ggg cat ttg gcg His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala 325 330 335	1008
tgt gga gag ttg ttg gcg acg atg ttt att gtg aat cac gtc att gag Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu 340 345 350	1056
ggt gtg agt tat gga acg aag gat ttg gtt ggt ggt gcg agt cat gta Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val 355 360 365	1104
gat gag aag aag att gtc aag cca acg act gta ttg gga gat aca cca Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro 370 375 380	1152
atg gta aag act cgc gag gag gca ttg aaa agc aac agc aat aac aac Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn 385 390 395 400	1200
aag aag aag gga gag aag aac tcg gta cca tcc gtt cca ttc aac gac Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp 405 410 415	1248
tgg gca gca gtc caa tgc cag acc tcc gtg aat tgg tct cca ggc tca Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser 420 425 430	1296
tgg ttc tgg aat cac ttt tct ggg gga ctc tct cat cag att gag cat Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His 435 440 445	1344
cac ttg ttc ccc agc att tgt cat aca aac tac tgt cat atc cag gat His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp 450 455 460	1392
gtt gtg gag agt acg tgt gct gag tac gga gtt ccg tat cag agt gag Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu 465 470 475 480	1440
agt aat ttg ttt gtt gct tat gga aag atg att agt cat ttg aag ttt Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe 485 490 495	1488
ttg ggt aaa gcc aag tgt gag tag Leu Gly Lys Ala Lys Cys Glu 500	1512

&lt;210&gt; SEQ ID NO 104

&lt;211&gt; LENGTH: 503

-continued

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 104

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Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr
1      5      10      15

Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu
20      25      30

Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser
35      40      45

Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His
50      55      60

Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp
65      70      75      80

Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr
85      90      95

Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile
100     105     110

Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr
115     120     125

Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu
130     135     140

Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys
145     150     155     160

Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr
165     170     175

Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile
180     185     190

Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp
195     200     205

Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala
210     215     220

Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu
225     230     235     240

Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val
245     250     255

Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys
260     265     270

Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp
275     280     285

Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala
290     295     300

Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe
305     310     315     320

His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala
325     330     335

Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu
340     345     350

Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val
355     360     365

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

Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn
385     390     395     400

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Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp  
 405 410 415  
 Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser  
 420 425 430  
 Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His  
 435 440 445  
 His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp  
 450 455 460  
 Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu  
 465 470 475 480  
 Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe  
 485 490 495  
 Leu Gly Lys Ala Lys Cys Glu  
 500

<210> SEQ ID NO 105  
 <211> LENGTH: 1257  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1257)  
 <223> OTHER INFORMATION: Omega-3 desaturase

<400> SEQUENCE: 105

atg tac aga tta aca tcc acc ttc ctc atc gca ttg gca ttc tcc tcc	48
Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser	
1 5 10 15	
tcc atc aat gcc ttc tct cca caa cgg cca cca cgt act atc acc aaa	96
Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys	
20 25 30	
agt aaa gtc caa agc acc gtg cta ccc ata ccg acc aag gat gat ctg	144
Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu	
35 40 45	
aac ttt ctc caa cca caa ctc gat gag aat gat ctc tac ctc gac gat	192
Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp	
50 55 60	
gtc aac act cca cca aga gca ggt acc atc atg aag atg ttg ccg aag	240
Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys	
65 70 75 80	
gaa acg ttc aac att gat aca gca act tca ttg ggt tac ttt ggt atg	288
Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met	
85 90 95	
gat atg gca gcg gtt gta tcg tcc atg acg ttg cta aat gct att gta	336
Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val	
100 105 110	
act tcg gat cag tac cat gct ctt cca ctt cct ctc caa gca gca aca	384
Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr	
115 120 125	
gtg att ccc ttt cag cta ttg gct ggg ttc gcc atg tgg tgt atg tgg	432
Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp	
130 135 140	
tgc att gga cac gat gct gga cat tct act gtt tcg aag aca aag tgg	480
Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp	
145 150 155 160	
atc aac cga gtc gtt ggt gaa gtg gct cat tct gtt gtt tgt ctc acg	528
Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr	
165 170 175	
ccg ttc gtg cct tgg cag atg tcg cat agg aaa cac cat ttg aat cac	576





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Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp  
 50 55 60  
 Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys  
 65 70 75 80  
 Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met  
 85 90 95  
 Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val  
 100 105 110  
 Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr  
 115 120 125  
 Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp  
 130 135 140  
 Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp  
 145 150 155 160  
 Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr  
 165 170 175  
 Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His  
 180 185 190  
 Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu  
 195 200 205  
 Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg  
 210 215 220  
 Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile  
 225 230 235 240  
 Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val  
 245 250 255  
 Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys  
 260 265 270  
 Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr  
 275 280 285  
 Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met  
 290 295 300  
 Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp  
 305 310 315 320  
 Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser  
 325 330 335  
 Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His  
 340 345 350  
 Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu  
 355 360 365  
 Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys  
 370 375 380  
 His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val  
 385 390 395 400  
 Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys  
 405 410 415  
 Arg Glu

<210> SEQ ID NO 107  
 <211> LENGTH: 1086  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1086)

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&lt;223&gt; OTHER INFORMATION: Delta-12 desaturase

&lt;400&gt; SEQUENCE: 107

atg	cag	gag	ggg	gtg	cga	aac	att	ccg	aac	gag	tgc	ttt	gag	acg	gga	48
Met	Gln	Glu	Gly	Val	Arg	Asn	Ile	Pro	Asn	Glu	Cys	Phe	Glu	Thr	Gly	
1			5					10					15			
cat	ctt	gaa	aga	ccc	tgg	cgt	tcc	ggc	cgg	tgt	ggg	cgc	gat	ccc	ggt	96
His	Leu	Glu	Arg	Pro	Trp	Arg	Ser	Gly	Arg	Cys	Gly	Arg	Asp	Pro	Gly	
		20					25						30			
tcg	aat	tgg	ggc	gct	ggc	ttc	cgc	ttt	ttt	tcg	ctc	aag	ggg	ttt	tgg	144
Ser	Asn	Trp	Gly	Ala	Gly	Phe	Arg	Phe	Phe	Ser	Leu	Lys	Gly	Phe	Trp	
		35					40					45				
tgg	ccg	gcg	tgg	tgg	gcg	tac	gcg	ttc	gtg	acg	ggg	acg	gcg	gcc	act	192
Trp	Pro	Ala	Trp	Trp	Ala	Tyr	Ala	Phe	Val	Thr	Gly	Thr	Ala	Ala	Thr	
	50					55					60					
ggg	tgt	tgg	gtc	gcc	gcg	cac	gag	tgc	ggg	cac	ggc	gcg	ttc	agc	gat	240
Gly	Cys	Trp	Val	Ala	Ala	His	Glu	Cys	Gly	His	Gly	Ala	Phe	Ser	Asp	
65					70					75					80	
aac	aag	acg	ttg	caa	gat	gcg	ggt	gga	tac	gtg	ttg	cac	tcg	ttg	ctc	288
Asn	Lys	Thr	Leu	Gln	Asp	Ala	Val	Gly	Tyr	Val	Leu	His	Ser	Leu	Leu	
				85					90					95		
ttg	gtg	ccg	tac	ttt	tct	tgg	cag	cga	tca	cac	gcg	gtg	cat	cac	tcg	336
Leu	Val	Pro	Tyr	Phe	Ser	Trp	Gln	Arg	Ser	His	Ala	Val	His	His	Ser	
			100					105					110			
agg	acg	aat	cac	ggt	ctt	gag	ggc	gag	acg	cac	gtg	ccg	gcg	cgc	ttg	384
Arg	Thr	Asn	His	Val	Leu	Glu	Gly	Glu	Thr	His	Val	Pro	Ala	Arg	Leu	
		115					120					125				
ggg	acg	gaa	gac	gcc	aac	gtc	gtg	ttc	aag	ctt	cgc	gaa	ttg	atc	ggt	432
Gly	Thr	Glu	Asp	Ala	Asn	Val	Val	Phe	Lys	Leu	Arg	Glu	Leu	Ile	Gly	
	130					135					140					
gaa	ggg	ccg	ttc	acg	ttt	ttc	aac	ctc	gtc	ggc	gtc	ttc	gcg	ctc	gga	480
Glu	Gly	Pro	Phe	Thr	Phe	Phe	Asn	Leu	Val	Gly	Val	Phe	Ala	Leu	Gly	
	145					150					155				160	
tgg	ccg	att	tac	ttg	ctc	acc	ggc	gcg	agc	ggc	gga	ccg	gtg	cgc	ggt	528
Trp	Pro	Ile	Tyr	Leu	Leu	Thr	Gly	Ala	Ser	Gly	Gly	Pro	Val	Arg	Gly	
			165						170					175		
aac	acg	aac	cac	ttc	tta	ccc	ttc	atg	ggc	gag	aaa	ggt	aag	cac	gcg	576
Asn	Thr	Asn	His	Phe	Leu	Pro	Phe	Met	Gly	Glu	Lys	Gly	Lys	His	Ala	
			180					185					190			
ctg	ttc	ccg	ggt	aag	tgg	gcg	aag	aag	gtg	tgg	cag	tct	gac	atc	ggc	624
Leu	Phe	Pro	Gly	Lys	Trp	Ala	Lys	Lys	Val	Trp	Gln	Ser	Asp	Ile	Gly	
		195					200					205				
ggt	ggt	gcc	gtc	ctg	ggc	gcg	ctc	gcg	gct	tgg	gcg	gcg	cac	agc	ggg	672
Val	Val	Ala	Val	Leu	Gly	Ala	Leu	Ala	Ala	Trp	Ala	Ala	His	Ser	Gly	
	210					215					220					
att	gcc	aca	gtg	atg	gca	ctc	tac	gtc	ggc	ccg	tac	atg	gtg	acc	aac	720
Ile	Ala	Thr	Val	Met	Ala	Leu	Tyr	Val	Gly	Pro	Tyr	Met	Val	Thr	Asn	
	225				230					235					240	
ttt	tgg	ctc	gtc	ttg	tac	acg	tgg	tta	cag	cac	acc	gac	ggt	gac	gtg	768
Phe	Trp	Leu	Val	Leu	Tyr	Thr	Trp	Leu	Gln	His	Thr	Asp	Val	Asp	Val	
			245						250					255		
ccg	cac	ttc	gag	ggc	gac	gat	tgg	aac	ttg	gtc	aag	ggg	gca	ttc	atg	816
Pro	His	Phe	Glu	Gly	Asp	Asp	Trp	Asn	Leu	Val	Lys	Gly	Ala	Phe	Met	
			260					265					270			
acg	atc	gat	cgc	ccg	tac	ggc	cca	ggt	ttt	gat	ttc	ttg	cac	cac	cgc	864
Thr	Ile	Asp	Arg	Pro	Tyr	Gly	Pro	Val	Phe	Asp	Phe	Leu	His	His	Arg	
		275					280					285				
atc	ggc	agc	acg	cac	gtc	gcg	cac	cac	atc	aac	aca	cca	ttc	ccg	cat	912
Ile	Gly	Ser	Thr	His	Val	Ala	His	His	Ile	Asn	Thr	Pro	Phe	Pro	His	
	290					295						300				

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tac aag gct caa atg gcg acg gat gcg cta aag gag gcg tat ccc gac      960
Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp
305                310                315                320

ctc tac ctt tac gat cca act ccg atc gcg acc gct acg tgg cgc gtg      1008
Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val
                325                330                335

ggg agc aag tgc atc gcc gtc gtg aag aag gga gac gaa tgg gtg ttc      1056
Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe
                340                345                350

acg gat aag caa ctc ccg gtc gcg gcg tga      1086
Thr Asp Lys Gln Leu Pro Val Ala Ala
                355                360

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&lt;210&gt; SEQ ID NO 108

&lt;211&gt; LENGTH: 361

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 108

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Met Gln Glu Gly Val Arg Asn Ile Pro Asn Glu Cys Phe Glu Thr Gly
1                5                10                15

His Leu Glu Arg Pro Trp Arg Ser Gly Arg Cys Gly Arg Asp Pro Gly
                20                25                30

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

Trp Pro Ala Trp Trp Ala Tyr Ala Phe Val Thr Gly Thr Ala Ala Thr
                50                55                60

Gly Cys Trp Val Ala Ala His Glu Cys Gly His Gly Ala Phe Ser Asp
65                70                75                80

Asn Lys Thr Leu Gln Asp Ala Val Gly Tyr Val Leu His Ser Leu Leu
                85                90                95

Leu Val Pro Tyr Phe Ser Trp Gln Arg Ser His Ala Val His His Ser
                100                105                110

Arg Thr Asn His Val Leu Glu Gly Glu Thr His Val Pro Ala Arg Leu
                115                120                125

Gly Thr Glu Asp Ala Asn Val Val Phe Lys Leu Arg Glu Leu Ile Gly
                130                135                140

Glu Gly Pro Phe Thr Phe Phe Asn Leu Val Gly Val Phe Ala Leu Gly
145                150                155                160

Trp Pro Ile Tyr Leu Leu Thr Gly Ala Ser Gly Gly Pro Val Arg Gly
                165                170                175

Asn Thr Asn His Phe Leu Pro Phe Met Gly Glu Lys Gly Lys His Ala
                180                185                190

Leu Phe Pro Gly Lys Trp Ala Lys Lys Val Trp Gln Ser Asp Ile Gly
                195                200                205

Val Val Ala Val Leu Gly Ala Leu Ala Ala Trp Ala Ala His Ser Gly
                210                215                220

Ile Ala Thr Val Met Ala Leu Tyr Val Gly Pro Tyr Met Val Thr Asn
225                230                235                240

Phe Trp Leu Val Leu Tyr Thr Trp Leu Gln His Thr Asp Val Asp Val
                245                250                255

Pro His Phe Glu Gly Asp Asp Trp Asn Leu Val Lys Gly Ala Phe Met
                260                265                270

Thr Ile Asp Arg Pro Tyr Gly Pro Val Phe Asp Phe Leu His His Arg
                275                280                285

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Ile Gly Ser Thr His Val Ala His His Ile Asn Thr Pro Phe Pro His  
 290 295 300  
 Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp  
 305 310 315 320  
 Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val  
 325 330 335  
 Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe  
 340 345 350  
 Thr Asp Lys Gln Leu Pro Val Ala Ala  
 355 360

<210> SEQ ID NO 109  
 <211> LENGTH: 1305  
 <212> TYPE: DNA  
 <213> ORGANISM: Thalassiosira pseudonana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1305)  
 <223> OTHER INFORMATION: Delta-12 desaturase

