US009458436B2

(12) **United States Patent**
Cirpus et al.

(10) **Patent No.: US 9,458,436 B2**
(45) **Date of Patent: *Oct. 4, 2016**

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

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 1278 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **10/590,457**

(22) PCT Filed: **Feb. 23, 2005**

(86) PCT No.: **PCT/EP2005/001863**

§ 371 (c)(1),
(2), (4) Date: **Aug. 25, 2006**

(87) PCT Pub. No.: **WO2005/083093**

PCT Pub. Date: **Sep. 9, 2005**

(65) **Prior Publication Data**

US 2009/0222951 A1 Sep. 3, 2009

(30) **Foreign Application Priority Data**

Feb. 27, 2004	(DE)	10 2004 009 457
Mar. 13, 2004	(DE)	10 2004 012 370
Apr. 8, 2004	(DE)	10 2004 017 518
May 14, 2004	(DE)	10 2004 024 014
Jul. 16, 2004	(EP)	PCT/EP2004/007957
Dec. 24, 2004	(DE)	10 2004 062 543

(51) **Int. Cl.**

C12N 15/82	(2006.01)
C12N 9/02	(2006.01)
A23D 9/00	(2006.01)
A61K 8/92	(2006.01)
A61Q 19/00	(2006.01)
C12N 9/10	(2006.01)
A61K 8/36	(2006.01)
A61K 31/202	(2006.01)

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

CPC ***C12N 9/0071*** (2013.01); ***A23D 9/00*** (2013.01); ***A61K 8/361*** (2013.01); ***A61K 8/922*** (2013.01); ***A61K 31/202*** (2013.01); ***A61Q 19/00*** (2013.01); ***C12N 9/0083*** (2013.01); ***C12N 9/1029*** (2013.01); ***C12N 15/8247*** (2013.01); *A61K 2800/86* (2013.01); *C12Y 114/19* (2013.01)

(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 ω3-desaturase, Δ12-desaturase, Δ6-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-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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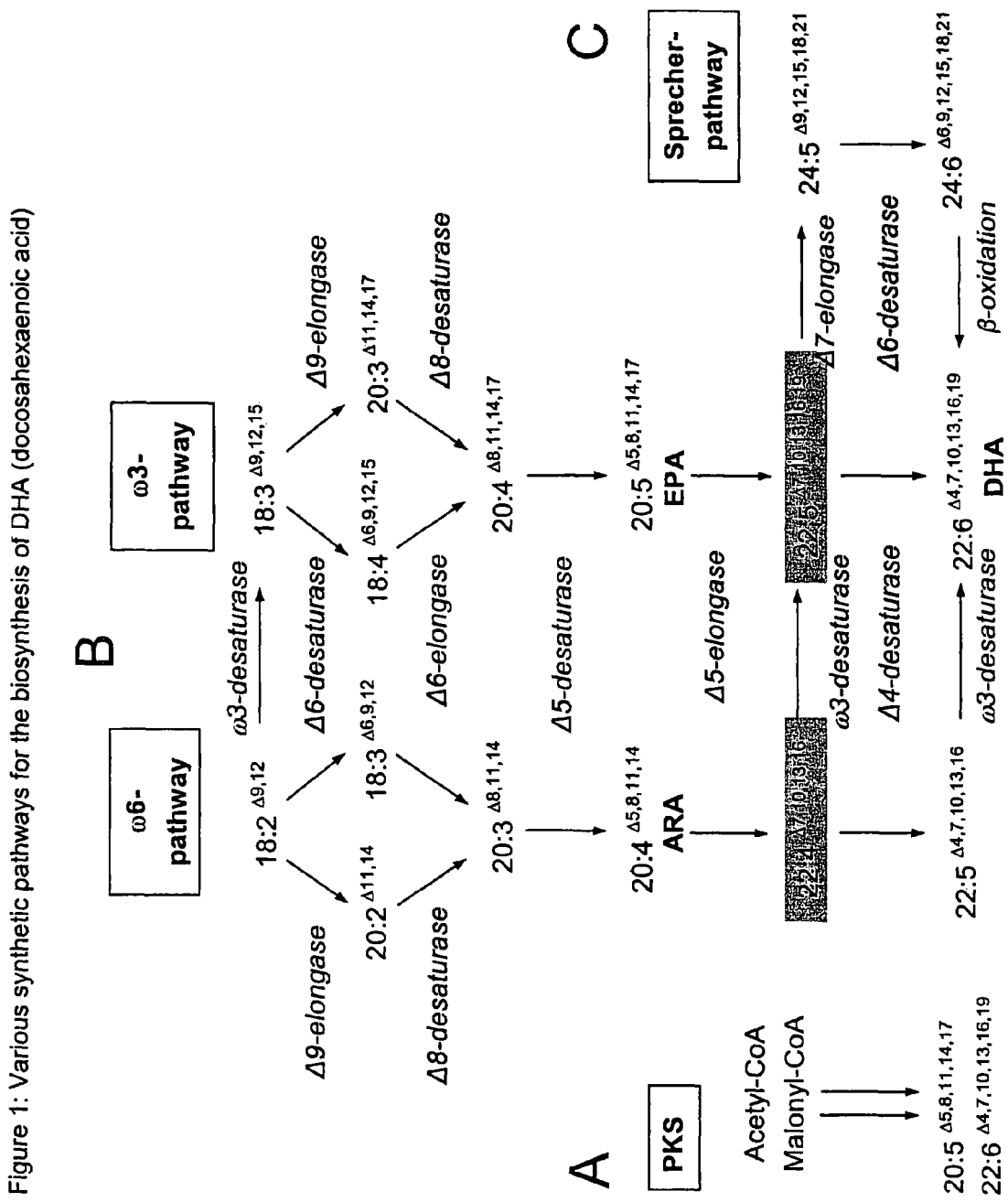


Figure 1: Various synthetic pathways for the biosynthesis of DHA (docosahexaenoic acid)

Figure 2: Substrate specificity of the Δ5-elongase (SEQ ID NO: 53) with regard to different fatty acids

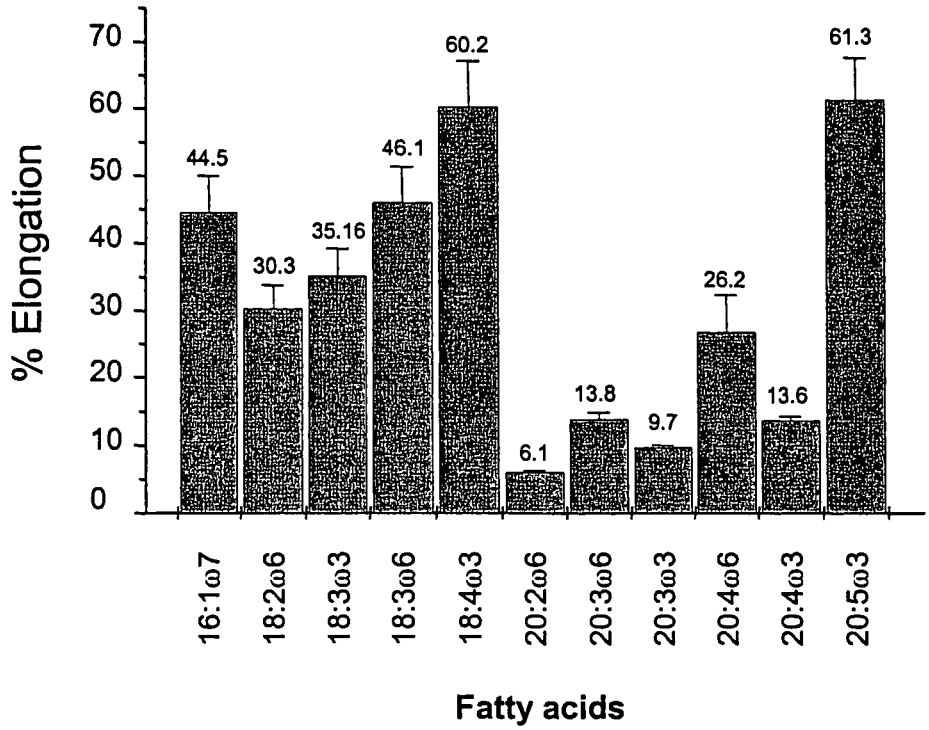


Figure 3: Reconstitution of DHA biosynthesis in yeast starting from 20:5ω3.

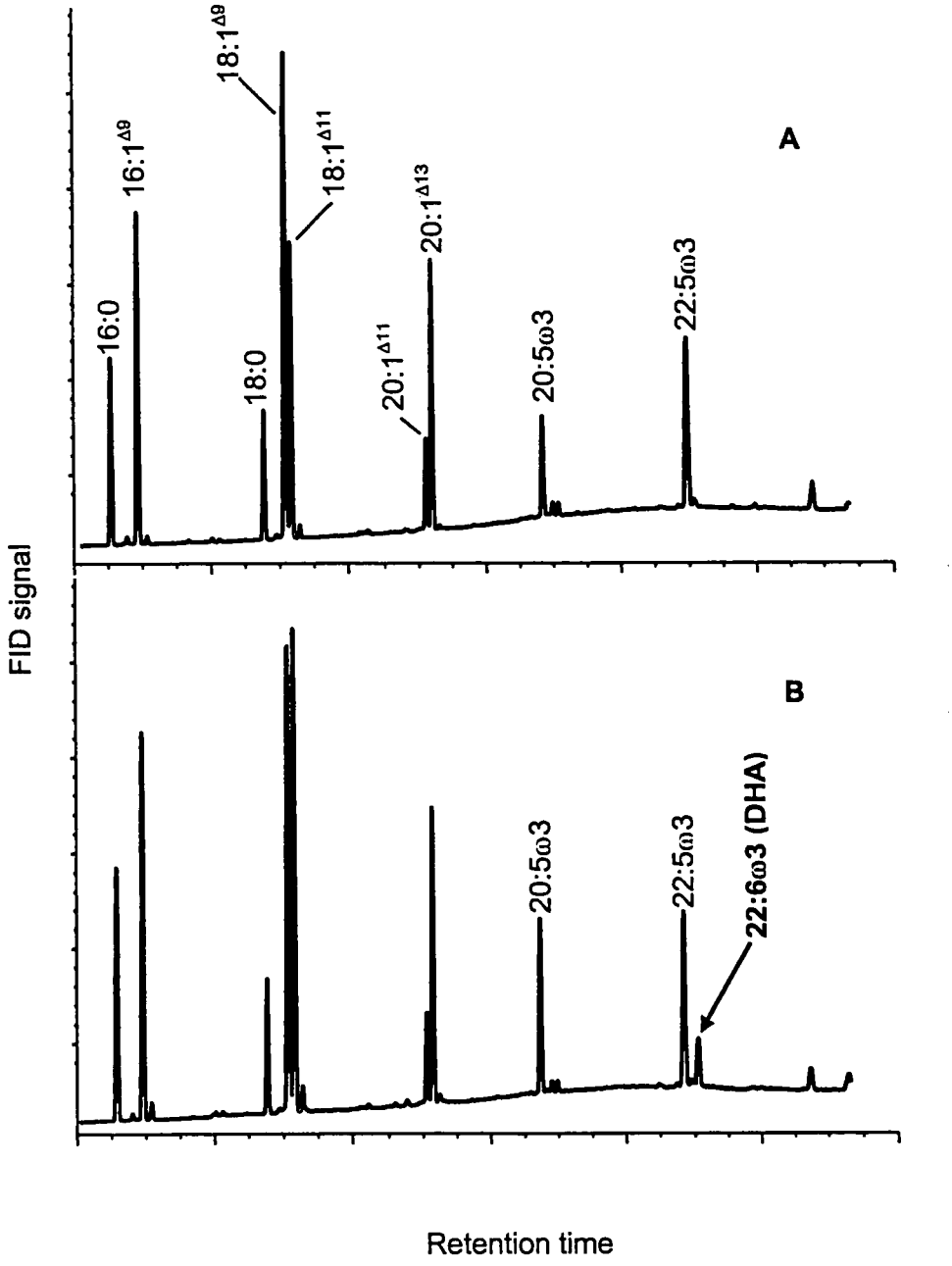


Figure 4: Reconstitution of DHA biosynthesis in yeast starting from 18:4ω3.

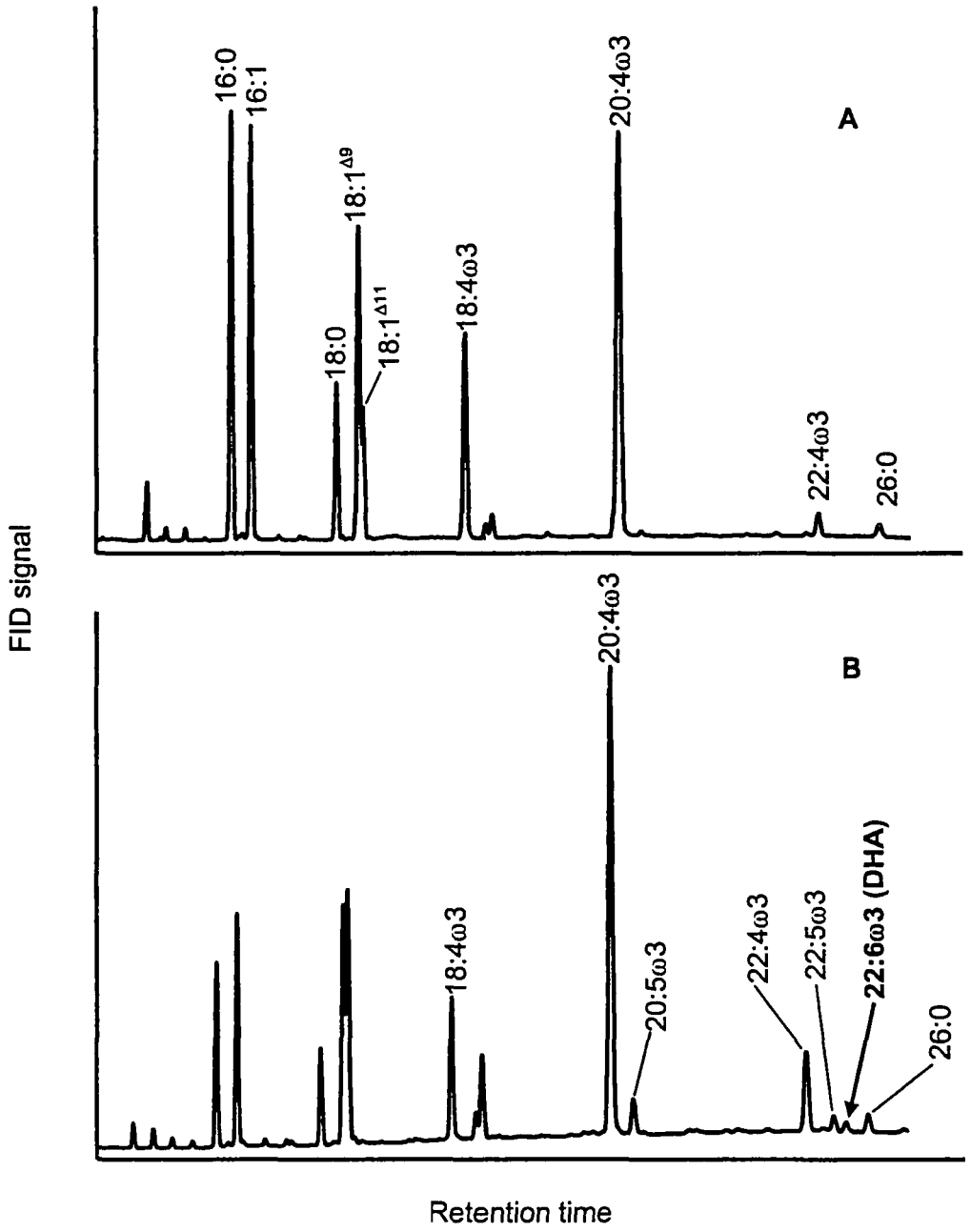


Figure 5: Fatty acid composition (in mol%) of transgenic yeasts which had been transformed with the vectors pYes3-OmELO3/pYes2-EgD4 or pYes3-OmELO3/pYes2-EgD4+pESCLeu-PtD5. The yeast cells were cultured in minimal medium without tryptophan and uracil/ and leucin in the presence of 250 μM $20:5^{\Delta5,8,11,14,17}$ and $18:4^{\Delta6,9,12,15}$, 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) ± standard deviation.

	pYes3-OmELO/pYes2-EgD4	pYes3-OmELO/pYes2-EgD4 EgD4 + pESCLeu-PtD5
Fatty acids	Feeding of $20:5^{\Delta5,8,11,14,17}$	Feeding of $18:4^{\Delta6,9,12,15}$
16:0	9.35 ± 1.61	7.35 ± 1.37
$16:1^{\Delta9}$	14.70 ± 2.72	10.02 ± 1.81
18:0	5.11 ± 1.09	4.27 ± 1.21
$18:1^{\Delta9}$	19.49 ± 3.01	10.81 ± 1.95
$18:1^{\Delta11}$	**18.93 ± 2.71**	**11.61 ± 1.48**
$18:4^{\Delta6,9,12,15}$	**-**	**7.79 ± 1.29**
$20:1^{\Delta11}$	**3.24 ± 0.41**	**1.56 ± 0.23**
$20:1^{\Delta13}$	**11.13± 2.07**	**4.40 ± 0.78**
$20:4^{\Delta8,11,14,17}$	**-**	**30.05 ± 3.16**
$20:5^{\Delta5,8,11,14,17}$	**6.91± 1.10**	**3.72 ± 0.59**
$22:4^{\Delta10,13,16,17}$	**-**	**5.71 ± 1.30**
$22:5^{\Delta7,10,13,16,19}$	**8.77 ± 1.32**	**1.10 ± 0.27**
$22:6^{\Delta4,7,10,13,16,19}$	**2.73 ± 0.39**	**0.58 ± 0.10**

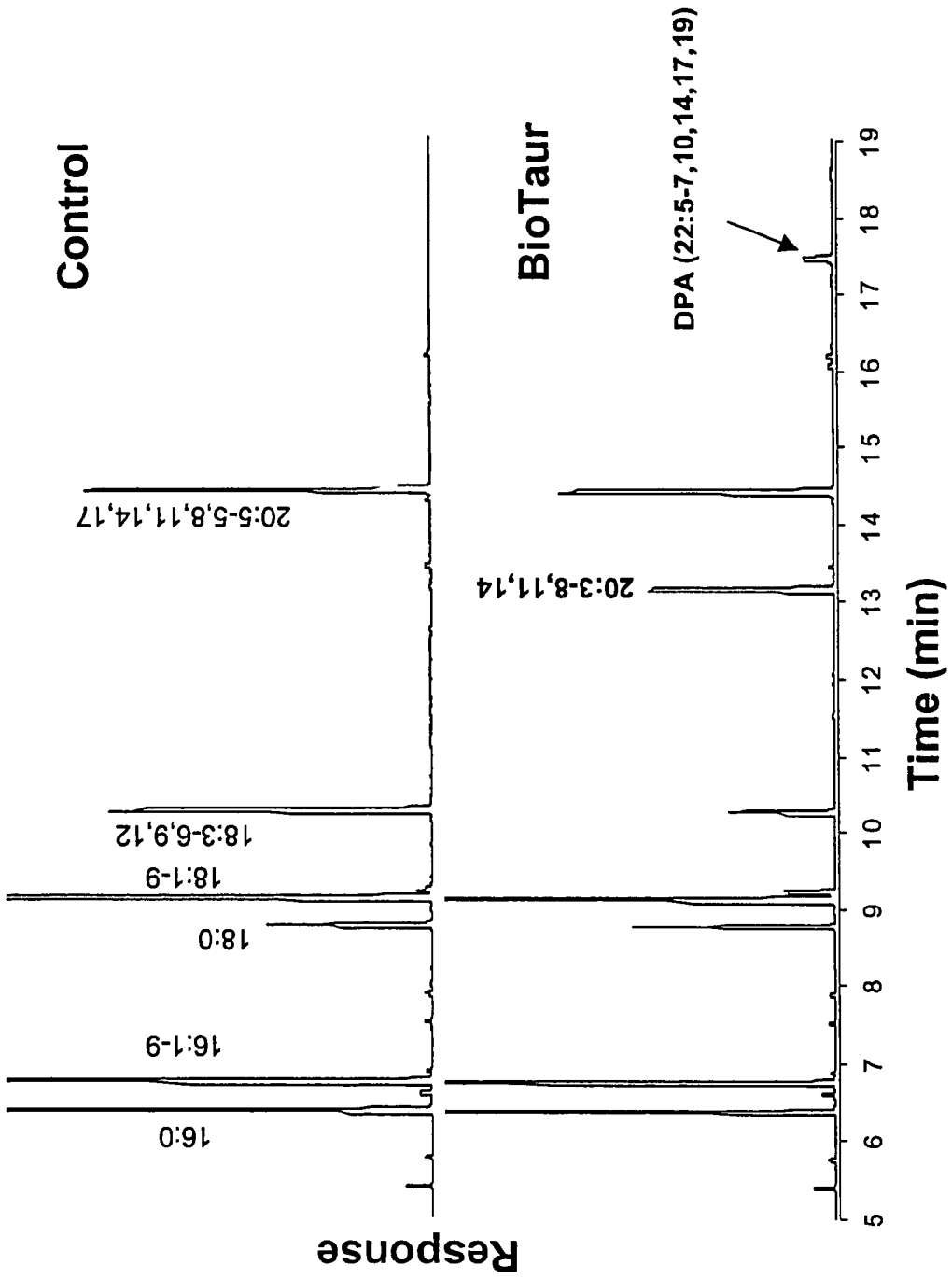


Figure 6: Feeding experiment for determining the functionality and substrate specificity with yeast strains

