

**Report Title**

**Updated Bioinformatics Evaluation of  $\Delta 6$  and  $\Delta 15$  Desaturases Utilizing the  
AD\_2009, TOX\_2009 and PRT\_2009 Databases**

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## 1.0 Summary

Monsanto has developed soybean, MON 87769, which produces stearidonic acid (SDA), an omega-3 fatty acid. Production of SDA in soybean seed was achieved through the introduction of genes encoding *Neurospora crassa*  $\Delta 15$  desaturase (Nc $\Delta 15$ D) and *Primula juliae*  $\Delta 6$  desaturase (Pj $\Delta 6$ D) via *Agrobacterium*-mediated transformation.

The bioinformatic evaluation of the Pj $\Delta 6$ D and Nc $\Delta 15$ D contained in MON 87769 was previously conducted by Silvanovich and McClain (2008). In the 2008 analysis it was concluded that the bioinformatic search data indicated the lack of both structurally and immunologically relevant similarities between the Pj $\Delta 6$ D and Nc $\Delta 15$ D protein sequences and known allergens, toxins, or other biologically active proteins that may have an adverse effect on the health of animals or humans.

The results of these most recent bioinformatics evaluations using the AD\_2009, TOX\_2009 and PRT\_2009 databases contained herein parallel those of Silvanovich and McClain (2008). When combined, these new data confirm the previously reported conclusion (Silvanovich and McClain, 2008) that no meaningful sequence or inferred structural similarity exists between Pj $\Delta 6$ D and Nc $\Delta 15$ D and allergenic or toxic proteins or proteins of concern to human or animal health.

## 2.0 Sequence Database Preparation

The allergen, gliadin, and glutenin sequence database (AD\_2009) was obtained from the Food Allergy Research and Resource Program Database (FARRP, 2009)<sup>1</sup> and was used as provided. The AD\_2009 database contains 1,386 sequences. A complete description of the AD\_2009 database can be found in Silvanovich (2009).

GenBank protein database, release 169.0 (December 16, 2008), was downloaded from NCBI (National Center for Biotechnology Information) and formatted for use. It is referred to herein as the PRT\_2009 database and contains 14,717,352 sequences. A complete description of the PRT\_2009 database can be found in Silvanovich (2009).

The toxin database is a subset of sequences derived from the PRT\_2009 database that was selected using a keyword search and filtered to remove likely non-toxin proteins. It is referred to herein as the TOX\_2009 database and contains 7,651 sequences. A complete description of the TOX\_2009 database can be found in Silvanovich (2009).

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<sup>1</sup> located at <http://www.allergenonline.com>

### 3.0 Sequence Database Searches

The PjΔ6D and NcΔ15D query sequences used in this analysis were the same as previously described in Silvanovich and McClain (2008). FASTA analyses using the AD\_2009, TOX\_2009, and PRT\_2009 databases were performed on a desktop computer loaded with a SUSE LINUX version 10.1 operating system. The structural similarity between the query peptides and sequences in the AD\_2009, TOX\_2009, and PRT\_2009 databases was assessed using the FASTA algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). FASTA comparisons are initiated by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Specific FASTA comparison parameters used in this study included a wordsize (k-tuple) of two, a gap creation penalty of 10, a gap extension penalty of two, and an expectation threshold (*E*-score) of one. FASTA comparisons were performed using the BLOSUM50 scoring matrix (Henikoff and Henikoff, 1992). The BLOSUM matrix series (Henikoff and Henikoff, 1992) was derived from a set of aligned, ungapped regions from protein families, called the BLOCKS database. Sequences from each block were clustered based on the percent of identical residues in the alignments (Henikoff and Henikoff, 1996). The BLOSUM50 matrix will identify blocks of conserved residues that are at least 50% identical. BLOSUM50 works well for identifying sequence similarities that include gaps, and thus recognizes distant evolutionary relationships (Pearson, 2000). In instances where greater than 25 alignments displaying an *E*-score less than one were recovered, alignment data is only shown for the top 25 alignments.

In addition to the FASTA comparisons of each query sequence to allergens (to assess overall structural similarity), an eight amino acid sliding window search was performed. An algorithm was developed to identify whether or not a linearly contiguous match of eight amino acids existed between the query sequence and sequences within the allergen database (AD\_2009). This program compares the query sequence to each protein sequence in the allergen database using a sliding-window of eight amino acids; that is, with a seven amino acid overlap relative to the preceding window.

### 4.0 Significance of the Alignment

An *E*-score of  $1 \times 10^{-5}$  was set as an initial high cut-off value for alignment significance. Although all alignments were inspected visually, any aligned sequence that yielded an *E*-score less than or equal to  $1 \times 10^{-5}$  was analyzed further to determine if such an alignment represented significant sequence homology.

### 5.0 Results and Discussion

Bioinformatics analysis was performed on PjΔ6D and NcΔ15D protein sequences (Figures 1 and 2) to assess the potential for structural similarity with known allergens, toxins, or other biologically active proteins. Summaries of the top alignments from the analyses are shown

in Tables 1-6. The supporting dataset output files for all of the analyses are presented in Appendices 1 and 2. The results of these assessments parallel those described in Silvanovich and McClain (2008).

### 5.1 *Assessment of Potential Allergenicity for the PjΔ6D protein sequence*

Potential structural identity and similarity shared between the PjΔ6D protein (Figure 1) and proteins in the allergen database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Appendix 1). None of these aligned proteins yielded an *E*-score of less than  $1 \times 10^{-5}$  nor did any alignments meet the Codex Alimentarius (2003) threshold for potential allergenicity.

No immunologically relevant sequences of eight contiguous amino acid identities were detected when the PjΔ6D protein sequence was compared to the AD\_2009 sequence using a sliding window search (Appendix 1).

### 5.2 *Assessment of Potential Toxicity for the PjΔ6D protein sequence:*

Potential structural identity and similarity shared between the PjΔ6D protein and proteins in the TOX\_2009 database was evaluated using the FASTA sequence alignment program. No alignments displaying an *E*-score of 1 or less were observed (Table 2 and Appendix 1).