<400> SEQUENCE: 109

atg gga aag gga gga aga tca gta acc cgc gct caa aca gca gaa aag 48  
 Met Gly Lys Gly Gly Arg Ser Val Thr Arg Ala Gln Thr Ala Glu Lys  
 1 5 10 15  
 tca gca cac acc atc caa acc ttc acc gac ggc cga tgg gtc tcc ccc 96  
 Ser Ala His Thr Ile Gln Thr Phe Thr Asp Gly Arg Trp Val Ser Pro  
 20 25 30  
 tac aac ccc ctc gca aaa gat gca cct gaa ctc ccc tcc aag ggt gaa 144  
 Tyr Asn Pro Leu Ala Lys Asp Ala Pro Glu Leu Pro Ser Lys Gly Glu  
 35 40 45  
 atc aag gcg gtc atc ccc aaa gag tgc ttc gaa cga agc tac ctc cac 192  
 Ile Lys Ala Val Ile Pro Lys Glu Cys Phe Glu Arg Ser Tyr Leu His  
 50 55 60  
 tcc atg tac ttc gtc ctc cgt gac acc gtc atg gcc gtg gcc tgc gcc 240  
 Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala  
 65 70 75 80  
 tac atc gcc cac tca acg ctc tcc acc gat att ccc tcc gag tta ctg 288  
 Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu  
 85 90 95  
 agc gtg gac gca ctc aaa tgg ttc ctc gga tgg aac acc tac gcc ttt 336  
 Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe  
 100 105 110  
 tgg atg ggg tgc att ctc acc gga cac tgg gtc cta gcc cat gaa tgt 384  
 Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys  
 115 120 125  
 gga cat ggt gca ttc tct ccc tct cag acg ttt aat gac ttt tgg ggg 432  
 Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly  
 130 135 140  
 ttc att atg cat cag gcg gtg ttg gtt ccg tat ttc gcc tgg cag tac 480  
 Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr  
 145 150 155 160  
 tct cat gcg aag cat cat cga cgt acc aac aac att atg gat ggg gag 528  
 Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu  
 165 170 175  
 agc cat gtg ccc aat atc gcc aag gaa atg gga ttg aac gag aag aat 576  
 Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn  
 180 185 190  
 gag cgc agt gga gga tat gcc gcc att cat gag gct att gga gat gga 624  
 Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly  
 195 200 205

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ccc ttt gcg atg ttt caa atc ttt gct cac ttg gtg atc ggg tgg cct	672
Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro	
210 215 220	
att tac ttg atg gga ttt gct tcc act gga cgt ctc ggt cag gat ggg	720
Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly	
225 230 235 240	
aag gaa ctt cag gct gga gag atc atc gac cat tac cgt cct tgg agt	768
Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser	
245 250 255	
aag atg ttc ccc acc aag ttg cga ttc aaa att gct ctt tcg aca ctt	816
Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu	
260 265 270	
gga gtg att gcc gcc tgg gtt ggg ttg tac ttt gct gca caa gag tat	864
Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr	
275 280 285	
gga gtc ttg ccc gtg gtt ctt tgg tac att ggc cca ctc atg tgg aat	912
Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn	
290 295 300	
cag gcg tgg ctt gtg ctc tac act tgg ctt cag cac aat gat ccc tcc	960
Gln Ala Trp Leu Val Leu Tyr Thr Trp Leu Gln His Asn Asp Pro Ser	
305 310 315 320	
gtg cct caa tat gga agt gac gaa tgg aca tgg gtc aag gga gct ttg	1008
Val Pro Gln Tyr Gly Ser Asp Glu Trp Thr Trp Val Lys Gly Ala Leu	
325 330 335	
tcg acg att gat cgc ccg tat ggt atc ttt gac ttc ttc cat cac aag	1056
Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys	
340 345 350	
att gga agc act cac gta gct cat cat ttg ttc cac gag atg cca ttt	1104
Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe	
355 360 365	
tac aag gcg gat gtg gct act gcg tcg atc aag ggt ttc ttg gag ccg	1152
Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro	
370 375 380	
aag gga ctt tac aac tat gat cca acg cct tgg tat gtg gcc atg tgg	1200
Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp	
385 390 395 400	
agg gtg gcc aag act tgt cat tat att gag gat gtg gat gga gtt cag	1248
Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln	
405 410 415	
tat tat aag agt ttg gag gat gtg cct ttg aag aag gat gcc aag aag	1296
Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys	
420 425 430	
tct gat tag	1305
Ser Asp	

&lt;210&gt; SEQ ID NO 110

&lt;211&gt; LENGTH: 434

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Thalassiosira pseudonana*

&lt;400&gt; SEQUENCE: 110

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

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Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala
65          70          75          80

Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu
85          90

Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe
100        105        110

Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys
115        120        125

Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly
130        135        140

Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr
145        150        155        160

Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu
165        170        175

Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn
180        185        190

Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly
195        200        205

Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro
210        215        220

Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly
225        230        235        240

Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser
245        250        255

Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu
260        265        270

Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr
275        280        285

Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn
290        295        300

Gln Ala Trp Leu Val Leu Tyr Thr Trp Leu Gln His Asn Asp Pro Ser
305        310        315        320

Val Pro Gln Tyr Gly Ser Asp Glu Trp Thr Trp Val Lys Gly Ala Leu
325        330        335

Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys
340        345        350

Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe
355        360        365

Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro
370        375        380

Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp
385        390        395        400

Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln
405        410        415

Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys
420        425        430

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Ser Asp

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<210> SEQ ID NO 111
<211> LENGTH: 879
<212> TYPE: DNA
<213> ORGANISM: Ostreococcus tauri
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(879)

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&lt;223&gt; OTHER INFORMATION: Delta-6 elongase

&lt;400&gt; SEQUENCE: 111

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atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag      48
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
1           5           10           15

tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt      96
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
           20           25           30

cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc     144
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
           35           40           45

att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc     192
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
           50           55           60

aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa     240
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
65           70           75           80

att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg     288
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
           85           90           95

ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa     336
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
           100          105          110

gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg     384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
           115          120          125

gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata     432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
           130          135          140

tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg     480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
145           150           155           160

caa gta agt ttc cta cac att tat cac cac agc acg att tcc ttt att     528
Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile
           165          170          175

tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc     576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
           180          185          190

gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta     624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
           195          200          205

tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt     672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu
210           215           220

tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc     720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
225           230           235           240

aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag     768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
           245          250          255

ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc gcc ttg     816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
           260          265          270

ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag     864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
           275          280          285

aaa aaa cag cag tga                                             879
Lys Lys Gln Gln
290

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<210> SEQ ID NO 112  
 <211> LENGTH: 292  
 <212> TYPE: PRT  
 <213> ORGANISM: *Ostreococcus tauri*

<400> SEQUENCE: 112

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

<210> SEQ ID NO 113  
 <211> LENGTH: 903  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(903)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 113

atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac

48

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Met	Ser	Ala	Ser	Gly	Ala	Leu	Leu	Pro	Ala	Ile	Ala	Phe	Ala	Ala	Tyr		
1				5					10					15			
gcg	tac	gcg	acg	tac	gcc	tac	gcc	ttt	gag	tgg	tcg	cac	gcg	aat	ggc		96
Ala	Tyr	Ala	Thr	Tyr	Ala	Tyr	Ala	Phe	Glu	Trp	Ser	His	Ala	Asn	Gly		
			20					25					30				
atc	gac	aac	gtc	gac	gcg	cgc	gag	tgg	atc	ggt	gcg	ctg	tcg	ttg	agg		144
Ile	Asp	Asn	Val	Asp	Ala	Arg	Glu	Trp	Ile	Gly	Ala	Leu	Ser	Leu	Arg		
		35					40					45					
ctc	ccg	gcg	atc	gcg	acg	acg	atg	tac	ctg	ttg	ttc	tgc	ctg	gtc	gga		192
Leu	Pro	Ala	Ile	Ala	Thr	Thr	Met	Tyr	Leu	Leu	Phe	Cys	Leu	Val	Gly		
	50						55				60						
ccg	agg	ttg	atg	gcg	aag	cgc	gag	gcg	ttc	gac	ccg	aag	ggg	ttc	atg		240
Pro	Arg	Leu	Met	Ala	Lys	Arg	Glu	Ala	Phe	Asp	Pro	Lys	Gly	Phe	Met		
65					70					75					80		
ctg	gcg	tac	aat	gcg	tat	cag	acg	gcg	ttc	aac	gtc	gtc	gtg	ctc	ggg		288
Leu	Ala	Tyr	Asn	Ala	Tyr	Gln	Thr	Ala	Phe	Asn	Val	Val	Val	Leu	Gly		
			85						90					95			
atg	ttc	gcg	cga	gag	atc	tcg	ggg	ctg	ggg	cag	ccc	gtg	tgg	ggg	tca		336
Met	Phe	Ala	Arg	Glu	Ile	Ser	Gly	Leu	Gly	Gln	Pro	Val	Trp	Gly	Ser		
			100					105						110			
acc	atg	ccg	tgg	agc	gat	aga	aaa	tcg	ttt	aag	atc	ctc	ctc	ggg	gtg		384
Thr	Met	Pro	Trp	Ser	Asp	Arg	Lys	Ser	Phe	Lys	Ile	Leu	Leu	Gly	Val		
		115					120							125			
tgg	ttg	cac	tac	aac	aac	aaa	tat	ttg	gag	cta	ttg	gac	act	gtg	ttc		432
Trp	Leu	His	Tyr	Asn	Asn	Lys	Tyr	Leu	Glu	Leu	Leu	Asp	Thr	Val	Phe		
		130				135								140			
atg	gtt	gcg	cgc	aag	aag	acg	aag	cag	ttg	agc	ttc	ttg	cac	gtt	tat		480
Met	Val	Ala	Arg	Lys	Thr	Lys	Gln	Leu	Ser	Phe	Leu	His	Val	Tyr			
		145			150					155				160			
cat	cac	gcc	ctg	ttg	atc	tgg	gcg	tgg	tgg	ttg	gtg	tgt	cac	ttg	atg		528
His	His	Ala	Leu	Leu	Ile	Trp	Ala	Trp	Trp	Leu	Val	Cys	His	Leu	Met		
			165						170					175			
gcc	acg	aac	gat	tgt	atc	gat	gcc	tac	ttc	ggc	gcg	gcg	tgc	aac	tcg		576
Ala	Thr	Asn	Asp	Cys	Ile	Asp	Ala	Tyr	Phe	Gly	Ala	Ala	Cys	Asn	Ser		
			180					185						190			
ttc	att	cac	atc	gtg	atg	tac	tcg	tat	tat	ctc	atg	tcg	gcg	ctc	ggc		624
Phe	Ile	His	Ile	Val	Met	Tyr	Ser	Tyr	Tyr	Leu	Met	Ser	Ala	Leu	Gly		
		195					200						205				
att	cga	tgc	ccg	tgg	aag	cga	tac	atc	acc	cag	gct	caa	atg	ctc	caa		672
Ile	Arg	Cys	Pro	Trp	Lys	Arg	Tyr	Ile	Thr	Gln	Ala	Gln	Met	Leu	Gln		
		210				215						220					
ttc	gtc	att	gtc	ttc	gcg	cac	gcc	gtg	ttc	gtg	ctg	cg	cag	aag	cac		720
Phe	Val	Ile	Val	Phe	Ala	His	Ala	Val	Phe	Val	Leu	Arg	Gln	Lys	His		
		225			230					235				240			
tgc	ccg	gtc	acc	ctt	cct	tgg	gcg	caa	atg	ttc	gtc	atg	acg	aac	atg		768
Cys	Pro	Val	Thr	Leu	Pro	Trp	Ala	Gln	Met	Phe	Val	Met	Thr	Asn	Met		
				245					250					255			
ctc	gtg	ctc	ttc	ggg	aac	ttc	tac	ctc	aag	gcg	tac	tcg	aac	aag	tcg		816
Leu	Val	Leu	Phe	Gly	Asn	Phe	Tyr	Leu	Lys	Ala	Tyr	Ser	Asn	Lys	Ser		
			260					265						270			
cgc	ggc	gac	ggc	gcg	agt	tcc	gtg	aaa	cca	gcc	gag	acc	acg	cgc	gcg		864
Arg	Gly	Asp	Gly	Ala	Ser	Ser	Val	Lys	Pro	Ala	Glu	Thr	Thr	Arg	Ala		
		275					280						285				
ccc	agc	gtg	cga	cgc	acg	cga	tct	cga	aaa	att	gac	taa					903
Pro	Ser	Val	Arg	Arg	Thr	Arg	Ser	Arg	Lys	Ile	Asp						
		290				295					300						

&lt;210&gt; SEQ ID NO 114

&lt;211&gt; LENGTH: 300

&lt;212&gt; TYPE: PRT

-continued

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 114

```

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

```

&lt;210&gt; SEQ ID NO 115

&lt;211&gt; LENGTH: 13

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Consensus sequence

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;222&gt; LOCATION: (2)..(2)

&lt;223&gt; OTHER INFORMATION: Xaa is Ser, Cys, Leu or Gly, preferably is Cys or Leu

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;222&gt; LOCATION: (3)..(3)

&lt;223&gt; OTHER INFORMATION: Xaa is Thr, Phe, Ile, Ser, Val, Trp or Gly, preferably is Phe or Trp

&lt;220&gt; FEATURE:

-continued

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<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa is Val or Ile
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is Val, Ile or Thr, preferably is Val or
Ile
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa is Ile, Phe, Val, Leu or Cys, preferably
is Cys or Val
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa is Ser, Gly, Tyr, Thr, Ala, preferably is
Thr or Ser
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is Phe, Met, Thr, Leu, Ala or Gly,
preferably is Leu

```

&lt;400&gt; SEQUENCE: 115

```

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
1           5           10

```

```

<210> SEQ ID NO 116
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Ala, Ser or Thr, preferably is Ala or
Ser, more preferably is Ala
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa is Thr, Met, Val, Leu, Ile or Ser,
preferably is Leu or Thr, more preferably is Leu
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is Val, Thr, Met, Leu or Ile, preferably
is Ile or Ser, more
preferably is Ile
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is Val, Met, Leu, Ile, Ala, Pro, Ser or
Phe, preferably is Ile or Ser, more preferably is Ile

```

&lt;400&gt; SEQUENCE: 116

```

His His Xaa Xaa Xaa Xaa Trp Ala Trp Trp
1           5           10

```

```

<210> SEQ ID NO 117
<211> LENGTH: 909
<212> TYPE: DNA
<213> ORGANISM: Xenopus laevis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(909)
<223> OTHER INFORMATION: Delta-5 elongase

```

&lt;400&gt; SEQUENCE: 117