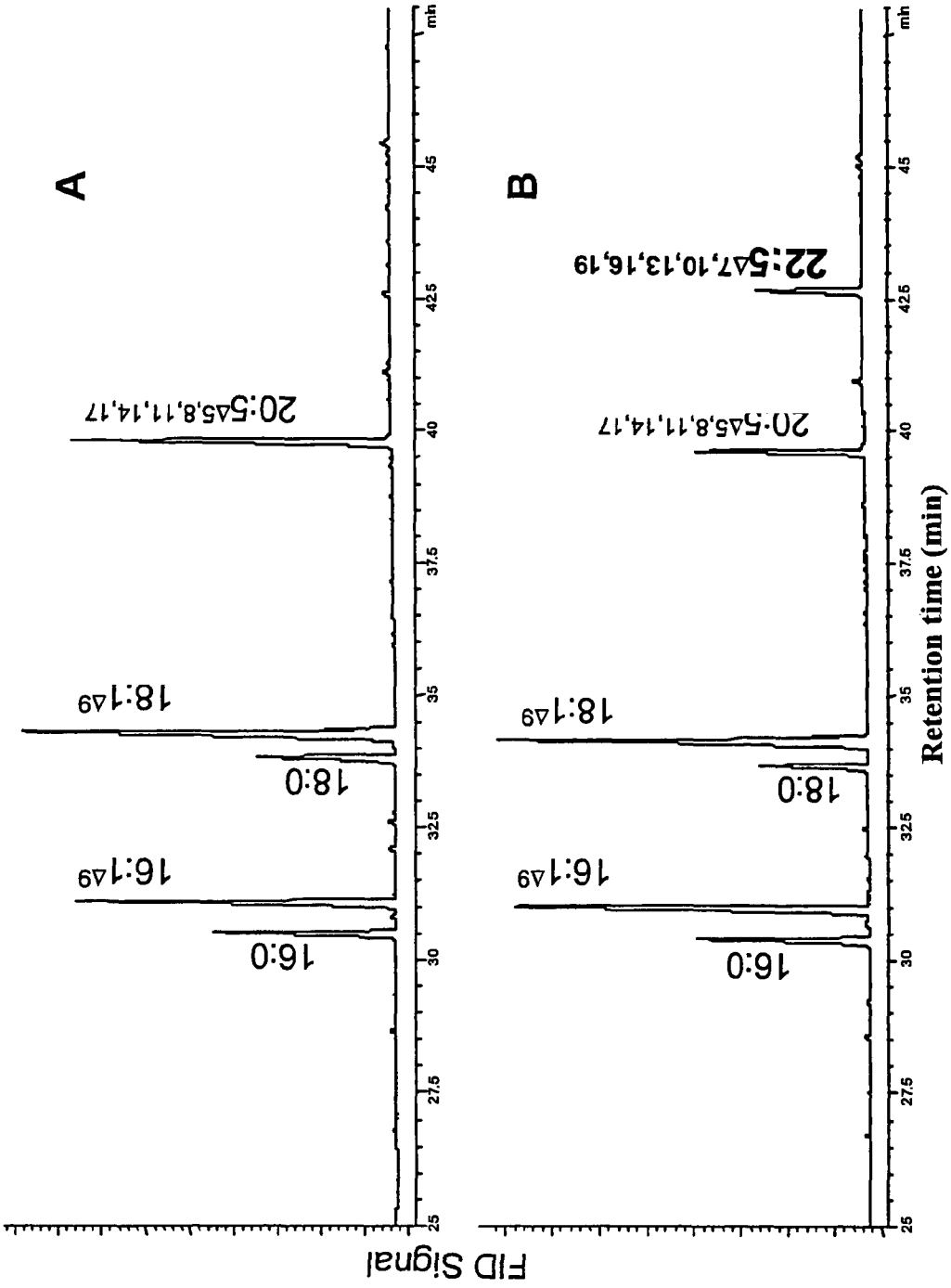


Figure 7: Elongation of eicosapentaenoic acid by OtElo1

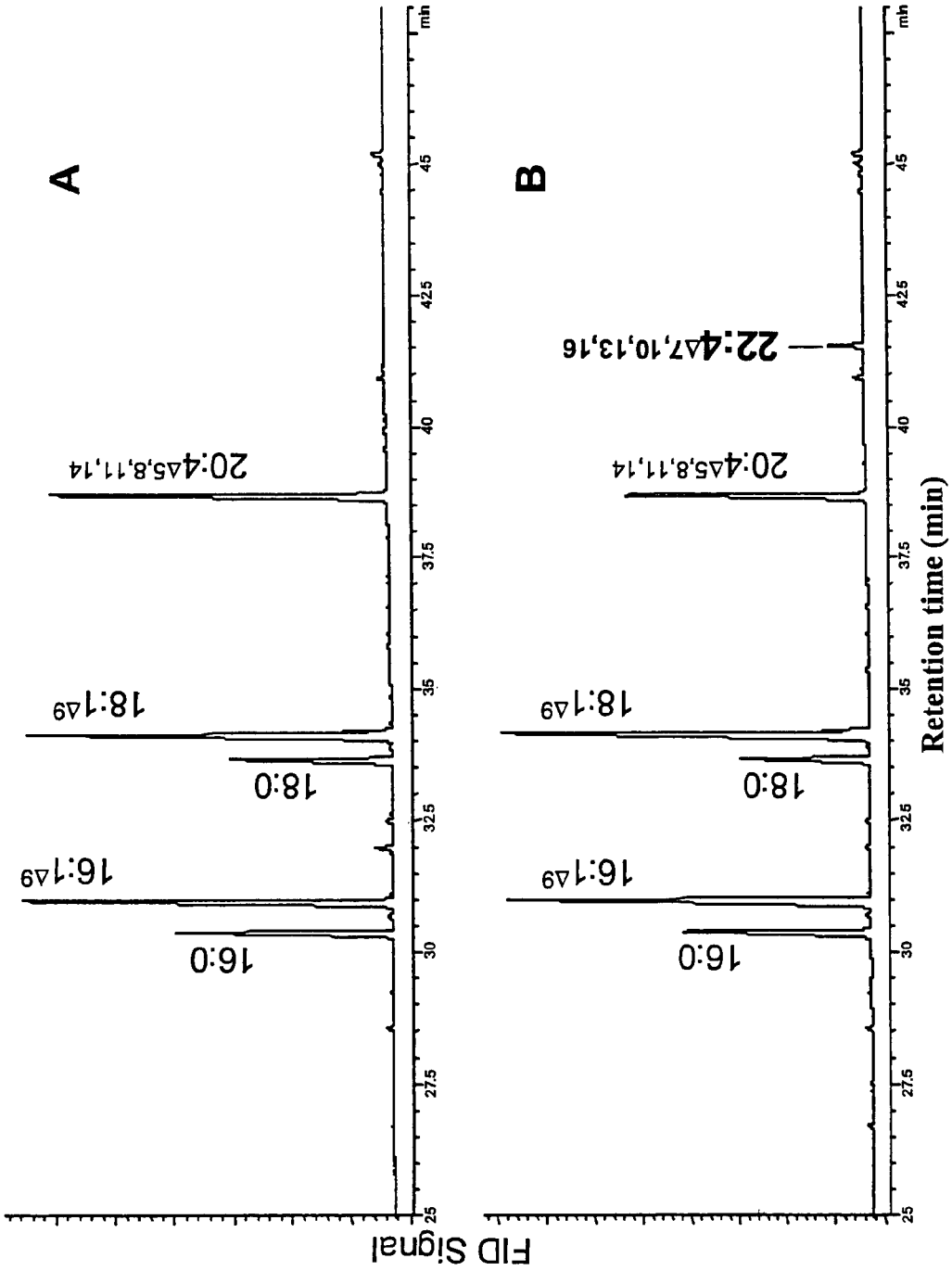


Figure 8: Elongation of arachidonic acid by OtElo1

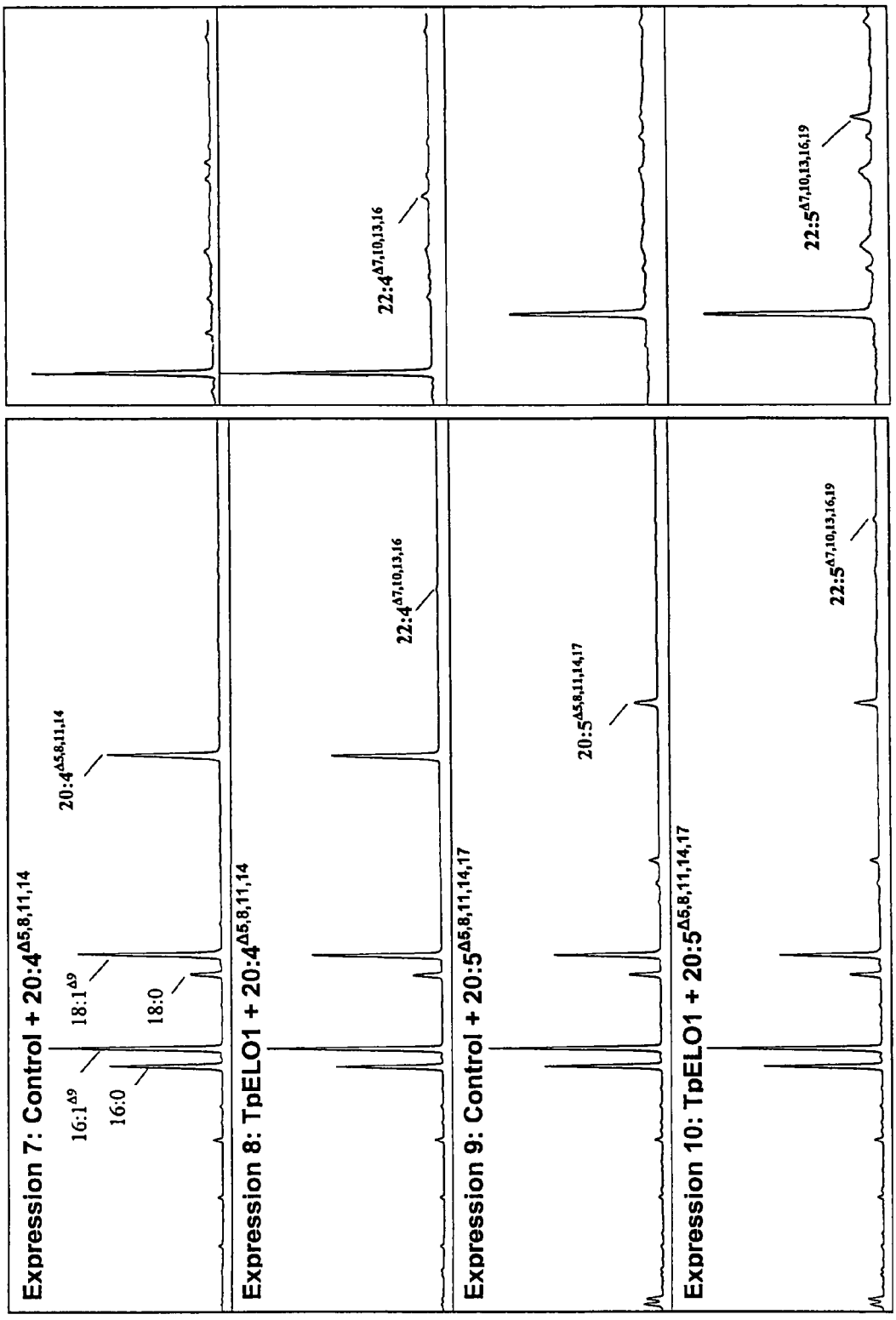


Figure 9: Expression of TpELO1 in yeast

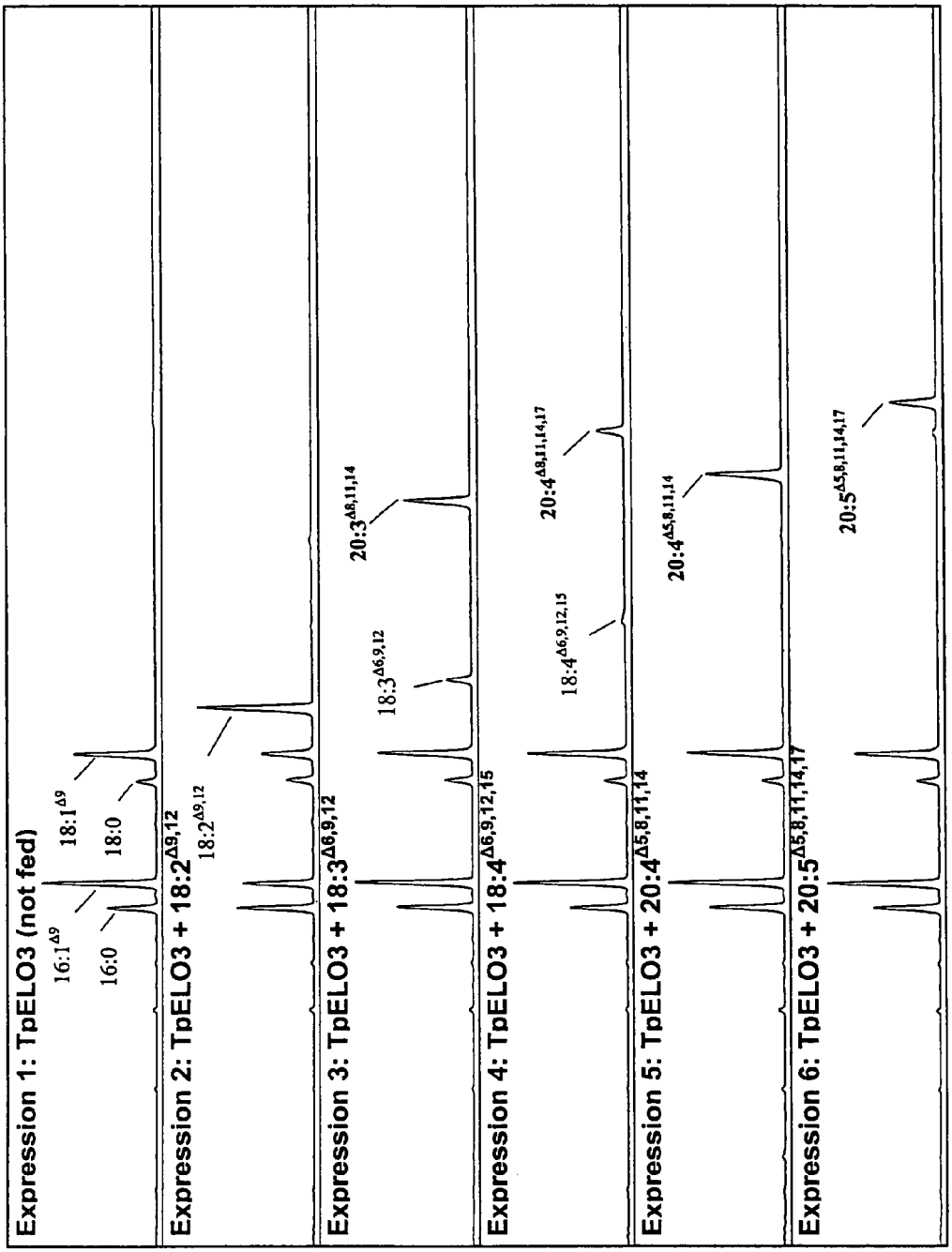


Figure 10: Expression of TpELO3 in yeast

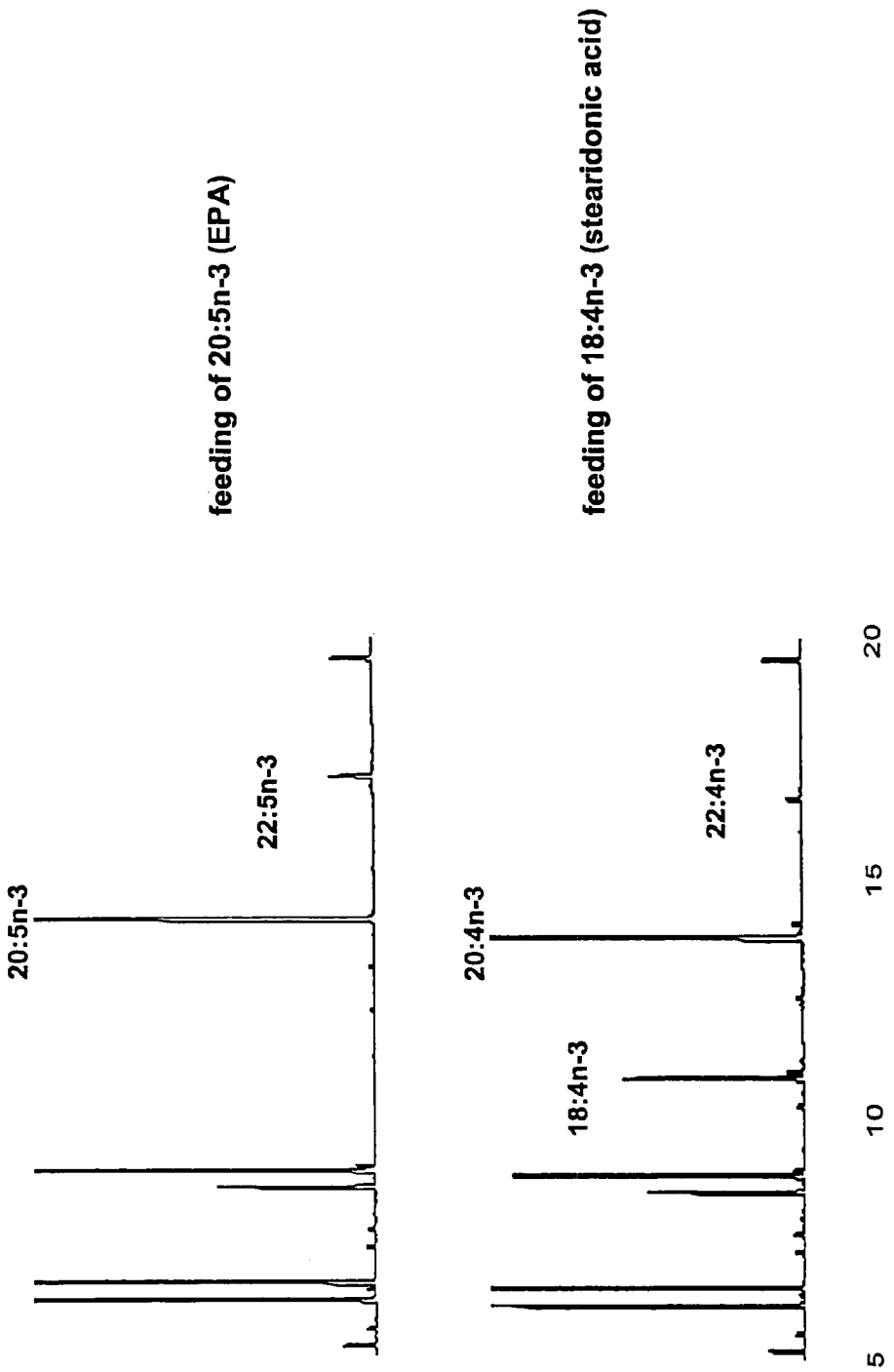


Figure 11: Expression of Thraustochytrium Δ5-elongase TL16/pYES2.1 in yeast

Figure 12: Desaturation of γ-linolenic acid (18:2 ω6-fatty acid) to give α-linolenic acid (18:3 ω3-fatty acid) by Pi-omega3Des.

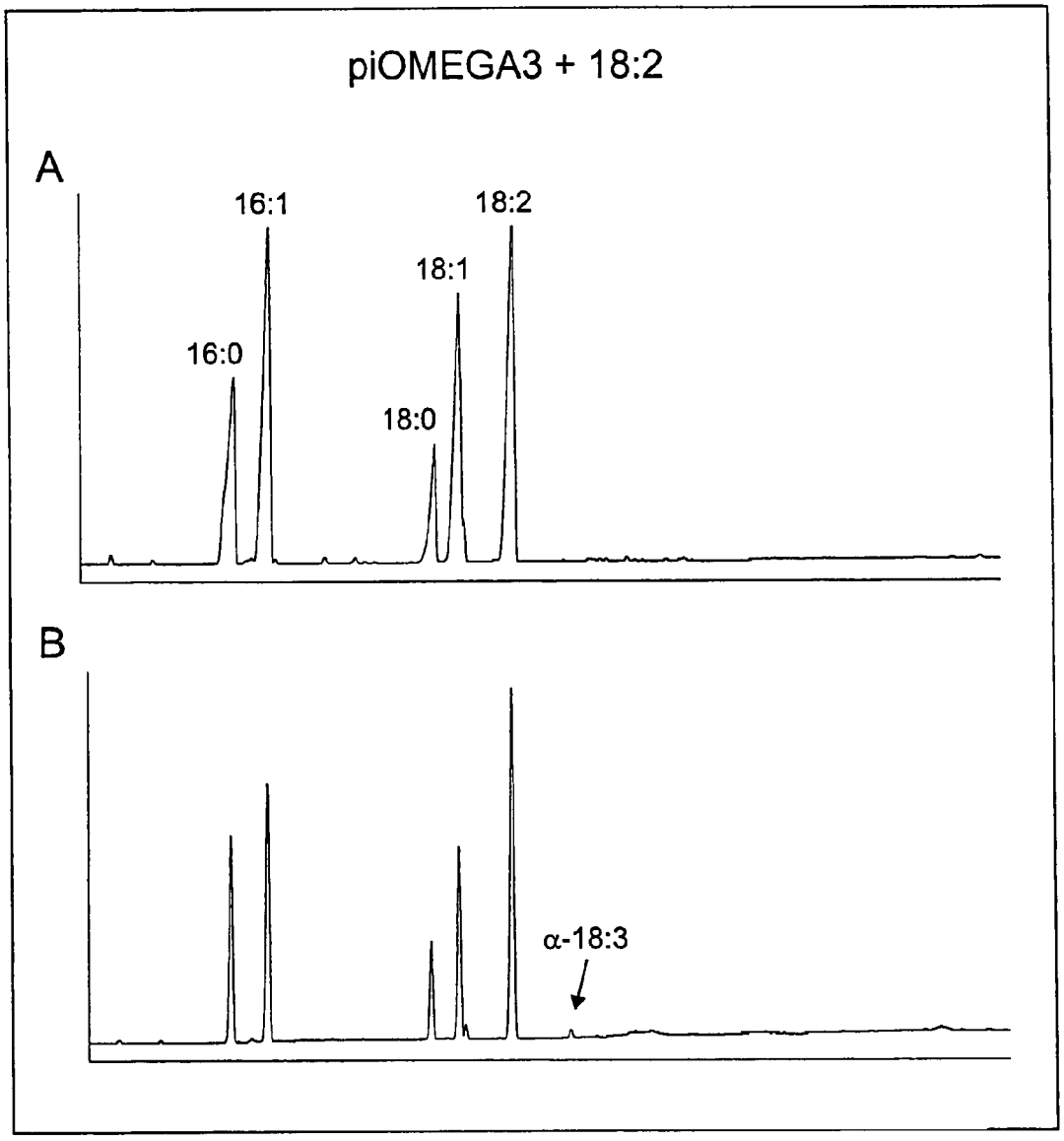


Figure 13: Desaturation of γ-linolenic acid (18:2 ω6-fatty acid) to give stearidonic acid (18:4 ω3-fatty acid) by Pi-omega3Des.

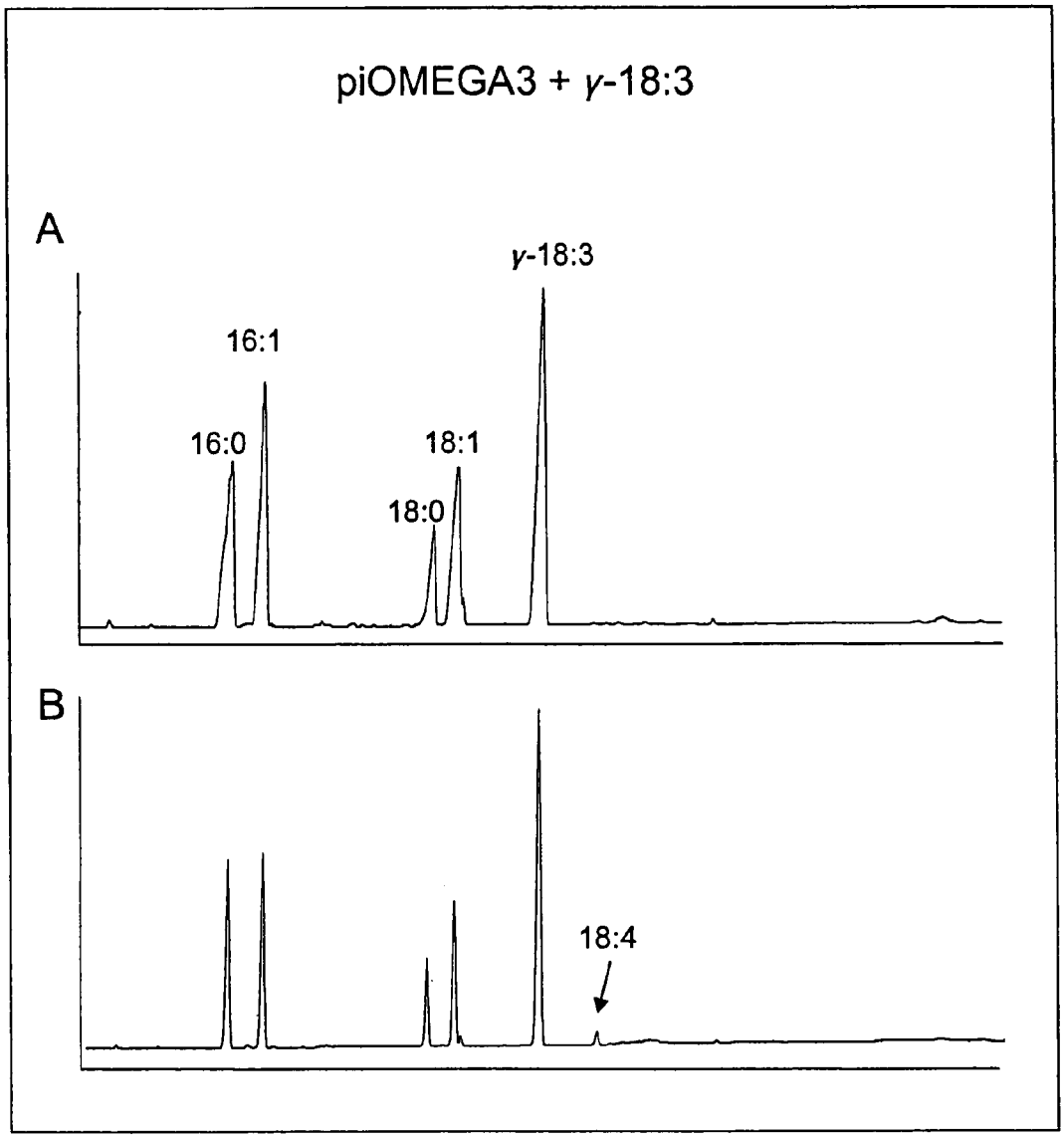


Figure 14: Desaturation of C20:2 ω6-fatty acid to give C20:3 ω3-fatty acid by Pi-omega3Des.

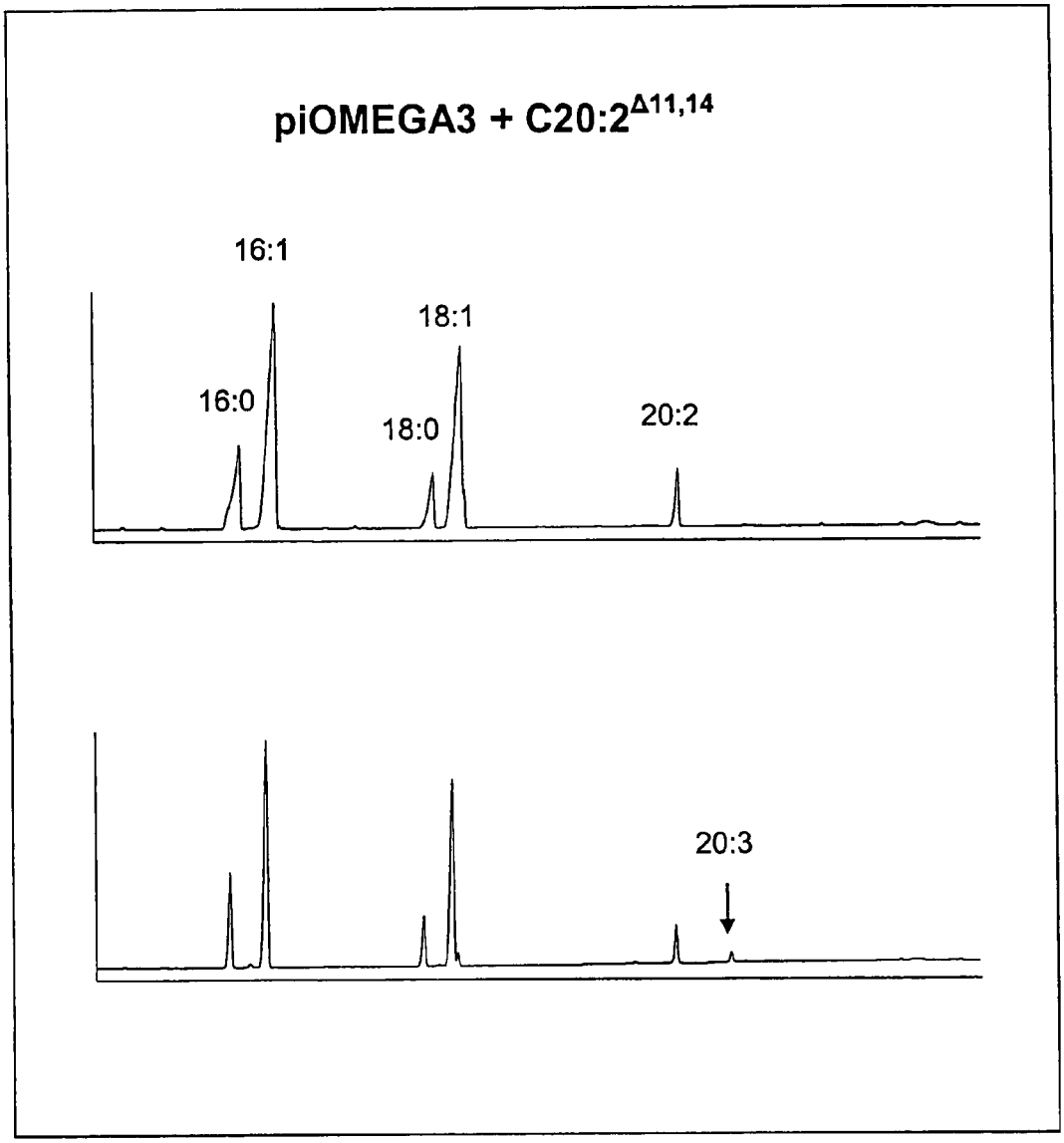


Figure 15: Desaturation of C20:3 ω6-fatty acid to give C20:4 ω3-fatty acid by Pi-omega3Des.

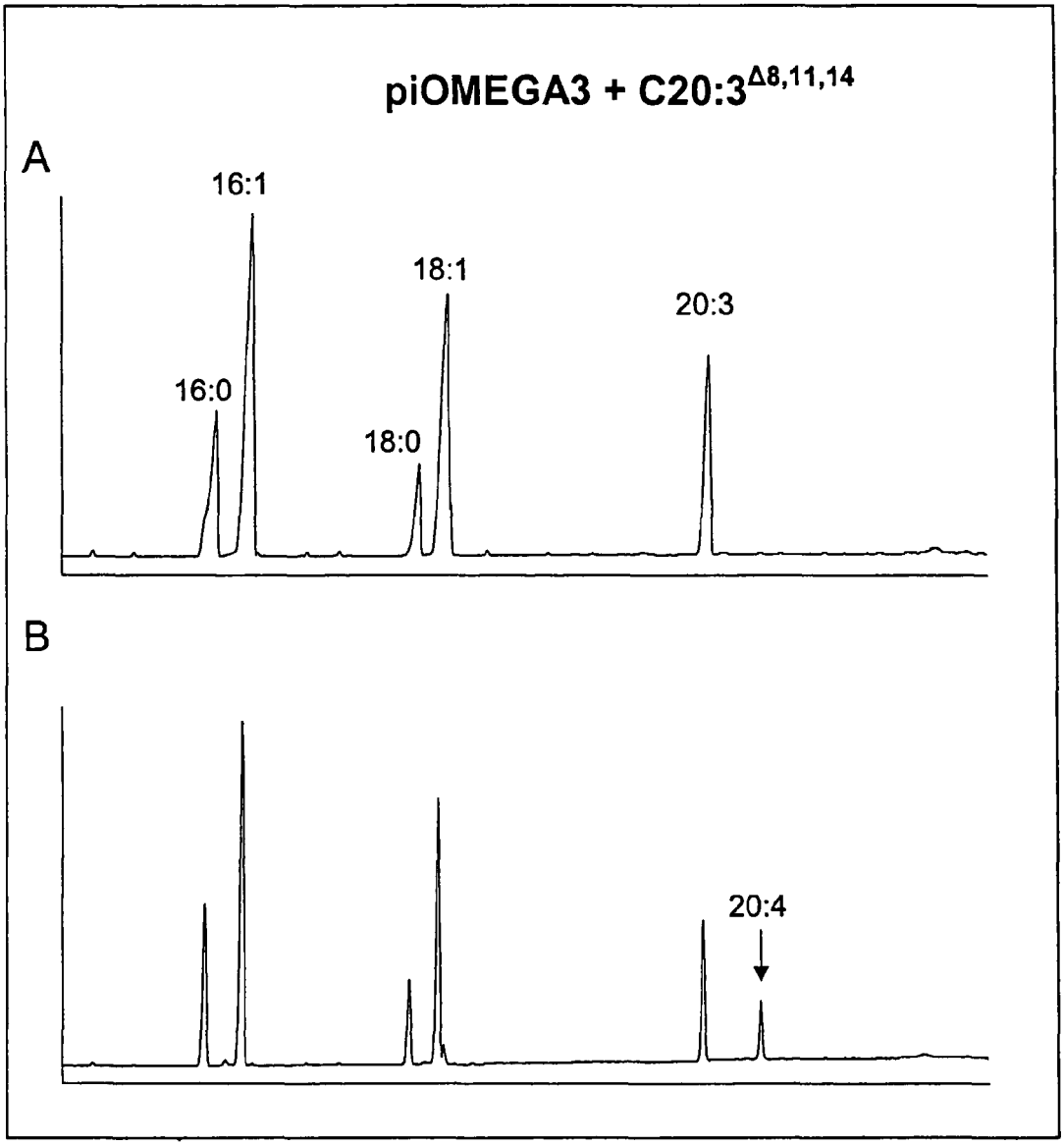


Figure 16: Desaturation of arachidonic acid (C20:4 ω6-fatty acid) to give eicosapentaenoic acid (C20:5 ω3-fatty acid) by Pi-omega3Des.