### 5.3 *Assessment of Potential Adverse Biological Activity for the PjΔ6D protein sequence:*

Potential structural similarities shared between the PjΔ6D protein and proteins in the PRT\_2009 database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Table 3 and Appendix 1).

The FASTA algorithm identified and aligned a total of 2566 proteins in the PRT\_2009 database that yielded an alignment *E*-score of 1 or less and of those, 779 displayed an *E*-score of  $1 \times 10^{-5}$  or less. Visual inspection of these alignments revealed that many alignments were with proteins described as being fatty acid desaturases. The top alignment observed for the PjΔ6D sequence was to an unnamed protein product (GI-151416086) from *Primula luteola* (Table 2). The alignment demonstrated 89.438% identity over the full length of both the query and aligned proteins with an *E*-score of  $6.2 \times 10^{-188}$ . The next six alignments were identical to one another and one of these, with GI -30350277, was identified as being a delta-6 desaturase. Based upon the top seven alignments, it is concluded that the PjΔ6D is a Δ6 desaturase and that there is no indication of the potential for harmful biological activity.

#### 5.4 *Assessment of Potential Allergenicity for the NcΔ15D protein sequence:*

Potential structural identity and similarity shared between the NcΔ15D protein (Figure 2) and proteins in the allergen database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Appendix 2). None of these aligned proteins yielded an *E*-score of less than or equal to  $1 \times 10^{-5}$  nor did any alignments meet the Codex Alimentarius (2003) threshold for potential allergenicity.

As was described in Silvanovich and McClain (2008), a single potential immunologically relevant sequence of eight contiguous amino acid identities was detected when the NcΔ15D protein sequence (Figure 2) was compared to the AD\_2009 sequence database (Appendix 2) using a sliding window search. The alignment consisted of eight consecutive serine residues (SSSSSSSS) in the NcΔ15D query sequence with a region of nine consecutive serine residues in *Triticum aestivum* serine carboxypeptidase. Polyserine tracts such as that contained in the NcΔ15D are a common motif that are found in numerous proteins. Proteins containing stretches of eight or more serine residue represent functionally diverse classes, including enzymes, signaling molecules, structural proteins and transport molecules (Faux et al., 2005).

#### 5.5 *Assessment of Potential Toxicity for the NcΔ15D protein sequence:*

Potential structural identity and similarity shared between the NcΔ15D protein and proteins in the TOX\_2009 database was evaluated using the FASTA sequence alignment program. No alignments displaying an *E*-score of 1 or less were observed (Table 5 and Appendix 2).

#### 5.6 *Assessment of Potential Adverse Biological Activity for the NcΔ15D protein sequence:*

Potential structural similarities shared between the NcΔ15D protein and proteins in the PRT\_2009 database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Table 6 and Appendix 2).

The FASTA algorithm identified and aligned a total of 1,786 proteins in the PRT\_2009 database that yielded an alignment *E*-score of  $\leq 1$  and of those 1,303 displayed an *E*-score less than  $1 \times 10^{-5}$ . Visual inspection of these alignments revealed that most alignments were with proteins described as being a fatty acid desaturase. The top alignment observed for the NcΔ15D sequence was to a hypothetical protein CHGG\_0 (GI-88181398) from *Chaetomium globosum* (Table

6). Annotation associated with GI-88181398 describes the protein sequence as being Delta12 Fatty Acid Desaturase-like. The alignment demonstrated 67.519% identity over the 391 amino acids with an *E*-score of  $1.2 \times 10^{-120}$ . Based upon the top alignment, it is concluded that the NcΔ15D is a Δ15 desaturase and that there is no indication of the potential for harmful biological activity.

## 6.0 Conclusions

A bioinformatics analysis of PjΔ6D and NcΔ15D protein sequences was conducted to determine if either protein shared significant structural similarities with known allergens, toxins, or biologically active protein sequences contained in the AD\_2009, TOX\_2009 and PRT\_2009 databases, respectively. The bioinformatics results indicate that no biologically relevant sequence similarities were observed between the PjΔ6D and NcΔ15D protein sequences and any known allergens, biologically active proteins, or human and animal toxins. These results and conclusions of this current analysis parallel those described in Silvanovich and McClain (2008).



## 7.0 References

- Codex Alimentarius (2003). Guideline for the conduct of food safety assessment of foods derived from recombinant-DNA plants. CAC/GL 45-2003.
- FARRP, (Food Allergy Research and Resource Program Database) (2009). [www.allergenonline.com](http://www.allergenonline.com). University of Nebraska.
- Faux N.G., Bottomley S.P., Lesk A.M., Irving J.A., Morrison J.R., de la Banda M.G., and Whisstock J.C. (2005). Functional insights from the distribution and role of homopeptide repeat-containing proteins. *Genome Res* 15:537-551.
- Henikoff, S., and Henikoff, J.G. (1992). Amino acid substitution matrices from protein blocks. *Proc Natl Acad Sci USA* 89:10915-10919.
- Henikoff, J.G., and Henikoff, S. (1996). Blocks database and its applications. *Methods Enzymol* 266:88-105.
- Lipman D.J. and Pearson W.R. (1985). Rapid and sensitive protein similarity searches. *Science* Mar 227:1435-1441.
- Pearson, W.R., and Lipman, D.J. (1988). Improved tools for biological sequence comparison. *Proc Natl Acad Sci USA* 85:2444-2448.
- Pearson, W.R. (2000). Flexible sequence similarity searching with the FASTA3 program package. *Methods Mol Biol* 132:185-219.
- Silvanovich, A. (2009). The assembly of AD\_2009, TOX\_2009 and PRT\_2009. Monsanto Technical Report MSL0021840, St. Louis, MO.
- Silvanovich, A. and McClain, J. S. (2008). Bioinformatics Evaluation of Delta 6 and Delta 15 desaturases Utilizing the AD8, TOXIN6 and PROTEIN Databases. Monsanto Technical Report MSL0021252, St. Louis, MO.