```

atg gcc ttc aag gag ctc aca tca agg gca gtg ctc ctg tat gat gaa      48
Met Ala Phe Lys Glu Leu Thr Ser Arg Ala Val Leu Leu Tyr Asp Glu
1           5           10           15

```

-continued

tgg att aaa gat gct gat cct agg gtt gaa gac tgg cca ctc atg tcc	96
Trp Ile Lys Asp Ala Asp Pro Arg Val Glu Asp Trp Pro Leu Met Ser	
20 25 30	
tct cct atc cta caa acc atc atc atc ggc gct tac atc tac ttt gtc	144
Ser Pro Ile Leu Gln Thr Ile Ile Ile Gly Ala Tyr Ile Tyr Phe Val	
35 40 45	
aca tca ttg ggc cca agg atc atg gag aac agg aag ccg ttt gct ctg	192
Thr Ser Leu Gly Pro Arg Ile Met Glu Asn Arg Lys Pro Phe Ala Leu	
50 55 60	
aag gag atc atg gca tgt tac aac tta ttc atg gtt ctg ttt tct gtg	240
Lys Glu Ile Met Ala Cys Tyr Asn Leu Phe Met Val Leu Phe Ser Val	
65 70 75 80	
tac atg tgc tat gag ttt ctc atg tcg ggc tgg gct act gga tat tcc	288
Tyr Met Cys Tyr Glu Phe Leu Met Ser Gly Trp Ala Thr Gly Tyr Ser	
85 90 95	
ttt aga tgt gac att gtt gac tac tct cag tca cct cag gcg tta cgg	336
Phe Arg Cys Asp Ile Val Asp Tyr Ser Gln Ser Pro Gln Ala Leu Arg	
100 105 110	
atg gcc tgg acc tgc tgg ctc ttc tat ttt tca aag ttc att gaa tta	384
Met Ala Trp Thr Cys Trp Leu Phe Tyr Phe Ser Lys Phe Ile Glu Leu	
115 120 125	
tta gac act gtt ttc ttt gtg ctg cgt aag aag aac agc cag att aca	432
Leu Asp Thr Val Phe Phe Val Leu Arg Lys Lys Asn Ser Gln Ile Thr	
130 135 140	
ttc ctg cac gtc tat cac cac tcc att atg cct tgg acg tgg tgg ttt	480
Phe Leu His Val Tyr His His Ser Ile Met Pro Trp Thr Trp Trp Phe	
145 150 155 160	
gga gtc aaa ttt gct cca ggt ggt ttg ggc aca ttc cat gca ctg gtg	528
Gly Val Lys Phe Ala Pro Gly Gly Leu Gly Thr Phe His Ala Leu Val	
165 170 175	
aac tgt gtg gtc cat gtt atc atg tac agc tac tac ggc ctg tca gcc	576
Asn Cys Val Val His Val Ile Met Tyr Ser Tyr Tyr Gly Leu Ser Ala	
180 185 190	
ttg ggg cct gcc tac cag aag tac ctg tgg tgg aaa aag tac atg acg	624
Leu Gly Pro Ala Tyr Gln Lys Tyr Leu Trp Trp Lys Lys Tyr Met Thr	
195 200 205	
tct atc caa ctg acc cag ttc ttg atg gtt act ttt cac atc ggc cag	672
Ser Ile Gln Leu Thr Gln Phe Leu Met Val Thr Phe His Ile Gly Gln	
210 215 220	
ttc ttc ttc atg gag aat tgc ccg tac cag tat ccc gtc ttc ttg tat	720
Phe Phe Phe Met Glu Asn Cys Pro Tyr Gln Tyr Pro Val Phe Leu Tyr	
225 230 235 240	
gtc att tgg ctg tac ggg ttc gtt ttc tta atc ttg ttc ctc aac ttc	768
Val Ile Trp Leu Tyr Gly Phe Val Phe Leu Ile Leu Phe Leu Asn Phe	
245 250 255	
tgg ttc cac gct tac atc aaa gga cag agg ctg ccg aaa gcc gtc caa	816
Trp Phe His Ala Tyr Ile Lys Gly Gln Arg Leu Pro Lys Ala Val Gln	
260 265 270	
aat ggc cac tgc aag aac aac aac aac caa gaa aac act tgg tgc aag	864
Asn Gly His Cys Lys Asn Asn Asn Asn Gln Glu Asn Thr Trp Cys Lys	
275 280 285	
aac aaa aac cag aaa aac ggt gca ttg aaa agc aaa aac cat tga	909
Asn Lys Asn Gln Lys Asn Gly Ala Leu Lys Ser Lys Asn His	
290 295 300	

&lt;210&gt; SEQ ID NO 118

&lt;211&gt; LENGTH: 302

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Xenopus laevis

&lt;400&gt; SEQUENCE: 118

-continued

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

&lt;210&gt; SEQ ID NO 119

&lt;211&gt; LENGTH: 870

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Ciona intestinalis

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(870)

&lt;223&gt; OTHER INFORMATION: Delta-5 elongase

&lt;400&gt; SEQUENCE: 119

atg gac gta ctt cat cgt ttc tta gga ttc tac gaa tgg acg ctg act 48  
 Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr  
 1 5 10 15  
 ttc gcg gac ccc cga gtg gca aaa tgg cct tta ata gaa aac ccc ctt 96  
 Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu  
 20 25 30  
 cct aca att gct att gtg ttg ctg tac ctg gcg ttt gtt ctg tat att 144

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Pro	Thr	Ile	Ala	Ile	Val	Leu	Leu	Tyr	Leu	Ala	Phe	Val	Leu	Tyr	Ile	
		35					40					45				
ggg	ccg	cgt	ttt	atg	cga	aaa	aga	gca	cca	ggt	gac	ttt	ggt	tta	ttc	192
Gly	Pro	Arg	Phe	Met	Arg	Lys	Arg	Ala	Pro	Val	Asp	Phe	Gly	Leu	Phe	
	50					55					60					
ctc	cct	gga	tat	aac	ttt	gct	ttg	ggt	gca	tta	aat	tat	tat	atc	ctg	240
Leu	Pro	Gly	Tyr	Asn	Phe	Ala	Leu	Val	Ala	Leu	Asn	Tyr	Tyr	Ile	Leu	
	65			70					75					80		
caa	gaa	gtg	gtc	act	ggg	agt	tat	ggg	gct	ggg	tat	gat	ttg	ggt	tgc	288
Gln	Glu	Val	Val	Thr	Gly	Ser	Tyr	Gly	Ala	Gly	Tyr	Asp	Leu	Val	Cys	
				85				90						95		
aca	cca	ctt	cga	agt	gat	tcc	tac	gat	ccc	aat	gaa	atg	aag	ggt	gca	336
Thr	Pro	Leu	Arg	Ser	Asp	Ser	Tyr	Asp	Pro	Asn	Glu	Met	Lys	Val	Ala	
			100				105						110			
aac	gct	gta	tgg	tgg	tat	tat	gta	tcc	aag	ata	ata	gag	ttg	ttt	gat	384
Asn	Ala	Val	Trp	Trp	Tyr	Tyr	Val	Ser	Lys	Ile	Ile	Glu	Leu	Phe	Asp	
		115					120						125			
act	gtg	ttg	ttc	act	cta	cgc	aaa	cga	gac	cga	caa	gta	act	ttc	ctt	432
Thr	Val	Leu	Phe	Thr	Leu	Arg	Lys	Arg	Asp	Arg	Gln	Val	Thr	Phe	Leu	
		130				135					140					
cat	ggt	tat	cac	cat	tct	acc	atg	ccc	ctg	ttg	tgg	tgg	att	ggg	gca	480
His	Val	Tyr	His	His	Ser	Thr	Met	Pro	Leu	Leu	Trp	Trp	Ile	Gly	Ala	
					150				155						160	
aag	tgg	gtg	cct	ggt	ggg	caa	tca	ttt	ggt	ggc	atc	ata	ctg	aac	tcc	528
Lys	Trp	Val	Pro	Gly	Gly	Gln	Ser	Phe	Val	Gly	Ile	Ile	Leu	Asn	Ser	
			165						170					175		
agt	ggt	cat	ggt	atc	atg	tat	acg	tac	tat	gga	ttg	tca	gcc	ttg	ggg	576
Ser	Val	His	Val	Ile	Met	Tyr	Thr	Tyr	Tyr	Gly	Leu	Ser	Ala	Leu	Gly	
			180				185						190			
cct	cac	atg	cag	aag	ttt	cta	tgg	tgg	aag	aaa	tat	atc	aca	atg	ttg	624
Pro	His	Met	Gln	Lys	Phe	Leu	Trp	Trp	Lys	Lys	Tyr	Ile	Thr	Met	Leu	
			195				200						205			
caa	ctg	ggt	caa	ttt	ggt	ctt	gcc	atc	tac	cat	act	gct	cga	tca	ttg	672
Gln	Leu	Val	Gln	Phe	Val	Leu	Ala	Ile	Tyr	His	Thr	Ala	Arg	Ser	Leu	
		210				215					220					
tac	ggt	aaa	tgt	ccc	tcg	cct	ggt	tgg	atg	cac	tgg	gca	ctt	atc	ttg	720
Tyr	Val	Lys	Cys	Pro	Ser	Pro	Val	Trp	Met	His	Trp	Ala	Leu	Ile	Leu	
					230					235				240		
tac	gct	ttc	tca	ttc	att	ttg	ctt	ttc	tca	aac	ttc	tac	atg	cat	gcc	768
Tyr	Ala	Phe	Ser	Phe	Ile	Leu	Leu	Phe	Ser	Asn	Phe	Tyr	Met	His	Ala	
				245					250					255		
tat	atc	aag	aaa	tca	aga	aaa	ggg	aaa	gag	aat	ggc	agt	cga	gga	aaa	816
Tyr	Ile	Lys	Lys	Ser	Arg	Lys	Gly	Lys	Glu	Asn	Gly	Ser	Arg	Gly	Lys	
			260				265						270			
ggt	ggt	gta	agt	aat	gga	aag	gaa	aag	ctg	cac	gct	aat	ggt	aaa	acc	864
Gly	Gly	Val	Ser	Asn	Gly	Lys	Glu	Lys	Leu	His	Ala	Asn	Gly	Lys	Thr	
		275					280						285			
gat	taa															870
Asp																

&lt;210&gt; SEQ ID NO 120

&lt;211&gt; LENGTH: 289

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Ciona intestinalis

&lt;400&gt; SEQUENCE: 120

Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr  
1 5 10 15

Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu  
20 25 30

-continued

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

Asp

<210> SEQ ID NO 121  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

&lt;400&gt; SEQUENCE: 121

aggatccatg gccttcaagg agctcacatc

30

<210> SEQ ID NO 122  
 <211> LENGTH: 35  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

&lt;400&gt; SEQUENCE: 122

cctcgagtca atggtttttg cttttcaatg caccg

35

<210> SEQ ID NO 123  
 <211> LENGTH: 25  
 <212> TYPE: DNA



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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 123  
  
 taagcttatg gacgtacttc atcgt 25

<210> SEQ ID NO 124  
 <211> LENGTH: 26  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 124  
  
 tcagatcttt aatcggtttt accatt 26

<210> SEQ ID NO 125  
 <211> LENGTH: 34  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 125  
  
 gcggccgcac catggccttc aaggagctca catc 34

<210> SEQ ID NO 126  
 <211> LENGTH: 38  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 126  
  
 gcggccgcct tcaatggttt ttgcttttca atgcaccg 38

<210> SEQ ID NO 127  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 127  
  
 gcggccgcac catggacgta cttcatcgt 29

<210> SEQ ID NO 128  
 <211> LENGTH: 27  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 128  
  
 gcggccgctt taatcggttt taccatt 27

<210> SEQ ID NO 129  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 129  
  
 gtcgaccgcg ggactagtgg gccctctaga cccgggggat ccggatctgc tggetatgaa 60

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<210> SEQ ID NO 130  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 130

gtcgaccgcg ggactagtgg gccctctaga cccgggggat cgggatctgc tggctatgaa 60

<210> SEQ ID NO 131  
 <211> LENGTH: 789  
 <212> TYPE: DNA  
 <213> ORGANISM: Euglena gracilis  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(789)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 131

atg ctg ggg gcc atc gcg gac gtc gtg ctc cgg ggg ccc gcc gca ttc 48  
 Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe  
 1 5 10 15

cac tgg gac cct gcc acc acc ccg ctc gca tgg atc gtc agc ccc tgt 96  
 His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys  
 20 25 30

gtg gcc tcc gtg gcg tac ctg ggg gcc atc ggg ctg ctg aag cgc cgc 144  
 Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg  
 35 40 45

act gga ccg gag gtc cgc tcc aag ccc ttc gag ctg cta cac aac ggg 192  
 Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly  
 50 55 60

ctg ctg gtg ggc tgg tcc ctc gtg gtg ctg ctc ggg acg ctg tac ggc 240  
 Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly  
 65 70 75 80

gcg ttc cag cgc gtg cag gag gac ggc cgg ggg gtg cag gcc ctc ctg 288  
 Ala Phe Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu  
 85 90 95

tgc acc cag ccg cca cca tct cag atc tgg gac ggc ccg gtg ggg tac 336  
 Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr  
 100 105 110

ttc acg tac ctc ttc tac ctc gcg aag tac tgg gag ctg gcg gac act 384  
 Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Ala Asp Thr  
 115 120 125

gtc atc ctc gcc ctc cgc cag aag ccc acc atc ccc ctc cac gtc tac 432  
 Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr  
 130 135 140

cat cac gcc gtc atg ctg ttc atc gtg tgg tgg tgg ttc gcg cac ccc 480  
 His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro  
 145 150 155 160

tgg ctc gag ggg agc tgg tgg tgc tcc ctg gtc aac tct ttc atc cac 528  
 Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His  
 165 170 175

acg gtg atg tac tgg tac tac acc ctg acg gtg gtt ggc atc aac cct 576  
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro  
 180 185 190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg 624  
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr  
 195 200 205

ggc tgc gtg tac gtc atg gcg ttc ttc ggc cta tat tat gcc ggg gcg 672  
 Gly Cys Val Tyr Val Met Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala

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210	215	220		
ggc tgc acc tcc aac gtg tac act gcc tgg ttc tcg atg ggg gtc aac				720
Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn				
225	230	235		240
ctc agc ttt ctg tgg etc ttc gct ctt ttc ttc cgc cgg tca tac agc				768
Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser				
	245	250		255
aaa cct agc cgg aag gag tag				789
Lys Pro Ser Arg Lys Glu				
	260			

&lt;210&gt; SEQ ID NO 132

&lt;211&gt; LENGTH: 262

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Euglena gracilis*

&lt;400&gt; SEQUENCE: 132

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

&lt;210&gt; SEQ ID NO 133

&lt;211&gt; LENGTH: 789

&lt;212&gt; TYPE: DNA

<213> ORGANISM: *Euglena gracilis*

&lt;220&gt; FEATURE:

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<221> NAME/KEY: CDS
<222> LOCATION: (1)..(789)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 133

atg ctg ggg gcc atc gcg gac gtc gtg ctc cgg ggg ccc gcc gca ttc      48
Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe
1          5          10          15

cac tgg gac cct gcc acc acc cgg ctc gca tcg atc gtc agc ccc tgt      96
His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys
20          25          30

gtg gcc tcc gtg gcg tac ctg ggg gcc atc ggg ctg ctg aag cgc cgc      144
Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg
35          40          45

act gga cgg gag gtc cgc tcc aag ccc ttc gag ctg cta cac aac ggg      192
Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly
50          55          60

ctg ctg gtg ggc tgg tcc ctc gtg gtg ctg ctc ggg acg ctg tac ggc      240
Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly
65          70          75          80

gcg tac cag cgc gtg cag gag gac ggc cgg ggg gtg cag gcc ctg ctg      288
Ala Tyr Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu
85          90          95

tgc acc cag cgg cca cca tct cag atc tgg gac ggc cgg gtg ggg tac      336
Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr
100         105         110

ttc acg tac ctt ttc tac ctc gcg aag tac tgg gag ctg gtg gac act      384
Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Val Asp Thr
115         120         125

gtc atc ctc gcc ctc cgc cag aag ccc acc atc ccc ctc cac gtc tac      432
Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr
130         135         140

cat cac gcc gtc atg ctg ttc att gtg tgg tcg tgg ttc gcg cac ccc      480
His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro
145         150         155         160

tgg ctc gag ggg agc tgg tgg tgc tcc ctg gtc aac tct ttc atc cac      528
Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His
165         170         175

acg gtg atg tac tcg tat tac acc ctg acg gtg gtt ggc atc aac cct      576
Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro
180         185         190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg      624
Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr
195         200         205

ggc tgc gtg tac gtc acg gcg ttc ttc ggc cta tac tat gcc ggg gcg      672
Gly Cys Val Tyr Val Thr Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala
210         215         220

ggc tgc acc tcc aac gtg tac act gcc tgg ttc tcg atg ggg gtc aac      720
Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn
225         230         235         240

ctc agc ttt ctg tgg ctc ttc gct ctt ttc ttc cgc cgg tcg tac agc      768
Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser
245         250         255

aaa cct agc cgg aag gag tag      789
Lys Pro Ser Arg Lys Glu