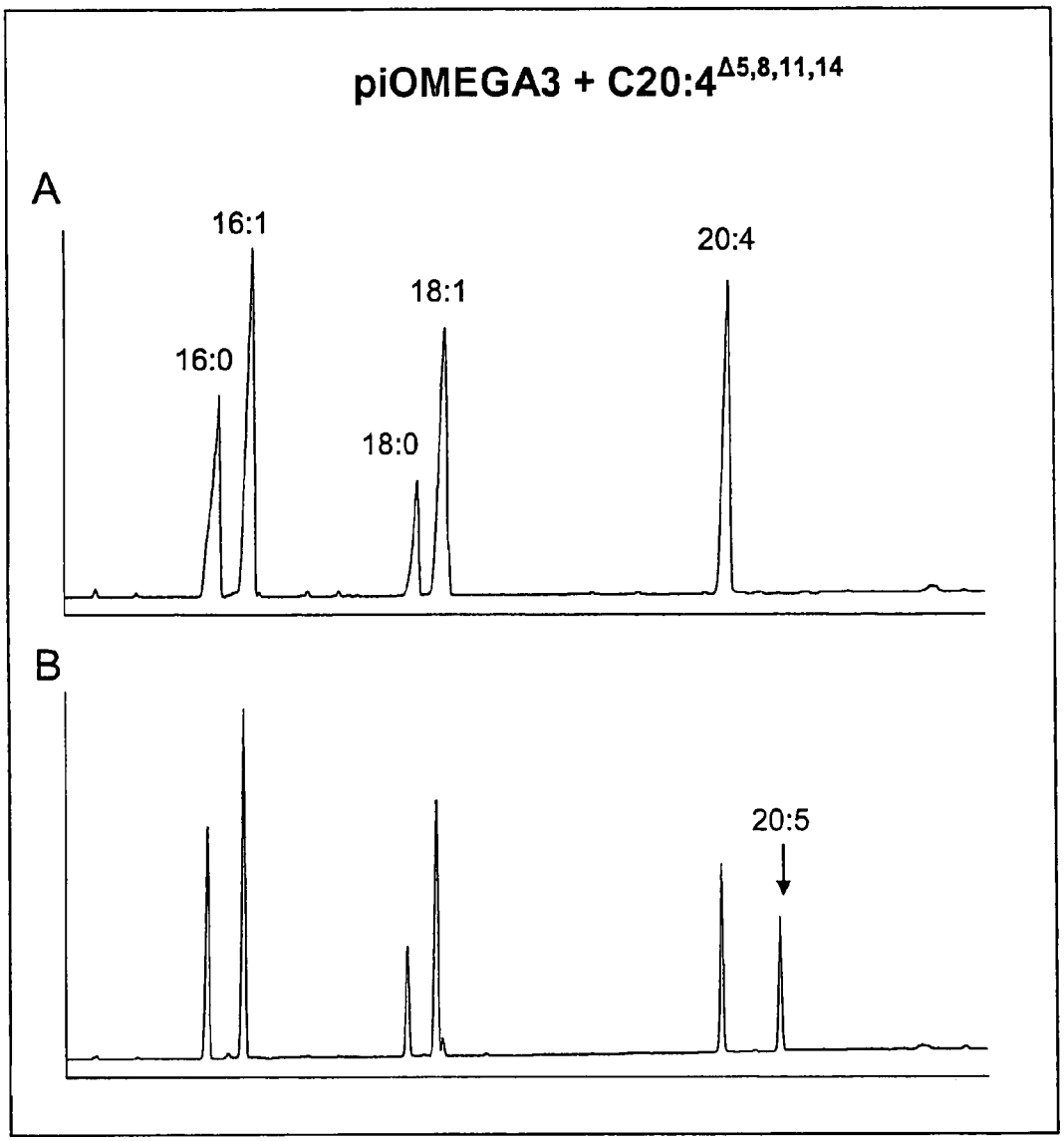
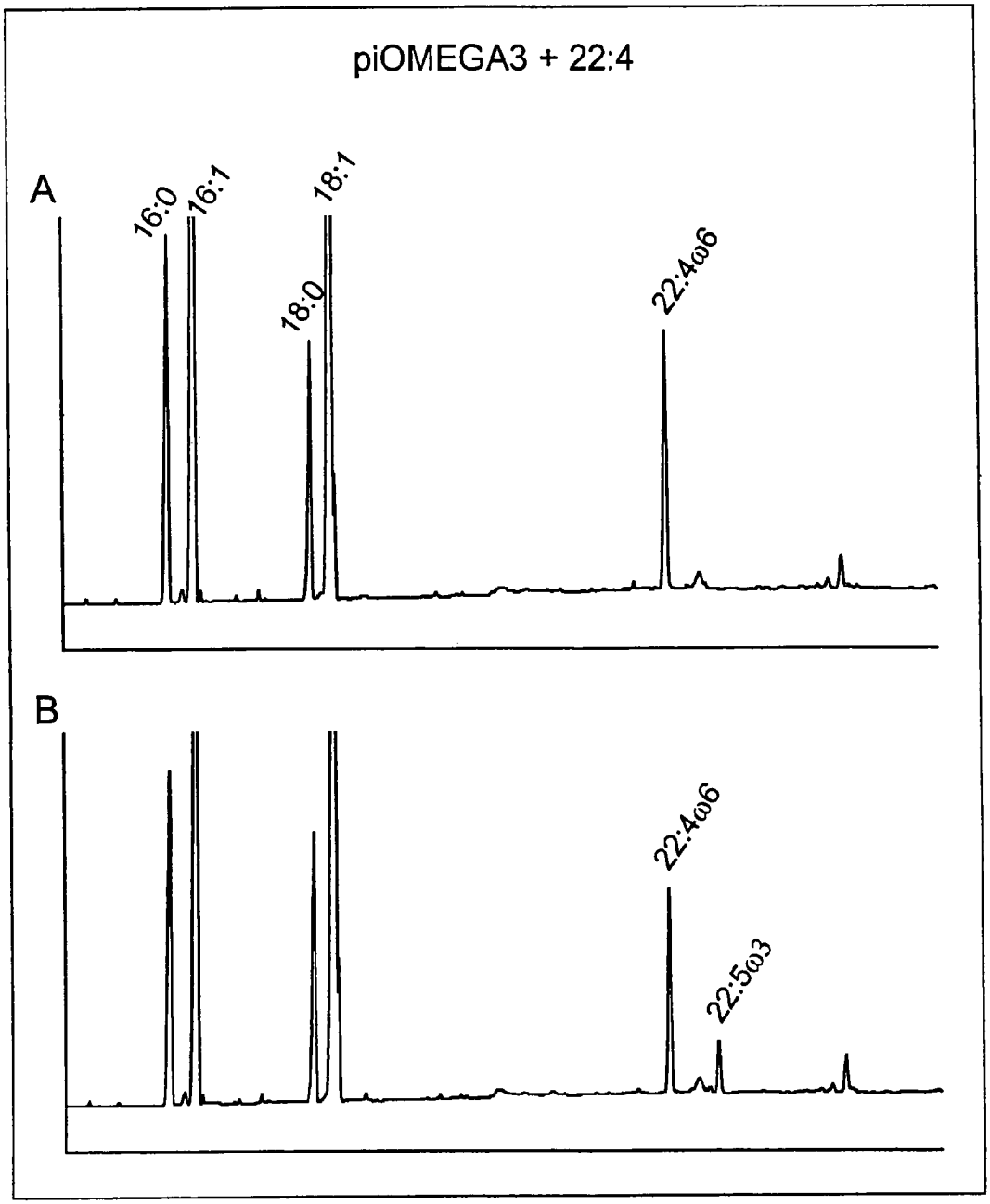


Figure 17: Desaturation of docosatetraenoic acid (C22:4 ω6-fatty acid) to give docosapentaenoic acid (C22:5 ω3-fatty acid) by Pi-omega3Des.



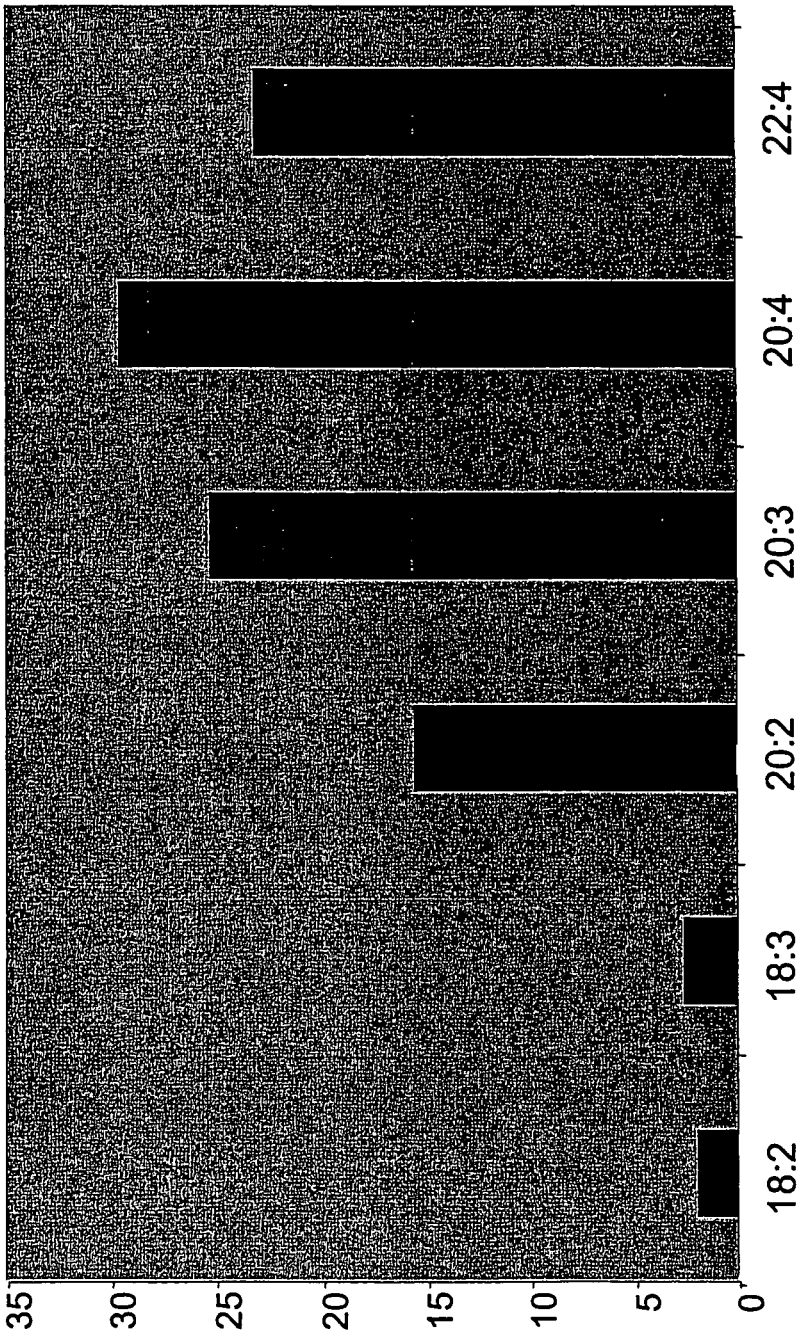


Figure 18: Substrate specificity of Pi-omega3Des with regard to different fatty acids

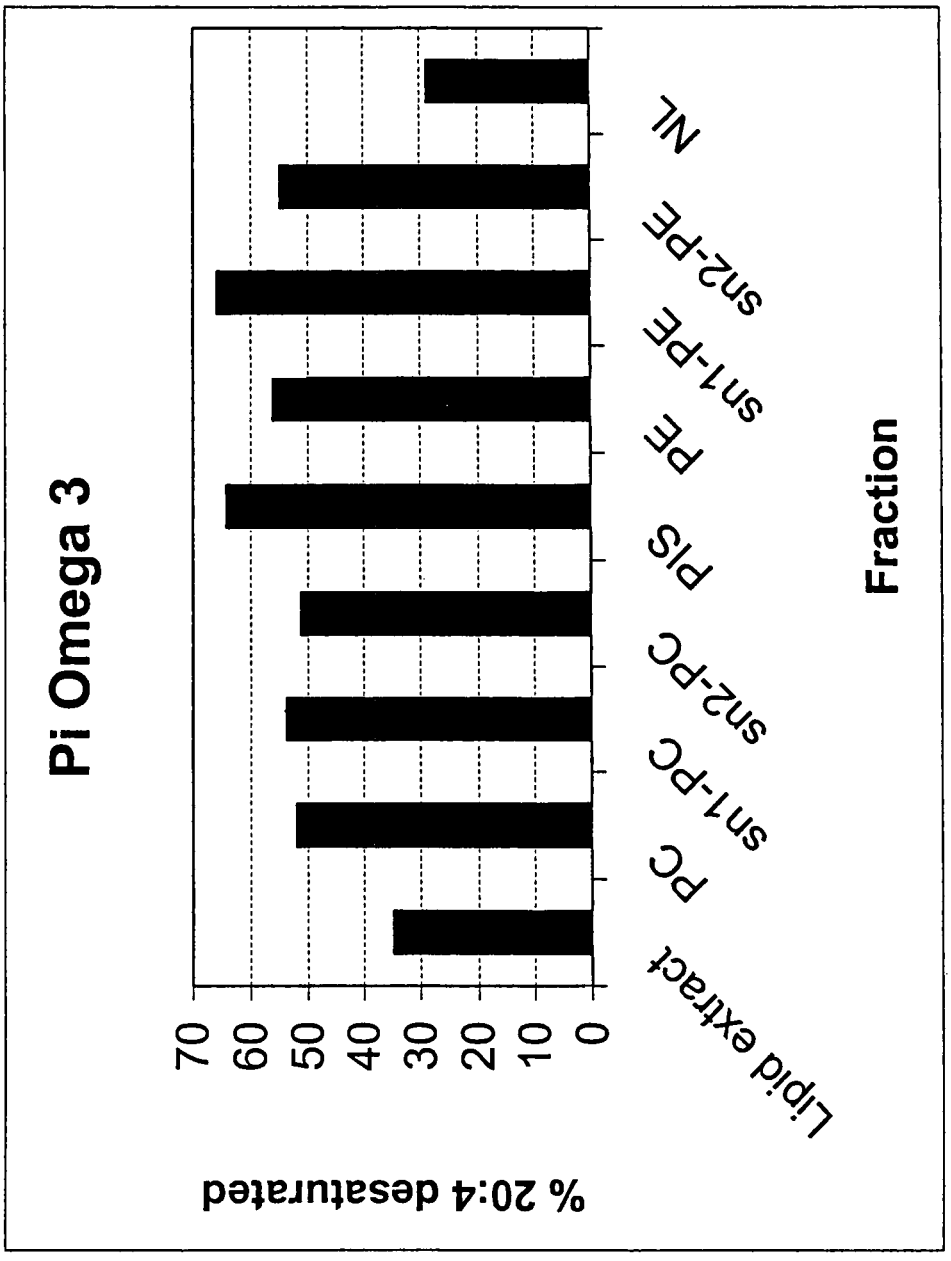


Figure 19: Desaturation of phospholipid-bound arachidonic acid to give EPA by Pi-Omega3Des

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

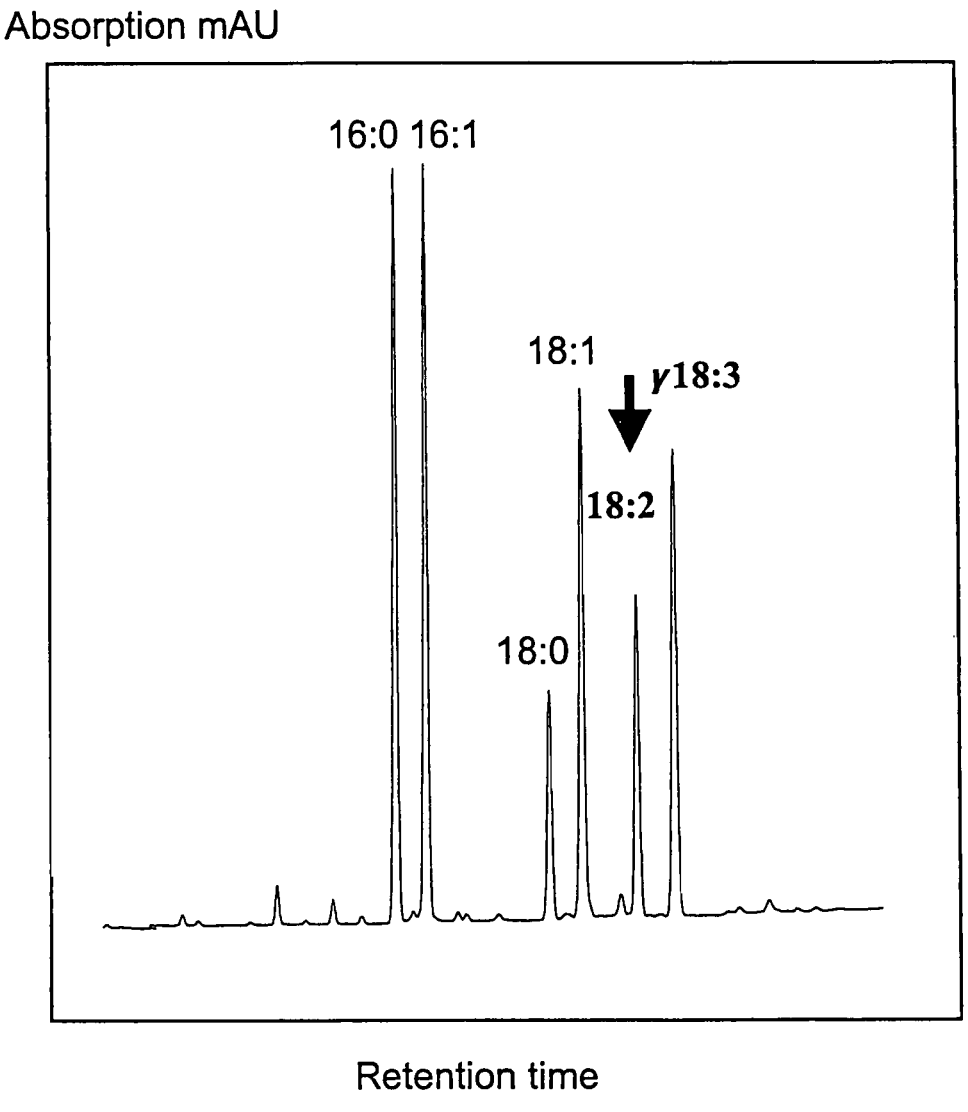


Figure 21: Conversion of linoleic acid and α-linolenic acid (A and C), and reconstitution of the ARA and EPA synthetic pathways, respectively, in yeast (B and D) in the presence of OtD6.1.

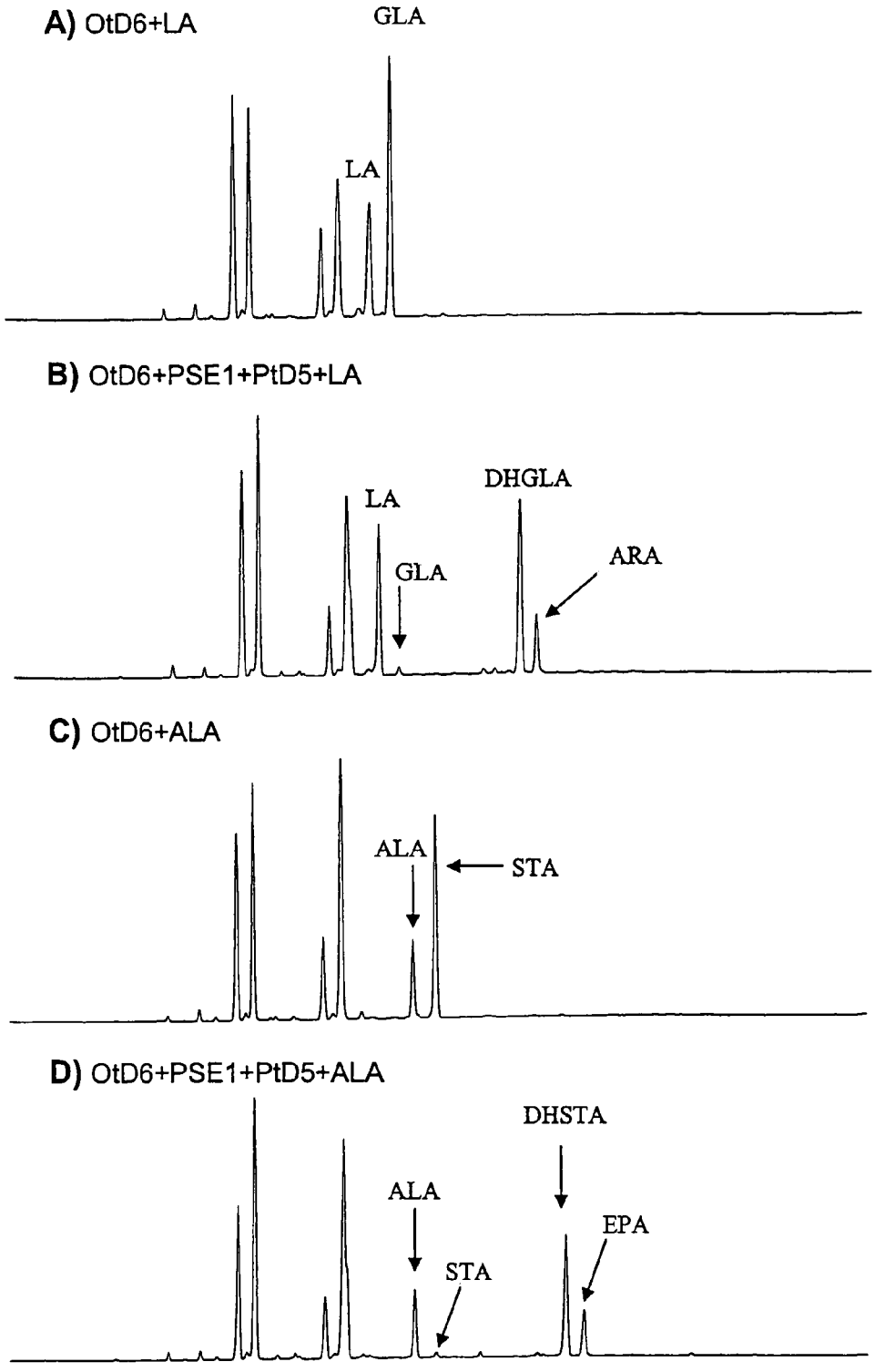


Figure 22: Expression of ELO(XI) in yeast

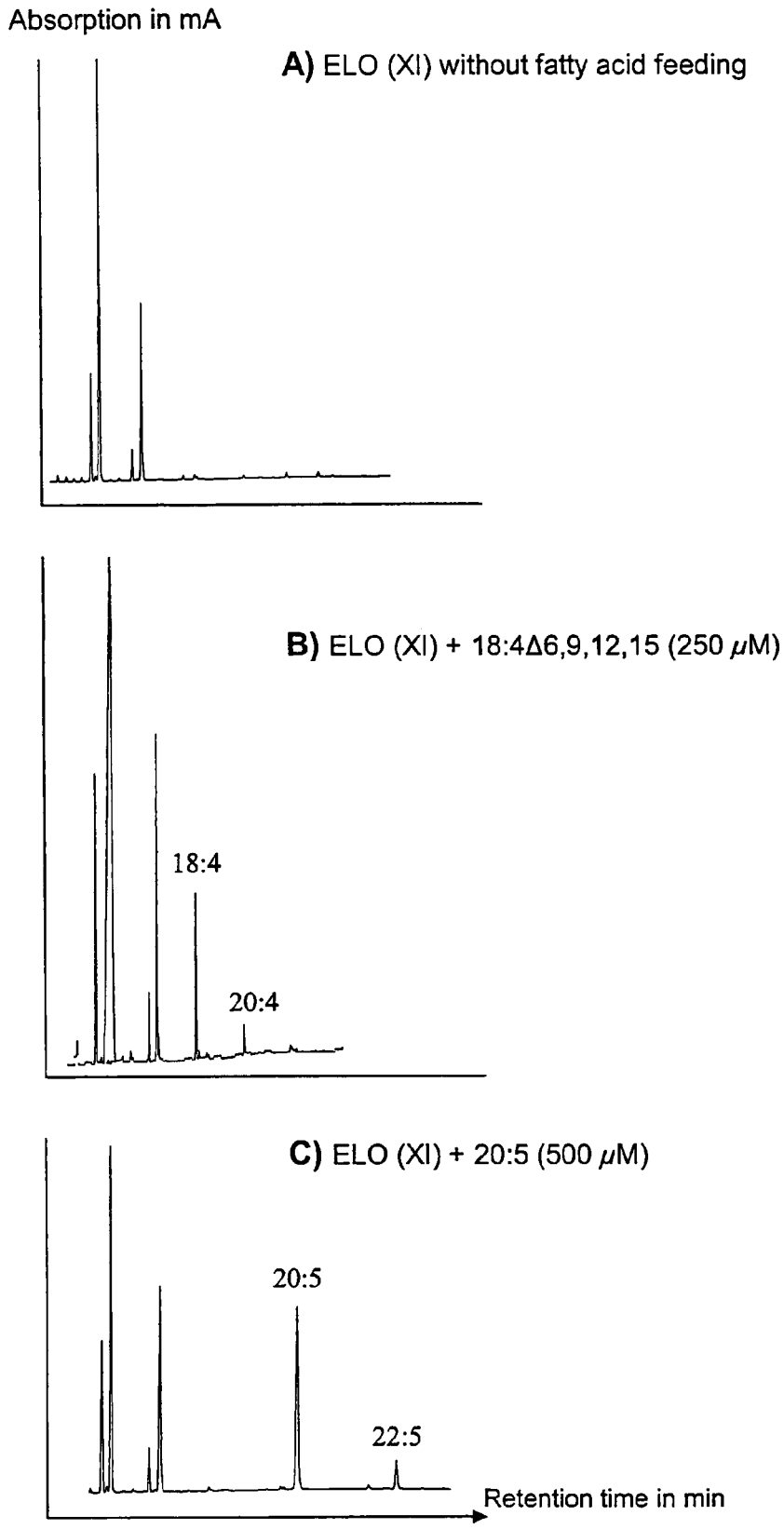


Figure 23:

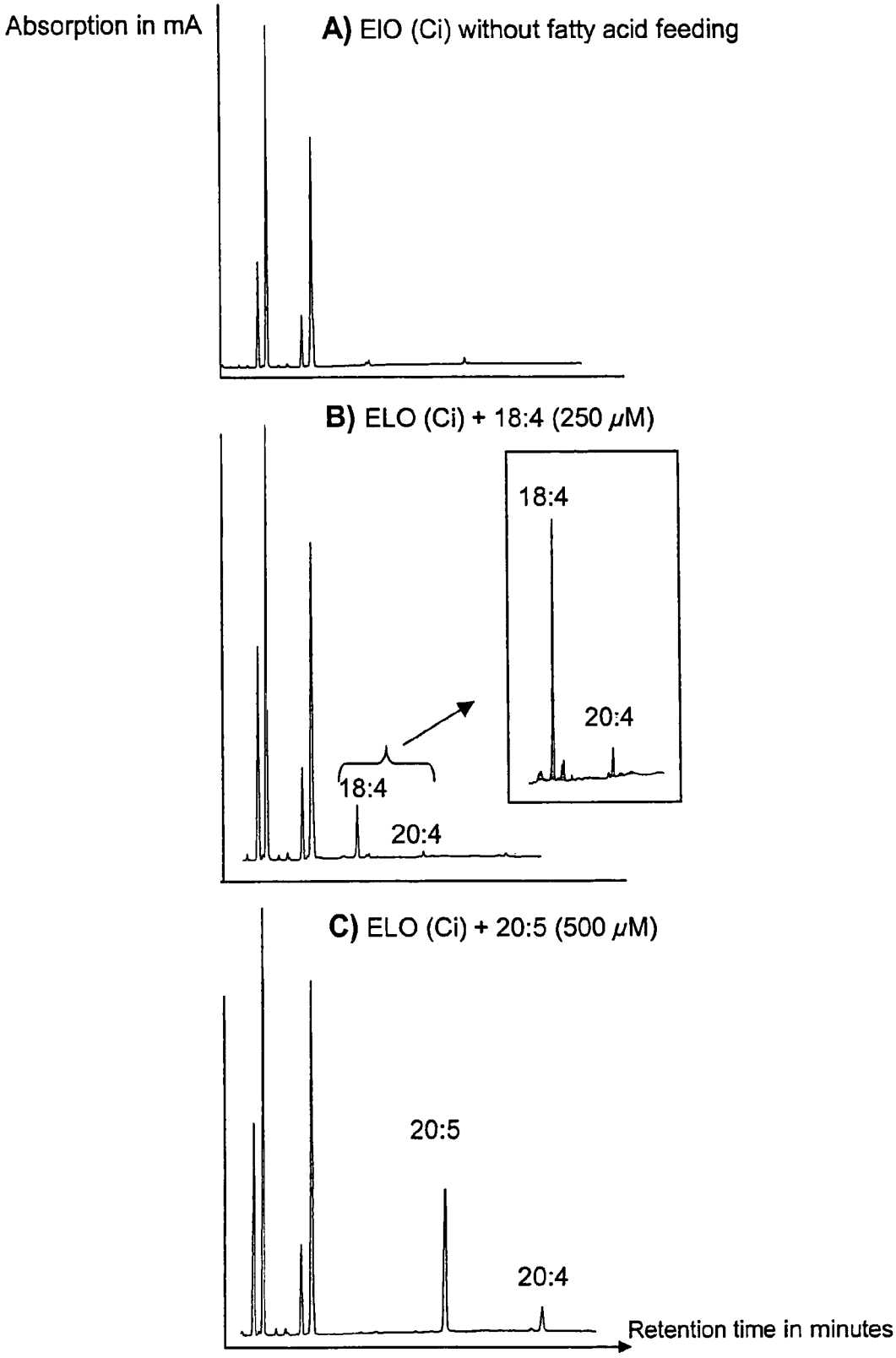
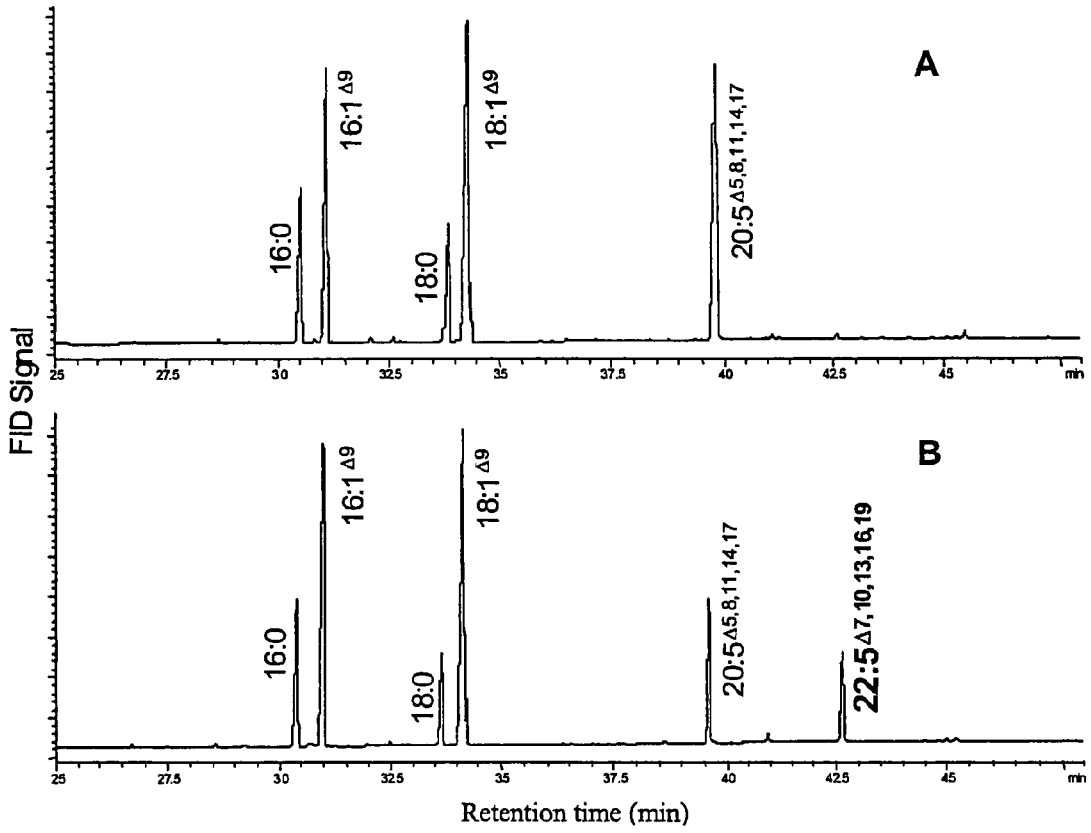


Figure 24: Elongation of eicosapentaenoic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:5ω3).