Figure 1 Amino Acid Sequence of *Primula juliae* PjΔ6D Protein

```
>del_6
MTKTIYITSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTDAFL
AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMG MFRARGHTAYATFVIM
ILMLVSSVTGVLCSNPVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRFQIL
SSNCLQGIGSIGWWKWNHNAHHIACNSLEYD PDLQYIPLLVS PKFFNSLTSRFYDKKLN
FDGVS RFLVQYQHWSFY PVMC VARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFP
LLLSCLPNWGERIMFLLASYSVTGIQH VQFSLNHFSSDVYVGPPVGNDWFKKQTAGTLN
ISCPAWMDWFHGG LQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
LTLET LRNTAIEARDLSNPIPKNMVWEAVKNVG
```

Figure 2 Amino Acid Sequence of the *Neurospora crassa* NcΔ15D Protein

&gt;del\_15

MAVTTRSHKAAAATEPEVVSTGVDAVSAAAPSSSSSSSSSQKSAEPIEYPDIKTIRDAIP  
DHCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTG  
IWILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHHRFTGHMEKDMAFV  
PATEADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSK  
QWETGKGGMGWL RVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYILYQAAQVVGWQMVG  
LLYFQQYFWVHHWLVAITYLHHTHEEVHHFDADSWTFVKGALATVDRDFGFIGKHLFHN  
IIDHHVVHHLFPRI PFYYAEEATNSIRPMLGPLYHRDDRSFMGQLWYNFTHCKWVVPDP  
QVPGALIWAHTVQSTQ

**Table 1** Top alignment observed for the PjΔ6D protein sequence from a FASTA search against the AD\_2009 allergen database.

| Database | GI #     | Description   | E-score | % Identity | aa Overlap |
|----------|----------|---|---------|------------|------------|
| AD_2009  | 82492267 | major pollen<br>allergen Phl p 4<br>precursor<br>[Phleum<br>pratense] | 0.09    | 24.038     | 208        |

**Table 2** Top alignment observed for the PjΔ6D protein sequence from a FASTA search against the TOX\_2009 database.

| Database | Accession # | Description | E-score | % Identity | aa Overlap |
|----------|-------------|-------------|---------|------------|------------|
| TOX_2009 | -           | -           | -       | -          | -          |

**Table 3** Top alignment observed for the PjΔ6D desaturase protein sequence from a FASTA search against the PRT\_2009 database.

| Database | GI #      | Description                | E-score  | % Identity | aa Overlap |
|----------|-----------|----------------------------|----------|------------|------------|
| PRT_2009 | 151416086 | unnamed protein<br>product | 6.2e-188 | 89.438     | 445        |

**Table 4** Top alignment observed for the NcΔ15D protein sequence from a FASTA search against the AD\_2009 allergen database.

| Database | GI #     | Description                      | E-score | % Identity | aa Overlap |
|----------|----------|----------------------------------|---------|------------|------------|
| AD_2009  | 30794292 | lactotransferrin<br>[Bos taurus] | 0.25    | 25.225     | 111        |

**Table 5** Top alignment observed for the NcΔ15D protein sequence from a FASTA search against the TOX\_2009 database.

| Database | Accession # | Description | E-score | % Identity | aa Overlap |
|----------|-------------|-------------|---------|------------|------------|
| TOX_2009 | -           | -           | -       | -          | -          |

**Table 6** Top alignment observed for the NcΔ15ΔDprotein sequence from a FASTA search against the PRT\_2009 database.

| Database | GI #     | Description                    | E-score  | % Identity | aa Overlap |
|----------|----------|--------------------------------|----------|------------|------------|
| PRT_2009 | 88181398 | hypothetical<br>protein CHGG_0 | 1.2e-120 | 67.519     | 391        |

## Appendix 1. Bioinformatic analysis of PjΔ6D (polypeptide del\_6)

```
>del_6
MTKTIYITSSSELEKHNKPGDLWISIHGQYVDVSSWAALHPGGIAPLLALAGHDVTD AFLAYHPPSTSRLLPPFSTNLL
LEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYATFVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCQGWIG
HDSGHYRIMTDRKWNRFQILSSNCLQGIGISIGWWKWNHNAHHIACNSLEYDPDLQYIPLLVSPPKFFNSLTSTRFYDKK
LNFDGVSRLVQYQHSFYPMVCVARLNMLAQSFILFSRREVANRVQEILGLAVFWLWFPLLLSCLPNWGERIMFLL
ASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTLNISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISP
FVRDLCKKHNLTYNIASFTKANVLTLETLRNTAIEARDLSNPDKNMVWEAVKNVG
```

Sliding 8 amino acid window search  
Database searched = AD\_2009  
Query = del\_6

Start time: Tue Oct 20 14:14:08 CDT 2009 Finish time: Tue Oct 20 14:14:08 CDT 2009

No 8 amino acid matches exist between del\_6 and the AD\_2009 database

```
# fasta34 del_6.pep /home/andre/db/AD_2009 -Q -E 1 -O del_6.pep_ad.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
del_6, 446 aa
vs /home/andre/db/AD_2009 library
```