260

<210> SEQ ID NO 134
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Euglena gracilis

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<400> SEQUENCE: 134

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

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<210> SEQ ID NO 135

<211> LENGTH: 897

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(897)

<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 135

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atg gca tct gtt tac tcc acc cta acc tac tgg ctc gtc cac cac ccc      48
Met Ala Ser Val Tyr Ser Thr Leu Thr Tyr Trp Leu Val His His Pro
1           5           10           15
tac att gcc aac ttc acg tgg acc gaa ggt gaa aca cta ggc tcc acc      96
Tyr Ile Ala Asn Phe Thr Trp Thr Glu Gly Glu Thr Leu Gly Ser Thr
20           25           30
gtt ttc ttt gtc ttt gtc gtc gtc tcc ctt tac ctc tcc gcc aca ttc      144
Val Phe Phe Val Phe Val Val Val Ser Leu Tyr Leu Ser Ala Thr Phe
35           40           45
ctc ctc cga tac acc gtc gat tca ctc ccc aca ctc ggt ccc cgc att      192

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Leu	Leu	Arg	Tyr	Thr	Val	Asp	Ser	Leu	Pro	Thr	Leu	Gly	Pro	Arg	Ile	
50						55					60					
ctc	aaa	cca	atc	aca	gcc	ggt	cac	agc	ctc	att	ctc	ttc	ctc	ctc	tcc	240
Leu	Lys	Pro	Ile	Thr	Ala	Val	His	Ser	Leu	Ile	Leu	Phe	Leu	Leu	Ser	
65				70					75						80	
tta	acc	atg	gcc	ggt	ggt	tgc	act	ctc	tcc	cta	atc	tct	tcc	tcg	gac	288
Leu	Thr	Met	Ala	Val	Gly	Cys	Thr	Leu	Ser	Leu	Ile	Ser	Ser	Ser	Asp	
			85						90					95		
ccg	aag	gcg	cgt	ctc	ttc	gac	gcc	ggt	tgt	ttc	ccc	ctc	gac	gtg	aaa	336
Pro	Lys	Ala	Arg	Leu	Phe	Asp	Ala	Val	Cys	Phe	Pro	Leu	Asp	Val	Lys	
		100						105					110			
cct	aag	gga	ccg	ctt	ttc	ttt	tgg	gct	caa	gtc	ttt	tac	ctc	tcg	aag	384
Pro	Lys	Gly	Pro	Leu	Phe	Phe	Trp	Ala	Gln	Val	Phe	Tyr	Leu	Ser	Lys	
		115					120					125				
atc	ctt	gag	ttc	gta	gac	aca	ctt	ctc	atc	ata	ctc	aac	aaa	tca	atc	432
Ile	Leu	Glu	Phe	Val	Asp	Thr	Leu	Leu	Ile	Ile	Leu	Asn	Lys	Ser	Ile	
	130					135								140		
caa	cgg	ctc	tcg	ttc	ctc	cac	gtc	tac	cac	cac	gca	acg	ggt	gtg	att	480
Gln	Arg	Leu	Ser	Phe	Leu	His	Val	Tyr	His	His	Ala	Thr	Val	Val	Ile	
	145				150					155					160	
ttg	tgc	tac	ctc	tgg	tta	cga	aca	cgt	caa	tcg	atg	ttt	cct	ggt	ggg	528
Leu	Cys	Tyr	Leu	Trp	Leu	Arg	Thr	Arg	Gln	Ser	Met	Phe	Pro	Val	Gly	
			165						170					175		
ctc	gtg	ttg	aac	tcg	acg	gtc	cat	gtg	att	atg	tac	ggg	tac	tat	ttc	576
Leu	Val	Leu	Asn	Ser	Thr	Val	His	Val	Ile	Met	Tyr	Gly	Tyr	Tyr	Phe	
			180						185					190		
ctc	tgc	gct	atc	gga	tcg	agg	ccc	aag	tgg	aag	aag	ttg	gtg	acg	aat	624
Leu	Cys	Ala	Ile	Gly	Ser	Arg	Pro	Lys	Trp	Lys	Lys	Leu	Val	Thr	Asn	
		195					200					205				
ttt	caa	atg	ggt	cag	ttt	gct	ttc	ggc	atg	ggg	tta	gga	gcc	gct	tgg	672
Phe	Gln	Met	Val	Gln	Phe	Ala	Phe	Gly	Met	Gly	Leu	Gly	Ala	Ala	Trp	
	210					215					220					
atg	ctc	cca	gag	cat	tat	ttc	ggg	tcg	ggt	tgc	gcc	ggg	att	tgg	aca	720
Met	Leu	Pro	Glu	His	Tyr	Phe	Gly	Ser	Gly	Cys	Ala	Gly	Ile	Trp	Thr	
	225				230					235				240		
ggt	tat	ttc	aat	ggt	gtg	ttt	act	gct	tct	cta	ttg	gct	ctc	ttc	tac	768
Val	Tyr	Phe	Asn	Gly	Val	Phe	Thr	Ala	Ser	Leu	Leu	Ala	Leu	Phe	Tyr	
			245						250					255		
aac	ttc	cac	tcc	aag	aac	tat	gag	aag	act	aca	acg	tcg	cct	ttg	tat	816
Asn	Phe	His	Ser	Lys	Asn	Tyr	Glu	Lys	Thr	Thr	Thr	Ser	Pro	Leu	Tyr	
			260					265					270			
aag	atc	gaa	tcc	ttt	ata	ttt	att	cac	gga	gag	agg	tgg	gca	aat	aaa	864
Lys	Ile	Glu	Ser	Phe	Ile	Phe	Ile	His	Gly	Glu	Arg	Trp	Ala	Asn	Lys	
		275					280					285				
gcg	att	aca	tta	ttt	tcc	aag	aaa	aac	gat	taa						897
Ala	Ile	Thr	Leu	Phe	Ser	Lys	Lys	Asn	Asp							
	290					295										

&lt;210&gt; SEQ ID NO 136

&lt;211&gt; LENGTH: 298

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 136

Met	Ala	Ser	Val	Tyr	Ser	Thr	Leu	Thr	Tyr	Trp	Leu	Val	His	His	Pro
1				5					10					15	
Tyr	Ile	Ala	Asn	Phe	Thr	Trp	Thr	Glu	Gly	Glu	Thr	Leu	Gly	Ser	Thr
		20						25					30		
Val	Phe	Phe	Val	Phe	Val	Val	Val	Ser	Leu	Tyr	Leu	Ser	Ala	Thr	Phe
		35					40					45			

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

<210> SEQ ID NO 137  
 <211> LENGTH: 837  
 <212> TYPE: DNA  
 <213> ORGANISM: Arabidopsis thaliana  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(837)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 137

atg gca tca att tac tcc tct tta acc tac tgg ctc gtt aac cac ccc 48  
 Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro  
 1 5 10 15  
 tac atc tcc aat ttt act tgg atc gaa ggt gaa acc cta ggc tcc acc 96  
 Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr  
 20 25 30  
 gtc ttt ttc gta tcc gtc gta gtc tcc gtt tac ctc tcc gcc acg ttc 144  
 Val Phe Phe Val Ser Val Val Ser Val Tyr Leu Ser Ala Thr Phe  
 35 40 45  
 ctc ctc cga tcc gcc atc gat tca ctc cca tca ctc agt cca cgt atc 192  
 Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile  
 50 55 60  
 ctc aaa ccg atc aca gcc gtc cac agc cta atc ctc tgt ctc ctc tcc 240  
 Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser

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65	70	75	80	
tta gtc atg gcc gtc ggt tgc act ctc tca ata acc tca tct cac gcg				288
Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala	85	90	95	
tct tca gat ccg atg gcg cgt ttc ctt cac gcg att tgc ttt ccc gtc				336
Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val	100	105	110	
gac gtt aaa cct aac gga ccg ctt ttc ttc tgg gct caa gtc ttc tac				384
Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr	115	120	125	
ctc tcg aag atc ctc gag ttc gga gac acg atc ctc atc ata ctc ggc				432
Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly	130	135	140	
aaa tca atc caa cgg cta tcc ttc ctc cac gtg tac cac cac gcg acg				480
Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr	145	150	155	160
gtt gtg gtc atg tgt tat ctc tgg ctc cga act cgc caa tcg atg ttt				528
Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe	165	170	175	
ccg att gcg ctc gtg acg aat tcg acg gta cac gtc atc atg tac ggt				576
Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly	180	185	190	
tac tac ttc ctc tgc gcc gtt gga tcg agg ccc aag tgg aag aga ttg				624
Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu	195	200	205	
gtg acg gat tgt cag att gtt cag ttt gtt ttc agt ttc ggg tta tcc				672
Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser	210	215	220	
ggt tgg atg ctc cga gag cac tta ttc ggg tcg ggt tgc acc ggg att				720
Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile	225	230	235	240
tgg gga tgg tgt ttc aac gct gca ttt aat gct tct ctt ttg gct ctc				768
Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu	245	250	255	
ttt tcc aac ttc cat tca aag aat tat gtc aag aag cca acg aga gag				816
Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu	260	265	270	
gat ggc aaa aaa agc gat tag				837
Asp Gly Lys Lys Ser Asp	275			

&lt;210&gt; SEQ ID NO 138

&lt;211&gt; LENGTH: 278

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Arabidopsis thaliana

&lt;400&gt; SEQUENCE: 138

Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro	1	5	10	15
Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr	20	25	30	
Val Phe Phe Val Ser Val Val Val Ser Val Tyr Leu Ser Ala Thr Phe	35	40	45	
Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile	50	55	60	
Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser	65	70	75	80
Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala	85	90	95	



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Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val  
 100 105 110

Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr  
 115 120 125

Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly  
 130 135 140

Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr  
 145 150 155 160

Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe  
 165 170 175

Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly  
 180 185 190

Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu  
 195 200 205

Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser  
 210 215 220

Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile  
 225 230 235 240

Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu  
 245 250 255

Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu  
 260 265 270

Asp Gly Lys Lys Ser Asp  
 275

<210> SEQ ID NO 139  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Consensus sequence  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <222> LOCATION: (3)..(3)  
 <223> OTHER INFORMATION: Xaa is Val, Try or Ile, preferably is Val or  
 Thr  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <222> LOCATION: (4)..(4)  
 <223> OTHER INFORMATION: Xaa is Tyr or Phe, preferably is Tyr

<400> SEQUENCE: 139

Leu His Xaa Xaa His His  
 1 5

<210> SEQ ID NO 140  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Consensus sequence  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <222> LOCATION: (2)..(2)  
 <223> OTHER INFORMATION: Xaa is Asn, Asp, Thr, Gln, Met, Ser or Ala,  
 preferably is Gln  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <222> LOCATION: (3)..(3)  
 <223> OTHER INFORMATION: Xaa is Thr, Cys, Leu, Met, Ala, Ile, Val or  
 Phe, preferably is Ala or Met  
 <220> FEATURE:  
 <221> NAME/KEY: MISC\_FEATURE  
 <222> LOCATION: (5)..(5)

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<223> OTHER INFORMATION: Xaa is Met, Ile or Leu, preferably is Met
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is Val, Ile, Leu, Thr or Phe, preferably
is Leu

<400> SEQUENCE: 140

Thr Xaa Xaa Gln Xaa Xaa Gln Phe
1                5

<210> SEQ ID NO 141
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Leu, Ile, Val, Tyr, Phe or Ala,
preferably is Phe

<400> SEQUENCE: 141

Asp Thr Xaa Phe Met Val
1                5

<210> SEQ ID NO 142
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is Met, Ile or Leu, preferably is Met or
Leu, more preferably is Met
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is Val, Ile, Leu, Thr or Phe, preferably
is Leu

<400> SEQUENCE: 142

Thr Gln Ala Gln Xaa Xaa Gln Phe
1                5

<210> SEQ ID NO 143
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 143

gtcgaccgc ggactagtgg gccctctaga cccgggggat cgggatctgc tggctatgaa      60

<210> SEQ ID NO 144
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 144

gtcgaccgc ggactagtgg gccctctaga cccgggggat cgggatctgc tggctatgaa      60

<210> SEQ ID NO 145

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<211> LENGTH: 36  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 145  
  
 ggtaccacat aatgtgcgtg gagacggaaa ataacg 36

<210> SEQ ID NO 146  
 <211> LENGTH: 33  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 146  
  
 ctcgagttac gccgtctttc cggagtgttg gcc 33

<210> SEQ ID NO 147  
 <211> LENGTH: 24  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 147  
  
 gcggccgctt acgtggactt ggtc 24

<210> SEQ ID NO 148  
 <211> LENGTH: 24  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 148  
  
 gcggccgcat ggcgacgaag gagg 24

<210> SEQ ID NO 149  
 <211> LENGTH: 25  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 149  
  
 taagcttaca tggcgacgaa ggagg 25

<210> SEQ ID NO 150  
 <211> LENGTH: 24  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 150  
  
 tggatccact tacgtggact tggt 24

<210> SEQ ID NO 151  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 151

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gtcgaccgcg ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> SEQ ID NO 152  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 152

gcggccgcac catgtgctca ccaccgccgt c 31

<210> SEQ ID NO 153  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 153

gcggccgcct acatggcacc agtaac 26

<210> SEQ ID NO 154  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 154

gcggccgcac catgtgctca tcaccgccgt c 31

<210> SEQ ID NO 155  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 155

gcggccgcct acatggcacc agtaac 26

<210> SEQ ID NO 156  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 156

gcggccgcac catggacgcc tacaacgctg c 31

<210> SEQ ID NO 157  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 157

gcggccgcct aagcactctt cttcttt 27

<210> SEQ ID NO 158  
<211> LENGTH: 23  
<212> TYPE: DNA

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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 158  
  
 accatgtgct caccaccgcc gtc 23

<210> SEQ ID NO 159  
 <211> LENGTH: 18  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 159  
  
 ctacatggca ccagtaac 18

<210> SEQ ID NO 160  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 160  
  
 accatgtgct catcaccgcc gtc 23

<210> SEQ ID NO 161  
 <211> LENGTH: 18  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 161  
  
 ctacatggca ccagtaac 18

<210> SEQ ID NO 162  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 162  
  
 accatggacg cctacaacgc tgc 23

<210> SEQ ID NO 163  
 <211> LENGTH: 19  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 163  
  
 ctaagcactc ttcttcttt 19

<210> SEQ ID NO 164  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 164  
  
 gtcgaccgc ggactagtgg gccctctaga cccgggggat cgggatctgc tggetatgaa 60

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<210> SEQ ID NO 165  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 165

gtcgaccgcg ggactagtgg gccctctaga cccgggggat cgggatctgc tggctatgaa 60

<210> SEQ ID NO 166  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 166

gcggccgcat aatgacgagc aacatgagc 29

<210> SEQ ID NO 167  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 167

gcggccgctt aggccgactt ggccttggg 29

<210> SEQ ID NO 168  
 <211> LENGTH: 34  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 168

gcggccgcac catggacgtc gtcgagcagc aatg 34

<210> SEQ ID NO 169  
 <211> LENGTH: 36  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 169

gcggccgctt agatggtcct ctgcttcttg ggcgcc 36

<210> SEQ ID NO 170  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 170

gacataatga cgagcaacat gag 23

<210> SEQ ID NO 171  
 <211> LENGTH: 25  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:

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<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 171

cggccttaggc cgaacttgcc ttggg 25

<210> SEQ ID NO 172  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 172

agacataatg gacgtcgtcg agcagcaatg 30

<210> SEQ ID NO 173  
 <211> LENGTH: 28  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 173

ttagatggtc ttctgcttct tggcgccc 28

<210> SEQ ID NO 174  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 174

gtcgaccgc ggactagtag gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> SEQ ID NO 175  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 175

gcgccgcgat aatggcttca acatggcaa 29

<210> SEQ ID NO 176  
 <211> LENGTH: 32  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 176

gcgccgctt atgtcttctt getcttctg tt 32

<210> SEQ ID NO 177  
 <211> LENGTH: 26  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 177

gcgccgcgat aatggagact tttaat 26

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<210> SEQ ID NO 178
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 178

gcggccgctc agtccccct cactttcc                28

<210> SEQ ID NO 179
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 179

aagcttacat aatggcttca acatggcaa                29

<210> SEQ ID NO 180
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 180

ggatccttat gtcttcttgc tcttctgtt                30

<210> SEQ ID NO 181
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 181

aagcttacat aatggagact tttaat                    26

<210> SEQ ID NO 182
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 182

ggatccttca gtccccctc actttcc                    27

<210> SEQ ID NO 183
<211> LENGTH: 993
<212> TYPE: DNA
<213> ORGANISM: Phaeodactylum tricornutum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (103)..(939)
<223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 183

ggtcttttgt ggtagctatc gtcacacac gcaggtcgtt gtcactatc gtgatccgta    60

tattgaccgt gcacttgtgt aaaacagaga tatttcaaga gt atg atg gta cct    114
Met Met Val Pro
1

tca agt tat gac gag tat atc gtc atg gtc aac gac ctt ggc gac tct    162
Ser Ser Tyr Asp Glu Tyr Ile Val Met Val Asn Asp Leu Gly Asp Ser

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5	10	15	20	
att ctg agc tgg gcc gac cct gat cac tat cgt gga cat acc gag gga				210
Ile Leu Ser Trp Ala Asp Pro Asp His Tyr Arg Gly His Thr Glu Gly	25	30	35	
tgg gag ttc act gac ttt tct gct gct ttt agc att gcc gtc gcg tac				258
Trp Glu Phe Thr Asp Phe Ser Ala Ala Phe Ser Ile Ala Val Ala Tyr	40	45	50	
ctc ctg ttt gtc ttt gtt gga tct ctc att atg agt atg gga gtc ccc				306
Leu Leu Phe Val Phe Val Gly Ser Leu Ile Met Ser Met Gly Val Pro	55	60	65	
gca att gac cct tat ccg ctc aag ttt gtc tac aat gtt tca cag att				354
Ala Ile Asp Pro Tyr Pro Leu Lys Phe Val Tyr Asn Val Ser Gln Ile	70	75	80	
atg ctt tgt gct tac atg acc att gaa gcc agt ctt cta gct tat cgt				402
Met Leu Cys Ala Tyr Met Thr Ile Glu Ala Ser Leu Leu Ala Tyr Arg	85	90	95	100
aac ggc tac aca ttc tgg cct tgc aac gat tgg gac ttt gaa aag ccg				450
Asn Gly Tyr Thr Phe Trp Pro Cys Asn Asp Trp Asp Phe Glu Lys Pro	105	110	115	
cct atc gct aag ctc ctc tgg ctc ttt tac gtt tcc aaa att tgg gat				498
Pro Ile Ala Lys Leu Leu Trp Leu Phe Tyr Val Ser Lys Ile Trp Asp	120	125	130	
ttt tgg gac acc atc ttt att gtt ctc ggg aag aag tgg cgt caa ctt				546
Phe Trp Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu	135	140	145	
tcc ttc ctg cac gtc tac cat cac acc acc atc ttt ctc ttc tac tgg				594
Ser Phe Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp	150	155	160	
ttg aat gca cat gta aac ttt gat ggt gat att ttc ctc acc atc gtc				642
Leu Asn Ala His Val Asn Phe Asp Gly Asp Ile Phe Leu Thr Ile Val	165	170	175	180
ttg aac ggt ttc atc cac acc gtc atg tac acg tac tac ttc att tgc				690
Leu Asn Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys	185	190	195	
atg cac acc aag gtc cca gag acc ggc aaa tcc ttg ccc att tgg tgg				738
Met His Thr Lys Val Pro Glu Thr Gly Lys Ser Leu Pro Ile Trp Trp	200	205	210	
aaa tct agt ttg aca agc atg cag ctg gtg cag ttc atc acg atg atg				786
Lys Ser Ser Leu Thr Ser Met Gln Leu Val Gln Phe Ile Thr Met Met	215	220	225	
acg cag gct atc atg atc ttg tac aag ggc tgt gct gct ccc cat agc				834
Thr Gln Ala Ile Met Ile Leu Tyr Lys Gly Cys Ala Ala Pro His Ser	230	235	240	
cgg gtg gtg aca tcg tac ttg gtt tac att ttg tcg ctc ttt att ttg				882
Arg Val Val Thr Ser Tyr Leu Val Tyr Ile Leu Ser Leu Phe Ile Leu	245	250	255	260
ttc gcc cag ttc ttt gtc agc tca tac ctc aag ccg aag aag aag aag				930
Phe Ala Gln Phe Phe Val Ser Ser Tyr Leu Lys Phe Pro Lys Lys Lys Lys	265	270	275	
aca gct taa gcgaaatttg ggtctacggt aaaacaatta cgttacaaaa				979
Thr Ala				
aaaaaaaaaaaa aaaa				993
<210> SEQ ID NO 184				
<211> LENGTH: 278				
<212> TYPE: PRT				
<213> ORGANISM: Phaeodactylum tricornutum				
<400> SEQUENCE: 184				

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

<210> SEQ ID NO 185  
 <211> LENGTH: 20  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
 <220> FEATURE:  
 <221> NAME/KEY: misc\_feature  
 <222> LOCATION: (1)..(20)  
 <223> OTHER INFORMATION: N in positions 3 and 18 is C or T.

<400> SEQUENCE: 185

aanctuctut ggctuttnta

20

<210> SEQ ID NO 186  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
 <220> FEATURE:  
 <221> NAME/KEY: misc\_feature

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<222> LOCATION: (1)..(23)  
 <223> OTHER INFORMATION: N in positions 3 and 15 is C or T. N in positions 9, 12 and 21 is A or G.

<400> SEQUENCE: 186

gantguacna anaantgugc naa 23

<210> SEQ ID NO 187  
 <211> LENGTH: 446  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <221> NAME/KEY: misc\_feature  
 <222> LOCATION: (1)..(446)  
 <223> OTHER INFORMATION: PCR fragment

<400> SEQUENCE: 187

aagctcctct ggctctttaa cgtttccaaa atttgggatt tttgggacac catctttatt 60  
 gttctcggga agaagtggcg tcaactttcc ttctgcacg tctaccatca caccaccatc 120  
 tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt cctcaccatc 180  
 gtcttgaacg gtttcatcca caccgcatg tacacgtact acttcatttg catgcacacc 240  
 aaggtcccag agaccggcaa atccttgccc atttggtgga aatctagttt gacaagcatg 300  
 cagctggtgc agttcatcac gatgatgacg caggctatca tgatcttgta caagggtgt 360  
 gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc gctctttatt 420  
 ttgttcgccc agttctttgt cagctc 446

<210> SEQ ID NO 188  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 188

gcgccgcac ataatgatgg taccttcaag 30

<210> SEQ ID NO 189  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 189

gaagacagct taatagacta gt 22

<210> SEQ ID NO 190  
 <211> LENGTH: 31  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 190

gcgccgcac catgatggta ccttcaagtt a 31

<210> SEQ ID NO 191  
 <211> LENGTH: 24  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

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&lt;400&gt; SEQUENCE: 191

gaagacagct taataggcgg ccgc 24

&lt;210&gt; SEQ ID NO 192

&lt;211&gt; LENGTH: 859

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: PCR product

&lt;400&gt; SEQUENCE: 192

gcggccgcac ataatgatgg tacctcaag ttatgacgag tatatcgta tggccaacga 60

ccttgccgac tctattctga gctgggccga cctgatcac tategtggac ataccgaggg 120

atgggagttc actgactttt ctgctgcttt tagcattgcc gtcgcgtacc tctgtttgt 180

ctttgttggg tctctcatta tgagtatgg agtccccgca attgaccctt atccgctcaa 240

gtttgtctac aatgtttcac agattatgct ttgtgcttac atgaccattg aagccagtct 300

tctagcctat cgtaacggct acacattctg gccttgcaac gattgggact ttgaaaagcc 360

gcctatcgct aagctcctct ggctctttta cgtttccaaa atttgggatt ttgggacac 420

catctttatt gttctcggga agaagtggcg tcaactttcc ttctgcacg tctaccatca 480

caccaccatc tttctctct actggttgaa tgcacatgta aactttgatg gtgatatttt 540

cctcaccatc gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg 600

catgcacacc aaggtcccag agaccggcaa atccttgccc atttgggtgga aatctagttt 660

gacaagcatg cagctgggtc agttcatcac gatgatgacg caggctatca tgatcttgta 720

caagggtgt gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc 780

gctctttatt ttgttcgccc agttctttgt cagctcatac ctcaagccga agaagaagaa 840

gacagcttaa tagactagt 859

&lt;210&gt; SEQ ID NO 193

&lt;211&gt; LENGTH: 1380

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Phytium irregulare

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(1380)

&lt;223&gt; OTHER INFORMATION: Delta-6 desaturase

&lt;400&gt; SEQUENCE: 193

atg gtg gac ctc aag cct gga gtg aag cgc ctg gtg agc tgg aag gag 48  
Met Val Asp Leu Lys Pro Gly Val Lys Arg Leu Val Ser Trp Lys Glu  
1 5 10 15atc cgc gag cac gcg acg ccc gcg acc gcg tgg atc gtg att cac cac 96  
Ile Arg Glu His Ala Thr Pro Ala Thr Ala Trp Ile Val Ile His His  
20 25 30aag gtc tac gac atc tcc aag tgg gac tcg cac ccg ggt ggc tcc gtg 144  
Lys Val Tyr Asp Ile Ser Lys Trp Asp Ser His Pro Gly Gly Ser Val  
35 40 45atg ctc acg cag gcc ggc gag gac gcc acg gac gcc ttc gcg gtc ttc 192  
Met Leu Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe  
50 55 60cac ccg tcc tcg gcg ctc aag ctg ctc gag cag ttc tac gtc ggc gac 240  
His Pro Ser Ser Ala Leu Lys Leu Leu Glu Gln Phe Tyr Val Gly Asp  
65 70 75 80gtg gac gaa acc tcc aag gcc gag atc gag ggg gag ccg gcg agc gac 288  
Val Asp Glu Thr Ser Lys Ala Glu Ile Glu Gly Glu Pro Ala Ser Asp

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85			90			95										
gag	gag	cgc	gcg	cgc	cgc	gag	cgc	atc	aac	gag	ttc	atc	gcg	tcc	tac	336
Glu	Glu	Arg	Ala	Arg	Arg	Glu	Arg	Ile	Asn	Glu	Phe	Ile	Ala	Ser	Tyr	
		100						105					110			
cgc	cgt	ctg	cgc	gtc	aag	gtc	aag	ggc	atg	ggg	ctc	tac	gac	gcc	agc	384
Arg	Arg	Leu	Arg	Val	Lys	Val	Lys	Gly	Met	Gly	Leu	Tyr	Asp	Ala	Ser	
		115						120					125			
gcg	ctc	tac	tac	gcg	tgg	aag	ctc	gtg	agc	acg	ttc	ggc	atc	gcg	gtg	432
Ala	Leu	Tyr	Tyr	Ala	Trp	Lys	Leu	Val	Ser	Thr	Phe	Gly	Ile	Ala	Val	
	130					135					140					
ctc	tcg	atg	gcg	atc	tgc	ttc	ttc	ttc	aac	agt	ttc	gcc	atg	tac	atg	480
Leu	Ser	Met	Ala	Ile	Cys	Phe	Phe	Phe	Asn	Ser	Phe	Ala	Met	Tyr	Met	
	145				150					155					160	
gtc	gcc	ggc	gtg	att	atg	ggg	ctc	ttc	tac	cag	cag	tcc	gga	tgg	ctg	528
Val	Ala	Gly	Val	Ile	Met	Gly	Leu	Phe	Tyr	Gln	Gln	Ser	Gly	Trp	Leu	
				165					170					175		
gcg	cac	gac	ttc	ttg	cac	aac	cag	gtg	tgc	gag	aac	cgc	acg	ctc	ggc	576
Ala	His	Asp	Phe	Leu	His	Asn	Gln	Val	Cys	Glu	Asn	Arg	Thr	Leu	Gly	
		180						185					190			
aac	ctt	atc	ggc	tgc	ctc	gtg	ggc	aac	gcc	tgg	cag	ggc	ttc	agc	atg	624
Asn	Leu	Ile	Gly	Cys	Leu	Val	Gly	Asn	Ala	Trp	Gln	Gly	Phe	Ser	Met	
	195						200					205				
cag	tgg	tgg	aag	aac	aag	cac	aac	ctg	cac	cac	gcg	gtg	ccg	aac	ctg	672
Gln	Trp	Trp	Lys	Asn	Lys	His	Asn	Leu	His	His	Ala	Val	Pro	Asn	Leu	
	210					215					220					
cac	agc	gcc	aag	gac	gag	ggc	ttc	atc	ggc	gac	ccg	gac	atc	gac	acc	720
His	Ser	Ala	Lys	Asp	Glu	Gly	Phe	Ile	Gly	Asp	Pro	Asp	Ile	Asp	Thr	
	225			230						235				240		
atg	ccg	ctg	ctg	gcg	tgg	tct	aag	gag	atg	gcg	cgc	aag	gcg	ttc	gag	768
Met	Pro	Leu	Leu	Ala	Trp	Ser	Lys	Glu	Met	Ala	Arg	Lys	Ala	Phe	Glu	
			245						250					255		
tcg	gcg	cac	ggc	ccg	ttc	ttc	atc	cgc	aac	cag	gcg	ttc	cta	tac	ttc	816
Ser	Ala	His	Gly	Pro	Phe	Phe	Ile	Arg	Asn	Gln	Ala	Phe	Leu	Tyr	Phe	
		260						265					270			
ccg	ctg	ctg	ctg	ctc	gcg	cgc	ctg	agc	tgg	ctc	gcg	cag	tcg	ttc	ttc	864
Pro	Leu	Leu	Leu	Leu	Ala	Arg	Leu	Ser	Trp	Leu	Ala	Gln	Ser	Phe	Phe	
		275					280						285			
tac	gtg	ttc	acc	gag	ttc	tcg	ttc	ggc	atc	ttc	gac	aag	gtc	gag	ttc	912
Tyr	Val	Phe	Thr	Glu	Phe	Ser	Phe	Gly	Ile	Phe	Asp	Lys	Val	Glu	Phe	
	290					295				300						
gac	gga	ccg	gag	aag	gcg	ggt	ctg	atc	gtg	cac	tac	atc	tgg	cag	ctc	960
Asp	Gly	Pro	Glu	Lys	Ala	Gly	Leu	Ile	Val	His	Tyr	Ile	Trp	Gln	Leu	
	305				310					315					320	
gcg	atc	ccg	tac	ttc	tgc	aac	atg	agc	ctg	ttt	gag	ggc	gtg	gca	tac	1008
Ala	Ile	Pro	Tyr	Phe	Cys	Asn	Met	Ser	Leu	Phe	Glu	Gly	Val	Ala	Tyr	
			325						330					335		
ttc	ctc	atg	ggc	cag	gcg	tcc	tgc	ggc	ttg	ctc	ctg	gcg	ctg	gtg	ttc	1056
Phe	Leu	Met	Gly	Gln	Ala	Ser	Cys	Gly	Leu	Leu	Leu	Ala	Leu	Val	Phe	
			340					345					350			
agt	att	ggc	cac	aac	ggc	atg	tcg	gtg	tac	gag	cgc	gaa	acc	aag	ccg	1104
Ser	Ile	Gly	His	Asn	Gly	Met	Ser	Val	Tyr	Glu	Arg	Glu	Thr	Lys	Pro	
		355						360					365			
gac	ttc	tgg	cag	ctg	cag	gtg	acc	acg	acg	cgc	aac	atc	cgc	gcg	tcg	1152
Asp	Phe	Trp	Gln	Leu	Gln	Val	Thr	Thr	Thr	Arg	Asn	Ile	Arg	Ala	Ser	
		370				375						380				
gta	ttc	atg	gac	tgg	ttc	acc	ggt	ggc	ttg	aac	tac	cag	atc	gac	cat	1200
Val	Phe	Met	Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Tyr	Gln	Ile	Asp	His	
	385				390					395					400	
cac	ctg	ttc	ccg	ctc	gtg	ccg	cgc	cac	aac	ttg	cca	aag	gtc	aac	gtg	1248

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His Leu Phe Pro Leu Val Pro Arg His Asn Leu Pro Lys Val Asn Val
      405                                410                                415

ctc atc aag tcg cta tgc aag gag ttc gac atc ccg ttc cac gag acc      1296
Leu Ile Lys Ser Leu Cys Lys Glu Phe Asp Ile Pro Phe His Glu Thr
      420                                425                                430

ggc ttc tgg gag ggc atc tac gag gtc gtg gac cac ctg gcg gac atc      1344
Gly Phe Trp Glu Gly Ile Tyr Glu Val Val Asp His Leu Ala Asp Ile
      435                                440                                445

agc aag gaa ttt atc acc gag ttc cca gcg atg taa                        1380
Ser Lys Glu Phe Ile Thr Glu Phe Pro Ala Met
      450                                455

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&lt;210&gt; SEQ ID NO 194

&lt;211&gt; LENGTH: 459

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Phytium irregulare

&lt;400&gt; SEQUENCE: 194

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Met Val Asp Leu Lys Pro Gly Val Lys Arg Leu Val Ser Trp Lys Glu
 1      5      10      15

Ile Arg Glu His Ala Thr Pro Ala Thr Ala Trp Ile Val Ile His His
 20     25     30

Lys Val Tyr Asp Ile Ser Lys Trp Asp Ser His Pro Gly Gly Ser Val
 35     40     45

Met Leu Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe
 50     55     60

His Pro Ser Ser Ala Leu Lys Leu Leu Glu Gln Phe Tyr Val Gly Asp
 65     70     75     80

Val Asp Glu Thr Ser Lys Ala Glu Ile Glu Gly Glu Pro Ala Ser Asp
 85     90     95