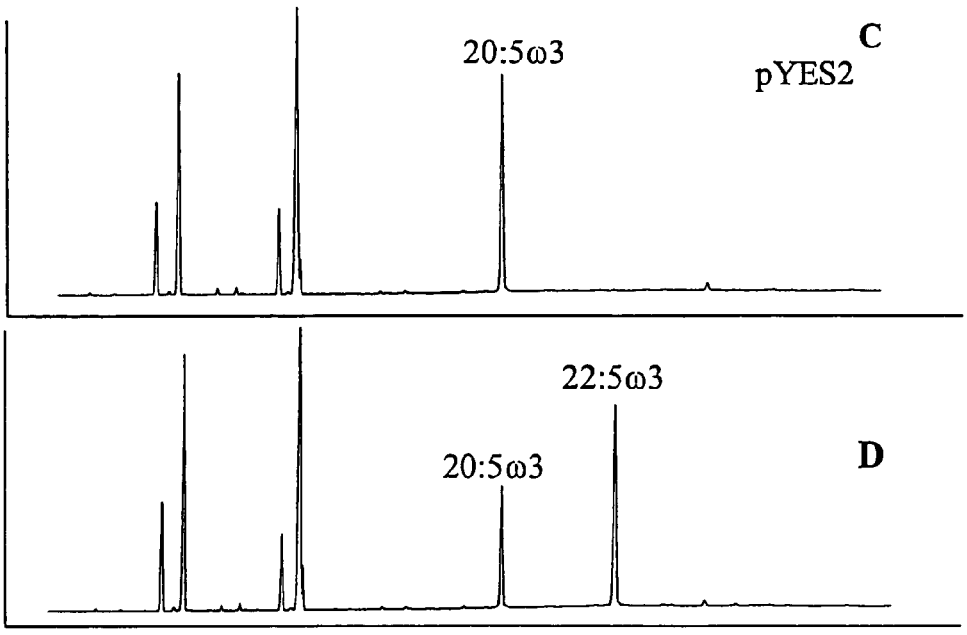


Figure 25: Elongation of arachidonic acid by OtElo1 (B) and OtElo1.2 (D), respectively. The controls (A, C) do not show the elongation product (22:4ω6).

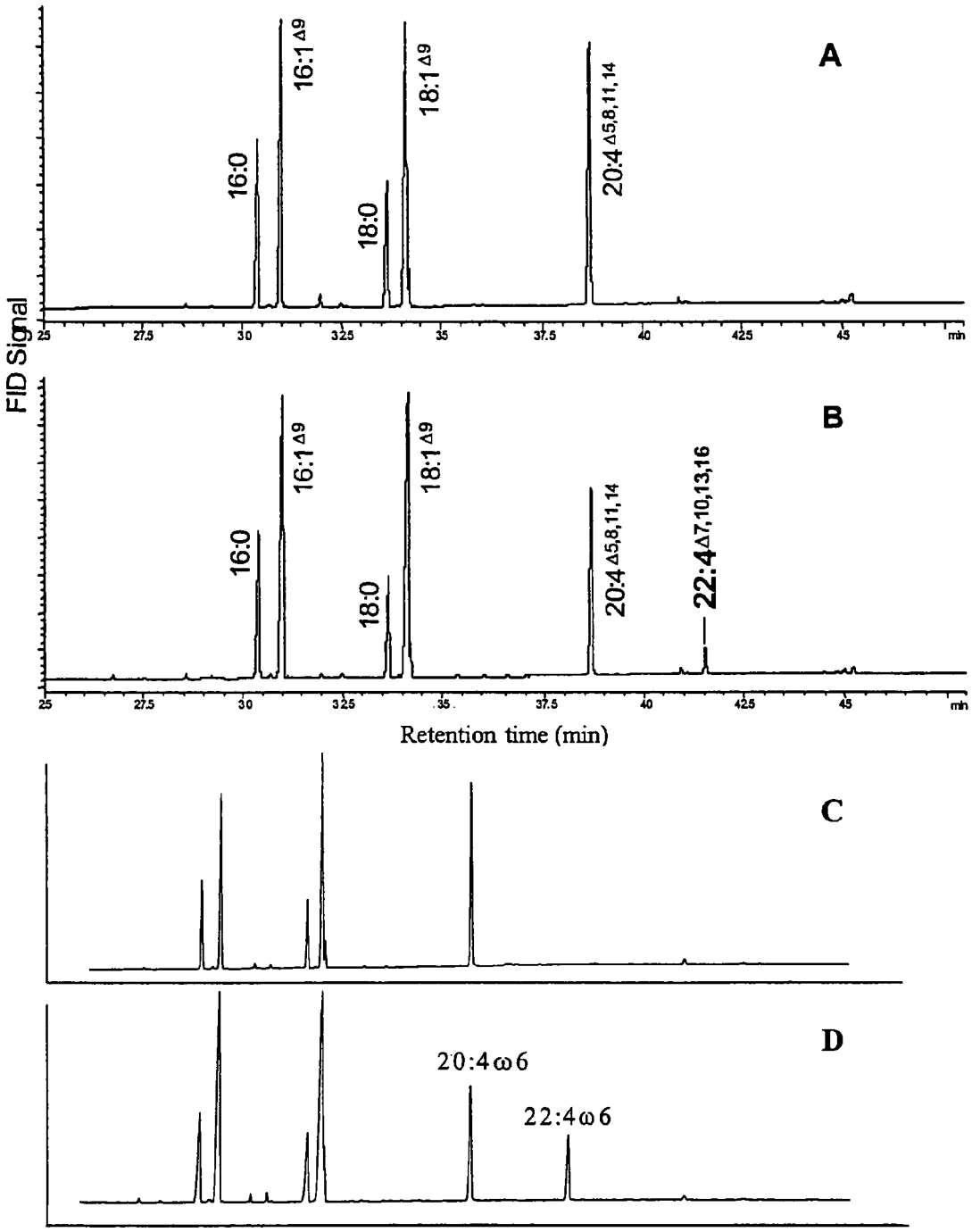


Figure 26: Elongation of 20:5n-3 by the elongases At3g06470.

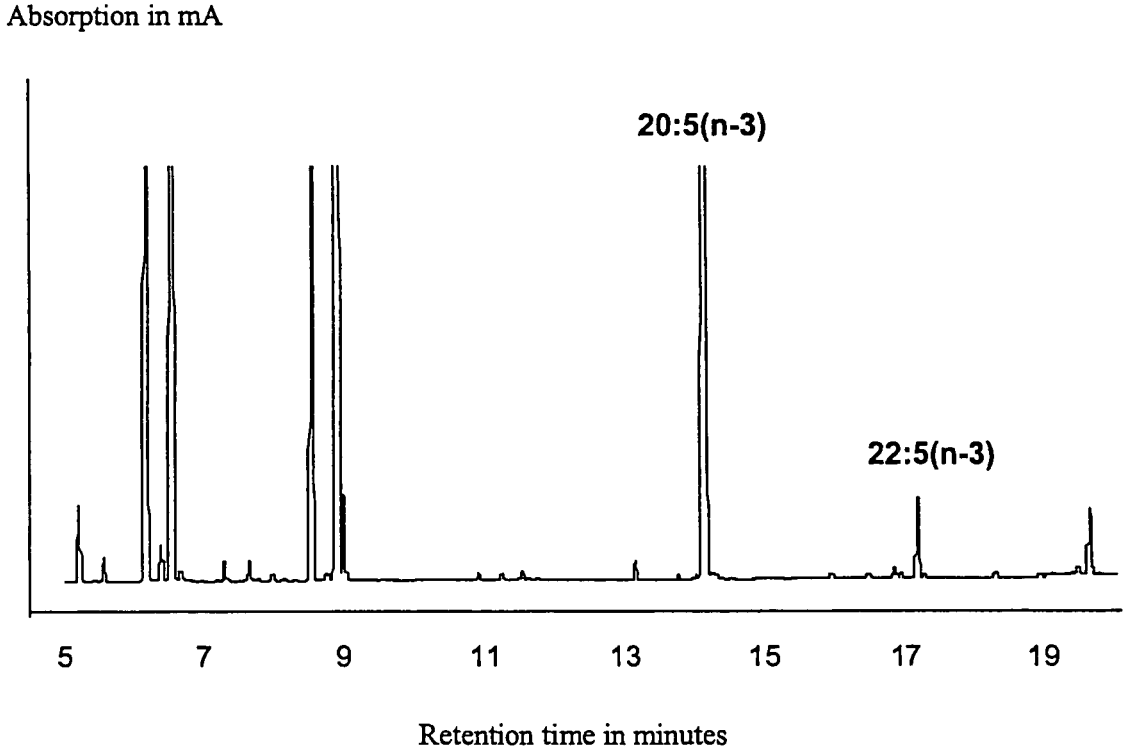


Figure 27: Substrate specificity of the Xenopus Elongase (A), Ciona Elongase (B) und Oncorhynchus Elongase (C)

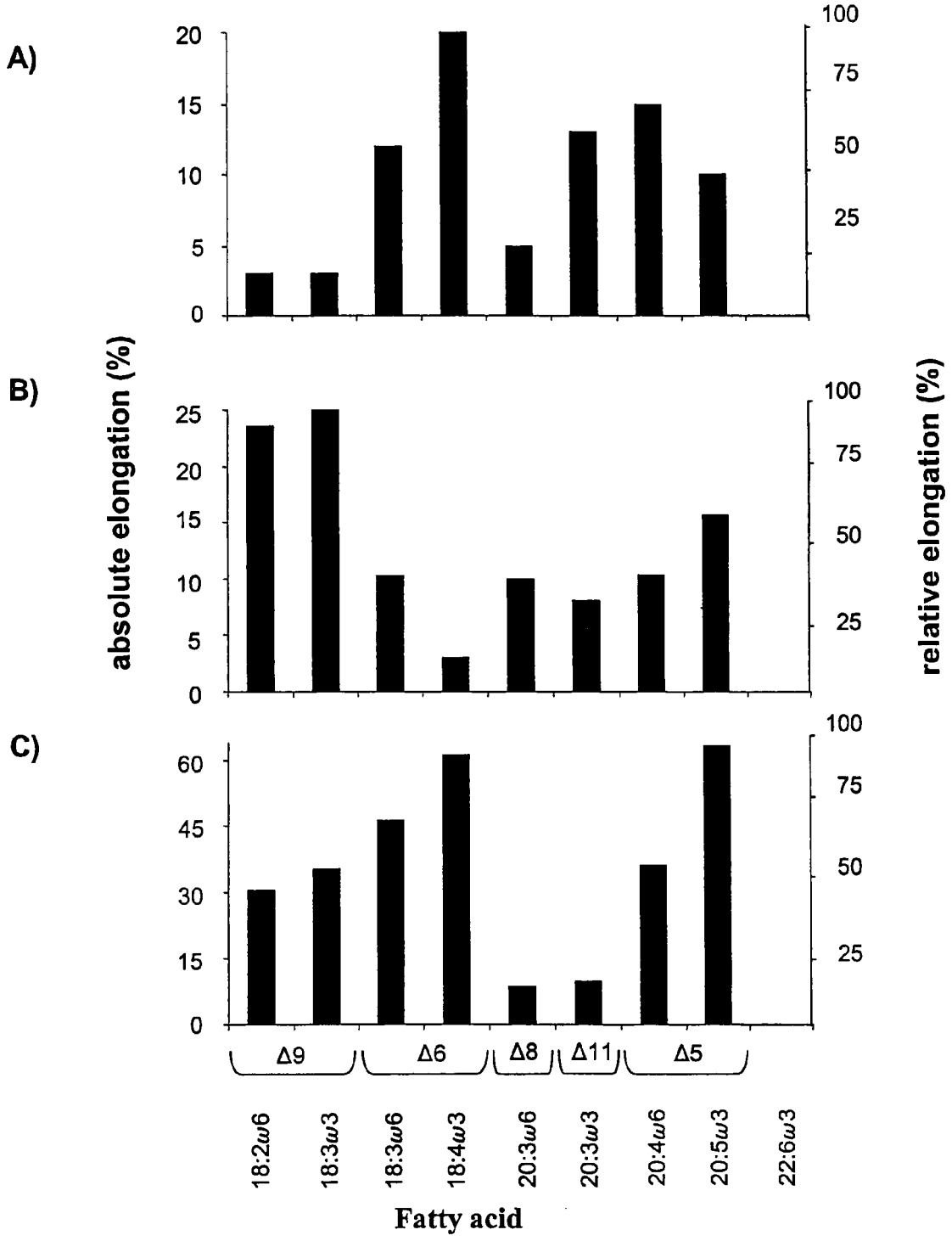


Figure 28: Substrate specificity of the Ostreococcus Δ5-elongase (A), the Ostreococcus Δ6-elongase (B), the Thalassiosira Δ5-elongase (C) and the Thalassiosira Ostreococcus Δ6-elongase (D)

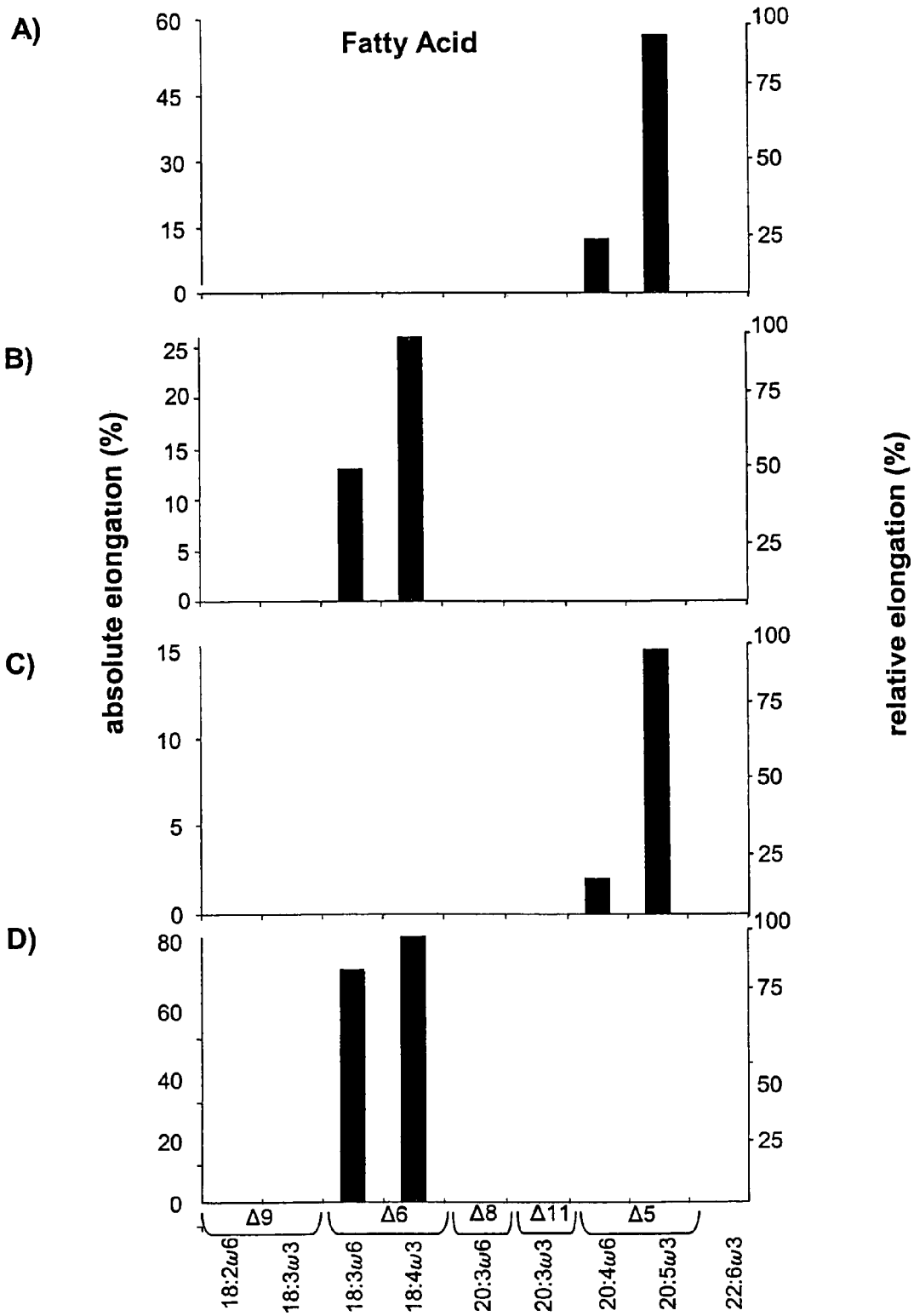
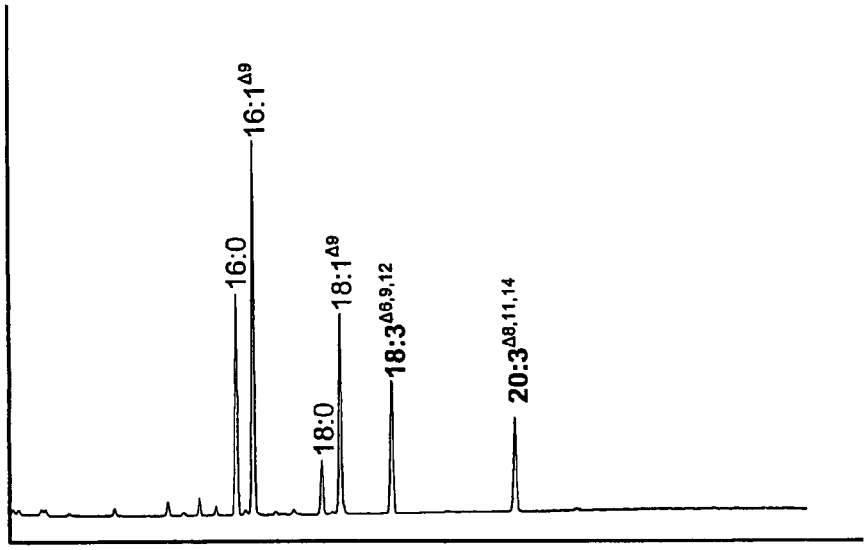


Figure 29: Expression of the Phaeodactylum tricornutum Δ6-elongase (PtELO6) in yeast. A) shows the elongation of the C18:3$^{\Delta 6,9,12}$ fatty acid and B) the elongation of the C18:3$^{\Delta 6,9,12,15}$ fatty acid

A)



B)

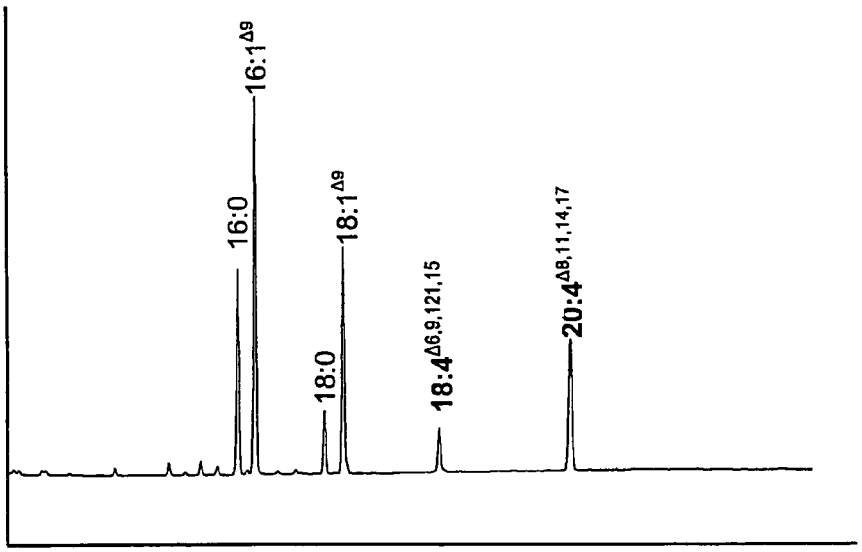
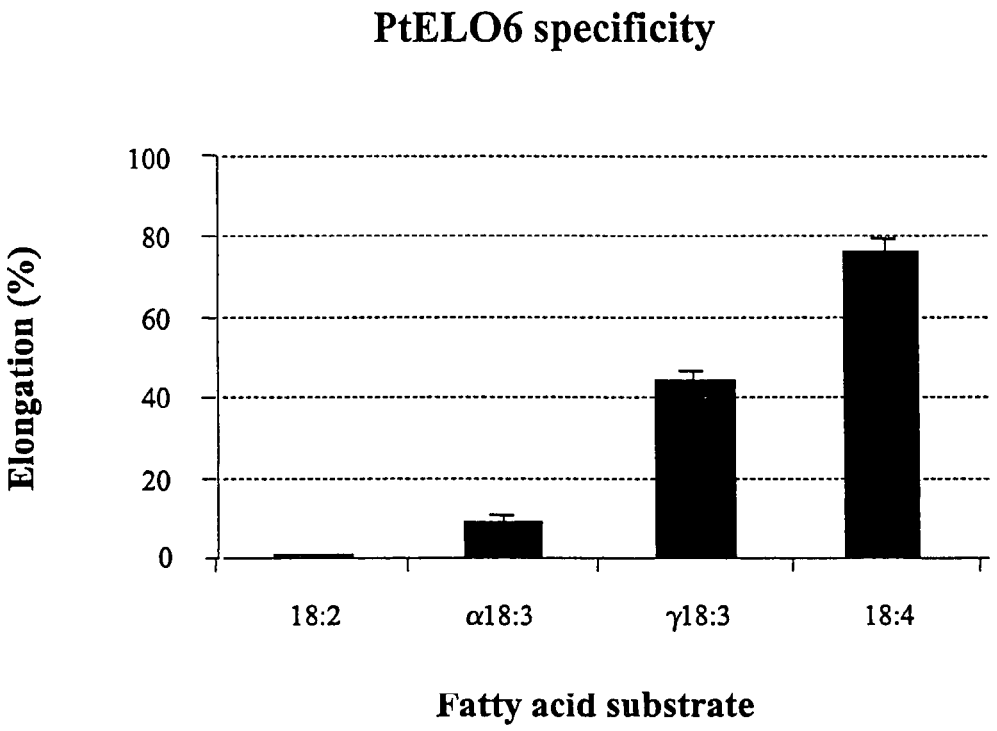


Figure 30: Figure 30 shows the substrate specificity of PtELO6 with regard to the substrates fed.



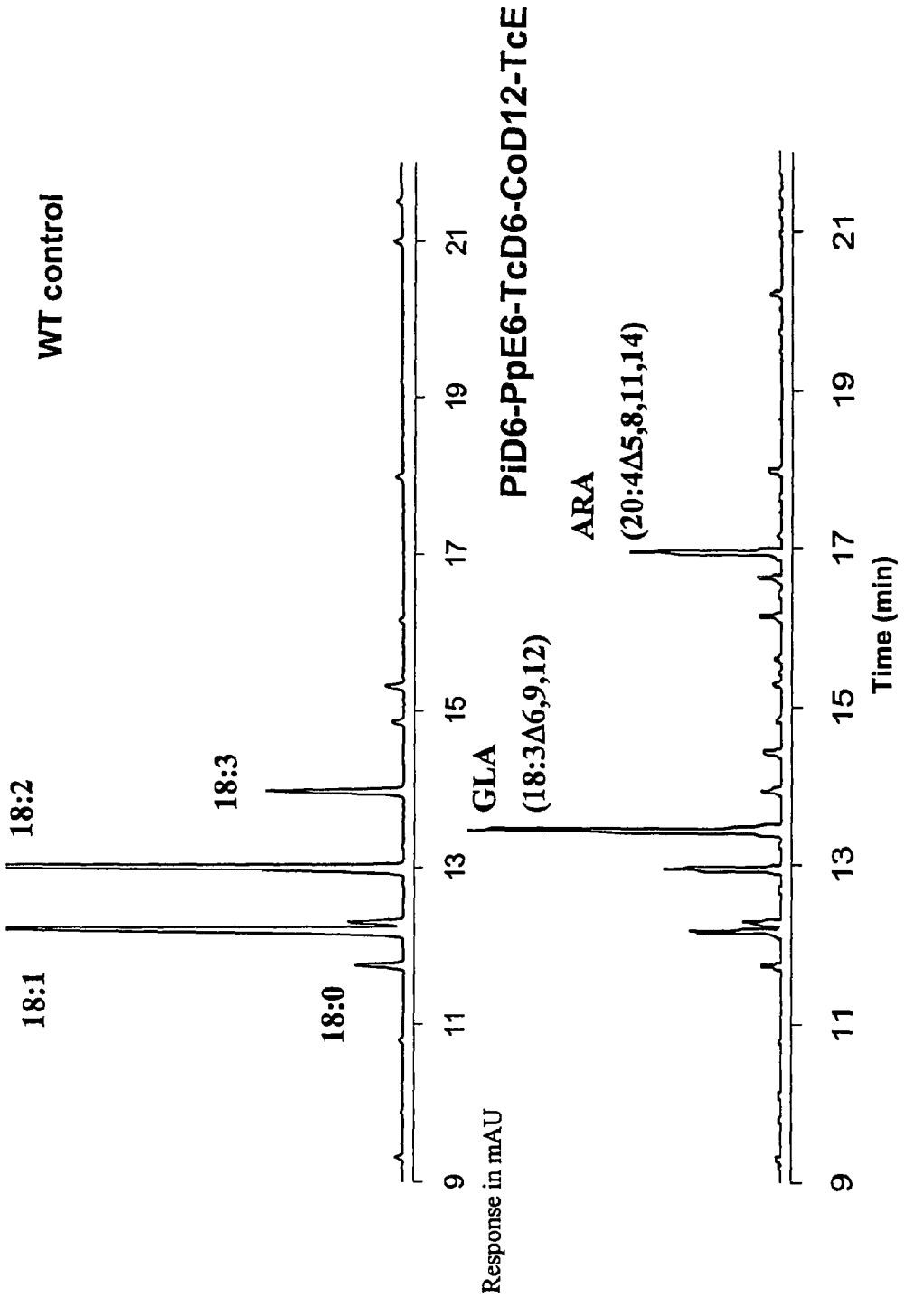


Figure 31: Gas-chromatographic analysis of the seed of a transgenic plant, transformed with pSUN-5G.