|      | opt | E()         |                                      |
|------|-----|-------------|--------------------------------------|
| < 20 | 3   | 0:==        |                                      |
| 22   | 0   | 0:          | one = represents 3 library sequences |
| 24   | 0   | 0:          |                                      |
| 26   | 0   | 0:          |                                      |
| 28   | 4   | 0:==        |                                      |
| 30   | 2   | 2:*         |                                      |
| 32   | 4   | 7:==*       |                                      |
| 34   | 13  | 20:===== *  |                                      |
| 36   | 36  | 41:===== *  |                                      |
| 38   | 57  | 68:===== *  |                                      |
| 40   | 82  | 95:===== *  |                                      |
| 42   | 122 | 116:=====*  |                                      |
| 44   | 146 | 128:=====*  |                                      |
| 46   | 114 | 130:===== * |                                      |
| 48   | 109 | 125:===== * |                                      |
| 50   | 115 | 114:=====*  |                                      |
| 52   | 100 | 100:=====*  |                                      |
| 54   | 106 | 85:=====*   |                                      |
| 56   | 72  | 71:=====*   |                                      |
| 58   | 62  | 59:=====*   |                                      |
| 60   | 58  | 47:=====*   |                                      |
| 62   | 48  | 38:=====*   |                                      |

```
64 22 30:===== *
66 23 24:=====*
68 17 19:=====*
70 10 15:=====*
72 15 12:=====*
74 14 9:=====*
76 1 7:== *
78 11 5:=====
80 7 4:=====
82 1 3:==
84 4 3:==
86 1 2:==
88 2 2:== inset = represents 1 library sequences
90 0 1:==
92 0 1:== :*
94 0 1:== :*
96 0 1:== :*
98 1 0:== *=
100 3 0:== =====
102 0 0:== *
104 0 0:== *
106 0 0:== *
108 0 0:== *
110 0 0:== *
112 0 0:== *
114 0 0:== *
116 0 0:== *
118 0 0:== *
>120 1 0:== *=
307888 residues in 1386 sequences
Expectation_n fit: rho(ln(x))= 3.45140.00395; mu= 17.5972 0.204
mean_var=51.640512.245, 0's: 3 Z-trim: 4 B-trim: 0 in 0/44
Lambda= 0.178476
Kolmogorov-Smirnov statistic: 0.0308 (N=29) at 48

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
The best scores are: opt bits E(1386)
gi|82492267|gb|ABB78007.1| major pollen allergen P ( 525) 90 31.7 0.09

>>gi|82492267|gb|ABB78007.1| major pollen allergen Phl p (525 aa)
initn: 53 initl: 53 opt: 90 Z-score: 120.7 bits: 31.7 E(): 0.09
Smith-Waterman score: 90; 24.038% identity (48.558% similar) in 208 aa
overlap (68-262:246-440)
```

|        | 40                  | 50                | 60                   | 70     | 80       | 90  |
|--------|---------------------|-------------------|----------------------|--------|----------|-----|
| del_6  | LHPGGIAPLLALAGHDVTD | AFLAYHPPSTSRLLP   | -PFSTNLLLEKHSVSETSSD | ----   | YR       |     |
|        |                     |                   |                      | ....   | .....    | ..  |
| gi 824 | HDKKSMGDDHFWAVRG    | GGGSGFGIVVAWQVKLL | FPVPTVTIFKISKT       | VSEGA  | VDIINKWQ |     |
|        | 220                 | 230               | 240                  | 250    | 260      | 270 |
|        | 100                 | 110               | 120                  | 130    | 140      | 150 |
| del_6  | KLDSFHKMGMFRRAGHT   | AYATFVIMILMLVSSVT | GVLCSENPWVHLVCGA     | AMGFAW | IQ       |     |
|        | ..                  | ..                | ..                   | ..     | ..       | ..  |
| gi 824 | VVAPQLPADLMIRIIAQ   | GPKATFEAMYLGTCKT  | LTPLMSSKFPELGMNP     | SHCNEM | SWIQS    |     |
|        | 280                 | 290               | 300                  | 310    | 320      | 330 |

```

      160      170      180      190      200
del_6  GWIGHDSGHYRIMTDRKWNR-----FAQILSSNCLQGISIGWWKWNHNAHHIACNS--L
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|824  IPFVH-LGHRDALEDDLLNRNNSFKPFAEYKSDYVYQPFPKTVWEQILNTWLKPGAGIM
      340      350      360      370      380      390

      210      220      230      240      250      260
del_6  EYDPLQYIPLLVSPKFFNSLTSRFYDKKLNFDGVSRLFVQYQHWSFYPMCVARLNML
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|824  IFDP---YGATISATPE---SATP-FPHRK---GVL-FNIQYVNYWFAPGAAAAPLSWS
      400      410      420      430      440

      270      280      290      300      310      320
del_6  AQSFIILLFSRREVANRVQEILGLAVFWLWFPLLLSCLPNWGERIMFLLASYSVTGIQHVQ
gi|824  KDIYNMEFYPVSKNPRQAYANYRIDLGRNEVVNDVSTYASGKVGWQKYFKGNFERLAIT
      450      460      470      480      490      500

```

446 residues in 1 query sequences  
307888 residues in 1386 library sequences  
Scomplib [34t26]  
start: Tue Oct 20 14:14:07 2009 done: Tue Oct 20 14:14:07 2009  
Total Scan time: 0.130 Total Display time: 0.010

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 del_6.pep /home/andre/db/TOX_2009 -Q -E 1 -O del_6.pep_tx.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

del\_6, 446 aa  
vs /home/andre/db/TOX\_2009 library

```

      opt      E()
< 20      61      0:=====
22      0      0:
24      0      0:
26      1      0:=
28      4      2:*
30      18      11:*=
32      169      41:====*=====
34      223      110:=====*=====
36      189      227:===== *
38      260      375:===== *
40      397      523:===== *
42      583      639:===== *
44      610      705:===== *
46      697      718:===== *
48      683      688:===== *
50      491      627:===== *
52      553      552:=====*=

```

one = represents 12 library sequences

```

54      632      471:=====*=
56      470      394:=====*=
58      316      323:=====*=
60      240      262:===== *
62      216      210:=====*=
64      238      167:=====*=
66      122      132:=====*=
68      90      104:=====*=
70      66      81:=====*=
72      61      64:=====*=
74      55      50:=====*=
76      41      39:=====*=
78      59      30:=====*=
80      24      23:=====*=
82      30      18:=====*=
84      11      14:=====*=
86      4      11:=====*=
88      7      8:=====*=
90      13      7:=====*=
92      4      5:=====*=
94      3      4:=====*=
96      4      3:=====*=
98      1      2:=====*=
100     0      2:=====*=
102     0      1:=====*=
104     0      1:=====*=
106     0      1:=====*=
108     0      1:=====*=
110     0      1:=====*=
112     0      0:=====*=
114     0      0:=====*=
116     0      0:=====*=
118     0      0:=====*=
>120    0      0:=====*=

```

inset = represents 1 library sequences

1891534 residues in 7651 sequences  
Expectation\_n fit: rho(ln(x))= 4.69740.000632; mu= 11.8328 0.032  
mean\_var=46.976210.284, 0's: 59 Z-trim: 60 B-trim: 317 in 2/60  
Lambda= 0.187127  
Kolmogorov-Smirnov statistic: 0.0450 (N=29) at 50

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16  
!! No sequences with E() < 1.000000