Glu Glu Arg Ala Arg Arg Glu Arg Ile Asn Glu Phe Ile Ala Ser Tyr
100    105    110

Arg Arg Leu Arg Val Lys Val Lys Gly Met Gly Leu Tyr Asp Ala Ser
115    120    125

Ala Leu Tyr Tyr Ala Trp Lys Leu Val Ser Thr Phe Gly Ile Ala Val
130    135    140

Leu Ser Met Ala Ile Cys Phe Phe Phe Asn Ser Phe Ala Met Tyr Met
145    150    155    160

Val Ala Gly Val Ile Met Gly Leu Phe Tyr Gln Gln Ser Gly Trp Leu
165    170    175

Ala His Asp Phe Leu His Asn Gln Val Cys Glu Asn Arg Thr Leu Gly
180    185    190

Asn Leu Ile Gly Cys Leu Val Gly Asn Ala Trp Gln Gly Phe Ser Met
195    200    205

Gln Trp Trp Lys Asn Lys His Asn Leu His His Ala Val Pro Asn Leu
210    215    220

His Ser Ala Lys Asp Glu Gly Phe Ile Gly Asp Pro Asp Ile Asp Thr
225    230    235    240

Met Pro Leu Leu Ala Trp Ser Lys Glu Met Ala Arg Lys Ala Phe Glu
245    250    255

Ser Ala His Gly Pro Phe Phe Ile Arg Asn Gln Ala Phe Leu Tyr Phe
260    265    270

Pro Leu Leu Leu Leu Ala Arg Leu Ser Trp Leu Ala Gln Ser Phe Phe
275    280    285

Tyr Val Phe Thr Glu Phe Ser Phe Gly Ile Phe Asp Lys Val Glu Phe
290    295    300

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Asp Gly Pro Glu Lys Ala Gly Leu Ile Val His Tyr Ile Trp Gln Leu  
 305 310 315 320  
 Ala Ile Pro Tyr Phe Cys Asn Met Ser Leu Phe Glu Gly Val Ala Tyr  
 325 330 335  
 Phe Leu Met Gly Gln Ala Ser Cys Gly Leu Leu Leu Ala Leu Val Phe  
 340 345 350  
 Ser Ile Gly His Asn Gly Met Ser Val Tyr Glu Arg Glu Thr Lys Pro  
 355 360 365  
 Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Arg Ala Ser  
 370 375 380  
 Val Phe Met Asp Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Asp His  
 385 390 395 400  
 His Leu Phe Pro Leu Val Pro Arg His Asn Leu Pro Lys Val Asn Val  
 405 410 415  
 Leu Ile Lys Ser Leu Cys Lys Glu Phe Asp Ile Pro Phe His Glu Thr  
 420 425 430  
 Gly Phe Trp Glu Gly Ile Tyr Glu Val Val Asp His Leu Ala Asp Ile  
 435 440 445  
 Ser Lys Glu Phe Ile Thr Glu Phe Pro Ala Met  
 450 455

<210> SEQ ID NO 195  
 <211> LENGTH: 1152  
 <212> TYPE: DNA  
 <213> ORGANISM: Calendula officinalis  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1152)  
 <223> OTHER INFORMATION: Delta-12 desaturase

<400> SEQUENCE: 195

atg ggt gca ggc ggt cga atg caa gat ccc acc aac ggt ggc aac aaa 48  
 Met Gly Ala Gly Gly Arg Met Gln Asp Pro Thr Asn Gly Gly Asn Lys  
 1 5 10 15  
 acc gag ccc gaa cca atc caa cgg gtc cca cat gaa aaa ccc cca ttc 96  
 Thr Glu Pro Glu Pro Ile Gln Arg Val Pro His Glu Lys Pro Pro Phe  
 20 25 30  
 aca gtt gga gac atc aag aaa gcg atc cca cct cat tgt ttc aac cga 144  
 Thr Val Gly Asp Ile Lys Lys Ala Ile Pro Pro His Cys Phe Asn Arg  
 35 40 45  
 tcg gta att cgt tca ttt tca tac gtc ttt tac gac ctc aca atc gcg 192  
 Ser Val Ile Arg Ser Phe Ser Tyr Val Phe Tyr Asp Leu Thr Ile Ala  
 50 55 60  
 tca atc ttg tac tac att gcc aac aat tac atc tct acc ctc cct agc 240  
 Ser Ile Leu Tyr Tyr Ile Ala Asn Asn Tyr Ile Ser Thr Leu Pro Ser  
 65 70 75 80  
 ccg ctc gcc tac gtg gca tgg ccc gtt tac tgg gcc gtc caa ggg tgc 288  
 Pro Leu Ala Tyr Val Ala Trp Pro Val Tyr Trp Ala Val Gln Gly Cys  
 85 90 95  
 gtc tta acc ggg gtg tgg gtc ata gcc cac gaa tgt ggc cat cat gct 336  
 Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala  
 100 105 110  
 ttt agc gac cac caa tgg ctc gat gac acc gtg ggt ctc gtc ttg cac 384  
 Phe Ser Asp His Gln Trp Leu Asp Asp Thr Val Gly Leu Val Leu His  
 115 120 125  
 tcg ttc cta ctc gtg ccc tac ttt tcg tgg aaa tat agc cac cgt agg 432  
 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
 130 135 140

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cac cac tcg aac acg ggc tcg atc gag cac gat gag gtt ttc gtc ccg 480
His His Ser Asn Thr Gly Ser Ile Glu His Asp Glu Val Phe Val Pro
145 150 155 160

aag ttg aaa tcg ggc gtc cgg tca acc gcc cgg tac cta aac aac cca 528
Lys Leu Lys Ser Gly Val Arg Ser Thr Ala Arg Tyr Leu Asn Asn Pro
165 170 175

ccg ggc cga atc ttg acc cta ctc gta acc cta acc ctc ggt tgg cct 576
Pro Gly Arg Ile Leu Thr Leu Leu Val Thr Leu Thr Leu Gly Trp Pro
180 185 190

cta tac ctc acg ttc aac gtt tcg ggc cgt tac tac gac cgg ttc gcg 624
Leu Tyr Leu Thr Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Phe Ala
195 200 205

tgc cat ttc gac ccg aat agc ccg atc tac tcg aag cgc gaa cgg gct 672
Cys His Phe Asp Pro Asn Ser Pro Ile Tyr Ser Lys Arg Glu Arg Ala
210 215 220

caa atc ttc ata tcc gac gcc ggg atc tta gcc gta gtc ttc gta ctc 720
Gln Ile Phe Ile Ser Asp Ala Gly Ile Leu Ala Val Val Phe Val Leu
225 230 235

ttc cga ctc gca atg acc aaa ggg ctc acg tgg gtc cta acc atg tac 768
Phe Arg Leu Ala Met Thr Lys Gly Leu Thr Trp Val Leu Thr Met Tyr
245 250 255

ggg ggc ccg tta ctc gtg gtc aac ggt ttc cta gtc ttg atc aca ttc 816
Gly Gly Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe
260 265 270

cta caa cac act cac cct tcg ctc ccg cac tat gac tca acc gaa tgg 864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
275 280 285

gat tgg tta cgt ggg gcc ctc acc aca atc gac cgt gat tac ggg atc 912
Asp Trp Leu Arg Gly Ala Leu Thr Thr Ile Asp Arg Asp Tyr Gly Ile
290 295 300

cta aac aaa gtg ttc cat aac ata acc gac act cac gtg gcc cac cat 960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305 310 315 320

ttg ttc tct aca atg cct cat tac cat gca atg gaa gcc acg aag gtg 1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Val
325 330 335

atc aaa ccg att ttg ggc gat tat tat cag ttt gac ggg acc tcg att 1056
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Ser Ile
340 345 350

ttt aag gcg atg tat ccg gaa aca aag gag tgc att tat gtt gat aag 1104
Phe Lys Ala Met Tyr Arg Glu Thr Lys Glu Cys Ile Tyr Val Asp Lys
355 360 365

gat gag gag gtg aaa gat ggt gtt tat tgg tat cgt aat aag att taa 1152
Asp Glu Glu Val Lys Asp Gly Val Tyr Trp Tyr Arg Asn Lys Ile
370 375 380

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<210> SEQ ID NO 196
<211> LENGTH: 383
<212> TYPE: PRT
<213> ORGANISM: Calendula officinalis

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<400> SEQUENCE: 196

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Met Gly Ala Gly Gly Arg Met Gln Asp Pro Thr Asn Gly Gly Asn Lys
1 5 10 15

Thr Glu Pro Glu Pro Ile Gln Arg Val Pro His Glu Lys Pro Pro Phe
20 25 30

Thr Val Gly Asp Ile Lys Lys Ala Ile Pro Pro His Cys Phe Asn Arg
35 40 45

Ser Val Ile Arg Ser Phe Ser Tyr Val Phe Tyr Asp Leu Thr Ile Ala
50 55 60

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

<210> SEQ ID NO 197  
 <211> LENGTH: 903  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(903)  
 <223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 197

atg tct gct tct gga gct ttg ttg cct gct att gct ttc gct gct tac 48  
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr  
 1 5 10 15  
 gct tac gct acc tac gct tat gct ttc gag tgg tct cat gct aac gga 96  
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly

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20					25					30						
atc	gat	aac	gtg	gat	gct	aga	gag	tgg	att	gga	gct	ttg	tct	ttg	aga	144
Ile	Asp	Asn	Val	Asp	Ala	Arg	Glu	Trp	Ile	Gly	Ala	Leu	Ser	Leu	Arg	
		35					40					45				
ctc	cct	gca	att	gct	acc	acc	atg	tac	ctc	ttg	ttc	tgc	ctt	gtg	gga	192
Leu	Pro	Ala	Ile	Ala	Thr	Thr	Met	Tyr	Leu	Leu	Phe	Cys	Leu	Val	Gly	
		50				55					60					
cct	aga	ttg	atg	gct	aag	agg	gag	gct	ttt	gat	cct	aag	gga	ttc	atg	240
Pro	Arg	Leu	Met	Ala	Lys	Arg	Glu	Ala	Phe	Asp	Pro	Lys	Gly	Phe	Met	
65					70					75					80	
ctc	gct	tac	aac	gct	tac	caa	acc	gct	ttc	aac	ggt	gtg	gtg	ctc	gga	288
Leu	Ala	Tyr	Asn	Ala	Tyr	Gln	Thr	Ala	Phe	Asn	Val	Val	Val	Val	Leu	Gly
			85						90						95	
atg	ttc	gct	aga	gag	atc	tct	gga	ttg	gga	caa	cct	ggt	tgg	gga	tct	336
Met	Phe	Ala	Arg	Glu	Ile	Ser	Gly	Leu	Gly	Gln	Pro	Val	Trp	Gly	Ser	
			100					105							110	
act	atg	cct	tgg	agc	gat	agg	aag	tcc	ttc	aag	att	ttg	ttg	gga	gtg	384
Thr	Met	Pro	Trp	Ser	Asp	Arg	Lys	Ser	Phe	Lys	Ile	Leu	Leu	Gly	Val	
			115				120								125	
tgg	ctc	cat	tac	aac	aat	aag	tac	ctc	gag	ttg	ttg	gat	act	gtg	ttc	432
Trp	Leu	His	Tyr	Asn	Asn	Lys	Tyr	Leu	Glu	Leu	Leu	Asp	Thr	Val	Phe	
		130				135									140	
atg	gtg	gct	agg	aaa	aag	acc	aag	cag	ctc	tct	ttc	ttg	cat	gtg	tac	480
Met	Val	Ala	Arg	Lys	Lys	Thr	Lys	Gln	Leu	Ser	Phe	Leu	His	Val	Tyr	
					150						155				160	
cat	cat	gct	ttg	ttg	att	tgg	gct	tgg	tgg	ctt	ggt	tgt	cat	ctc	atg	528
His	His	Ala	Leu	Leu	Ile	Trp	Ala	Trp	Trp	Leu	Val	Cys	His	Leu	Met	
			165						170						175	
gct	acc	aac	gat	tgc	atc	gat	gct	tat	ttc	gga	gct	gct	tgc	aac	tct	576
Ala	Thr	Asn	Asp	Cys	Ile	Asp	Ala	Tyr	Phe	Gly	Ala	Ala	Cys	Asn	Ser	
			180						185						190	
ttc	atc	cac	atc	gtg	atg	tac	tcc	tac	tac	ctc	atg	tct	gct	ttg	gga	624
Phe	Ile	His	Ile	Val	Met	Tyr	Ser	Tyr	Tyr	Leu	Met	Ser	Ala	Leu	Gly	
			195						200						205	
att	aga	tgc	cct	tgg	aag	aga	tat	atc	acc	cag	gct	cag	atg	ttg	caa	672
Ile	Arg	Cys	Pro	Trp	Lys	Arg	Tyr	Ile	Thr	Gln	Ala	Gln	Met	Leu	Gln	
			210				215								220	
ttc	gtg	atc	gtg	ttc	gct	cat	gct	ggt	ttc	gtg	ctc	aga	caa	aag	cac	720
Phe	Val	Ile	Val	Phe	Ala	His	Ala	Val	Phe	Val	Leu	Arg	Gln	Lys	His	
					230					235					240	
tgc	cct	ggt	act	ttg	cct	tgg	gca	caa	atg	ttc	gtg	atg	aca	aat	atg	768
Cys	Pro	Val	Thr	Leu	Pro	Trp	Ala	Gln	Met	Phe	Val	Met	Thr	Asn	Met	
				245						250					255	
ttg	gtg	ctc	ttc	gga	aac	ttc	tac	ctc	aag	gct	tac	tct	aac	aag	tct	816
Leu	Val	Leu	Phe	Gly	Asn	Phe	Tyr	Leu	Lys	Ala	Tyr	Ser	Asn	Lys	Ser	
			260						265						270	
agg	gga	gat	gga	gct	tct	tct	ggt	aag	cct	gct	gag	act	act	aga	gca	864
Arg	Gly	Asp	Gly	Ala	Ser	Ser	Val	Lys	Pro	Ala	Glu	Thr	Thr	Arg	Ala	
			275					280						285		
cct	tct	gtg	aga	aga	acc	agg	tcc	agg	aag	atc	gat	tga				903
Pro	Ser	Val	Arg	Arg	Thr	Arg	Ser	Arg	Lys	Ile	Asp					
			290					295								300

&lt;210&gt; SEQ ID NO 198

&lt;211&gt; LENGTH: 300

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 198

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr

-continued

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

<210> SEQ ID NO 199  
 <211> LENGTH: 879  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(879)  
 <223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 199

atg tct gga ttg agg gct cct aac ttc ttg cat agg ttc tgg acc aag	48
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys	
1 5 10 15	
tggtgat tac gct atc tct aag gtg gtg ttc act tgc gct gat tct ttc	96
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe	
20 25 30	
cag tgg gat atc gga cct gtt tct tct tct acc gct cat ttg cct gct	144
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala	
35 40 45	

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att gag tct cct act cct ttg gtg acc tct ttg ctc ttc tac ttg gtg      192
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
   50                               55                               60

act gtg ttc ttg tgg tac gga aga ttg acc aga tcc tcc gat aag aag      240
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
   65                               70                               75                               80

atc aga gag cct acc tgg ttg agg aga ttc atc atc tgc cac aac gct      288
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
                               85                               90                               95

ttc ttg att gtg ctc tcc ttg tac atg tgt ttg gga tgc gtt gct caa      336
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
                               100                              105                              110

gct tac caa aac gga tac acc ttg tgg gga aac gag ttc aag gct act      384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
                               115                              120                              125

gag acc caa ttg gct ctc tac atc tac atc ttc tac gtg tcc aag atc      432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
                               130                              135                              140

tac gag ttc gtg gat acc tac atc atg ctc ctc aag aac aac ctc agg      480
Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
   145                               150                               155                               160

caa gtg tct ttc ttg cac atc tac cac cac tct acc atc tct ttc atc      528
Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile
                               165                              170                              175

tgg tgg atc atc gct aga aga gca cct gga gga gat gct tat ttc tcc      576
Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
                               180                              185                              190

gct gct ctc aac tct tgg gtt cat gtg tgc atg tac act tac tac ctc      624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
   195                               200                               205

ctc tct acc ttg att gga aag gaa gat cct aag agg tct aac tac ctc      672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu
   210                               215                               220

tgg tgg gga agg cat ttg acc caa atg caa atg ctc cag ttc ttc ttc      720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
   225                               230                               235                               240

aac gtg ctc caa gct ctt tat tgc gct tcc ttc tcc act tac cct aag      768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
                               245                               250                               255

ttc ctc tcc aag atc ttg ctc gtg tac atg atg tct ttg ctc gga ctt      816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
   260                               265                               270

ttc gga cac ttc tac tac tct aag cac atc gct gct gct aag ttg caa      864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
   275                               280                               285

aag aag cag cag tga      879
Lys Lys Gln Gln
   290

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&lt;210&gt; SEQ ID NO 200

&lt;211&gt; LENGTH: 292

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 200