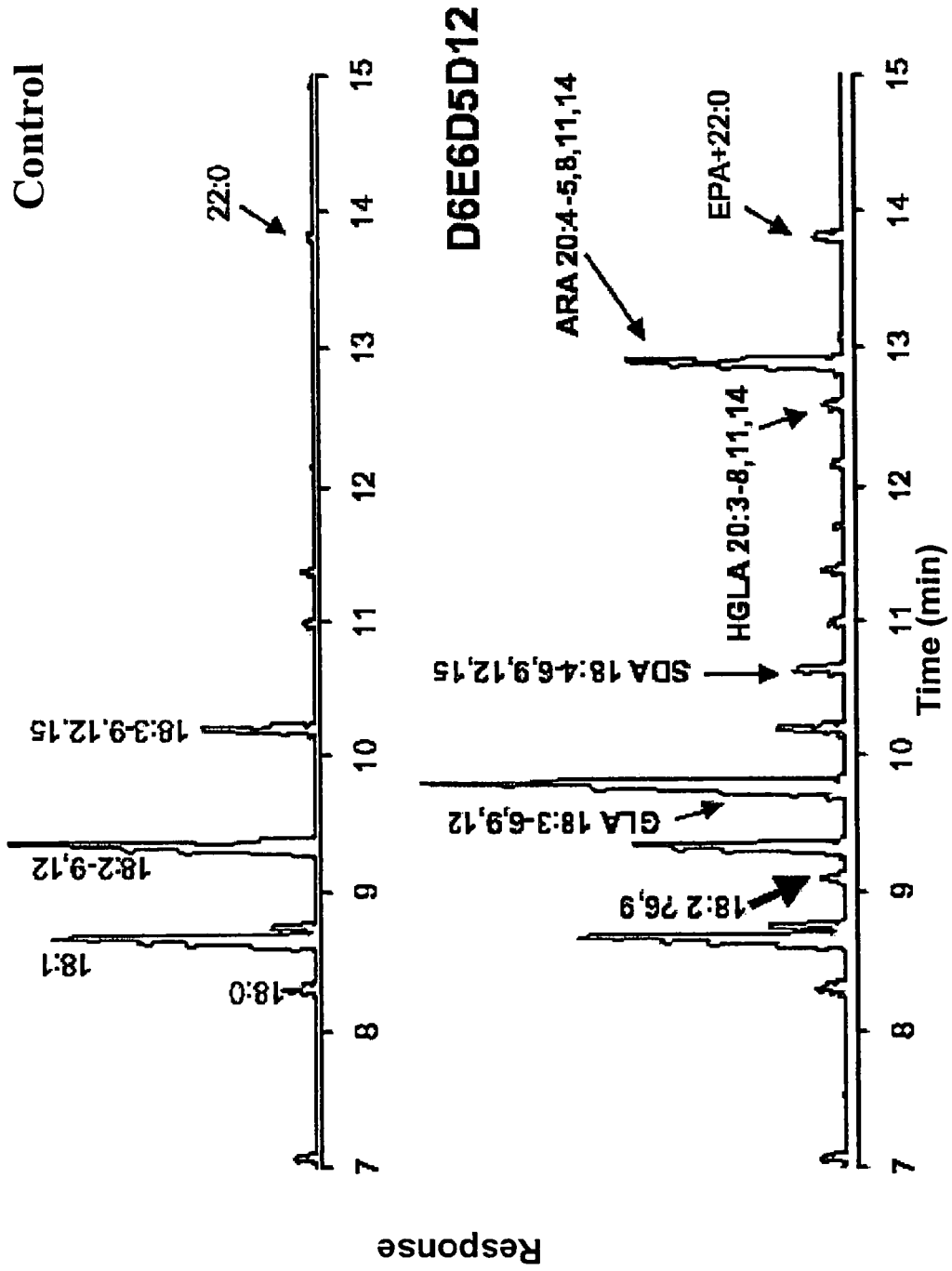


Figure 32: Gas-chromatographic analysis of the seed of a transgenic plant, transformed with pGPTV-D6Des(Pir)_D5Des(Tc)_D6Elo(PP)_12Des(Co)

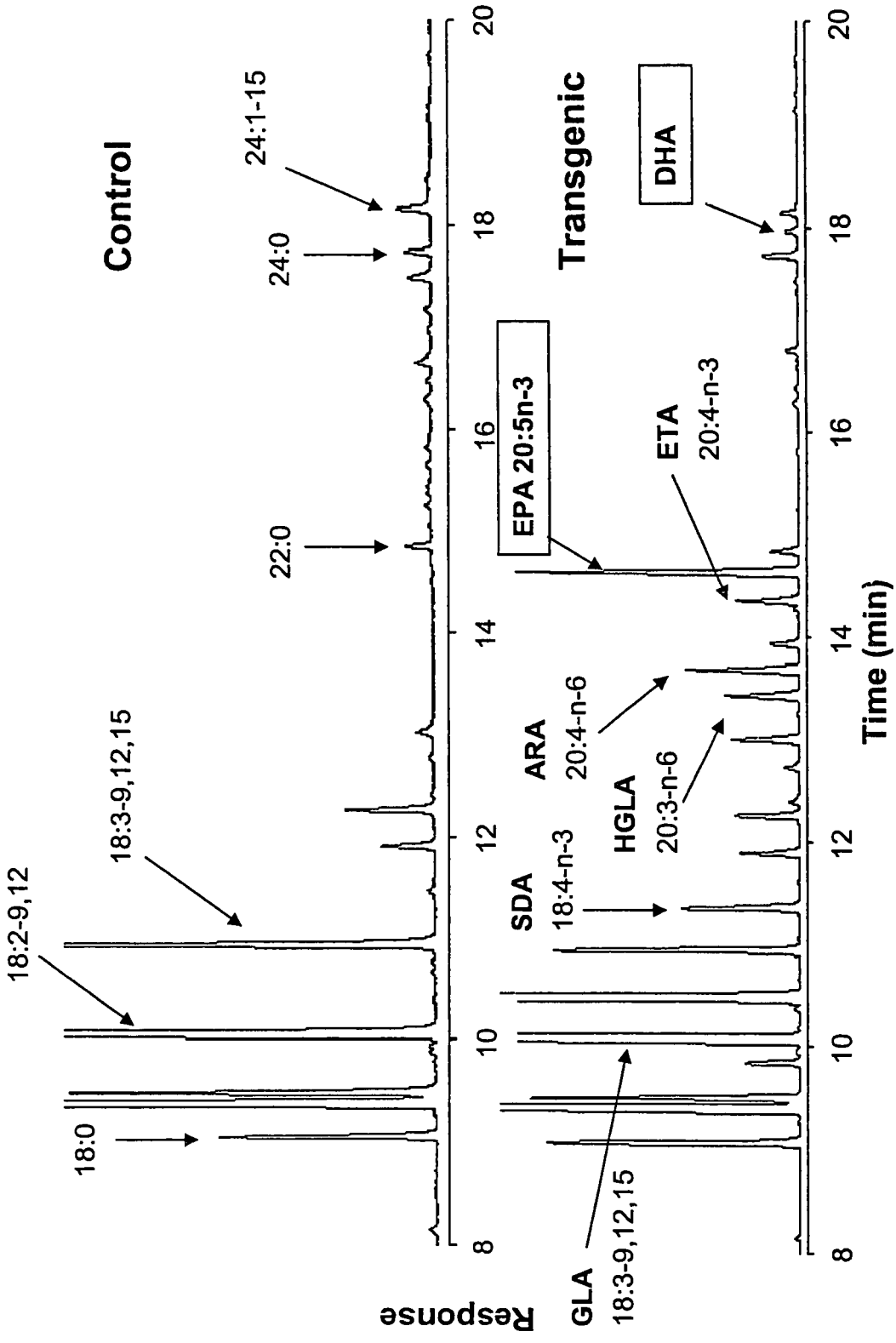


Figure 33: DHA in transgenic seeds of Brassica juncea. The plants were transformed with the construct pSUN-8G.

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 it s 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 ω3-desaturase, Δ12-desaturase, Δ6-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-desaturase activity, preferably polypeptides with Δ6-desaturase, Δ6-elongase and Δ5-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 Δ12-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 Δ6-desaturase, a Δ5-desaturase, Δ4-desaturase, Δ12-desaturase and/or Δ6-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 arichidonic 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 arichidonic 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.

The invention furthermore relates to recombinant nucleic acid molecules comprising the nucleic acid sequences which encode the polypeptides with Δ6-desaturase, Δ6-elongase, Δ5-desaturase and Δ5-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 Procaryotes. 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 ω3-fatty acids and ω6-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 ω3-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 ω3-fatty acids to the food (Shimikawa 2001, World Rev. Nutr. Diet. 88, 100-108).

ω3-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. Ω-6-fatty acids such as arachidonic acid tend to have a negative effect in connection with these rheumatological diseases.

ω3- and ω6-fatty acids are precursors of tissue hormones, known as eicosanoids, such as the prostaglandins, which are derived from dihomo-γ-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_2 series) which are formed from the ω6-fatty acids, generally promote inflammatory reactions, while eicosanoids (known as the PG_3 series) from ω3-fatty acids have little or no proinflammatory effect.

Polyunsaturated long-chain ω3-fatty acids such as eicosapentaenoic acid (=EPA, C20:$5^{\Delta5,8,11,14,17}$) or docosahexaenoic acid (=DHA, C22:$6^{\Delta4,7,10,13,16,19}$) 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 ω3-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:$6^{\Delta4,7,10,13,16,19}$) or eicosapentaenoic acid (=EPA, C20:$5^{\Delta5,8,11,14,17}$) 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 *Crypthecodinium* 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:$4^{\Delta5,8,11,14}$), dihomo-γ-linolenic acid (C20:$3^{\Delta8,11,14}$) or docosapentaenoic acid (DPA, C22:$5^{\Delta7,10,13,16,19}$) 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 ω3-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 ω3-fatty acids to the food. Also, ω3-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. ω3-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 Δ9-desaturase. WO 93/11245 claims a Δ15-desaturase and WO 94/11516 a Δ12-desaturase. Further desaturates 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. Δ6-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

contents of unsaturated fatty acids/lipids such as, for example, γ-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_{28}-C_{32}). 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, Porphiridium* species, *Thraustochytrium* species, *Schizochytrium* species or *Crypthecodinium* 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 adds 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 Δ6-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases or Δ4-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 Δ6-desaturase genes from the moss *Physcomitrella patens* and Δ6-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).

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 Δ6-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and Δ4-desaturase is the Sprecher pathway (Sprecher 2000, Biochim. Biophys. Acta 1486:219-231) in mammals. Instead of the Δ4-desaturation, a further elongation step is effected here to give C24, followed by a further Δ6-desaturation and finally β-oxidation to give the C_{22} 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 ω6- or ω3-fatty acids, which differ with regard to their metabolic and functional activities (FIG. **1**).

The starting material for the ω6-metabolic pathway is the fatty acid linoleic acid ($18:2^{\Delta 9,12}$) while the ω3-pathway proceeds via linolenic acid ($18:3^{\Delta 9,12,15}$). Linolenic acid is formed by the activity of an ω3-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 (Δ12- and ω3-desaturase) and must take up these fatty acids (essential fatty acids) via the food. Starting with these precursors, the physiologically important polyunsaturated fatty acids arachidonic acid (=ARA, $20:4^{\Delta 5,8,11,14}$), an ω6-fatty acid and the two ω3-fatty acids eicosapentaenoic acid (=EPA, $20:5^{\Delta 5,8,11,14,17}$) and docosahexaenoic acid (DHA, $22:6^{\Delta 4,7,10,13,17,19}$) are synthesized via the sequence of desaturase and elongase reactions. The application of ω3-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 ω6-synthetic pathway and the ω-3-synthetic pathway (see FIG. **1**) so that more ω3-fatty acids are produced. The enzymatic activities of various ω3-desaturases which desaturate $C_{18:2}$-, $C_{22:4}$- or $C_{22:5}$-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 ω6-synthetic pathway into the corresponding fatty acids of the ω3-synthetic pathway.

The elongation of fatty acids, by elongases, by 2 or 4 C atoms is of crucial importance for the production of C_{20}- and C_{22}-PUFAs, respectively. This process proceeds via 4 steps. The first step is the condensation of malonyl-CoA 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_{20}- or C_{24}-fatty acids have been described to date. A Δ5-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_{20}- and C_{22}-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-γ-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 20:5ω3.

FIG. **4** shows reconstitution of DHA biosynthesis in yeast starting from 18:4ω3.

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 leucin 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)±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 γ-linolenic acid (18:2 ω6-fatty acid) to give α-linolenic acid (18:3 ω3-fatty acid) by Pi-omega3Des.

FIG. **13** shows desaturation of γ-linolenic acid (18:2 ω6-fatty acid) to give stearidonic acid (18:4 ω3-fatty acid) by Pi-omega3Des.

FIG. **14** shows desaturation of C20:2 ω6-fatty acid to give C20:3 ω3-fatty acid by Pi-omega3Des.

FIG. **15** shows desaturation of C20:3 ω6-fatty acid to give C20:4 ω3-fatty acid by Pi-omega3Des.

FIG. **16** shows desaturation of arachidonic acid (C20:4 ω6-fatty acid) to give eicosapentaenoic acid (C20:5 ω3-fatty acid) by Pi-omega3Des.

FIG. **17** shows desaturation of docosatetraenoic acid (C22:4 ω6-fatty acid) to give docosapentaenoic acid (C22:5 ω3-fatty acid) by Pi-omega3Des.

FIG. **18** shows substrate specificity of Pi-omega3Des with regard to 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 γ-linolenic acid (γ-18:3) by OtDes6.1.

FIG. **21** shows conversion of linoleic acid and α-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 (22:5ω3).

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 (22:4ω6).

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* Δ5-elongase (A), the *Ostreococcus* Δ6-elongase (B), the *Thalassiosira* Δ5-elongase (C) and the *Thalassiosira* Δ6-elongase (D).

FIG. **29** shows expression of the *Phaeodactylum tricornutum* Δ6-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^{Δ}6,9,12,15 fatty acid.

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

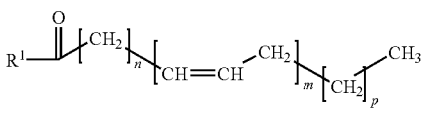
FIG. **31** shows gas-chromatographic analysis of the seed of a transgenic plant, transformed with pSUN-5G.

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



(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 Δ9-elongase and Δ6-desaturase activity, and

b) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ8-desaturase and Δ6-elongase activity, and

c) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ5-desaturase activity, and

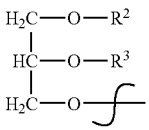
d) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ5-elongase activity, and

e) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ4-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

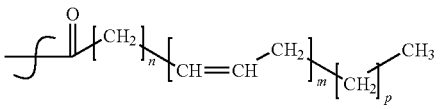
(II)



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:

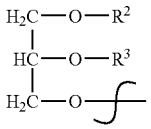
(Ia)



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

(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-docosanylcarbdnyl or h-tetracosanylcarbbnyl, 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 four, five or six double bonds, very 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,

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 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^1, R^2 and R^3 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 Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-desaturase activity.

Nucleic acid sequences which are advantageously used in the process according to the invention are nucleic acid sequences which encode polypeptides with Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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, 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,

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 Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-desaturase activity.

Advantageously, the substituents R^2 or R^3 in the general formulae I and II independently of one another are saturated or unsaturated C_{18}-C_{22}-alkylcarbonyl; especially advantageously, are independently of one another C_{18}-, C_{20}- or C_{22}-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 ω3-desaturase activity, selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or
b) nucleic acid sequences which can be derived form 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
c) 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 ω3-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 Δ12-desaturase activity, selected from the group consisting of:

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 60% at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have Δ12-desaturase activity

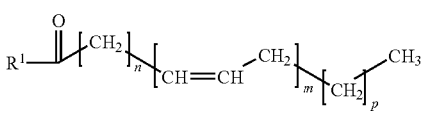
is additionally introduced into the transgenic plant.

These abovementioned Δ12-desaturase sequences can be used alone or in combination with ω3-desaturase sequences together with the nucleic acid sequences used in the process which encode Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases or Δ4-desaturases.

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

No.	Organism	Activity	Sequence number
1.	*Euglena gracilis*	Δ8-Desaturase	SEQ ID NO: 1
2.	*Isochrysis galbana*	Δ9-Elongase	SEQ ID NO: 3
3.	*Phaeodactylum tricornutum*	Δ5-Desaturase	SEQ ID NO: 5
4.	*Ceratodon purpureus*	Δ5-Desaturase	SEQ ID NO: 7
5.	*Physcomitrella patens*	Δ5-Desaturase	SEQ ID NO: 9
6.	*Thraustrochytrium* sp.	Δ5-Desaturase	SEQ ID NO: 11
7.	*Mortierella alpina*	Δ5-Desaturase	SEQ ID NO: 13
8.	*Caenorhabditis elegans*	Δ5-Desaturase	SEQ ID NO: 15
9.	*Borago officinalis*	Δ6-Desaturase	SEQ ID NO: 17
10.	*Ceratodon purpureus*	Δ6-Desaturase	SEQ ID NO: 19
11.	*Phaeodactylum tricornutum*	Δ6-Desaturase	SEQ ID NO: 21
12.	*Physcomitrella patens*	Δ6-Desaturase	SEQ ID NO: 23
13.	*Caenorhabditis elegans*	Δ6-Desaturase	SEQ ID NO: 25
14.	*Physcomitrella patens*	Δ6-Elongase	SEQ ID NO: 27
15.	*Thraustrochytrium* sp.	Δ6-Elongase	SEQ ID NO: 29
16.	*Phytophtora infestans*	Δ6-Elongase	SEQ ID NO: 31
17.	*Mortierella alpina*	Δ6-Elongase	SEQ ID NO: 33
18.	*Mortierella alpina*	Δ6-Elongase	SEQ ID NO: 35
19.	*Caenorhabditis elegans*	Δ6-Elongase	SEQ ID NO: 37
20.	*Euglena gracilis*	Δ4-Desaturase	SEQ ID NO: 39
21.	*Thraustrochytrium* sp.	Δ4-Desaturase	SEQ ID NO: 41
22.	*Thalassiosira pseudonana*	Δ5-Elongase	SEQ ID NO: 43
23.	*Thalassiosira pseudonana*	Δ6-Elongase	SEQ ID NO: 45
24.	*Crypthecodinium cohnii*	Δ5-Elongase	SEQ ID NO: 47
25.	*Crypthecodinium cohnii*	Δ5-Elongase	SEQ ID NO: 49
26.	*Oncorhynchus mykiss*	Δ5-Elongase	SEQ ID NO: 51
27.	*Oncorhynchus mykiss*	Δ5-Elongase	SEQ ID NO: 53
28.	*Thalassiosira pseudonana*	Δ5-Elongase	SEQ ID NO: 59
29.	*Thalassiosira pseudonana*	Δ5-Elongase	SEQ ID NO: 61
30.	*Thalassiosira pseudonana*	Δ5-Elongase	SEQ ID NO: 63
31.	*Thraustrochytrium aureum*	Δ5-Elongase	SEQ ID NO: 65
32.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 67
33.	*Ostreococcus tauri*	Δ6-Elongase	SEQ ID NO: 69
34.	*Primula farinosa*	Δ6-Desaturase	SEQ ID NO: 71
35.	*Primula vialii*	Δ6-Desaturase	SEQ ID NO: 73
36.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 75
37.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 77
38.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 79
39.	*Ostreococcus tauri*	Δ6-Elongase	SEQ ID NO: 81
40.	*Thraustrochytrium* sp.	Δ5-Elongase	SEQ ID NO: 83
41.	*Thalassiosira pseudonana*	Δ5-Elongase	SEQ ID NO: 85
42.	*Phytophtora infestans*	ω3-Desaturase	SEQ ID NO: 87
43.	*Ostreococcus tauri*	Δ6-Desaturase	SEQ ID NO: 89
44.	*Ostreococcus tauri*	Δ5-Desaturase	SEQ ID NO: 91
45.	*Ostreococcus tauri*	Δ5-Desaturase	SEQ ID NO: 93
46.	*Ostreococcus tauri*	Δ4-Desaturase	SEQ ID NO: 95
47.	*Thalassiosira pseudonana*	Δ6-Desaturase	SEQ ID NO: 97
48.	*Thalassiosira pseudonana*	Δ5-Desaturase	SEQ ID NO: 99
49.	*Thalassiosira pseudonana*	Δ5-Desaturase	SEQ ID NO: 101
50.	*Thalassiosira pseudonana*	Δ4-Desaturase	SEQ ID NO: 103
51.	*Thalassiosira pseudonana*	ω3-Desaturase	SEQ ID NO: 105
52.	*Ostreococcus tauri*	Δ12-Desaturase	SEQ ID NO: 107
53.	*Thalassiosira pseudonana*	Δ12-Desaturase	SEQ ID NO: 109
54.	*Ostreococcus tauri*	Δ6-Elongase	SEQ ID NO: 111
55.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 113
56.	*Xenopus laevis* (BC044967)	Δ5-Elongase	SEQ ID NO: 117
57.	*Ciona intestinalis* (AK112719)	Δ5-Elongase	SEQ ID NO: 119
58.	*Euglena gracilis*	Δ5-Elongase	SEQ ID NO: 131
59.	*Euglena gracilis*	Δ5-Elongase	SEQ ID NO: 133
60.	*Arabidopsis thaliana*	Δ5-Elongase	SEQ ID NO: 135
61.	*Arabidopsis thaliana*	Δ5-Elongase	SEQ ID NO: 137
62.	*Phaeodactylum tricornutum*	Δ6-Elongase	SEQ ID NO: 183
63.	*Phytium irregulare*	Δ6-Desaturase	SEQ ID NO: 193
64.	*Calendula officinalis*	Δ12-Desaturase	SEQ ID NO: 195
65.	*Ostreococcus tauri*	Δ5-Elongase	SEQ ID NO: 197
66.	*Ostreococcus tauri*	Δ6-Elongase	SEQ ID NO: 199
67.	*Ostreococcus tauri*	Δ6-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



(I)

in transgenic plants, the process comprising:

a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a Δ6-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 Δ6-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 Δ5-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 (Δ5-desaturase from *Thraustochytrium* ssp., SEQ ID NO: 11 and Δ6-desaturase from *Phytium irregulare*, SEQ ID NO: 193) and in WO 01/59128 (Δ6-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 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 Δ12-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 Δ12-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 Δ12-desaturases used in the process according to the invention advantageously convert oleic acid ($C18:1^{\Delta 9}$) into linoleic acid ($C18:2^{\Delta 9,12}$) or $C18:2^{\Delta 6,9}$ into $C18:3^{\Delta 6,9,12}$ (gamma-linolenic acid=GLA), the starting materials for the synthesis of ARA, EPA and DHA. The Δ12-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 Δ12-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 Δ5-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 Δ5-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: 6.5, 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 Δ5-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×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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase and/or Δ6-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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase and/or Δ6-elongase which are the result of natural variation and which do not essentially modify the enzymatic activity.

Essential enzymatic activity of the Δ12-desaturase, Δ6-desaturase, Δ6-elongase, Δ5-elongase or Δ5-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_{18}-, C_{20}- or C_{22}-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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase and/or Δ6-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× sodium chloride/sodium citrate (=SSC) at approximately 45° C., followed by one or more washing steps in 0.2×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×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×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×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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase and/or Δ6-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), unpolar 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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase or Δ6-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 Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase or Δ6-elongase, for example by saturation mutagenesis, and the resulting mutants can be screened by recombinant expression for the hereindescribed Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase or Δ6-elongase activity in order to identify mutants which have retained the Δ12-desaturase, Δ6-desaturase, Δ5-desaturase, Δ5-elongase or Δ6-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_{18}-, C_{20}- and/or C_{22}-fatty acids, very especially preferred are the long-chain fatty acids LCPUFAs of C_{20}- and/or C_{22}-fatty acids such as ARA, EPA, DHA or their combination.

The process according to the invention advantageously yields fatty acid esters with polyunsaturated C_{18}-, C_{20}- and/or C_{22}-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, $C18:2^{\Delta 9,12}$), γ-linolenic acid (=GLA, $C18:3^{\Delta 6,9,12}$), stearidonic acid (=SDA, $C18:4^{\Delta 6,9,12,15}$), dihomo-γ-linolenic acid (=DGLA, $20:3^{\Delta 8,11,14}$), ω3-eicosatetraenoic acid (=ETA, $C20:4^{\Delta 5,8,11,14}$), arachidonic acid (ARA, $C20:4^{\Delta 5,8,11,14}$), eicosapentaenoic acid (EPA, $C20:4^{\Delta 5,8,11,14}$) or mixtures of

these, ω3-eicosapentaenoic acid (=ETA, C20:$4^{\Delta 5,8,11,14,17}$), arachidonic acid (ARA, C20:$4^{\Delta 5,8,11,14}$), eicosapentaenoic acid (EPA, C20:$5^{\Delta 5,8,11,14,17}$)) ω6-docosapentaenoic acid (C22:$5^{\Delta 4,7,10,13,16}$), ω6-docosapentaenoic acid (C22:$4^{\Delta 7,10,13,16}$), ω3-docosapentaenoic acid (=DPA, C22:$5^{\Delta 7,10,13,16,19}$), docosahexaenoic acid (=DHA, C22:$6^{\Delta 4,7,10,13,16,19}$) or their mixtures are preferably produced, and ARA, EPA and/or DHA are very especially produced. ω3-Fatty acids such as EPA and/or DHA, preferably DHA, are advantageously produced.

The fatty acid esters with polyunsaturated C_{18}-, C_{20}- and/or C_{22}-fatty acid molecules, advantageously with polyunsaturated-C_{20}- and/or C_{22}-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_{18}- and/or C_{20}-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_{20}-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_{20}- and/or C_{22}-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, 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), ω6-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_{20}- and/or C_{22}-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

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), sterculic 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 (t11-octadecen-9-ynoic acid), 6,9-octadecenynoic acid, pyrulic acid (t10-heptadecen-8-ynoic acid), crepenyninic acid (9-octadecen-12-ynoic acid), 13,14-dihydrooropheic acid, octadecen-13-ene-9,11-diynoic 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), 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$^{\Delta 4,8,12,15,21}$) and no nisinic acid (tetracosahexaenoic acid, C23:6$^{\Delta 3,8,12,15,18,21}$).

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 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 thanliana* or *Linum usitatissimum* when compared by means of GC analysis; see Examples.

Advantageously, as described above, the polyunsaturated C_{20}- and/or C_{22}-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$^{\Delta 3}$trans, C16:4$^{\Delta 4,7,10,13}$ and C18:5$^{\Delta 3,6,9,12,15}$. Besides oleic acid (C18:1$^{\Delta 9}$), the isomers (C18:1$^{\Delta 7}$, 18:1$^{\Delta 11}$) 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

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, advantageous 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

	Oleic acid			Linoleic acid			α-Linolenic acid		
No.	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, *Anarcardium occidentale, Argania spinosa, Bombax malabaricum, Brassica napus, Butyrospermum parkii*, high-oleic safflower (*Carthamus tinctorius*), *Citrullus colocythis, Corylus avellana, Curcurbita foetidissima, Curcurbita pepo, Guizotia abyssinica*, high-oleic sunflower (*Helianthus annus*), *Macadamia intergrifolia, Nigella sativa, Olea europaea, Papaver somniferium, Passiflora edulis, Persea americana, Prunus amygdalis, Prunus armeniaca, Prunus dulcis, Prunus communis, Sesamum indicum, Simarouba glauca, Thea sasumgua*, or *Theobroma cacao*. Further advantageous plants have a higher content of the unsaturated fatty acids oleic acid, linoleic acid and α-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 bigelovii, Salvia hispanica* are also those which have a high α-linolenic acid content in the lipid and/or oil of the plant, that is to say an α-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 Adelotheciaceae, 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 Solaneae, 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 annus* [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, Cerinthe, Cynoglossum, Echium, Gastrocatyle, Lithospermum, Moltkia, Nonea, Onosma, Onosmodium, Paracaryum, Pectocarya, Symphytum* for example the genus and species *Adelocarym coelestinum, Alkanna orientalis, Anchusa anzurea, Anchusa capensis, Anchusa hybrida, Borago officinalis* [borage], *Brunnera orientalis, Cerinthe minor, Cynoglossum amabile, Cynoglossum lanceolatum, Echium rubrum, Echium vulgare, Gastrocatyle hispida, Lithospermum arvense, Lithosperumum purpureocaeruleum, Mbltkia 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*, such as the genus and species, *Carica papaya* [pawpaw], Cannabaceae, such as the genus *Cannabis*, such as the genus and species *Cannabis sativa* [hemp], Convolvulaceae, such as the genera *Ipomea, Convolvulus*, for example the genera and species *Ipomoea batatus, Ipomoea pandurata, Convolvulus batatas, Convolvulus tiliaceus, Ipomoea fastigiata, Ipomoea tiliacea, Ipomoea triloba* or *Convolvulus panduratus* [sweet potato, batate], Chenopodiaceae, such as the genus *Beta*, such as the genera and species *Beta vulgaris, Beta vulgaris* var. *altissima, Beta vulgaris* var. *vulgaris, Beta maritima, Beta vulgaris* var. *perennis, Beta vulgaris* var. conditiva or *Beta vulgaris* var. *esculenta* [sugarbeet], Crypthecodiniaceae, such as the genus *Crypthecodinium*, for example the genus and species *Cryptecodinium cohnii*, 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 chamaerhodendros* 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, Medicajo, 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, Albizzia berteriana, Cathormion berteriana, Feuillea berteriana, Inga fragrans, Pithecellobium berterianum, Pithecellobium fragrans, Pithecolobium berterianum, Pseudalbizzia berteriana, Acacia julibrissin, Acacia nemu, Albizia nemu, Feuilleea julibrissin, Mimosa julibrissin, Mimosa speciosa, Sericanrda julibrissin, Acacia lebbeck, Acacia macrophylla, Albizia lebbeck, Feuilleea 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], Lythrarieae, such as the genus *Punica*, for example the genus and species *Punica granatum* [pomegranate], Malvaceae, such as the genus *Gossypium*, for example the genera and species *Gossypium hirsutum, Gossypium arboreum, Gossypium barbadense, Gossypium herbaceum* or *Gossypium thurberi* [cotton], Marchantiaceae, such as the genus *Marchantia*, for example the genera and species *Marchantia berteroana, 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*

[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,Triticumt turgidum, Triticum hybernum, Triticum macha, Triticum sativum* or *Triticum vulgare* [wheat]; Porphyridiaceae, such as the genera *Chrodthece, Flintiella, Petrovanella, Porphyridium, Rhodella, Rhodosorus, Vanhoeffenia*, for example the genus and species *Porphyridium cruentum*, Proteaceae, such as the genus *Macadamia*, for example the genus and species *Macadamia intergrifolia [macadamia*], Rosaceae, such as the genus *Prunus*, for example the genus and species *Prunus armeriiaca, 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 phlomoides, 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 alata, Nicotiana attenuata, Nicotiana glauca, Nicotiana langsdorffii, Nicotiana obtusifolia, Nicotiana quadrivalvis, Nicotiana repanda, Nicotiana rustica, Nicotiana sylvestris* [tobacco], *Solanum tuberosum* [potato], *Solanum melongena* [eggplant] *Lycopersicon esculentum, Lycopersicon lycopersicum, Lycopersicon pyriforme, Solanum integrifolium* or *Solarium 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 lupus, Hyptis spicigera* and *Shorea stenoptera.*

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 perrenial 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 ω3-desaturases and/or the Δ12-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 Δ5-elongase(s), Δ6-elongase(s) and/or ω3-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 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) are advantageously used in combination with the Δ5-elongase, Δ6-elongase and/or ω3-desaturase. Genes selected from the group of the Δ4-desaturases, Δ5-desaturases, Δ6-desaturases, Δ8-desaturases, Δ9-desaturases, Δ12-desaturases, Δ6-elongases or Δ9-elongases are especially preferably used in combination with the above genes for the Δ5-elongase, Δ6-elongase and/or ω3-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 Δ6-elongase, Δ5-elongase, Δ5-desaturase, Δ6-desaturase and/or Δ12-desaturase used in accordance with the invention.