446 residues in 1 query sequences  
1891534 residues in 7651 library sequences  
Scomplib [34t26]  
start: Tue Oct 20 14:14:08 2009 done: Tue Oct 20 14:14:09 2009  
Total Scan time: 0.740 Total Display time: 0.000

Function used was FASTA [version 3.4t26 July 7, 2006]

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# fasta34 del_6.pep /home/andre/db/PRT_2009 -Q -E 1 -O del_6.pep_prt.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:  
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

del\_6, 446 aa  
vs /home/andre/db/PRT\_2009 library

```

      opt      E()
< 20 221466    0:=====
 22   193      0:=          one = represents 22740 library sequences
 24   349     14:*
 26   741     309:*
 28  3029     3336:*
 30 14774    20264:*
 32 57974    78356:====*
 34 163664   212491:===== *
 36 359115   436407:===== *
 38 623546   721218:===== *
 40 911007   1006036:===== *
 42 1157242  1229756:===== *
 44 1320669
1356536:===== *
 46 1364349
1381665:===== *
 48 1322937
1322785:===== *
 50 1223641  1207047:===== *
 52 1079789  1061196:===== *
 54 916033   906447:===== *
 56 777304   757161:===== *
 58 653895   621615:===== *
 60 532387   503545:===== *
 62 434796   403693:===== *
 64 335406   321055:===== *
 66 267599   253752:===== *
 68 209055   199596:===== *
 70 164773   156415:===== *
 72 127412   122224:===== *
 74 104149   95294:===== *
 76 83345    74169:===== *
 78 63975    57651:===== *
 80 48570    44765:===== *
 82 38769    34244:===== *
 84 29472    27126:===== *
 86 22720    20988:===== *
 88 17284    16240:===== *
 90 14466    12565:===== *
 92 11005    9722:===== *
 94 7810     7523:===== *
 96 5804     5821:===== *
 98 4266     4504:===== *
100 3246     3485:===== *
102 2586     2696:===== *
104 1921     2086:===== *
106 1675     1614:===== *
108 1214     1249:===== *
110 1002     966:===== *
112 756      748:===== *
114 526      579:===== *
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inset = represents 221 library sequences

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116   520   448:*          :==*
118   520   346:*          :==*
>120  5672   268:*          :==*=====
3787527556 residues in 14717352 library sequences
statistics sampled from 60000 to 14708932 sequences
Expectation_n fit: rho(ln(x))= 5.13510.000191; mu= 11.0947 0.010
mean_var=64.341913.335, 0's: 845 Z-trim: 861 B-trim: 2610 in 1/63
Lambda= 0.159892
Kolmogorov-Smirnov statistic: 0.0324 (N=29) at 46
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FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16

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The best scores are:
opt bits
E(14717352)
gi|151416086|emb|CAO78348.1| unnamed protein produ ( 449) 2838 663.3 6.2e-188
gi|118627908|emb|CAL85354.1| unnamed protein produ ( 453) 2836 662.8 8.6e-188
gi|126633766|emb|CAM55839.1| unnamed protein produ ( 453) 2836 662.8 8.6e-188
gi|39750753|emb|CAE84827.1| unnamed protein produc ( 453) 2836 662.8 8.6e-188
gi|60220786|emb|CAI58892.1| unnamed protein produc ( 453) 2836 662.8 8.6e-188
gi|30350277|gb|AAP23034.1| fatty acid delta-6 desa ( 453) 2836 662.8 8.6e-188
gi|76059286|emb|CAJ30837.1| unnamed protein produc ( 453) 2836 662.8 8.6e-188
gi|118627910|emb|CAL85355.1| unnamed protein produ ( 453) 2821 659.4 9.5e-187
gi|39750755|emb|CAE84828.1| unnamed protein produc ( 453) 2821 659.4 9.5e-187
gi|126633768|emb|CAM55840.1| unnamed protein produ ( 453) 2813 657.5 3.4e-186
gi|30350281|gb|AAP23036.1| fatty acid delta-6 desa ( 453) 2813 657.5 3.4e-186
gi|60220788|emb|CAI58893.1| unnamed protein produc ( 453) 2813 657.5 3.4e-186
gi|76059288|emb|CAJ30838.1| unnamed protein produc ( 453) 2813 657.5 3.4e-186
gi|30350275|gb|AAP23033.1| sphingolipid delta-8 de ( 452) 2504 586.3 9.8e-165
gi|30350279|gb|AAP23035.1| sphingolipid delta-8 de ( 452) 2486 582.1 1.7e-163
gi|129593742|gb|ABO31111.1| sphingolipid delta-8 d ( 447) 2189 513.6 7.2e-143
gi|144583293|gb|ABP01349.1| D8-sphingolipid desatu ( 447) 2175 510.4 6.8e-142
gi|157339279|emb|CAO43820.1| unnamed protein produ ( 447) 2166 508.3 2.9e-141
gi|4101626|gb|AAD01240.1| desaturase/cytochrome b5 ( 446) 2143 503.0 1.1e-139
gi|37727301|gb|AAO13090.1| delta-6-desaturase [Cam ( 448) 2136 501.4 3.5e-139
gi|4102021|gb|AAD01410.1| delta 6-desaturase [Bora ( 448) 2120 497.7 4.5e-138
gi|126633756|emb|CAM55834.1| unnamed protein produ ( 448) 2120 497.7 4.5e-138
gi|70795233|gb|AAZ08559.1| delta-6 desaturase [Ech ( 448) 2120 497.7 4.5e-138
gi|76059232|emb|CAJ30813.1| unnamed protein produc ( 448) 2120 497.7 4.5e-138