```

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
 1                               5                               10                               15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
 20                               25                               30

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Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala  
 35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val  
 50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys  
 65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala  
 85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln  
 100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr  
 115 120 125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile  
 130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg  
 145 150 155 160

Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile  
 165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser  
 180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu  
 195 200 205

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

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe  
 225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys  
 245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu  
 260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln  
 275 280 285

Lys Lys Gln Gln  
 290

<210> SEQ ID NO 201  
 <211> LENGTH: 1421  
 <212> TYPE: DNA  
 <213> ORGANISM: *Ostreococcus tauri*  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (26)..(1399)  
 <223> OTHER INFORMATION: Delta-6 desaturase

<400> SEQUENCE: 201

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ggatccttaa ttaaggcgcg ccaaa atg tgt gtt gag acc gag aac aac gat      52
Met Cys Val Glu Thr Glu Asn Asn Asp
1 5

gga atc cct act gtg gag atc gct ttc gat gga gag aga gaa aga gct      100
Gly Ile Pro Thr Val Glu Ile Ala Phe Asp Gly Glu Arg Glu Arg Ala
10 15 20 25

gag gct aac gtg aag ttg tct gct gag aag atg gaa cct gct gct ttg      148
Glu Ala Asn Val Lys Leu Ser Ala Glu Lys Met Glu Pro Ala Ala Leu
30 35 40

gct aag acc ttc gct aga aga tac gtg gtt atc gag gga gtt gag tac      196
Ala Lys Thr Phe Ala Arg Arg Tyr Val Val Ile Glu Gly Val Glu Tyr
45 50 55
    
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gat	gtg	acc	gat	ttc	aaa	cat	cct	gga	gga	acc	gtg	att	ttc	tac	gct	244
Asp	Val	Thr	Asp	Phe	Lys	His	Pro	Gly	Gly	Thr	Val	Ile	Phe	Tyr	Ala	
	60						65				70					
ctc	tct	aac	act	gga	gct	gat	gct	act	gag	gct	ttc	aag	gag	ttc	cac	292
Leu	Ser	Asn	Thr	Gly	Ala	Asp	Ala	Thr	Glu	Ala	Phe	Lys	Glu	Phe	His	
	75				80					85						
cac	aga	tct	aga	aag	gct	agg	aag	gct	ttg	gct	gct	ttg	cct	tct	aga	340
His	Arg	Ser	Arg	Lys	Ala	Arg	Lys	Ala	Leu	Ala	Ala	Leu	Pro	Ser	Arg	
90					95				100						105	
cct	gct	aag	acc	gct	aaa	gtg	gat	gat	gct	gag	atg	ctc	cag	gat	ttc	388
Pro	Ala	Lys	Thr	Ala	Lys	Val	Asp	Asp	Ala	Glu	Met	Leu	Gln	Asp	Phe	
				110					115						120	
gct	aag	tgg	aga	aag	gag	ttg	gag	agg	gac	gga	ttc	ttc	aag	cct	tct	436
Ala	Lys	Trp	Arg	Lys	Glu	Leu	Glu	Arg	Asp	Gly	Phe	Phe	Lys	Pro	Ser	
		125						130							135	
cct	gct	cat	ggt	gct	tac	aga	ttc	gct	gag	ttg	gct	gct	atg	tac	gct	484
Pro	Ala	His	Val	Ala	Tyr	Arg	Phe	Ala	Glu	Leu	Ala	Ala	Met	Tyr	Ala	
		140					145								150	
ttg	gga	acc	tac	ttg	atg	tac	gct	aga	tac	gtt	gtg	tcc	tct	gtg	ttg	532
Leu	Gly	Thr	Tyr	Leu	Met	Tyr	Ala	Arg	Tyr	Val	Val	Ser	Ser	Val	Leu	
	155					160						165				
gtt	tac	gct	tgc	ttc	ttc	gga	gct	aga	tgt	gga	tgg	gtt	caa	cat	gag	580
Val	Tyr	Ala	Cys	Phe	Phe	Gly	Ala	Arg	Cys	Gly	Trp	Val	Gln	His	Glu	
170					175					180					185	
gga	gga	cat	tct	tct	ttg	acc	gga	aac	atc	tgg	tgg	gat	aag	aga	atc	628
Gly	Gly	His	Ser	Ser	Leu	Thr	Gly	Asn	Ile	Trp	Trp	Asp	Lys	Arg	Ile	
				190					195						200	
caa	gct	ttc	act	gct	gga	ttc	gga	ttg	gct	gga	tct	gga	gat	atg	tgg	676
Gln	Ala	Phe	Thr	Ala	Gly	Phe	Gly	Leu	Ala	Gly	Ser	Gly	Asp	Met	Trp	
			205					210							215	
aac	tcc	atg	cac	aac	aag	cac	cat	gct	act	cct	caa	aaa	gtg	agg	cac	724
Asn	Ser	Met	His	Asn	Lys	His	His	Ala	Thr	Pro	Gln	Lys	Val	Arg	His	
		220						225							230	
gat	atg	gat	ttg	gat	acc	act	cct	gct	gtt	gct	ttc	ttc	aac	acc	gct	772
Asp	Met	Asp	Leu	Asp	Thr	Thr	Pro	Ala	Val	Ala	Phe	Phe	Asn	Thr	Ala	
		235				240									245	
gtg	gag	gat	aat	aga	cct	agg	gga	ttc	tct	aag	tac	tgg	ctc	aga	ttg	820
Val	Glu	Asp	Asn	Arg	Pro	Arg	Gly	Phe	Ser	Lys	Tyr	Trp	Leu	Arg	Leu	
250					255										265	
caa	gct	tgg	acc	ttc	att	cct	gtg	act	tct	gga	ttg	gtg	ttg	ctc	ttc	868
Gln	Ala	Trp	Thr	Phe	Ile	Pro	Val	Thr	Ser	Gly	Leu	Val	Leu	Leu	Phe	
				270					275						280	
tgg	atg	ttc	ttc	ctc	cat	cct	tct	aag	gct	ttg	aag	gga	gga	aag	tac	916
Trp	Met	Phe	Phe	Leu	His	Pro	Ser	Lys	Ala	Leu	Lys	Gly	Gly	Lys	Tyr	
			285					290							295	
gag	gag	ctt	gtg	tgg	atg	ttg	gct	gct	cat	gtg	att	aga	acc	tgg	acc	964
Glu	Glu	Leu	Val	Trp	Met	Leu	Ala	Ala	His	Val	Ile	Arg	Thr	Trp	Thr	
		300						305							310	
att	aag	gct	ggt	act	gga	ttc	acc	gct	atg	caa	tcc	tac	gga	ctc	ttc	1012
Ile	Lys	Ala	Val	Thr	Gly	Phe	Thr	Ala	Met	Gln	Ser	Tyr	Gly	Leu	Phe	
		315				320									325	
ttg	gct	act	tct	tgg	gtt	tcc	gga	tgc	tac	ttg	ttc	gct	cac	ttc	tct	1060
Leu	Ala	Thr	Ser	Trp	Val	Ser	Gly	Cys	Tyr	Leu	Phe	Ala	His	Phe	Ser	
330					335					340					345	
act	tct	cac	acc	cat	ttg	gat	gtt	gtt	cct	gct	gat	gag	cat	ttg	tct	1108
Thr	Ser	His	Thr	His	Leu	Asp	Val	Val	Pro	Ala	Asp	Glu	His	Leu	Ser	
				350						355					360	
tgg	gtt	agg	tac	gct	gtg	gat	cac	acc	att	gat	atc	gat	cct	tct	cag	1156
Trp	Val	Arg	Tyr	Ala	Val	Asp	His	Thr	Ile	Asp	Ile	Asp	Pro	Ser	Gln	
			365					370							375	

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gga tgg gtt aac tgg ttg atg gga tac ttg aac tgc caa gtg att cat    1204
Gly Trp Val Asn Trp Leu Met Gly Tyr Leu Asn Cys Gln Val Ile His
      380                      385                      390

cac ctc ttc cct tct atg cct caa ttc aga caa cct gag gtg tcc aga    1252
His Leu Phe Pro Ser Met Pro Gln Phe Arg Gln Pro Glu Val Ser Arg
      395                      400                      405

aga ttc gtt gct ttc gct aag aag tgg aac ctc aac tac aag gtg atg    1300
Arg Phe Val Ala Phe Ala Lys Lys Trp Asn Leu Asn Tyr Lys Val Met
      410                      415                      420

act tat gct gga gct tgg aag gct act ttg gga aac ctc gat aat gtg    1348
Thr Tyr Ala Gly Ala Trp Lys Ala Thr Leu Gly Asn Leu Asp Asn Val
      430                      435                      440

gga aag cac tac tac gtg cac gga caa cat tct gga aag acc gct tga    1396
Gly Lys His Tyr Tyr Val His Gly Gln His Ser Gly Lys Thr Ala
      445                      450                      455

taa ttaattaagg cgcgccgaat tc    1421

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&lt;210&gt; SEQ ID NO 202

&lt;211&gt; LENGTH: 456

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Ostreococcus tauri*

&lt;400&gt; SEQUENCE: 202

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Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
 1      5      10      15

Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser
 20      25      30

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
 35      40      45

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His
 50      55      60

Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp
 65      70      75      80

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg
 85      90      95

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val
 100     105     110

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu
 115     120     125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg
 130     135     140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr
 145     150     155     160

Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly
 165     170     175

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr
 180     185     190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
 195     200     205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
 210     215     220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
 225     230     235     240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
 245     250     255

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Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro  
 260 265 270

Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro  
 275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu  
 290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe  
 305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser  
 325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp  
 340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp  
 355 360 365