Genes selected from the group of the Δ8-desaturases, Δ9-desaturases, Δ5-elongase or Δ9-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 Δ6-elongase, Δ6-desaturase, Δ5-desaturase and/or Δ12-desaturase activity, advantageously in combination with nucleic acid sequences which encode polypeptides of the fatty acid or lipid metabolism, such as polypeptides with Δ8-desaturase, or Δ5- or Δ9-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:$2^{\Delta 9,12}$) 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. If only α-linolenic acid (=ALA, C18:$3^{\Delta 9,12,15}$) 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 Δ6-desaturase and Δ6-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 Δ5-desaturase is additionally introduced into the plant, ARA and/or EPA are also formed. If, moreover, genes which encode a Δ5-elongase and/or Δ4-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:$2^{\Delta 9,12}$), γ-linolenic acid (C18:$3^{\Delta 8,9,12}$) and dihomo-γ-linolenic acid (20:$3^{\Delta 8,11,14}$). Substrates which are preferred for the production of EPA are linolenic acid (C18:$3^{\Delta 9,12,15}$), stearidonic acid (C18:$4^{\Delta 6,9,12,15}$) and eicosatetraenoic acid (C20:$4^{\Delta 8,11,14,17}$). Substrates which are preferred for the production of DHA are linolenic acid (C18:$3^{\Delta 9,12,15}$), stearidonic acid (C18:$4^{\Delta 6,9,12,15}$), eicosatetraenoic acid (C20:$4^{\Delta 8,11,14,17}$), EPA and DPA.

In comparison with the human elongases or elongases from non-human animals, such as those from *Oncorhynchus, Xenopus* or *Ciona*, the Δ5-elongases according to the invention have the advantageous characteristic that they do not elongate C_{22}-fatty acids to the corresponding C_{24}-fatty acids. Furthermore, they advantageously do not convert fatty acids with a double bond in the Δ6-position, as is the case with the human elongases or the elongases from non-human animals. Especially advantageously Δ5-elongases preferentially only convert unsaturated C_{20}-fatty acids. These advantageous Δ5-elongases contain some putative transmembrane helices (5-7). Advantageously, only C_{20}-fatty acids with one double bond in the Δ5-position are converted, with ω3-C_{20}-fatty acids being preferred (EPA). Moreover, in a preferred embodiment of the invention, they have the characteristic that, besides the Δ5-elongase activity, they advantageously have no, or only relatively low, Δ6-elongase activity. In contrast, the human elongases or non-human animal elongases have approximately the same activity towards fatty acids with a Δ6- or Δ5-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_{16}- and C_{18}-fatty acids, for example with Δ9- or Δ11-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:$5^{\Delta 7,10,13,16,19}$), advantageously at least 20% by weight, especially, advantageously at least 25% by weight. If v-linolenic acid (=GLA, C18:$3^{\Delta 6,9,12}$ is added as the substrate, this acid is advantageously not elongated at all. Likewise, C18:$3^{\Delta 6,9,12}$ is not elongated. In another advantageous embodiment, less than 60% by weight of the added GLA is converted into dihomo-Y-linolenic acid (=C20:$3^{\Delta 8,11,14}$), 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 Δ5-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* Δ5-elongase. This enzyme only converts fatty acids with a double bond in the Δ5-position. Advantageously, only C_{20}-fatty acids are converted. A similarly high substrate specificity is shown by the *Thallasiosira pseudonana* Δ5-elongase (FIG. **28**. C). Both the *Ostreococcus tauri* Δ6-elongase (FIG. **28** B) as that of *Thallasiosira pseudonana* (FIG. **28** D) advantageously only convert fatty acids with a double bond in the Δ6-position. Advantageously, only C^{18}-fatty acids are converted. The Δ5-elongases from *Arabidopsis thaliana* and *Euglena gracilis* are also distinguished by their specificities.

Likewise, advantageous Δ6-elongases according to the invention are distinguished by a high specificity, that is to say that C_{18}-fatty acids are preferentially elongated. They

advantageously convert fatty acids with a double bond in the Δ6-position. Especially advantageous Δ6-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 Δ6-position. Moreover, in a preferred embodiment of the invention, they have the characteristic that, besides the Δ6-elongase activity, they advantageously have no, or only relatively low, Δ5-elongase activity. In contrast, the human elongases or non-human animal elongases have approximately the same activity towards fatty acids with a Δ6- or Δ5-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 Δ9- or Δ11-double bonds. In a yeast feeding text, in which EPA has been added to the yeasts as the substrate, the monofunctional elongases convert at least 10% by weight of the added α-linolenic acid (=ALA, $C18:3^{\Delta 9,12,15}$) or at least 40% by weight of added γ-linolenic acid (=GLA, $C18:3^{\Delta 6,9,12}$), 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 $C18:4^{\Delta 6,9,12,15}$ (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 Δ6-elongases show no, or only very low activity (less than 0.1% by weight conversion rate) toward the following substrates: $C18:1^{\Delta 6}$, $C18:1^{\Delta 9}$, $C18:1^{\Delta 11}$, $C20:2^{\Delta 11,14}$, $C20:3^{\Delta 11,14,17}$, $C20:3^{\Delta 8,11,14}$, $C20:4^{\Delta 5,8,11,14}$, $C20:5^{\Delta 5,8,11,14,17}$ or $C22:4^{\Delta 7,10,13,16}$.

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

In comparison with the known ω3-desaturase, the ω3-desaturase used in the process according to the invention has the advantageous characteristic that it is capable of desaturating a broad spectrum of ω6-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 ω3-desaturase, it is advantageously possible to shift the fatty acid spectrum within an organism, advantageously within a plant or a fungus, from the ω6-fatty acids towards the ω3-fatty acids. The ω3-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 ω3-fatty acids. In comparison with the C_{18}-fatty acids, the activity of ω3-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 ω3-fatty acids. Preferred substrates of the ω3-desaturase according to the invention are the ω6-fatty acids bound in phospholipids. With reference to the desaturation of dihomo-γ-linolenic acid [$C_{20:4}^{\Delta 8,11,14}$], FIG. **19** shows clearly that ω3-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 ω3-desaturase converts a broad range of phospholipids such as phosphatidylcholine (=PC), phosphatidylinositol (=PIS) or phosphatidylethanolamine (=PE). Finally, desaturation products are also found in the neutral lipids (=NL), i.e. in the triglycerides.

In comparison with the known Δ4-desaturases, Δ5-desaturases and Δ6-desaturases, the advantage of the Δ4-desaturases, Δ5-desaturases and Δ6-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 Δ12-desaturases used in the process according to the invention advantageously convert oleic acid ($C18:1^{\Delta 9}$) into linoleic acid ($C18:2^{\Delta 9,12}$) or $C18:2^{\Delta 6,9}$ into $C18:3^{\Delta 6,9,12}$ (=GLA). The Δ12-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 Δ5-elongase, Δ6-elongase and/or ω3-desaturase activity, advantageously in combination with nucleic acid sequences which encode polypeptides of the fatty acid or lipid metabolism, such as additionally polypeptides with Δ4-, Δ5-, Δ6-, Δ8-, Δ12-desaturase or Δ5-, Δ6- or Δ9-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 (C18:2- or C18:3-fatty acids), fatty acids which are derived from C18:2-fatty acids, such as GLA, DGLA or ARA, or which are derived from C18:3-fatty acids, such as SDA, ETA, EPA or DHA, are thus obtained. If only linoleic acid (=LA, $C18:2^{\Delta 9,12}$) 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 ω3-desaturase in plants, the fatty acid spectrum can be shifted towards α-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 α-linolenic acid content. If only α-linolenic acid (=ALA, $C18:3^{\Delta 9,12,15}$) 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 Δ5-elongase which plays a role in the synthesis, advantageously in combination with Δ4-, Δ5-, Δ6-, Δ12-desaturase and/or Δ6-elongase, or Δ4-, Δ5-, Δ8-, Δ12-desaturase, and/or Δ9-elongase, it is possible to produce; in a targeted fashion, only individual products in the abovementioned plants. Owing to the activity of Δ6-desaturase and Δ6-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 Δ5-desaturase, Δ5-elongase and Δ4-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 Δ8-desaturase and Δ9-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

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:$4^{\Delta 6,9,12,15}$- and C20:$5^{\Delta 5,8,11,14,17}$-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:$2^{\Delta 9,12}$), γ-linolenic acid (C18:$3^{\Delta 8,9,12}$), eicosadienoic acid (C20:$2^{\Delta 11,14}$); dihomo-γ-linolenic acid (C20:$3^{\Delta 8,11,14}$), arachidonic acid; (C20:$4^{\Delta 5,8,11,14}$), docosatetraenoic acid (C22:$4^{\Delta 7,10,13,16}$) and docosapentaenoic acid (C22:$5^{\Delta 4,7,10,13,15}$).

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 species *Heteromastix longifillis, Mamiella gilva, Mantoniella squamata, Micromonas pusilla, Nephroselmis olivacea, Nephroselmis pyriformis, Nephroselmis rotunda, Ostreococcus tauri, Ostreococcus* sp. *Prasinocladus ascus, Prasinocladus lubricus, Pycnococcus provasolii, Pyramimonas amylifera, 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 geniculate, 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 *Crypthecodinium*, 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 *Crypthecodinium*.

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 alpiina, 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 Δ12-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase and/or ω-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 Δ12-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase and/or ω3-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 Δ5-desaturase, Δ6-desaturase, Δ5-elongase or Δ6-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, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s). Biosynthesis genes of the fatty acid or lipid metabolism selected from the group Δ8-desaturase, Δ9-desaturase, Δ9-elongase or ω3-desaturase are advantageously additionally present.

The nucleic acid sequences used in the process which encode proteins with Δ5-desaturase, Δ6-desaturase, Δ12-desaturase, Δ5-elongase or Δ6-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 Δ12-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase and/or Δ6-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 Δ12-desaturase, Δ5-elongase, Δ6-elongase, Δ5-desaturase and/or Δ6-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 Δ12-Desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase or Δ5-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 Δ12-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase and/or Δ5-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 Δ12-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase or Δ5-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 Δ12-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase or Δ5-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 Δ12-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase and/or Δ6-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 Δ12-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase or Δ5-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 monocotyledanous 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 Ipt1 (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 α-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 Δ12-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-elongase and/or Δ5-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 inductors, 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, ω3-desaturase, Δ8-desaturase, Δ4-desaturase, Δ9-desaturase, Δ5-elongase and/or Δ9-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 Δ12-desaturases, Δ6-desaturases, Δ5-elongases, Δ6-elongases or Δ5-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, ω3-desaturases, Δ8-desaturases, Δ9-desaturases, ω3-desaturases, Δ4-desaturases, Δ5-elongases and/or Δ9-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 exchangeably 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 Δ12-desaturases, Δ6-desaturases, Δ5-elongases, Δ6-elongases and/or Δ5-desaturases can be expressed in single-celled plant cells (such as algae), see Falciatore et al., 1999, Marine Biotechnology 1 (3):239-251 and references cited therein, and in plant cells from higher plants (for example spermatophytes such as arable crops). Examples of plant expression vectors comprise those which are described in detail in: Becker, D., Kemper, E., Schell, J., and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", Plant Mol. Biol. 20:1195-1197; and Bevan, M. W. (1984) "Binary *Agrobacterium* vectors for plant transformation", Nucl. Acids Res. 12:8711-8721; Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, Vol. 1, Engineering and Utilization, 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 multiparallel expression of the Δ12-desaturases, Δ6-desaturases, Δ5-elongases, Δ6-elongases and/or Δ5-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 Δ12-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase and/or Δ6-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 Δ12-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ8-desaturase, U)-3-desaturase, Δ9-elongase, Δ6-elongase and/or Δ5-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, cotelydons, 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, cotelydons, 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_{18}-, C_{20}- or C_{22}-fatty acid molecules, advantageously C_{20}- or C_{22}-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_{18}-, C_{20}- or C_{22}-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), sterculic 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 (t11-octadecen-9-ynoic acid), 6,9-octadecenynoic acid, pyrulic acid (t10-heptadecen-8-ynoic acid), crepenyninic acid (9-octadecen-12-ynoic acid), 13,14-dihydrooropheic acid, octadecen-13-ene-9,11-diynoic 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), 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 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:$5^{\Delta4,8,12,15,21}$) and no nisinic acid (tetracosahexaenoic acid, C23:$6^{\Delta3,8,12,15,18,21}$).

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:$5^{\Delta4,8,12,15,21}$) and no nisinic acid (tetracosahexaenoic acid, C23:$6^{\Delta3,8,12,15,18,21}$).

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 thanliana* 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 α-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_{20}- and/or C_{22}-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:$1^{\Delta3}$trans, C16:$4^{\Delta4,7,10,13}$ and C18:$5^{\Delta3,6,9,12,15}$. Besides oleic acid (C18:$1^{\Delta9}$), the isomers (C18:$1^{\Delta7}$, C18:$1^{\Delta11}$) 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-γ-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 α-tocopherol, β-tocopherol, γ-tocopherol and/or δ-tocopherol or phytosterols such as brassicasterol, campesterol, stigmasterol, β-sitosterol, sitostanol, Δ^5-avenasterol, Δ^5,24-stigmastadienol, Δ^7-stigmasternol or Δ^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, amyrin, 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 unpolar lipids such as phospholipids, for example phosphatidylcholine, phosphatidylethanolamine, phosphatidiylinositol, 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, C15:0, 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 C19:0 and C19:1 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, γ-linolenic acid, dihomo-γ-linolenic acid, arachidonic acid, α-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 ω3-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ8-desaturase, Δ12-desaturase, Δ5-elongase, Δ6-elongase and/or Δ9-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 adds 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 Δ5-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 Δ5-elongase, the Δ5-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 Δ5-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 Δ6-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 Δ6-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:

a) one or more copies of a promoter which is active in plant cells, preferably in seed cells,
b) at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201 which encodes a Δ6-desaturase activity,
c) at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 11 which encodes a Δ5-desaturase activity,
d) at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199 which encodes a Δ6-elongase activity, and
e) 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 Δ12-desaturase may also advantageously be present in the recombinant abovementioned nucleic acid molecule.

In a further advantageous embodiment, an additional nucleic acid sequence with the sequence shown in SEQ ID NO: 197 and which encodes a Δ5-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: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) 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 Δ4-desaturase, Δ8-desaturase, Δ9-desaturase or Δ9-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, Crypthecodinium, Euglena* or *Ostreococcus*, fungi such as the genus *Phytophtora* or from diatoms such as the genera *Thalassiosira* or *Phaeodactylum.*

The nucleic acid sequences used in the process which encode proteins with ω3-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ8-desaturase, Δ9-desaturase, Δ12-desaturase, Δ5-elongase, Δ6-elongase or Δ9-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 Δ12-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ5-elongase, Δ6-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 Δ12-desaturase, Δ5-elongase, Δ6-elongase, Δ5-desaturase, Δ4-desaturase, Δ6-desaturase and/or ω3-desaturase protein according to the invention and of the further proteins used in the process, such as the Δ12-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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 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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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: 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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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

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: 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 ere 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 ah, 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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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 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, Cryphthecodinium*, specifically from the genera and species *Oncorhynchus mykiss, Xenopus laevis, Ciona intestinalis, Thalassiosira pseudonona, Mantoniella squamata, Ostreococcus* sp., *Ostreococcus tauri, Euglena gracilis, Physcomitrella patens, Phytophtora infestans, Fusarium graminaeum, Cryptocodinium cohnii, Ceratodon purpureus, Isochrysis galbana, Aleurita farinosa, Thraustochytrium* sp., *Muscarioides viallii, Mortierella alpina, Borago officinalis, Phaeodactylum tricornutum, Caenorhabditis elegans* or especially advantageously from *Oncorhynchus mykiss, Euglena gracilis, Thalassiosira pseudonona* or *Crypthecodinium cohnii*.

As an alternative, it is possible to use, in the process according to the invention, nucleotide sequences which encode a Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ4-desaturase, Δ5-desaturase, Δ6-desaturase, Δ8-desaturase, Δ5-elongase, Δ6-elongase and/or Δ9-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, ah 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 *Arobidopsis*), 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 β-conglycinin α-subunit, of the β-conglycinin β-subunit, of the Kunitz trypsin inhibitor, of annexin, of glysinin, 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 AlS3'.

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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-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 Δ12-desaturases, ω3-desaturases, Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases or Δ4-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 acyltransferases, ω3-desaturases, Δ4-desaturases, Δ5-desaturases, Δ6-desaturases, Δ8-desaturases, Δ9-desaturases, Δ12-desaturases, ω3-desaturases, Δ5-elongases, Δ6-elongases and/or Δ9-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 Δ12-desaturases, ω3-desaturases, Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases and/or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-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, Suctoria, Tetrahymena, Paramecium, Colpidium*, Glaucoma, *Platyophrya, Potomacus, Desaturaseudocohnilembus, Euplotes, Engelmaniella* 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. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press (1993), 128-43; Potrykus, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991), 205-225 (and references cited therein)). Suitable host cells are furthermore discussed in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, 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 λ-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, λgt11 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 pYeDesaturasec1 (Baldari et al. (1987) Embo J. 6:229-234), pMFa (Kurjan and Herskowitz (1982) Cell 30:933-943), pJRY88 (Schultz et al. (1987) Gene 54:113-123) and pYES2 (Invitrogen Corporation, San Diego, 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 Δ12-desaturases, u)-3-desaturases, Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases and/or Δ4-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, 2nd edition, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

To detect the enzyme activity, Δ12-desaturases, u)-3-desaturases, Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases and/or Δ4-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 Kermode, 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 oryzin 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 Δ12-desaturases, ω3-desaturases, Δ9-elongases, Δ6-desaturases, Δ8-desaturases, Δ6-elongases, Δ5-desaturases, Δ5-elongases and/or Δ4-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, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Gold 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 Δ5-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 Δ6-double bond, or C_{22}-fatty acids, are not converted either. Advantageously, only polyunsaturated C_{20}-fatty acids with one Δ5-double bond are elongated by the enzymatic activity. Further subject matters of the invention are, as described above, a Δ6-elongase, Δ6-desaturase and a Δ12-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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:

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: 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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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: 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: 7-9, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 9T, 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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase,

Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-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 Δ12-desaturase, ω3-desaturase, Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase and/or Δ4-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 usitatissumum*) 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 desaturates 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 Procaryotes. 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_{18}-carbon fatty acids must be elongated to C_{20} and C_{22} 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 Δ12-, ω3-, Δ4-, Δ5-, Δ6- and Δ8-desaturases and/or the Δ5-, Δ6-, Δ9-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_{20}- and/or C_{22}-fatty acids with at least two, advantageously at least three, four, five or six double bonds in the fatty acid molecule, preferably C_{20}- or C_{22}-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_{20}- to C_{22}-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_{16}-, C_{18}- or C_{20}-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_{20}- to C_{22}-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 alkylaeylglycerophospholipids.

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.

EXAMPLES

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.

Example 4

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' aagcttacataatggcttcaacatggcaa	(SEQ ID NO: 179)
3' r* OmELO2	5' ggatccttatgtcttcttgctcttcctgtt	(SEQ ID NO: 180)
5' f OmELO3	5' aagcttacataatggagacttttaat	(SEQ ID NO: 181)
3' r OmELO3	5' ggatccttcagtccccctcactttcc	(SEQ ID NO: 182)

*f: forward, r: reverse

Composition of the PCR Mix (50 µl):

5.00 µl template cDNA

5.00 µl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$

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 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.

Example 5

Cloning Expression Plasmids for the Seed-Specific Expression in Plants

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'-GCGGCCGCTTATGTCTTCTTGCTCTTCCTGTT

PSUN-OmELO3

(SEQ ID NO: 177)
Forward: 5'-GCGGCCGCataatggagacttttaat

(SEQ ID NO: 178)
Reverse: 3'-GCGGCCGCtcagtccccctcactttcc

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 octopin 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 metabolytes 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.

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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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 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 tricornutum* 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-OmEIO/pYes2-EgD4 strain and complete minimal dropout tryptophan, uracil and leucine medium in the case of the pYes3-OmEIO/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

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 Δ5-desaturase from *P. tricomutum* (PtD5) were expressed together. The transgenic yeasts were fed stearidonic acid (18:4 ω3) and analyzed (FIG. **4**). The fatty acid composition of these yeasts is shown in FIG. **5**. OmElo3 elongated the fed fatty acid 18:4 ω3 to give 20:4 ω3 (60% elongation). The latter was desaturated by PtD5 to give 20:5 ω3. The PtD5 activity amounted to 15%. Furthermore, 20:5 ω3 was elongated by EmElo3 to give 22:5 ω3. Thereafter, the newly synthesized 22:5 ω3 was desaturated to give 22:6 ω3 (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. Petiols or hypocotyls of freshly germinated sterile oilseed rape plants (in each case approx. 1 cm^2) 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 μM 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 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 Δ5-elongase or Δ6-elongase activity. In this manner, lines with elevated contents of polyunsaturated C_{20}- and C_{22}-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 Δ5-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 Δ5-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' cggcttaggccgacttggccttggg	(SEQ ID NO: 171)
5' f* TL16y2	5' agacataatggacgtcgtcgagcagcaatg	(SEQ ID NO: 172)
3' r* TL16y2	5' ttagatggtcttctgcttcttgggcgcc	(SEQ ID NO: 173)

*f: forward, r: reverse

Composition of the PCR Mix (50 μl):

5.00 μl template cDNA

5.00 μl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$

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'-GCGGCCGCATAATGACGAGCAACATGAGC

Reverse:
                                (SEQ ID NO: 167)
3'-GCGGCCGCTTAGGCCGACTTGGCCTTGGG

PSUN-TL16y2 -
Forward:
                                (SEQ ID NO: 168)
5'-GCGGCCGCACCATGGACGTCGTCGAGCAGCAATG

Reverse:
                                (SEQ ID NO: 169)
5'-GCGGCCGCTTAGATGGTCTTCTGCTTCTTGGGCGCC
```

Composition of the PCR Mix (50 μl):

5.00 μl template cDNA

5.00 μl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$

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 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-BioTaurELO1 and pSUN-TL16y2 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 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'-GTCGAC-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 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

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 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 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 Δ5- and Δ6-fatty acids with one ω-3-double bond. Moreover, ω6-fatty acids (C18 and C20) were also elongated. γ-Linolenic acid (C18:3 ω6) is converted with a conversion rate of 65.28%, stearidonic acid (C18:4 ω3) with a conversion rate of 65.66% and eicosapentaenoic acid (C20:5 ω3) 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 μm EPA						13.79		
TL16y2	250 μm EPA						25.81		**2.25**
pYES	50 μm EPA						5.07		
TL16y2	50 μm EPA						2.48		**1.73**
pYES	250 μm GLA	8.31							
TL16y2	250 μm GLA	3.59		**10.71**					
pYES	250 μm ARA				16.03				
TL16y2	250 μm ARA				15.2		**3.87**		
pYES	250 μm SDA		26.79			0.35			
TL16y2	250 μm SDA		7.74			**29.17**			

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 μm): 8%, b) conversion rate of EPA in % (50 μm): 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 Δ5-, Δ6- and Δ8-elongase activity. The activity is highest for C18-fatty acids with Δ6-double bond. Then, C20-fatty acids with a Δ5- or Δ8-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 Δ5-elongase activity or Δ6-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, (Δ5-elongase)	SEQ ID NO: 67	300
OtELO2, (Δ6-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° 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 μl of defrosted cells, 200 μm of dNTPs, 2.5 U Taq 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.

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_{600} 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 $MgCl_2$
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.

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 *Ostreococcys* 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'-GTCGAC-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 $NaHCO_3$, 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 nonderivatized fatty acids, the organic phases were washed in each case once with 2 ml of 100 mM $NaHCO_3$, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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 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	—
$16:1^{\Delta 9}$	—
18:0	—
$18:1^{\Delta 9}$	—
$18:1^{\Delta 11}$	—
$18:2^{\Delta 9,12}$	—
$18:3^{\Delta 6,9,12}$	—
$18:3^{\Delta 5,9,12}$	—
$20:3^{\Delta 8,11,14}$	—
$20:4^{\Delta 5,8,11,14}$	10.8 ± 0.6
$20:5^{\Delta 5,8,11,14,17}$	46.8 ± 3.6
$22:4^{\Delta 7,10,13,16}$	—
$22:6^{\Delta 4,7,10,13,16,19}$	—

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	—
$16:1^{\Delta 9}$	—
$16:3^{\Delta 7,10,13}$	
18:0	—
$18:1^{\Delta 0}$	—
$18:1^{\Delta 9}$	—
$18:1^{\Delta 11}$	—
$18:2^{\Delta 9,12}$	—
$18:3^{\Delta 6,9,12}$	15.3±
$18:3^{\Delta 5,9,12}$	—
$18:4^{\Delta 6,9,12,15}$	21.1±
$20:2^{\Delta 11,14}$	—
$20:3^{\Delta 8,11,14}$	—
$20:4^{\Delta 5,8,11,14}$	—
$20:5^{\Delta 5,8,11,14,17}$	—
$22:4^{\Delta 7,10,13,16}$	—
$22:5^{\Delta 7,10,13,16,19}$	—
$22:6^{\Delta 4,7,10,13,16,19}$	—

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^2. 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 (Δ5-elongase), SEQ ID NO: 59	F:5'-accatgtgctcaccaccgccgtc (SEQ ID NO: 158) R:5'-ctacatggcaccagtaac (SEQ ID NO: 159)
TpELO2 (Δ5-elongase), SEQ ID NO: 85	F:5'-accatgtgctcatcaccgccgtc (SEQ ID NO: 160) R:5'-ctacatggcaccagtaac (SEQ ID NO: 161)
TpELO3 (Δ6-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'-GCGGCCGCACCATGTGCTCATCACCGCCGTC

Reverse:
(SEQ ID NO: 155)
3'-GCGGCCGCCTACATGGCACCAGTAAC

-continued

PSUN-TPELO3
Forward:
(SEQ ID NO: 156)
5'-GCGGCCGCaccatggacgcctacaacgctgc

Reverse:
(SEQ ID NO: 157)
3'-GCGGCCGCCTAAGCACTCTTCTTCTTT

Composition of the PCR Mix (50 μl):
5.00 μl template cDNA
5.00 μl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 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'-GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATC

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 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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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 TpEIo1 reaction. This means that the gene TpEIo1 has been expressed functionally.

It can be seen from Table 10 that TpEIo1 shows a narrow substrate specificity. TpEIo1 was only capable of elongating the C_{20}-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.

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
$16:1^{\Delta 9}$	28.0	29.8	36.6	36.6
18:0	5.2	5.0	6.8	6.9
$18:1^{\Delta 9}$	25.5	23.6	24.6	23.9
$20:4^{\Delta 5,8,11,14}$	22.5	23.4	—	—
$22:4^{\Delta 7,10,13,16}$	—	0.4	—	—
$20:5^{\Delta 5,8,11,14,17}$	—	—	6.6	6.5
$22:5^{\Delta 7,10,13,16,19}$	—	—	—	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
$16:1^{\Delta 9}$	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
$18:1^{\Delta 9}$	33.3	16.8	24.2	31.8	25.5	26.4
$18:2^{\Delta 9,12}$	—	**36.1**	—	—	—	—
$18:3^{\Delta 6,9,12}$	—	—	**6.1**	—	—	
$18:4^{\Delta 6,9,12,15}$	—	—	—	**1.7**	—	
$20:2^{\Delta 11,14}$	—	**0**	—	—	—	
$20:3^{\Delta 8,11,14}$	—	—	**18.5**	—	—	
$20:4^{\Delta 8,11,14,17}$	—	—	—	**10.0**	—	
$20:4^{\Delta 5,8,11,14}$	—	—	—	—	**22.5**	
$22:4^{\Delta 7,10,13,16}$	—	—	—	—	**0**	
$20:5^{\Delta 5,8,11,14,17}$	—	—	—	—	—	**17.4**
$22:5^{\Delta 7,10,13,16,19}$	—	—	—	—	—	0
% conversion	**0**	**0**	**75**	**85**	**0**	**0**

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

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 $MgCl_2$
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 $MgCl_2$
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 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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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.

FIG. **12** represents the desaturation of linoleic acid (18:2 ω6-fatty acid) to give α-linolenic acid (18:3 ω3-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:$2^{\Delta 9,12}$-fatty acid (300 μm). Thereafter, the FAMEs were analyzed via GLC.

FIG. **13** represents the desaturation of γ-linolenic acid (18:3 ω6-fatty acid) to give stearidonic acid (18:4 ω3-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 γC18:$3^{\Delta 6,9,12}$-fatty acid (300 μm). Thereafter, the FAMEs were analyzed via GLC.

FIG. **14** represents the desaturation of C20:2-ω6-fatty acid to give C20:3-ω3-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 miminal medium in the presence of C20:$2^{\Delta 11,14}$-fatty acid (300 μm). Thereafter, the FAMEs were analyzed via GLC.

FIG. **15** represents the desaturation of C20:3-ω6-fatty acid to give C20:4-ω3-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 miminal medium in the presence of C20:$3^{\Delta 8,11,14}$-fatty acid (300 μm). 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-ω3-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:$4^{\Delta 5,8,11,14}$-fatty acid (300 μm). Thereafter, the FAMEs were analyzed via GLC.

FIG. **17** represents the desaturation of docosatetraenoic acid (C22:4-ω6-fatty acid) to give docosapentaenoic acid (C22:5-ω3-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:$4^{\Delta 7,10,13,16}$-fatty acid (300 μm). 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:

[product]/[product]+[substrate]*100.

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	Δ4-desaturase
OtD5.1	SEQ ID NO: 91	201	Δ5-desaturase
OtD5.2	SEQ ID NO: 93	237	Δ5-desaturase
OtD6.1	SEQ ID NO: 89	456	Δ6-desaturase
OtFad2	SEQ ID NO: 107	361	Δ12-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 μl of double-distilled water and stored at −20° 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 μl of defrosted cells, 200 μm of dNTPs, 2.5 U Taq 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.

The following primers were employed in the PCR:

OtDes6.1 Forward: (SEQ ID NO: 145)
5'ggtaccacataatgtgcgtggagacggaaaataacg3'

OtDes6.1 Reverse: (SEQ ID NO: 146)
5'ctcgagttacgccgtctttccggagtgttggcc3'

Example 29

Cloning Expression Plasmids for the Heterologous Expression in Yeasts

To characterize the function of the desaturase OtDes6.1 (=Δ6-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

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_{600} 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 $MgCl_2$
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 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'-GTCGAC-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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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 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 %
$16:1^{\Delta 9}$	5.6
$18:1^{\Delta 9}$	13.1
$18:2^{\Delta 9,12}$	68.7
$18:3^{\Delta 9,12,15}$	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. **21**A 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 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. **21**B) and dihomostearidonic acid (=DHSTA) and eicosapentaenoic acid (=EPA, FIG. **21**D), 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. **21**B 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)	HCANH (SEQ ID NO: 228)	WRYHHQVSHHQVEHHLFP (SEQ ID NO: 231)	(SEQ ID NO: 235)
OtD5.1	606	201	Δ5-desaturase	–	–	–	QVVHHLFP (SEQ ID NO: 236)
OtD5.2	714	237	Δ5-desaturase	–	–	WRYHHMVSHHQIEHHLPF (SEQ ID NO: 232)	(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)

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

double-distilled water and stored at −20° 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 μl of defrosted cells, 200 μm of dNTPs, 2.5 U Taq 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.

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° C., 200 rpm. 5 ml of liquid CMdum medium (without uracil) supplemented with 2% raffinose and 300 μm of various fatty acids are then inoculated with the precultures to an 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° 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 μl):
5.00 μl template cDNA
5.00 μl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$
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 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 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
GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATCTGC
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×g, 5 min, 20° C.) and washed with 100 mM $NaHCO_3$, 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° 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 $NaHCO_3$, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases are dried with Na_2SO_4, evaporated under argon and taken up in 100 μl of PE. The samples are 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 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 *Thalassiosira pseudonana desaturases*

Desaturase	cDNA (bp)	Protein (aa)	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)	HVAHHLFH (SEQ ID NO: 252)
TpO3	1257	419	—	HDAGH (SEQ ID NO: 243)	WLFMVTYLQHH (SEQ ID NO: 249)	HWHHLF (SEQ ID NO: 253)

TABLE 15

Length, axons, homology and identities of the cloned desaturases.

Des.	GDNA (bp)	Exon 1	Exon 2	First Blast Hit	Hom./ Iden.
TpD4	2633	496-1314	1571-2260	*Thrautochitrium* D4-des	56%/43%
TpD5-1	2630	490-800	900-2019	*Phaeodactylum* D5-des	74%/62%
TpD5-2	2643	532-765	854-2068	*Phaeodactylum* D5-des	72%/61%
TpD6	2371	379-480	630-1982	*Phaeodactylum* D6-des	83%/69%
TpFAD2	2667	728-2032	—	*Phaeodacrylum* FAD2	76%/61%
TpO3	2402	403-988	1073-1743	*Chaenorhabdidis* 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)	*Xenopus laevis*	BC044967	117	303
ELO(Ci)	*Ciona intestinalis*	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'-AGGATCCATGGCCTTCAAGGAGCTCACATC
SEQ ID NO: 122	R:5'-CCTCGAGTCAATGGTTTTTGCTTTTCAATGCACCG
ELO(Ci)	
SEQ ID NO: 123	F:5'-TAAGCTTATGGACGTACTTCATCGT
SEQ ID NO: 124	R:5'-TCAGATCTTTAATCGGTTTTACCATT

*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.

Example 40

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'-GCGGCCGCACCATGGCCTTCAAGGAGCTCACATC

Reverse:
                                        (SEQ ID NO: 126)
3'-GCGGCCGCCTTCAATGGTTTTTGCTTTTCAATGCACCG

pSUN-ELO(Ci)
Forward:
                                        (SEQ ID NO: 127)
5'-GCGGCCGCACCATGGACGTACTTCATCGT

Reverse:
                                        (SEQ ID NO: 128)
3'-GCGGCCGCTTTAATCGGTTTTACCATT
```