gi|156141045|gb|ABU51607.1| delta 6-desaturase [Bo ( 448) 2120 497.7 4.5e-138
gi|60220732|emb|CAI58865.1| unnamed protein produc ( 448) 2120 497.7 4.5e-138
gi|71068111|gb|AAZ23035.1| delta-6 desaturase [Ech ( 448) 2119 497.5 5.3e-138
gi|56664937|gb|AAW18134.1| Sequence 15 from patent ( 448) 2114 496.3 1.2e-137
gi|197038257|gb|ACH17687.1| Sequence 15 from paten ( 448) 2114 496.3 1.2e-137
gi|17223795|gb|AAL23580.1| delta-6-desaturase [Ech ( 448) 2114 496.3 1.2e-137
gi|40781920|emb|CAF05407.1| unnamed protein produc ( 448) 2114 496.3 1.2e-137
gi|62780293|gb|AAZ05063.1| Sequence 11 from patent ( 448) 2114 496.3 1.2e-137
gi|2062403|gb|AAC49700.1| delta 6 desaturase [Bora ( 448) 2114 496.3 1.2e-137
gi|42689976|gb|AAS32275.1| Sequence 5 from patent ( 448) 2112 495.8 1.6e-137
gi|158508159|gb|ABW65783.1| Sequence 5 from patent ( 448) 2112 495.8 1.6e-137
gi|3999225|gb|AAC92657.1|AR021719 Sequence 5 from ( 448) 2112 495.8 1.6e-137
gi|145009144|gb|ABP23376.1| Sequence 5 from patent ( 448) 2112 495.8 1.6e-137
gi|2096441|gb|AAB55273.1| Sequence 5 from patent U ( 448) 2112 495.8 1.6e-137
gi|20251303|gb|AAE96306.1| Sequence 5 from patent ( 448) 2112 495.8 1.6e-137
gi|17223797|gb|AAL23581.1| delta-6-desaturase [Ech ( 448) 2111 495.6 1.9e-137
gi|89077589|gb|ABD60318.1| delta-6 fatty acid desa ( 448) 2110 495.4 2.2e-137
gi|10056257|gb|AAE33163.1| Sequence 5 from patent ( 446) 2104 494.0 5.8e-137
gi|12808274|gb|AAE43494.1| Sequence 15 from patent ( 446) 2104 494.0 5.8e-137
gi|33757665|gb|AAQ51238.1| Sequence 5 from patent ( 446) 2104 494.0 5.8e-137
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|                             |                          |        |      |       |          |                             |                          |        |     |       |         |
|-----------------------------|--------------------------|--------|------|-------|----------|-----------------------------|--------------------------|--------|-----|-------|---------|
| gi 67592982 gb AAAY74580.1  | Sequence 7 from patent   | ( 447) | 2098 | 492.6 | 1.5e-136 | gi 194702868 gb ACF85518.1  | unknown [Zea mays]       | ( 194) | 925 | 221.8 | 2.2e-55 |
| gi 156972231 gb ABU98945.1  | delta-8 lipid desatura   | ( 455) | 2080 | 488.5 | 2.7e-135 | gi 148372324 gb ABQ63083.1  | delta-6-fatty acid des   | ( 522) | 868 | 208.9 | 4.4e-51 |
| gi 22296826 gb AAM94345.1   | delta-6-desaturase [Arg  | ( 448) | 2042 | 479.7 | 1.2e-132 | gi 71068119 gb AAZ23038.1   | delta-8 desaturase rela  | ( 169) | 852 | 204.9 | 2.3e-50 |
| gi 157349838 emb CAO39694.1 | unnamed protein produ    | ( 447) | 2017 | 473.9 | 6.3e-131 | gi 11527281 gb AAG36959.1   | AF290983_1 delta-6 desat | ( 523) | 854 | 205.7 | 4.1e-50 |
| gi 22652111 gb AANO33619.1  | AF406816_1 sphingolipid  | ( 446) | 2000 | 470.0 | 9.6e-130 | gi 28557112 dbj BACS7562.1  | delta-6 fatty acid des   | ( 523) | 854 | 205.7 | 4.1e-50 |
| gi 118487585 gb ABK95618.1  | unknown [Populus trich   | ( 447) | 1962 | 461.2 | 4.2e-127 | gi 11527283 gb AAG36960.1   | AF296076_1 delta-6 desat | ( 523) | 854 | 205.7 | 4.1e-50 |
| gi 33330963 gb AAQ10732.1   | delta-8-sphingolipid de  | ( 446) | 1948 | 458.0 | 3.9e-126 | gi 189498326 gb ACE06759.1  | delta-6 fatty acid des   | ( 523) | 853 | 205.5 | 4.9e-50 |
| gi 62780291 gb AAY05061.1   | Sequence 8 from patent   | ( 450) | 1938 | 455.7 | 2e-125   | gi 71068117 gb AAZ23037.1   | delta-8 desaturase rela  | ( 169) | 833 | 200.6 | 4.7e-49 |
| gi 76803801 gb ABA55805.1   | delta-8 sphingolipid de  | ( 469) | 1938 | 455.7 | 2e-125   | gi 71068115 gb AAZ23036.1   | delta-8 desaturase rela  | ( 169) | 802 | 193.4 | 6.7e-47 |
| gi 3702328 gb AAC62885.1    | putative fatty acid desa | ( 449) | 1925 | 452.7 | 1.6e-124 | gi 150850711 gb EDN25904.1  | hypothetical protein B   | ( 542) | 800 | 193.2 | 2.4e-46 |
| gi 71068109 gb AAZ23034.1   | delta-6 desaturase-rela  | ( 448) | 1924 | 452.5 | 1.8e-124 | gi 154699578 gb EDN99316.1  | hypothetical protein S   | ( 538) | 793 | 191.6 | 7.3e-46 |
| gi 9995127 emb CAC07391.1   | unnamed protein product  | ( 458) | 1910 | 449.2 | 1.7e-123 | gi 150409733 gb EDN05173.1  | hypothetical protein H   | ( 567) | 793 | 191.6 | 7.6e-46 |
| gi 62780295 gb AAY05065.1   | Sequence 13 from patent  | ( 458) | 1910 | 449.2 | 1.7e-123 | gi 144976092 gb ABP13187.1  | Sequence 10 from paten   | ( 178) | 775 | 187.2 | 5.2e-45 |
| gi 1040729 emb CAA60621.1   | delta-8 sphingolipid de  | ( 458) | 1910 | 449.2 | 1.7e-123 | gi 57223843 gb AAW41886.1   | delta 8-sphingolipid de  | ( 535) | 757 | 183.3 | 2.3e-43 |