His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met  
 370 375 380

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro  
 385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys  
 405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys  
 420 425 430

Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His  
 435 440 445

Gly Gln His Ser Gly Lys Thr Ala  
 450 455

<210> SEQ ID NO 203  
 <211> LENGTH: 61  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 203

gaattcggcg cgccgagctc ctcgagcaac ggttccggcg gtatagagtt gggtaattcg 60  
 a 61

<210> SEQ ID NO 204  
 <211> LENGTH: 45  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 204

cccgggatcg atgccgcag atctccacca ttttttggtg gtgat 45

<210> SEQ ID NO 205  
 <211> LENGTH: 40  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 205

aggcctccat ggctgcttt aatgagatat gcgagacgcc 40

<210> SEQ ID NO 206



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<211> LENGTH: 32  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 206  
  
 cccgggccgg acaatcagta aattgaacgg ag 32

<210> SEQ ID NO 207  
 <211> LENGTH: 26  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 207  
  
 aggcctcaac ggttccggcg gtatag 26

<210> SEQ ID NO 208  
 <211> LENGTH: 60  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 208  
  
 cccgggggta acgctagcgg gcccgatata ggateccatt ttttgggtgt gattggttct 60

<210> SEQ ID NO 209  
 <211> LENGTH: 31  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 209  
  
 aggcctcctg ctttaatgag atatgcgaga c 31

<210> SEQ ID NO 210  
 <211> LENGTH: 31  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 210  
  
 cccgggcgga caatcagtaa attgaacgga g 31

<210> SEQ ID NO 211  
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 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 211  
  
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<210> SEQ ID NO 212  
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 <212> TYPE: DNA  
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 <223> OTHER INFORMATION: Primer  
  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
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 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
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<210> SEQ ID NO 217  
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 <212> TYPE: DNA  
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 <220> FEATURE:  
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gggatccatg ggcaagggca gcgagggccg 30

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 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
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<210> SEQ ID NO 219  
 <211> LENGTH: 36  
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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 219  
  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
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<210> SEQ ID NO 223  
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 <223> OTHER INFORMATION: Primer  
  
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 <212> TYPE: DNA  
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 <223> OTHER INFORMATION: Primer  
  
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32

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 <212> TYPE: PRT  
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 <223> OTHER INFORMATION: Cyt. B5 domain

<400> SEQUENCE: 227

His Pro Gly Gly  
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<210> SEQ ID NO 228  
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 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box1

<400> SEQUENCE: 228

His Cys Ala Asn His  
 1 5

<210> SEQ ID NO 229  
 <211> LENGTH: 5  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box1

<400> SEQUENCE: 229

His Glu Gly Gly His  
 1 5

<210> SEQ ID NO 230  
 <211> LENGTH: 5  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box1

<400> SEQUENCE: 230

His Glu Cys Gly His  
 1 5

<210> SEQ ID NO 231  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 231

Trp Arg Tyr His His Gln Val Ser His His  
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<210> SEQ ID NO 232  
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 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 232

Trp Arg Tyr His His Met Val Ser His His  
 1                   5                   10

<210> SEQ ID NO 233  
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 <212> TYPE: PRT  
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 <223> OTHER INFORMATION: His box2

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Trp Asn Ser Met His Asn Lys His His  
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<210> SEQ ID NO 234  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 234

Trp Gln Arg Ser His Ala Val His His  
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<210> SEQ ID NO 235  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 235

Gln Val Glu His His Leu Phe Pro  
 1                   5

<210> SEQ ID NO 236  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 236

Gln Val Val His His Leu Phe Pro  
 1                   5

<210> SEQ ID NO 237  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 237

Gln Ile Glu His His Leu Pro Phe  
 1                   5

<210> SEQ ID NO 238

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<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: His box3

<400> SEQUENCE: 238

Gln Val Ile His His Leu Phe Pro  
1 5

<210> SEQ ID NO 239  
<211> LENGTH: 5  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: His box3

<400> SEQUENCE: 239

His Val Ala His His  
1 5

<210> SEQ ID NO 240  
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<223> OTHER INFORMATION: His box1

<400> SEQUENCE: 240

His Asp Gly Asn His  
1 5

<210> SEQ ID NO 241  
<211> LENGTH: 5  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: His box1

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His Asp Ala Asn His  
1 5

<210> SEQ ID NO 242  
<211> LENGTH: 5  
<212> TYPE: PRT  
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<220> FEATURE:  
<223> OTHER INFORMATION: His box1

<400> SEQUENCE: 242

His Asp Phe Leu His  
1 5

<210> SEQ ID NO 243  
<211> LENGTH: 5  
<212> TYPE: PRT  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: His box1

<400> SEQUENCE: 243

His Asp Ala Gly His  
1 5

<210> SEQ ID NO 244  
<211> LENGTH: 10

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<212> TYPE: PRT  
 <213> ORGANISM: Artificial  
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 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 244

Trp Glu Leu Gln His Met Leu Gly His His  
 1                   5                   10

<210> SEQ ID NO 245  
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 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 245

Trp Met Ala Gln His Trp Thr His His  
 1                   5

<210> SEQ ID NO 246  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 246

Trp Leu Ala Gln His Trp Thr His His  
 1                   5

<210> SEQ ID NO 247  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
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 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 247

Trp Lys Asn Lys His Asn Gly His His  
 1                   5

<210> SEQ ID NO 248  
 <211> LENGTH: 5  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 248

His Ala Lys His His  
 1                   5

<210> SEQ ID NO 249  
 <211> LENGTH: 11  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box2

<400> SEQUENCE: 249

Trp Leu Phe Met Val Thr Tyr Leu Gln His His  
 1                   5                   10

<210> SEQ ID NO 250  
 <211> LENGTH: 8  
 <212> TYPE: PRT

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<213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 250

Gln Ile Glu His His Leu Phe Pro  
 1 5

<210> SEQ ID NO 251  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 251

Gln Val Asp His His Leu Phe Pro  
 1 5

<210> SEQ ID NO 252  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 252

His Val Ala His His Leu Phe His  
 1 5

<210> SEQ ID NO 253  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: His box3

<400> SEQUENCE: 253

His Val Val His His Leu Phe  
 1 5

<210> SEQ ID NO 254  
 <211> LENGTH: 7  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Corresponding amino acids to primer Phaelo  
 forward1

<400> SEQUENCE: 254

Asn Leu Leu Trp Leu Phe Tyr  
 1 5

<210> SEQ ID NO 255  
 <211> LENGTH: 8  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Corresponding amino acids to primer Phaelo  
 reversel

<400> SEQUENCE: 255

Phe Ala Gln Phe Phe Val Gln Ser  
 1 5

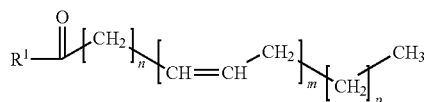
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We claim:

1. A process for the production of compounds of the general formula I

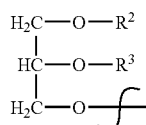


in seeds of a transgenic plant with a content of at least 20% by weight based on the total lipid content, which comprises the following process steps:

- introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 6$ -desaturase activity,
- introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 6$ -elongase activity,
- introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 5$ -desaturase activity,
- introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 5$ -elongase activity, wherein said  $\Delta 5$ -elongase activity elongates only unsaturated  $\text{C}^{20}$ -fatty acids, and
- introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 4$ -desaturase activity, and

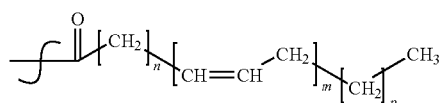
wherein the variables and substituents in formula I have the following meanings:

$\text{R}^1$ =hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the general formula II



$\text{R}^2$ =hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated  $\text{C}_2$ - $\text{C}_{24}$ -alkylcarbonyl,

$\text{R}^3$ =hydrogen, saturated or unsaturated  $\text{C}_2$ - $\text{C}_{24}$ -alkylcarbonyl, or  $\text{R}^2$  and  $\text{R}^3$  independently of one another are a radical of the general 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 the at least one nucleic acid sequence which encodes a polypeptide with  $\Delta 5$ -elongase activity comprises:

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- the nucleic acid sequence of SEQ ID NO: 67, 83, or 113;
- a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 68, 84, or 114;
- a nucleic acid sequence having at least 95% identity to the nucleic acid sequence of SEQ ID NO: 67, 83, or 113; or
- a nucleic acid sequence encoding an amino acid sequence having at least 95% identity to SEQ ID NO: 68, 84, or 114.

2. The process according to claim 1, wherein the variables  $n$ ,  $m$  and  $p$  have the following meanings:  
 $n=2, 3$  or  $5$ ,  $m=4, 5$  or  $6$  and  $p=0$  or  $3$ .

3. The process according to claim 1, wherein, in formula I, the variables  $n$ ,  $m$  and  $p$  have the following meanings:

- $m=4$ ,  $n=3$ ,  $p=3$  and the compound is arachidonic acid,
- $m=5$ ,  $n=3$ ,  $p=0$  and the compound is eicosapentaenoic acid,
- $m=5$ ,  $n=5$ ,  $p=0$  and the compound is docosapentaenoic acid, or
- $m=6$ ,  $n=3$ ,  $p=0$  and the compound is docosahexaenoic acid.

4. The process according to claim 2, wherein, in the seed of the transgenic plant, the content of all compounds of the formula I together amounts to at least 27% by weight based on the total lipid content.

5. The process according to claim 3, wherein, in the seed of the transgenic plant, the docosahexaenoic acid content amounts to at least 1% by weight based on the total lipid content.

6. The process according to claim 1, wherein the nucleic acid sequences which encode polypeptides with  $\Delta 6$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase, or  $\Delta 4$ -desaturase activity are selected from the group consisting of:

- a nucleic acid sequence with the sequence shown in SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 41, or SEQ ID NO: 193,
- nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 42, or SEQ ID NO: 194, and
- derivatives of the nucleic acid sequence shown in SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 41, or SEQ ID NO: 193, which encode polypeptides with at least 70% identity at the amino acid level with SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 42, or SEQ ID NO: 194, and which have  $\Delta 6$ -desaturase,  $\Delta 6$ -elongase,  $\Delta 5$ -desaturase or  $\Delta 4$ -desaturase activity.

7. The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with  $\omega 3$ -desaturase activity, selected from the group consisting of:

- a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or
- nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106, or
- derivatives of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, which encode polypeptides with at least 70% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and which have  $\omega 3$ -desaturase activity

is additionally introduced into the transgenic plant.

8. The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with  $\Delta 12$ -desaturase activity, selected from the group consisting of:

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- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, or
- b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196, or
- c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, which encode polypeptides with at least 70% identity at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have  $\Delta 12$ -desaturase activity

is additionally introduced into the transgenic plant.

9. The process according to claim 1, wherein a nucleic acid sequence which encodes proteins of the biosynthetic pathway 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, lipoxygenases, triacylglycerol lipases, alleloxide synthases, hydroperoxide lyases or fatty acid elongase(s) is additionally introduced into the transgenic plant.

10. The process according to claim 1, wherein the substituents R<sup>2</sup> or R<sup>3</sup> independently of one another are saturated or unsaturated C<sub>18</sub>-C<sub>22</sub>-alkylcarbonyl.

11. The process according to claim 1, wherein the substituents R<sup>2</sup> or R<sup>3</sup> independently of one another are unsaturated C<sub>18</sub>-, C<sub>20</sub>- or C<sub>22</sub>-alkylcarbonyl with at least two double bonds.

12. The process according to claim 1, wherein the transgenic plant is selected from the group consisting of an oil-producing plant, a vegetable plant and an ornamental.

13. The process according to claim 1, wherein the transgenic plant is selected from the group of the plant families consisting of: Anacardiaceae, Asteraceae, Boraginaceae, Brassicaceae, Cannabaceae, Compositae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Leguminosae, Linaceae, Malvaceae, Moringaceae, Marchantiaceae, Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae, Pedaliaceae, Poaceae and Solanaceae.

14. The process according to claim 1, wherein the compounds of the general formula I are isolated from the transgenic plant in the form of their oils, lipids or free fatty acids.

15. The process according to claim 1, wherein the polypeptide with  $\Delta 5$ -elongase activity elongates only unsaturated C<sub>20</sub>-fatty acids with one double bond in the  $\Delta 5$ -position.

16. The process according to claim 1, wherein the compounds of the general formula I comprise fatty acids having 20 or 22 carbon atoms in the fatty acid chain.

17. The process according to claim 1, wherein the plant is selected from the group consisting of soybean, peanut, oilseed rape, canola, linseed, evening primrose, mullein, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, *Punica*, oil palm, walnut and coconut.

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18. A process for the production of arachidonic acid (ARA), eicosapentaenoic acid (EPA) and/or docosahexaenoic acid (DHA) in seeds of a plant, comprising introducing into a plant:

- a nucleic acid encoding a polypeptide having  $\Delta 6$ -desaturase activity;
- a nucleic acid encoding a polypeptide having  $\Delta 6$ -elongase activity;
- a nucleic acid encoding a polypeptide having  $\Delta 5$ -desaturase activity;
- a nucleic acid encoding a polypeptide having  $\Delta 5$ -elongase activity; and
- a nucleic acid encoding a polypeptide having  $\Delta 4$ -desaturase activity;

wherein said nucleic acid encoding a polypeptide having  $\Delta 5$ -elongase activity comprises:

- the nucleotide sequence of SEQ ID NO: 67, 83, or 113;
- a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NO: 68, 84, or 114; or
- iii) a nucleic acid sequence encoding a polypeptide having at least 85% sequence identity to the amino acid sequence of SEQ ID NO: 68, 84, or 114.

19. The process of claim 18, wherein said nucleic acid encoding a polypeptide having  $\Delta 5$ -elongase activity comprises a nucleic acid sequence encoding a polypeptide having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 68, 84, or 114.

20. The process of claim 18, wherein said nucleic acid encoding a polypeptide having  $\Delta 5$ -elongase activity comprises a nucleic acid sequence encoding a polypeptide having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 68, 84, or 114.

21. The process of claim 1, wherein EPA and/or DHA is produced in the seeds of said transgenic plant.

22. A process for the production of an oil-, lipid- and fatty acid-composition, comprising:

- obtaining EPA and/or DHA produced by the process of claim 18; and
- formulating said EPA and/or DHA as an oil-, lipid- and fatty acid-composition.

23. A method for the production of feedstuffs, foodstuffs, cosmetics or pharmaceuticals, comprising:

- obtaining an oil-, lipid- and fatty acid-composition produced by the process of claim 22; and
- processing said oil-, lipid- and fatty acid-composition to produce feedstuffs, foodstuffs, cosmetics or pharmaceuticals.

24. A process for the production of an oil-, lipid- and fatty acid-composition, comprising:

- producing EPA and/or DHA in seeds of a transgenic plant according to the process of claim 18; and
- obtaining an oil-, lipid- and fatty acid-composition from the seeds of said transgenic plant.

25. A method for the production of feedstuffs, foodstuffs, cosmetics or pharmaceuticals, comprising:

- obtaining an oil-, lipid- and fatty acid-composition produced by the process of claim 24; and
- processing said oil-, lipid- and fatty acid-composition to produce feedstuffs, foodstuffs, cosmetics or pharmaceuticals.

\* \* \* \* \*