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$
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 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

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'-GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATC
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 (100×g, 5 min, 20° C.) and washed with 100 mM $NaHCO_3$, 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 $NaHCO_3$, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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.

It can be seen from Table 16 that ELO(XI) shows a broad substrate specificity. Both C18- and C_{20}-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
$16:1^{\Delta 9}$	0
18:0	2
$18:1^{\Delta 9}$	0
$18:2^{\Delta 9,12}$	3
$18:3^{\Delta 6,9,12}$	12
$18:3^{\Delta 5,9,12}$	13
$18:3^{\Delta 9,12,15}$	3
$18:4^{\Delta 6,9,12,15}$	20
$20:3^{\Delta 8,11,14}$	5
$20:3^{\Delta 11,14,17}$	13
$20:4^{\Delta 5,8,11,14}$	15
$20:5^{\Delta 5,8,11,14,17}$	10
$22:4^{\Delta 7,10,13,16}$	0
$22:6^{\Delta 4,7,10,13,16,19}$	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
$16:1^{\Delta 9}$	0
18:0	0
$18:1^{\Delta 9}$	0
$18:2^{\Delta 9,12}$	23
$18:3^{\Delta 6,9,12}$	10
$18:3^{\Delta 5,9,12}$	38
$18:3^{\Delta 9,12,15}$	25
$18:4^{\Delta 6,9,12,15}$	3
$20:3^{\Delta 8,11,14}$	10
$20:3^{\Delta 11,14,17}$	8
$20:4^{\Delta 5,8,11,14}$	10
$20:5^{\Delta 5,8,11,14,17}$	15
$22:4^{\Delta 7,10,13,16}$	0
$22:6^{\Delta 4,7,10,13,16,19}$	0

It can be seen from Table 17 that ELO(Ci) shows a broad substrate specificity. Both C18- and C20-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

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 Δ5-elongase activity or Δ6-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, (Δ5-elongase)	SEQ ID NO: 67	300
OtELO1.2, (Δ5-elongase)	SEQ ID NO: 113	300
OtELO2, (Δ6-elongase)	SEQ ID NO: 69	292
OtELO2.1, (Δ6-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 μl of double-distilled water and stored at −20° 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 μl of defrosted cells, 200 μM of dNTPs, 2.5 U Taq 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.

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.

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° C., 200 rpm. 5 ml of liquid CMdum medium (without uracil) supplemented with 2% raffinose and 300 μm of various fatty acids were then inoculated with the precultures to an OD_{600} 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 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 μl):

5.00 μl template cDNA

5.00 μl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$

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 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 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).

Primer sequence:

(SEQ ID NO: 130)

5'-GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATC

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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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 eicosapentaenoic acid (FIG. **24**A, **24**B) and arachidonic acid (FIG. **25**A, **25**B), 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	—	—
$16:1^{\Delta 9}$	—	—
18:0	—	—
$18:1^{\Delta 9}$	—	—
$18:1^{\Delta 11}$	—	—
$18:2^{\Delta 9,12}$	—	—
$18:3^{\Delta 6,9,12}$	—	—
$18:3^{\Delta 5,9,12}$	—	—
$20:3^{\Delta 8,11,14}$	—	—
$20:4^{\Delta 5,8,11,14}$	10.8 ± 0.6	38.0
$20:5^{\Delta 5,8,11,14,17}$	46.8 ± 3.6	68.6
$22:4^{\Delta 7,10,13,16}$	—	—
$22:6^{\Delta 4,7,10,13,16,19}$	—	—

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	—	—
$16:1^{\Delta 9}$	—	—
$16:3^{\Delta 7,10,13}$	—	—
18:0	—	—
$18:1^{\Delta 6}$	—	—
$18:1^{\Delta 9}$	—	—
$18:1^{\Delta 11}$	—	—
$18:2^{\Delta 9,12}$	—	—
$18:3^{\Delta 6,9,12}$	15.3	55.7
$18:3^{\Delta 5,9,12}$	—	—
$18:4^{\Delta 6,9,12,15}$	21.1	70.4
$20:2^{\Delta 11,14}$	—	—
$20:3^{\Delta 8,11,14}$	—	—

TABLE 19-continued

Fatty acid substrate	Conversion rate of OtElo2 (in %)	Conversion rate of OtElo2.2 (in %)
$20:4^{\Delta5,8,11,14}$	—	—
$20:5^{\Delta5,8,11,14,17}$	—	—
$22:4^{\Delta7,10,13,16}$	—	—
$22:5^{\Delta7,10,13,16,19}$	—	—
$22:6^{\Delta4,7,10,13,16,19}$	—	—

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 (22:5ω3).

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 (22:4ω6).

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 Δ5-elongase activity or Δ6-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 (*E. gracilis*)	SEQ ID NO: 131	262
EGY2019 (*E. gracilis*)	SEQ ID NO: 133	262
At3g06460 (*A. thaliana*)	SEQ ID NO: 135	298
At3g06470 (*A. thaliana*)	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−1m−2).

Total RNA of a four-day-old *Euglena* culture 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 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 μM of various fatty acids were then inoculated with the precultures to an OD_{600} 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 $NaHCO_3$, 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

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 $NaHCO_3$, pH 8.0 and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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
At3g06460	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 tricornutum*

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)
Phaelo reverse 1	GA(C/T)TGUAC(A/G)AA(A/G)AA (C/T)TGUG(A/G)AA (SEQ ID NO: 186)	FAQFFVQS (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. tricornutum* 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^2. 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 (Dynal, 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

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'-GCGGCCGCACATAATGATGGTACCTTCAA G (SEQ ID NO: 188) R: 3'-GAAGACAGCTTAATAGACTAGT (SEQ ID NO: 189)

*F = foward 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'-GCGGCCGCACCATGATGGTACCTTCAAGTTA

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 $MgCl_2$
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 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'-GTCGACCCGCGGACTAGTGGGCCCTCTAGACCCGGGGGATCCGGATC

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 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 $NaHCO_3$, 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 $NaHCO_3$, pH 8.0, and 2 ml of distilled water. Thereafter, the PE phases were dried with Na_2SO_4, 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:$3^{\Delta6,9,12}$ and C18.$4^{\Delta6,9,12,15}$. The substrates are elongated by in each case two carbon atoms; this results in the fatty acids C20:$3^{\Delta8,11,14}$ and C20:$4^{\Delta8,11,14,17}$, 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 PtEIO6 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	+18:4
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		0.4			
20:3			3.4		
20:3				9.7	
20:4					14.5
% elongation	**0.0**	**0.99**	**9.37**	**44.09**	**76.32**

The following fatty acids were fed, but not converted:
18:$1^{\Delta6}$, 18:$1^{\Delta9}$, 18:$1^{\Delta11}$
20:$2^{\Delta11,14}$, 20:$3^{\Delta11,14,17}$, 20:$3^{\Delta8,11,14}$, 20:$4^{\Delta5,8,11,14}$, 20:$5^{\Delta5,8,11,14,17}$
22:$4^{\Delta7,10,13,16}$

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:

Cnl1 C
(SEQ ID NO: 203)
5':gaattcggcgcgccgagctcctcgagcaacggttccggcggtataga

gttgggtaattcga

Cnl1 C
(SEQ ID NO: 204)
3':cccgggatcgatgccggcagatctccaccatttttggtggtgat

Composition of the PCR Mix (50 μl):
5.00 μl template cDNA
5.00 μl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$
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-Cnl1-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

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':aggcctccatggcctgctttaatgagatatgcgagacgcc

(SEQ ID NO: 206)
OCS_C 3':cccgggccggacaatcagtaaattgaacggag

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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':aggcctcaacggttccggcggtatag

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

ggtgattggttct

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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-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':aggcctcctgctttaatgagatatgcgagac

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

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+25 mM $MgCl_2$
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-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':aggcctcaacggttccggcggtatagag

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

ggt

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 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

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':aagcttggcgcgccgagctcgtcgacggacaatcagtaaattgaacg gaga

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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:

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

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

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 BglII 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 BglII 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:

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

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

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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:

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

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

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 Not 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':gtcgatcaacggttccggcggtatagagttg

(SEQ ID NO: 222)
Cnl1_OCS 3':gtcgatcggacaatcagtaaattgaacggaga

Composition of the PCR Mix (50 µl):
5.00 µl template cDNA
5.00 µl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 SalI. The vector pUC19 was incubated for 2 hours at 37° C. with the restriction enzyme SalI. 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_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':agatctatgggtgcaggcggtcgaatgc

(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 $MgCl_2$
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 SalI. 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':ccatggtccggg agaagcagaagaccatctaa

Composition of the PCR Mix (50 μl):
5.00 μl template cDNA
5.00 μl 10× buffer (Advantage polymerase)+ 25 mM $MgCl_2$
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 BglII and then for 2 hours at 37° C. with the restriction enzyme NcoII. The vector pUC19-Cnl1C_Cnl1B_Cnl1A_OCS3 was incubated for 2 hours at 37° C. with the restriction enzyme BglII and for 2 hours at 37° C. with the restriction enzyme NcoII. 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^2) 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 Δ4-desaturase from *Thraustochytrium* and Δ5-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 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.

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 *B. juncea* lines

B. juncea lines	No.	18:1	18:2 (LA)	γ18:3 (GLA)	α18:3 (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 = γ-linolenic acid,
ALA = α-linolenic acid,
SDA = stearidonic acid,
HGLA = dihomo-γ-linolenic acid,
ARA = arachidonic acid,
ETA = eicosatetraenoic acid,
EPA = eicosapentaenoic acid

TABLE 3

Fatty acid distribution in the seeds of the three different transgenic *B. juncea* lines

Sample	No.	18:1 Δ9	18:2 Δ6, 9	18:2 Δ9, 12 (LA)	18:3 Δ6, 9, 12 (GLA)	18:3 Δ9, 12, 15 (ALA)	18:4 Δ6, 9, 12, 15 (SDA)	20:3 Δ8, 11, 14 (HGLA)	20:4 Δ5, 8, 11, 14 (ARA)	20:4 Δ8, 11, 14, 17 (ETA)	20:5 Δ5, 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 = γ-linolenic acid,
ALA = α-linolenic acid,
SDA = stearidonic acid,
HGLA = dihomo-y-linolenic acid,
ARA = arachidonic acid,
ETA = eicosatetraenoic acid,
EPA = eicosapentaenoic acid

TABLE 4

Fatty acid analysis in seeds of *Brassica juncea*

	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 *Brassica juncea*

	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 = γ-linolenic acid,
ALA = α-linolenic acid,
SDA = stearidonic acid,
HGLA = dihomo-γ-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
[conversion rate] = [product]/[[substrate] + [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	**11.574**					**13.792**			
BioTaur	GLA + EPA	20.439	25.554	6.129	19.587	**3.521**		**6.620**			**10.149**			**1.127**
Vector	EPA	20.669	28.985	6.292	21.712						**16.225**			
BioTaur	EPA	20.472	26.913	6.570	23.131						**11.519**			**3.251**
Vector	ARA	23.169	23.332	6.587	12.735				**27.069**					
BioTaur	ARA	20.969	31.281	5.367	21.351				**9.648**			**1.632**		
Vector	SDA	18.519	12.626	6.642	6.344		**47.911**							
BioTaur	SDA	19.683	15.878	7.246	8.403		**13.569**			**25.946**			**0.876**	

TABLE 24

Fatty acid analysis of transgenic seeds which have been transformed with the construct pSUN-8G

I	16:0	18:0	18:1 Δ9	LA 18:2 Δ9, 12	GLA 18:3 Δ6, 9, 12	ALA 18:3 Δ9, 12, 15	SDA 18:4 Δ6, 9, 12, 15	HGLA 20:3 Δ8, 11, 14	ARA 20:4 Δ5, 8, 11, 14	EPA 20:5 Δ5, 8, 11, 14, 17	22:5 Δ7, 10, 13, 16, 19	DHA 22:6 Δ4, 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

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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

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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 gtt 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 gtt 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 gtt 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
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                405                 410                 415

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Ala Gly Lys Ala Leu
            420


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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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Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
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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                 240

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                 320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
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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
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Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
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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      240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65                  70                  75                  80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag      288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
                85                  90                  95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag      336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
            100                 105                 110

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg      384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
        115                 120                 125

agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat      432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
    130                 135                 140

gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg      480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145                 150                 155                 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc      528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
                165                 170                 175

acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg      576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
            180                 185                 190

cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc      624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
        195                 200                 205

aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct      672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
    210                 215                 220

ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt      720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
225                 230                 235                 240

ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag      768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
                245                 250                 255

cag ctc tag                                                         777
Gln Leu


<210> SEQ ID NO 4
<211> LENGTH: 258
<212> TYPE: PRT
<213> ORGANISM: Isochrysis galbana

<400> 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

atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta       48
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

ggt 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                                          1410
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 gtt gtt 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 gtt atg act cta ttc aga tgg caa cat gtt 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 gtt 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 gtt 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 gtt tct cat ctt gtt 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

gtt 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

gtt atg cca ctt gtt 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 gtt 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
```

<210> SEQ ID NO 8
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Ceratodon purpureus

<400> SEQUENCE: 8

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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


<210> SEQ ID NO 10
<211> LENGTH: 480
<212> TYPE: PRT
<213> ORGANISM: Physcomitrella patens

<400> 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 gcg 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 ggc 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


<210> SEQ ID NO 12
<211> LENGTH: 439
<212> TYPE: PRT
<213> ORGANISM: Thraustrochytrium

<400> 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 ctc      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 gtt 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 gtt 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 gtt gtt gag gaa gtt 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


<210> SEQ ID NO 14
<211> LENGTH: 446
<212> TYPE: PRT
<213> ORGANISM: Mortierella alpina

<400> SEQUENCE: 14

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                 320

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                 400

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


<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

<400> SEQUENCE: 15

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
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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
                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 gtt gtt 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 gtt atg act cta ttc aga tgg caa cat gtt 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 gtt 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 gtt 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 gtt tct cat ctt gtt 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

gtt 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

gtt atg cca ctt gtt 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 gtt 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
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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 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 aattacccttt         1398
Asn Leu Val Trp Glu Ala Leu His Thr His Gly
        440                 445

agttcatgta ataatttgag attatgtatc tcctatgttt gtgtcttgtc ttggttctac   1458

ttgttggagt cattgcaact tgtcttttat ggtttattag atgtttttta atatatttta   1518

gaggttttgc tttcatctcc attattgatg aataaggagt tgcatattgt caattgttgt   1578

gctcaatatc tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagctcat   1638

gtgtacttct atagactttg tttaaatggt tatgtcatgt tattt                   1683


<210> SEQ ID NO 18
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Borago officinalis
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<400> SEQUENCE: 18

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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 Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn
1               5                   10                  15

att gac gtt 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 gtt 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 gtt 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 gtt 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 gtt 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 gtt 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 gtt tcc att gtt 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 gtt 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
225                 230                 235                 240
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att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta      768
Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val
                245                 250                 255

ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac      816
Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn
            260                 265                 270

gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg      864
Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu
        275                 280                 285

cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat      912
His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp
    290                 295                 300

gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg      960
Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu
305                 310                 315                 320

gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac     1008
Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His
                325                 330                 335

cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt     1056
Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe
            340                 345                 350

tgg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag     1104
Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys
        355                 360                 365

ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt     1152
Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
    370                 375                 380

gtt gcg ttt tat ctg ctc ccc gga tgg aaa cca gtt gta tgg atg gtg     1200
Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
385                 390                 395                 400

gtc agc gag ctc atg tct ggt ttc ctg ctg gga tac gta ttt gta ctc     1248
Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
                405                 410                 415

agt cac aat gga atg gag gtg tac aat acg tca aag gac ttc gtg aat     1296
Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn
            420                 425                 430

gcc cag att gca tcg act cgc gac atc aaa gca ggg gtg ttt aat gat     1344
Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp
        435                 440                 445

tgg ttc acc gga ggt ctc aac aga cag att gag cat cat cta ttt cca     1392
Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro
    450                 455                 460

acg atg ccc agg cac aac ctt aat aaa att tct cct cac gtg gag act     1440
Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr
465                 470                 475                 480

ttg tgc aag aag cat gga ctg gtc tac gaa gac gtg agc atg gct tcg     1488
Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser
                485                 490                 495

ggc act tac cgg gtt ttg aaa aca ctt aag gac gtt gcc gat gct gct     1536
Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
            500                 505                 510

tca cac cag cag ctt gct gcg agt tga                                1563
Ser His Gln Gln Leu Ala Ala Ser
        515                 520
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<210> SEQ ID NO 20
<211> LENGTH: 520
<212> TYPE: PRT
<213> ORGANISM: Ceratodon purpureus

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<400> SEQUENCE: 20

```
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 gtt 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
385                 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
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<210> SEQ ID NO 22
<211> LENGTH: 477
<212> TYPE: PRT

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<213> ORGANISM: Phaeodactylum tricornutum

<400> 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      672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
    210                 215                 220

ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt      720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
225                 230                 235                 240

atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt      768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
                245                 250                 255

ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg      816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
            260                 265                 270

tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag      864
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
        275                 280                 285

gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act      912
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
    290                 295                 300

tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg      960
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
305                 310                 315                 320

agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc     1008
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
                325                 330                 335

ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt     1056
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
            340                 345                 350

ggt agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc     1104
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
        355                 360                 365

tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac     1152
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
    370                 375                 380

ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca     1200
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
385                 390                 395                 400

tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc     1248
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
                405                 410                 415

ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct     1296
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
            420                 425                 430

aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga     1344
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
        435                 440                 445

aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag     1392
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
    450                 455                 460

cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca     1440
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
465                 470                 475                 480

cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac     1488
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
                485                 490                 495

gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa     1536
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
            500                 505                 510

gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa             1578
Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
        515                 520                 525
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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                 480

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                  80

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
```

<210> SEQ ID NO 26
<211> LENGTH: 443
<212> TYPE: PRT
<213> ORGANISM: Caenorhabditis elegans

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<400> 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 Glu 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 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

gtagaccagc agcgccgagg acgcgtgccg cgttatcgcg aagcacgaaa taaagaagat    928

catttgattc aacgaggcta cttgcggcca cgagaaaaaa aaaaaaaaaa aaaaaaaaaa    988

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1048

c                                                                   1049


<210> SEQ ID NO 30
<211> LENGTH: 271
<212> TYPE: PRT
<213> ORGANISM: Thraustochytrium

<400> SEQUENCE: 30

Met Met Glu Pro Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala
1               5                   10                  15

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


<210> SEQ ID NO 31
<211> LENGTH: 837
<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 gcg 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
```

-continued

<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 48
Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
1 5 10 15

-continued

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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 ggc 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 ggc 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
```

<210> SEQ ID NO 34
<211> LENGTH: 317

-continued

<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

<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

<400> SEQUENCE: 35

atg gag tcg att gcg cca ttc ctc cca tca aag atg ccg caa gat ctg 48
Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu

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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

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

<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


<210> SEQ ID NO 38
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Caenorhabditis elegans
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<400> 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

<210> SEQ ID NO 39
<211> LENGTH: 1626
<212> TYPE: DNA
<213> ORGANISM: Euglena gracilis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1626)
<223> OTHER INFORMATION: Delta-4 desaturase

<400> 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 ccg ccg 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 gtt 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 gtt 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


<210> SEQ ID NO 40
<211> LENGTH: 541
<212> TYPE: PRT
<213> ORGANISM: Euglena gracilis

<400> 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 ggg 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 ggc 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

ggt 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 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


<210> SEQ ID NO 47
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-continued

<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 gcg 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 ggg 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 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
```

```
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

<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                  15

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 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 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

ggt 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 gtt tca caa aag aag gag tat cat cag aat ggc tct gtt 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
```

<210> SEQ ID NO 54
<211> LENGTH: 295
<212> TYPE: PRT
<213> ORGANISM: Oncorhynchus mykiss

<400> SEQUENCE: 54

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```
Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met
1               5                  10                  15

Gly Pro Arg Asp Glu Arg Val Gln Gly Trp Leu Leu Leu Asp Asn Tyr
            20                  25                  30

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

acggattaga agccgccgag cgggtgacag ccctccgaag gaagactctc ctccgtgcgt     60

cctcgtcctc accggtcgcg ttcctgaaac gcagatgtgc ctcgcgccgc actgctccga    120

acaataaaga ttctacaata ctagctttta tggttatgaa gaggaaaaat tggcagtaac    180

ctggccccac aaaccttcaa atgaacgaat caaattaaca accataggat gataatgcga    240

ttagtttttt agccttattt ctggggtaat taatcagcga agcgatgatt tttgatctat    300
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taacagatat ataaatgcaa aaactgcatt aaccacttta actaatactt tcaacatttt    360

cggtttgtat tacttcttat tcaaatgtaa taaaagtatc aacaaaaaat tgttaatata    420

cctctatact ttaacgtcaa ggagaaaaaa ccccggatcg gactactagc agctgtaata    480

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

tgg cac ggg gat tat aac ttc ttt tgc caa gac aca cac agt gca gga      821
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 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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Gly Val Thr Pro Thr Glu Thr Ile Thr His Arg Lys Val Arg Gly Asp
280                 285                 290                 295

tgaaggatcc actagtaacg gccgccagtg tgctggaatt ctgcagatat ccagcacagt   1457

ggcggccgct cgagtctaga gggcccttcg aaggtaagcc tatccctaac cctctcctcg   1517

gtctcgattc tacgcgtacc ggtcatcatc accatcacca ttgagtttaa acccgctgat   1577

cctagagggc cgcatcatgt aattagttat gtcacgctta cattcacgcc ctccccccac   1637

atccgctcta accgaaaagg aaggagttag acaacctgaa gtctaggtcc ctatttattt   1697

ttttatagtt atgttagtat taagaacgtt atttatattt caaatttttc ttttttttct   1757

gtacagacgc gtgtacgcat gtaacattat actgaaaacc ttgcttgaga aggttttggg   1817

acgctcgaag gctttaattt gcaagctgcg gccctgcatt aatgaatcgg ccaacgcgcg   1877

gggagaggcg gtttgcgtat tgggcgctct tccgcttcct cgctcactga ctcgctgcgc   1937

tcggtcgttc ggctgcggcg agcggtatca gctcactcaa aggcggtaat acggttatcc   1997

acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca aaagcccagg   2057

aaccgtaaaa aggccgcgtt gctggcgttt ttccataggc tccgcccccc tgacgagcat   2117

cacaaaaatc gacgctcaag tcagaggtgg cgaaacccga caggactata aagataccag   2177

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cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaaccc ggtaagacac   2417

gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag gtatgtaggc   2477

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tcatccatag ttgcctgact ccccgtcgtg tagataacta cgatacggga gcgcttacca   2957

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gaagattgta taagcaaata tttaaattgt aaacgttaat attttgttaa aattcgcgtt   6317

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taaatcaaaa gaatagaccg agatagggtt gagtgttgtt ccagtttcca acaagagtcc   6437

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cccactacgt gaaccatcac cctaatcaag ttttttgggg tcgaggtgcc gtaaagcagt   6557

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ggcgagaaag gaagggaaga aagcgaaagg agcgggggct agggcggtgg gaagtgtagg   6677

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gggatgatcc actagt                                                  6753


<210> SEQ ID NO 56
<211> LENGTH: 295
<212> TYPE: PRT
<213> ORGANISM: Oncorhynchus mykiss

<400> SEQUENCE: 56

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Gly Pro Arg Asp Glu Arg Val Gln Gly Trp Leu Leu Leu Asp Asn Tyr
            20                  25                  30

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
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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


<210> SEQ ID NO 57
<211> LENGTH: 6645
<212> TYPE: DNA
<213> ORGANISM: Oncorhynchus mykiss
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (513)..(1304)
<223> OTHER INFORMATION: Delta-5 elongase