| gi 6850849 emb CAB71088.1   | delta-8 sphingolipid de  | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 160707466 gb EAT91028.2  | hypothetical protein S   | ( 575) | 755 | 182.9 | 3.4e-43 |
| gi 28059272 gb AAO30042.1   | delta-8 sphingolipid de  | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 49650087 emb CAG79813.1  | YALIOE21131p [Yarrowia   | ( 535) | 748 | 181.2 | 9.7e-43 |
| gi 16226517 gb AAL16189.1   | AF428420_1 AT3g61580/F2A | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 146449687 gb EDK43943.1  | hypothetical protein L   | ( 597) | 748 | 181.3 | 1.1e-42 |
| gi 9995108 emb CAC07390.1   | unnamed protein product  | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 60172958 gb AA14504.1    | sphingolipid delta-8 de  | ( 493) | 747 | 180.1 | 1.1e-42 |
| gi 3819710 emb CAA11858.1   | delta-8 sphingolipid de  | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 90304858 gb EAS34489.1   | hypothetical protein CI  | ( 640) | 747 | 181.1 | 1.3e-42 |
| gi 23306384 gb AAN17419.1   | delta-8 sphingolipid de  | ( 449) | 1904 | 447.9 | 4.5e-123 | gi 211589395 emb CAP95536.1 | Pc21g06390 [Penicilli    | ( 553) | 743 | 180.1 | 2.2e-42 |
| gi 3819708 emb CAA11857.1   | delta-8 sphingolipid de  | ( 449) | 1901 | 447.2 | 7.2e-123 | gi 12311151 emb CAC22584.1  | unnamed protein produc   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 9995106 emb CAC07389.1   | unnamed protein product  | ( 449) | 1901 | 447.2 | 7.2e-123 | gi 144976088 gb ABP13183.1  | Sequence 2 from patent   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 1592945 gb AAM64895.1    | delta-8 sphingolipid de  | ( 449) | 1898 | 446.5 | 1.2e-122 | gi 8670977 emb CAF94992.1   | delta 6-fatty acetylena  | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 22002282 gb AAG43277.1   | AF133728_1 delta 8-sphin | ( 446) | 1896 | 446.0 | 1.6e-122 | gi 40781926 emb CAF05410.1  | unnamed protein produc   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 145009165 gb ABP23397.1  | Sequence 27 from paten   | ( 452) | 1893 | 445.3 | 2.6e-122 | gi 160814759 emb CAP40224.1 | unnamed protein produ    | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 42689997 gb AAS32296.1   | Sequence 27 from patent  | ( 452) | 1893 | 445.3 | 2.6e-122 | gi 12311153 emb CAC22585.1  | unnamed protein produc   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 20251324 gb AAE96327.1   | Sequence 27 from patent  | ( 452) | 1893 | 445.3 | 2.6e-122 | gi 40781928 emb CAF05411.1  | unnamed protein produc   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 158508180 gb ABW65804.1  | Sequence 27 from paten   | ( 452) | 1893 | 445.3 | 2.6e-122 | gi 144976089 gb ABP13184.1  | Sequence 4 from patent   | ( 483) | 742 | 179.8 | 2.3e-42 |
| gi 125563301 gb EAO8681.1   | hypothetical protein O   | ( 457) | 1851 | 435.6 | 2.2e-119 | gi 213504782 emb CAS91431.1 | unnamed protein produ    | ( 538) | 740 | 179.4 | 3.5e-42 |
| gi 113631148 dbj BAF24829.1 | Os09g0338500 [Oryza s    | ( 466) | 1851 | 435.6 | 2.2e-119 | gi 44984327 gb AAS53293.1   | AFL079Wp [Ashbya gossyp  | ( 538) | 740 | 179.4 | 3.5e-42 |
| gi 215765030 dbj BAG86727.1 | unnamed protein produ    | ( 466) | 1851 | 435.6 | 2.2e-119 | gi 211587722 emb CAP85769.1 | Pc20g04400 [Penicilli    | ( 555) | 739 | 179.2 | 4.2e-42 |
| gi 50252533 dbj BAD28708.1  | putative delta-6-desat   | ( 466) | 1851 | 435.6 | 2.2e-119 | gi 119413943 gb EAW23882.1  | fatty acid desaturase,   | ( 565) | 739 | 179.2 | 4.3e-42 |
| gi 33330961 gb AAQ10731.1   | delta-6-fatty acid desa  | ( 446) | 1840 | 433.1 | 1.2e-118 | gi 164651328 gb EDR15568.1  | delta 8-sphingoloid de   | ( 541) | 738 | 178.9 | 4.8e-42 |
| gi 194703370 gb ACF85769.1  | unknown [Zea mays]       | ( 464) | 1834 | 431.7 | 3.3e-118 | gi 159128761 gb EDP53875.1  | fatty acid desaturase,   | ( 565) | 731 | 177.3 | 1.5e-41 |
| gi 194689688 gb ACF78928.1  | unknown [Zea mays]       | ( 464) | 1834 | 431.7 | 3.3e-118 | gi 187973797 gb EDU41296.1  | fatty acid desaturase    | ( 568) | 731 | 177.3 | 1.5e-41 |
| gi 62780289 gb AAY05059.1   | Sequence 4 from patent   | ( 462) | 1833 | 431.5 | 3.9e-118 | gi 119401147 gb EAW11571.1  | fatty acid desaturase,   | ( 564) | 730 | 177.1 | 1.8e-41 |
| gi 195629792 gb ACG36537.1  | desaturase/cytochrome    | ( 462) | 1833 | 431.5 | 3.9e-118 | gi 150856702 gb EDN31894.1  | hypothetical protein B   | ( 563) | 729 | 176.9 | 2.1e-41 |
| gi 194690302 gb ACF79235.1  | unknown [Zea mays]       | ( 462) | 1833 | 431.5 | 3.9e-118 | gi 135365631 gb EBH15038.1  | hypothetical protein G   | ( 366) | 726 | 176.1 | 2.4e-41 |