<400> SEQUENCE: 57

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acaataaaga ttctacaata ctagctttta tggttatgaa gaggaaaaat tggcagtaac    180

ctggccccac aaaccttcaa atgaacgaat caaattaaca accataggat gataatgcga    240

ttagtttttt agccttattt ctggggtaat taatcagcga agcgatgatt tttgatctat    300

taacagatat ataaatgcaa aaactgcatt aaccacttta actaatactt tcaacatttt    360

cggtttgtat tacttcttat tcaaatgtaa taaaagtatc aacaaaaaat tgttaatata    420

cctctatact ttaacgtcaa ggagaaaaaa ccccggatcg gactactagc agctgtaata    480

cgactcacta tagggaatat taagcttaca ta atg gct tca aca tgg caa agc      533
                                    Met Ala Ser Thr Trp Gln Ser
                                    1               5

gtt cag tcc atg cgc cag tgg att tta gag aat gga gat aaa agg aca      581
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 ggt 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 gtt 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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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 tgcagatatc          1354
Thr

catcacactg gcggccgctc gagcatgcat ctagagggcc gcatcatgta attagttatg   1414

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tccaatgaag cacacaagtt tgtttgcttt tcgtgcatga tattaaatag cttggcagca 4354

acaggactag gatgagtagc agcacgttcc ttatatgtag ctttcgacat gatttatctt 4414

cgtttcctgc aggtttttgt tctgtgcagt tgggttaaga atactgggca atttcatgtt 4474

tcttcaacac tacatatgcg tatatatacc aatctaagtc tgtgctcctt ccttcgttct 4534

tccttctgtt cggagattac cgaatcaaaa aaatttcaaa gaaaccgaaa tcaaaaaaaa 4594

gaataaaaaa aaaatgatga attgaattga aaagctagct tatcgatgat aagctgtcaa 4654

agatgagaat taattccacg gactatagac tatactagat actccgtcta ctgtacgata 4714

cacttccgct caggtccttg tcctttaacg aggccttacc actcttttgt tactctattg 4774

atccagctca gcaaaggcag tgtgatctaa gattctatct tcgcgatgta gtaaaactag 4834

ctagaccgag aaagagacta gaaatgcaaa aggcacttct acaatggctg ccatcattat 4894

tatccgatgt gacgctgcag cttctcaatg atattcgaat acgctttgag gagatacagc 4954

ctaatatccg acaaactgtt ttacagattt acgatcgtac ttgttaccca tcattgaatt 5014

ttgaacatcc gaacctggga gttttccctg aaacagatag tatatttgaa cctgtataat 5074

aatatatagt ctagcgcttt acggaagaca atgtatgtat ttcggttcct ggagaaacta 5134

ttgcatctat tgcataggta atcttgcacg tcgcatcccc ggttcatttt ctgcgtttcc 5194

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atcttgcact tcaatagcat atctttgtta acgaagcatc tgtgcttcat tttgtagaac   5254

aaaaatgcaa cgcgagagcg ctaatttttc aaacaaagaa tctgagctgc atttttacag   5314

aacagaaatg caacgcgaaa gcgctatttt accaacgaag aatctgtgct tcatttttgt   5374

aaaacaaaaa tgcaacgcga cgagagcgct aatttttcaa acaaagaatc tgagctgcat   5434

ttttacagaa cagaaatgca acgcgagagc gctattttac caacaaagaa tctatacttc   5494

ttttttgttc tacaaaaatg catcccgaga gcgctatttt tctaacaaag catcttagat   5554

tacttttttt ctcctttgtg cgctctataa tgcagtctct tgataacttt ttgcactgta   5614

ggtccgttaa ggttagaaga aggctacttt ggtgtctatt ttctcttcca taaaaaaagc   5674

ctgactccac ttcccgcgtt 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 gcaagttcaa ggagcgaaag gtggatgggt aggttatata   6034

gggatatagc acagagatat atagcaaaga gatacttttg agcaatgttt gtggaagcgg   6094

tattcgcaat gggaagctcc accccggttg ataatcagaa aagccccaaa aacaggaaga   6154

ttgtataagc aaatatttaa attgtaaacg ttaatatttt gttaaaattc gcgttaaatt   6214

tttgttaaat cagctcattt tttaacgaat agcccgaaat cggcaaaatc ccttataaat   6274

caaaagaata gaccgagata gggttgagtg ttgttccagt ttccaacaag agtccactat   6334

taaagaacgt ggactccaac gtcaaagggc gaaaaagggt 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
```

<210> SEQ ID NO 58
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Oncorhynchus mykiss

<400> 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

cgg 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 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


<210> SEQ ID NO 60
<211> LENGTH: 358
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> 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 Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
    50                  55                  60

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 ggt 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 gtt 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 gtt 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 gtt 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 gtt act ggt gcc atg tag                                         933
Arg Val Thr Gly Ala Met
305                 310


<210> SEQ ID NO 62
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> 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 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
```

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```
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg      192
Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
    50                  55                  60

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 ggt 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 gtt 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 gtt 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 gtt 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 gtt act ggt gcc atg tag                                         933
Arg Val Thr Gly Ala Met
305                 310
```

<210> SEQ ID NO 64
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> 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


<210> SEQ ID NO 66
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Thraustochytrium aureum

<400> 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 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

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 68
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 68

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 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 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


<210> SEQ ID NO 70
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> 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 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 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 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
225                 230                 235                 240

aag ctg aac ttc gac ggc gtg tcg 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 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 gtt ttc gga ctt gcc gtg ttt tgg gtt 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 gtt 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
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 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                                          1362
Leu Lys Thr Leu Gly
    450


<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


<210> SEQ ID NO 74
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Primula vialii

<400> SEQUENCE: 74

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                  95

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 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


<210> SEQ ID NO 76
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 76

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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-continued

<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


<210> SEQ ID NO 80
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 80

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


<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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<400> 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 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 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
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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

<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

<400> SEQUENCE: 83

atg gac gtc gtc gag cag caa tgg cgc cgc ttc gtg gac gcc gtg gac 48
Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp

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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
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<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                  75                  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                 155                 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                 235                 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 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 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      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 ctg 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 cct 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

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 ggc 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

ttg 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
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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

<210> SEQ ID NO 87
<211> LENGTH: 1086

-continued

<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 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: Ostreococcus tauri
<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 cgg 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 ggc 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
```

<210> SEQ ID NO 90
<211> LENGTH: 456
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 90

```
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                  75                  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                 155                 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: Ostreococcus tauri
<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                  80

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                 160

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 cgg ctg cct cct cgg gtc tcg cgg      720
Tyr Ser Leu Pro Gly Val Pro Phe Arg Leu Pro Pro Arg Val Ser Arg
225                 230                 235                 240

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
385                 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 gtt 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 gtt 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


<210> SEQ ID NO 96
<211> LENGTH: 536
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri
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<400> SEQUENCE: 96

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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                 505                 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 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 ggt 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 gtt 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 ggt 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 ggt 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 ggt 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 ggt 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                                                    1455
Phe Pro Ala Met


<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 ggc 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      576
Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His
            180                 185                 190

gga gct gcc agt aag cgt ccc tgg gtg aat gac ttg ttg gga ttt gga      624
Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly
        195                 200                 205

acg gat ttg att gga tct aac aaa tgg aat tgg atg gca cag cat tgg      672
Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp
    210                 215                 220

act cat cac gct tac act aac cat agt gag aag gat ccc gat agc ttc      720
Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe
225                 230                 235                 240

agc tcg gaa cct atg ttt gca ttc aat gac tat ccc att gga cac ccg      768
Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro
                245                 250                 255

aag aga aag tgg tgg cat agg ttc cag gga ggg tac ttc ctc ttc atg      816
Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met
            260                 265                 270

ctt gga ctt tac tgg ctc tcg act gta ttc aat ccg caa ttc att gat      864
Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp
        275                 280                 285

ctt cgt caa cgt ggg gct cag tac gtc gga att caa atg gag aat gat      912
Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp
    290                 295                 300

ttc att gtc aag agg agg aag tac gcc gtt gca ttg agg atg atg tac      960
Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr
305                 310                 315                 320

att tac ttg aac att gtc agc ccc ttc atg aac aat ggt ttg agc tgg     1008
Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp
                325                 330                 335

tct acc ttt gga atc atc atg ttg atg gga atc agc gag agt ctc act     1056
Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr
            340                 345                 350

ctc agt gtg ctc ttc tcg ttg tct cac aac ttc atc aat tcg gat cgt     1104
Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg
        355                 360                 365

gat cct acg gct gac ttc aaa aag acc gga gaa caa gtg tgc tgg ttc     1152
Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe
    370                 375                 380

aag tcg cag gtg gag act tcg tct acc tat ggg ggt ttt att tcc gga     1200
Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly
385                 390                 395                 400

tgt ctt acg gga gga ctc aac ttt cag gtg gaa cat cat ctc ttt ccc     1248
Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro
                405                 410                 415

cgt atg agc agt gct tgg tat cct tac att gca cct acg gtt cgt gag     1296
Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu
            420                 425                 430

gtt tgc aag aag cac ggg gtg aac tac gct tat tat cct tgg att ggg     1344
Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly
        435                 440                 445

cag aat ttg gta tca aca ttc aaa tac atg cat cgc gct ggt agt gga     1392
Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly
    450                 455                 460

gcc aac tgg gag ctc aag ccg ttg tct gga agt gcc taa                 1431
Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala
465                 470                 475
```

<210> SEQ ID NO 100

-continued

<211> LENGTH: 476
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> SEQUENCE: 100

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
1               5                   10                  15

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 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 acc tac gat cat tgg tat caa agt ggt gta ttc      528
Cys Thr Thr Phe Thr 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      672
Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn
    210                 215                 220

tgg ttg gct cag cat tgg act cat cat gcg tat acc aat cac gct gat      720
Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp
225                 230                 235                 240

aaa gat cct gat agc ttt agt tcc gag ccg gtc ttc aac ttt aac gat      768
Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp
                245                 250                 255

tat ccc att ggt cac ccc aaa aga aag tgg tgg cat agg ttc caa ggg      816
Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly
            260                 265                 270

ctc tac ttc cta atc atg ctg agt ttc tat tgg gta tcg atg gta ttc      864
Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe
        275                 280                 285

aac cca caa gtt atc gac ctc cgt cat gct gga gct gcc tac gtt gga      912
Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly
    290                 295                 300

ttt cag atg gag aac gac ttt atc gtc aaa cgg aga aag tat gca atg      960
Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met
305                 310                 315                 320

gca ctt cgt gca atg tac ttc tat ttc aac atc tat tgt ccg att gtc     1008
Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val
                325                 330                 335

aac aat gga ttg act tgg tcg aca gtt gga atc atc ctc tta atg gga     1056
Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly
            340                 345                 350

gtt agc gaa agc ttc atg ctc tcc ggt cta ttc gta ctc tca cac aac     1104
Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn
        355                 360                 365

ttt gaa aat tcc gaa cgt gat cct acc tct gag tat cgc aag act ggt     1152
Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly
    370                 375                 380

gag caa gta tgt tgg ttc aag tct caa gtg gag act tct tct acc tac     1200
Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr
385                 390                 395                 400

gga ggt atc gtt gct ggg tgt ctc act ggt gga ctc aac ttt caa gtg     1248
Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val
                405                 410                 415

gag cat cat ttg ttc ccg agg atg agc agt gct tgg tat cct ttc atc     1296
Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile
            420                 425                 430

gcg ccg aag gtt aga gag att tgt aag aag cat gga gtt aga tac gct     1344
Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala
        435                 440                 445

tac tat ccg tac atc tgg cag aac ttg cat tct acc gtg agt tac atg     1392
Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met
    450                 455                 460

cat ggg acg gga acg gga gct aga tgg gag ctt cag ccg ttg tct gga     1440
His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly
465                 470                 475                 480

agg gcg tag                                                        1449
Arg Ala
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<210> SEQ ID NO 102
<211> LENGTH: 482
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

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<400> SEQUENCE: 102

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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      672
Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala
    210                 215                 220

ggg tgg acg ttg gat atg att ggt gcg agt gcg ttt acg tgg gag ctt      720
Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu
225                 230                 235                 240

cag cac atg ctg ggg cat cat cca tat acg aat gtg ttg gat ggg gtg      768
Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val
                245                 250                 255

gag gag gag agg aag gag agg ggg gag gat gtt gct ttg gaa gaa aag      816
Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys
            260                 265                 270

gat cag gat ttt gaa gtt gcc aca tcc gga cga tta tat cat att gat      864
Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp
        275                 280                 285

gcc aat gta cgt tat ggt tcg gta tgg aat gtc atg agg ttt tgg gct      912
Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala
    290                 295                 300

atg aag gtc att acg atg gga tat atg atg gga tta cca atc tac ttt      960
Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe
305                 310                 315                 320

cat gga gta ctg agg gga gtt gga ttg ttt gtt att ggg cat ttg gcg     1008
His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala
                325                 330                 335

tgt gga gag ttg ttg gcg acg atg ttt att gtg aat cac gtc att gag     1056
Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu
            340                 345                 350

ggt gtg agt tat gga acg aag gat ttg gtt ggt ggt gcg agt cat gta     1104
Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val
        355                 360                 365

gat gag aag aag att gtc aag cca acg act gta ttg gga gat aca cca     1152
Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro
    370                 375                 380

atg gta aag act cgc gag gag gca ttg aaa agc aac agc aat aac aac     1200
Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn
385                 390                 395                 400

aag aag aag gga gag aag aac tcg gta cca tcc gtt cca ttc aac gac     1248
Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp
                405                 410                 415

tgg gca gca gtc caa tgc cag acc tcc gtg aat tgg tct cca ggc tca     1296
Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser
            420                 425                 430

tgg ttc tgg aat cac ttt tct ggg gga ctc tct cat cag att gag cat     1344
Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His
        435                 440                 445

cac ttg ttc ccc agc att tgt cat aca aac tac tgt cat atc cag gat     1392
His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp
    450                 455                 460

gtt gtg gag agt acg tgt gct gag tac gga gtt ccg tat cag agt gag     1440
Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu
465                 470                 475                 480

agt aat ttg ttt gtt gct tat gga aag atg att agt cat ttg aag ttt     1488
Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe
                485                 490                 495

ttg ggt aaa gcc aag tgt gag tag                                    1512
Leu Gly Lys Ala Lys Cys Glu
            500
```

<210> SEQ ID NO 104
<211> LENGTH: 503

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<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> SEQUENCE: 104

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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Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His
            180                 185                 190

aat cat att gaa aag gac tac tct cat aag tgg tac agt cgc gac gag      624
Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu
        195                 200                 205

ttt gat gat atc cca caa ctc tat aag aca ttt ggc tac aac cca aga      672
Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg
    210                 215                 220

atg atg caa ctt cca ttc ctc tac ttc atg tat ctt gca ttg gga att      720
Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile
225                 230                 235                 240

cca gat ggt ggg cat gtt gtg ttc tac gga aga atg tgg gaa gga gtg      768
Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val
                245                 250                 255

tca ttg cag aag aag ttt gat gct gct att tct gtg gcc gta tca tgt      816
Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys
            260                 265                 270

gca act gct gga tcg ctt tgg atg aat atg ggt aca gca gac ttc acg      864
Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr
        275                 280                 285

gtg gta tgc atg gtt cct tgg cta gtt cta tcg tgg tgg ctc ttc atg      912
Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met
    290                 295                 300

gta aca tac ctt cag cat cat tca gaa gac gga aag cta tac act gat      960
Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp
305                 310                 315                 320

gaa acg ttt aca ttt gaa aag gga gcc ttc gag acc gtg gat cgt tcg     1008
Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser
                325                 330                 335

tac ggc aag ttg atc aac cga atg tcg cat cac atg atg gac ggt cac     1056
Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His
            340                 345                 350

gtg gtg cac cac ttg ttc ttt gaa cgt gta cct cac tac aga tta gag     1104
Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu
        355                 360                 365

gca gct acc gaa gct ctt gtg aaa gga atg gat gaa acg gga cag aaa     1152
Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys
    370                 375                 380

cat ttg tac aaa tac att gat act cct gat ttc aat gcc gag att gtc     1200
His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val
385                 390                 395                 400

aac gga ttt cgc gac aat tgg ttc ctt gtt gaa gag gag aac atc aaa     1248
Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys
                405                 410                 415

agg gag tag                                                        1257
Arg Glu


<210> SEQ ID NO 106
<211> LENGTH: 418
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> SEQUENCE: 106

Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser
1               5                   10                  15

Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys
            20                  25                  30

Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu
        35                  40                  45
```

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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)
```

-continued

<223> OTHER INFORMATION: Delta-12 desaturase

<400> 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 gtt 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 gtt 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

gtt gtt 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 gtt 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 gtt 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


<210> SEQ ID NO 108
<211> LENGTH: 361
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 108

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
```

<210> SEQ ID NO 110
<211> LENGTH: 434
<212> TYPE: PRT
<213> ORGANISM: Thalassiosira pseudonana

<400> 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
```

-continued

```
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                  95

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

Ser Asp


<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)
```

-continued

<223> OTHER INFORMATION: Delta-6 elongase

<400> SEQUENCE: 111

```
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 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
```

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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 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
```

<210> SEQ ID NO 114
<211> LENGTH: 300
<212> TYPE: PRT

-continued

<213> ORGANISM: Ostreococcus tauri

<400> 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

<210> SEQ ID NO 115
<211> LENGTH: 13
<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 Ser, Cys, Leu or Gly, preferably is Cys
or Leu
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is Thr, Phe, Ile, Ser, Val, Trp or Gly,
preferably is Phe or Trp
<220> FEATURE:

-continued

<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

<400> 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

<400> 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

<400> 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

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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
```

<210> SEQ ID NO 118
<211> LENGTH: 302
<212> TYPE: PRT
<213> ORGANISM: Xenopus laevis

<400> 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


<210> SEQ ID NO 119
<211> LENGTH: 870
<212> TYPE: DNA
<213> ORGANISM: Ciona intestinalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(870)
<223> OTHER INFORMATION: Delta-5 elongase

<400> 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 gtt 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 gtt 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 gtt 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 gtt 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 gtt 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
145                 150                 155                 160

aag tgg gtg cct ggt ggg caa tca ttt gtt 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 gtt cat gtt 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 gtt caa ttt gtt 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 gtt aaa tgt ccc tcg cct gtt 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
225                 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


<210> SEQ ID NO 120
<211> LENGTH: 289
<212> TYPE: PRT
<213> ORGANISM: Ciona intestinalis

<400> 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

<400> 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

<400> 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

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

-continued

<210> SEQ ID NO 130
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 130

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc 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 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 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 cgg 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 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 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 ctc 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


<210> SEQ ID NO 132
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Euglena gracilis

<400> 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


<210> SEQ ID NO 133
<211> LENGTH: 789
<212> TYPE: DNA
<213> ORGANISM: Euglena gracilis
<220> 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 ccg 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 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 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 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 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

-continued

<400> SEQUENCE: 134

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 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

<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

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 gtt 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 gtt 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 gtt 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 gtt 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 gtt 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 gtt 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

gtt 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


<210> SEQ ID NO 136
<211> LENGTH: 298
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> 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 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


<210> SEQ ID NO 138
<211> LENGTH: 278
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> 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)
```

-continued

<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

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc 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

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc 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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gtcgacccgc 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

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 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

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc 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 agatggtctt 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

cggcttaggc cgacttggcc 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 tgggcgcc 28

<210> SEQ ID NO 174
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 174

gtcgacccgc ggactagtgg 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

gcggccgcat 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

gcggccgctt atgtcttctt gctcttcctg 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

gcggccgcat 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 agtccccccct 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 tcttcctgtt 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 gtcatcacac gcaggtcgtt gctcactatc 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

-continued

```
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 Pro Lys Lys Lys Lys
                265                 270                 275

aca gct taa gcgaaatttg ggtctacgtt aaaacaatta cgttacaaaa              979
Thr Ala

aaaaaaaaaa aaaa                                                     993


<210> SEQ ID NO 184
<211> LENGTH: 278
<212> TYPE: PRT
<213> ORGANISM: Phaeodactylum tricornutum

<400> SEQUENCE: 184
```

-continued

```
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 ggctctttta cgtttccaaa atttgggatt tttgggacac catctttatt 60

gttctcggga agaagtggcg tcaactttcc ttcctgcacg tctaccatca caccaccatc 120

tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt cctcaccatc 180

gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg catgcacacc 240

aaggtcccag agaccggcaa atccttgccc atttggtgga aatctagttt gacaagcatg 300

cagctggtgc agttcatcac gatgatgacg caggctatca tgatcttgta caagggctgt 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

gcggccgcac 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

gcggccgcac 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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<400> SEQUENCE: 191

gaagacagct taataggcgg ccgc 24

<210> SEQ ID NO 192
<211> LENGTH: 859
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR product

<400> SEQUENCE: 192

gcggccgcac ataatgatgg taccttcaag ttatgacgag tatatcgtca tggtcaacga 60

ccttggcgac tctattctga gctgggccga ccctgatcac tatcgtggac ataccgaggg 120

atgggagttc actgactttt ctgctgcttt tagcattgcc gtcgcgtacc tcctgtttgt 180

ctttgttgga tctctcatta tgagtatggg agtccccgca attgaccctt atccgctcaa 240

gtttgtctac aatgtttcac agattatgct ttgtgcttac atgaccattg aagccagtct 300

tctagcttat cgtaacggct acacattctg gccttgcaac gattgggact ttgaaaagcc 360

gcctatcgct aagctcctct ggctctttta cgtttccaaa atttgggatt tttgggacac 420

catctttatt gttctcggga agaagtggcg tcaactttcc ttcctgcacg tctaccatca 480

caccaccatc tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt 540

cctcaccatc gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg 600

catgcacacc aaggtcccag agaccggcaa atccttgccc atttggtgga aatctagttt 660

gacaagcatg cagctggtgc agttcatcac gatgatgacg caggctatca tgatcttgta 720

caagggctgt gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc 780

gctctttatt ttgttcgccc agttctttgt cagctcatac ctcaagccga agaagaagaa 840

gacagcttaa tagactagt 859

<210> SEQ ID NO 193
<211> LENGTH: 1380
<212> TYPE: DNA
<213> ORGANISM: Phytium irregulare
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1380)
<223> OTHER INFORMATION: Delta-6 desaturase

<400> 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 15

atc 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 30

aag 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 45

atg 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 60

cac 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 80

gtg 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


<210> SEQ ID NO 194
<211> LENGTH: 459
<212> TYPE: PRT
<213> ORGANISM: Phytium irregulare

<400> SEQUENCE: 194

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                 240

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

ggt 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 cgg 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


<210> SEQ ID NO 196
<211> LENGTH: 383
<212> TYPE: PRT
<213> ORGANISM: Calendula officinalis

<400> SEQUENCE: 196

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 gtt gtg gtg ctc gga      288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
                85                  90                  95

atg ttc gct aga gag atc tct gga ttg gga caa cct gtt 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
145                 150                 155                 160

cat cat gct ttg ttg att tgg gct tgg tgg ctt gtt 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 gtt ttc gtg ctc aga caa aag cac      720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225                 230                 235                 240

tgc cct gtt 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 gtt 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


<210> SEQ ID NO 198
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 198

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
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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 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

tgg gat 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


<210> SEQ ID NO 200
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> 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

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 gtt 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                 260                 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 gtt 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                 425

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


<210> SEQ ID NO 202
<211> LENGTH: 456
<212> TYPE: PRT
<213> ORGANISM: Ostreococcus tauri

<400> SEQUENCE: 202

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 atgccggcag 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 ggcctgcttt 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

cccggggtta acgctagcgg gcccgatatc ggatcccatt ttttggtggt 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
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 211

aggcctcaac ggttccggcg gtatagag 28

<210> SEQ ID NO 212
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 212

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aggccttcta gactgcaggc ggccgcccgc atttttttggt ggtgattggt 50

<210> SEQ ID NO 213
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 213

ggcctcctgc tttaatgaga tatgcga 27

<210> SEQ ID NO 214
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 214

aagcttggcg cgccgagctc gtcgacggac aatcagtaaa ttgaacggag a 51

<210> SEQ ID NO 215
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 215

agatctatgg tggacctcaa gcctggagtg 30

<210> SEQ ID NO 216
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 216

ccatggcccg ggttacatcg ctgggaactc ggtgat 36

<210> SEQ ID NO 217
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 217

gggatccatg ggcaagggca gcgagggccg 30

<210> SEQ ID NO 218
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 218

ggcgccgaca ccaagaagca ggactgagat atc 33

<210> SEQ ID NO 219
<211> LENGTH: 36
<212> TYPE: DNA

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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 219

gcggccgcat ggaggtcgtg gagagattct acggtg 36

<210> SEQ ID NO 220
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 220

gcaaaaggga gctaaaactg agtgatctag a 31

<210> SEQ ID NO 221
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 221

gtcgatcaac ggttccggcg gtatagagtt g 31

<210> SEQ ID NO 222
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 222

gtcgatcgga caatcagtaa attgaacgga ga 32

<210> SEQ ID NO 223
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 223

agatctatgg gtgcaggcgg tcgaatgc 28

<210> SEQ ID NO 224
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 224

ccatggttaa atcttattac gatacc 26

<210> SEQ ID NO 225
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 225

agatctatgg acgtcgtcga gcagca 26

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<210> SEQ ID NO 226
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 226

ccatggcccg ggagaagcag aagaccatct aa 32

<210> SEQ ID NO 227
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Cyt. B5 domain

<400> SEQUENCE: 227

His Pro Gly Gly
1

<210> SEQ ID NO 228
<211> LENGTH: 5
<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
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: His box2

<400> SEQUENCE: 231

Trp Arg Tyr His His Gln Val Ser His His
1 5 10

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<210> SEQ ID NO 232
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<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
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: His box2

<400> SEQUENCE: 233

Trp Asn Ser Met His Asn Lys His His
1 5

<210> SEQ ID NO 234
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: His box2

<400> SEQUENCE: 234

Trp Gln Arg Ser His Ala Val His His
1 5

<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
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<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

<400> SEQUENCE: 241

His Asp Ala Asn His
1 5

<210> SEQ ID NO 242
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial
<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
<220> FEATURE:
<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
<211> LENGTH: 9
<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
<220> FEATURE:
<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

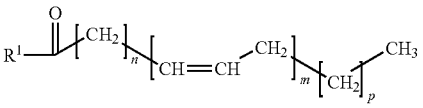
<210> SEQ ID NO 255
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Corresponding amino acids to primer Phaelo reverse1

<400> SEQUENCE: 255

Phe Ala Gln Phe Phe Val Gln Ser
1 5

We claim:

1. A process for the production of compounds of the general formula I



(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:

a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with Δ6-desaturase activity,

b) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with Δ6-elongase activity,

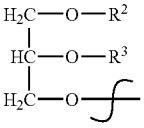
c) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with Δ5-desaturase activity,

d) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with Δ5-elongase activity, wherein said Δ5-elongase activity elongates only unsaturated C^{20}-fatty acids, and

e) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with Δ4-desaturase activity, and

wherein the variables and substituents in formula I have the following meanings:

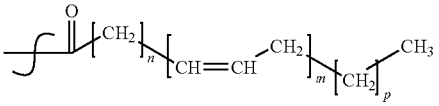
R^1=hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the general formula II



(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 general formula Ia:



(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 Δ5-elongase activity comprises:

i) the nucleic acid sequence of SEQ ID NO: 67, 83, or 113;

ii) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 68, 84, or 114;

iii) a nucleic acid sequence having at least 95% identity to the nucleic acid sequence of SEQ ID NO: 67, 83, or 113; or

iv) 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:

(a) m=4, n=3, p=3 and the compound is arachidonic acid,

(b) m=5, n=3, p=0 and the compound is eicosapentaenoic acid,

(c) m=5, n=5, p=0 and the compound is docosapentaenoic acid, or

(d) 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 Δ6-desaturase, Δ6-elongase, Δ5-desaturase, or Δ4-desaturase activity are selected from the group consisting of:

a) 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,

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: 12, SEQ ID NO: 28, SEQ ID NO: 42, or SEQ ID NO: 194, and

c) 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 Δ6-desaturase, Δ6-elongase, Δ5-desaturase or Δ4-desaturase activity.

7. The process according to claim **1**, wherein a nucleic acid sequence which encodes polypeptides with ω3-desaturase activity, selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, 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: 88 or SEQ ID NO: 106, or

c) 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 ω3-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 Δ12-desaturase activity, selected from the group consisting of:

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 Δ12-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, allenoxide 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^2 or R^3 independently of one another are saturated or unsaturated C_{18}-C_{22}-alkylcarbonyl.

11. The process according to claim **1**, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18}-, C_{20}- or C_{22}-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 Δ5-elongase activity elongates only unsaturated C_{20}-fatty acids with one double bond in the Δ5-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.

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) a nucleic acid encoding a polypeptide having Δ6-desaturase activity;

b) a nucleic acid encoding a polypeptide having Δ6-elongase activity;

c) a nucleic acid encoding a polypeptide having Δ5-desaturase activity;

d) a nucleic acid encoding a polypeptide having Δ5-elongase activity; and

e) a nucleic acid encoding a polypeptide having Δ4-desaturase activity;

wherein said nucleic acid encoding a polypeptide having Δ5-elongase activity comprises:

i) the nucleotide sequence of SEQ ID NO: 67, 83, or 113;

ii) 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 Δ5-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 Δ5-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:

a) obtaining EPA and/or DHA produced by the process of claim **18**; and

b) 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:

a) obtaining an oil-, lipid- and fatty acid-composition produced by the process of claim **22**; and

b) 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:

a) producing EPA and/or DHA in seeds of a transgenic plant according to the process of claim **18**; and

b) 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:

a) obtaining an oil-, lipid- and fatty acid-composition produced by the process of claim **24**; and

b) processing said oil-, lipid- and fatty acid-composition to produce feedstuffs, foodstuffs, cosmetics or pharmaceuticals.

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