| gi 195642946 gb ACG40941.1  | desaturase/cytochrome    | ( 463) | 1833 | 431.5 | 3.9e-118 | gi 210070696 gb EEA24786.1  | fatty acid desaturase,   | ( 557) | 728 | 176.6 | 2.5e-41 |
| gi 4100569 gb AAD00895.1    | fatty acid desaturase/cy | ( 446) | 1832 | 431.2 | 4.4e-118 | gi 134076236 emb CAK39522.1 | unnamed protein produ    | ( 557) | 727 | 176.4 | 2.9e-41 |
| gi 194701904 gb ACF85036.1  | unknown [Zea mays]       | ( 464) | 1830 | 430.8 | 6.3e-118 | gi 49643967 emb CAG99919.1  | KLLA0E19471p [Kluyvero   | ( 573) | 725 | 176.0 | 4.1e-41 |
| gi 62780294 gb AAY05064.1   | Sequence 12 from patent  | ( 469) | 1790 | 421.6 | 3.8e-115 | gi 83774861 dbj BAE64984.1  | unnamed protein produc   | ( 558) | 723 | 175.5 | 5.5e-41 |
| gi 4104056 gb AAD10250.1    | S276 [Triticum aestivum] | ( 469) | 1790 | 421.6 | 3.8e-115 | gi 190344838 gb EDK36596.2  | hypothetical protein P   | ( 599) | 720 | 174.8 | 9.4e-41 |
| gi 62780292 gb AAY05062.1   | Sequence 10 from patent  | ( 469) | 1788 | 421.1 | 5.3e-115 | gi 114191764 gb EAU33464.1  | hypothetical protein A   | ( 557) | 718 | 174.3 | 1.2e-40 |
| gi 62780288 gb AAY05061.1   | Sequence 2 from patent   | ( 448) | 1767 | 416.3 | 1.5e-113 | gi 213504774 gb CAS91423.1  | unnamed protein produ    | ( 597) | 718 | 174.3 | 1.3e-40 |
| gi 162670501 gb EDG57069.1  | predicted protein [Phy   | ( 469) | 1613 | 380.7 | 7.5e-103 | gi 154695397 gb EDN95135.1  | hypothetical protein S   | ( 563) | 716 | 173.9 | 1.7e-40 |
| gi 50882497 gb AAT85664.1   | putative desaturase [Ma  | ( 464) | 1579 | 372.9 | 1.7e-100 | gi 50882491 gb AAT85661.1   | delta6 fatty acid desat  | ( 481) | 714 | 173.4 | 2e-40   |
| gi 125605297 gb EAZ44333.1  | hypothetical protein O   | ( 433) | 1553 | 366.9 | 1e-98    | gi 160814735 emb CAP40212.1 | unnamed protein produ    | ( 481) | 714 | 173.4 | 2e-40   |
| gi 194702890 gb ACF85529.1  | unknown [Zea mays]       | ( 330) | 1495 | 353.4 | 8.8e-95  | gi 159124031 gb EDP49150.1  | fatty acid desaturase,   | ( 560) | 713 | 173.2 | 2.7e-40 |
| gi 217073182 gb ACJ84950.1  | unknown [Medicago trun   | ( 331) | 1490 | 352.3 | 2e-94    | gi 119409837 gb EAW19784.1  | fatty acid desaturase    | ( 507) | 712 | 172.9 | 2.9e-40 |
| gi 14477726 gb AAE61289.1   | Sequence 7 from patent   | ( 252) | 1228 | 291.8 | 2.4e-76  | gi 51831765 gb AAU10084.1   | delta 8-(E)-sphingolipi  | ( 542) | 711 | 172.7 | 3.6e-40 |
| gi 10055434 gb AAE32340.1   | Sequence 7 from patent   | ( 252) | 1228 | 291.8 | 2.4e-76  | gi 90304908 gb EAS34539.1   | hypothetical protein CI  | ( 560) | 711 | 172.7 | 3.7e-40 |
| gi 12808267 gb AAE43487.1   | Sequence 8 from patent   | ( 252) | 1228 | 291.8 | 2.4e-76  | gi 199433823 emb CAG90058.2 | DEHA2G01628p [Debaryo    | ( 582) | 710 | 172.5 | 4.5e-40 |
| gi 23313405 gb AAN19963.1   | Sequence 7 from patent   | ( 252) | 1228 | 291.8 | 2.4e-76  | gi 21104520 dbj BAB93117.1  | putative delta 8-sphin   | ( 568) | 708 | 172.0 | 6.1e-40 |
| gi 156227752 gb EDO48554.1  | predicted protein [Nem   | ( 455) | 1173 | 279.2 | 2.6e-72  | gi 21104522 dbj BAB93118.1  | putative delta 8-sphin   | ( 573) | 705 | 171.3 | 9.9e-40 |
| gi 190588831 gb EDV28853.1  | hypothetical protein T   | ( 472) | 1152 | 274.4 | 7.7e-71  | gi 145009867 gb EDJ94523.1  | hypothetical protein M   | ( 568) | 702 | 170.6 | 1.6e-39 |
| gi 144577779 gb ABO95845.1  | predicted protein [Ost   | ( 498) | 1063 | 253.9 | 1.2e-64  | gi 46406034 gb AAS93682.1   | delta-6-fatty acid desa  | ( 458) | 698 | 169.7 | 2.5e-39 |
| gi 62780290 gb AAY05060.1   | Sequence 6 from patent   | ( 253) | 935  | 224.2 | 5.4e-56  | gi 217271823 gb ACK28004.1  | Sequence 38 from paten   | ( 458) | 698 | 169.7 | 2.5e-39 |

|                             |                         |        |     |       |         |                             |                           |        |     |       |         |
|-----------------------------|-------------------------|--------|-----|-------|---------|-----------------------------|---------------------------|--------|-----|-------|---------|
| gi 160814737 emb CAP40213.1 | unnamed protein produ   | ( 458) | 698 | 169.7 | 2.5e-39 | gi 14477727 gb AAE61290.1   | Sequence 8 from patent    | ( 125) | 582 | 142.6 | 9.9e-32 |
| gi 32481183 gb AAP83964.1   | delta-6 fatty acid desa | ( 458) | 698 | 169.7 | 2.5e-39 | gi 10055435 gb AAE32341.1   | Sequence 8 from patent    | ( 125) | 582 | 142.6 | 9.9e-32 |
| gi 83772354 dbj BAE62484.1  | unnamed protein produc  | ( 560) | 698 | 169.7 | 3e-39   | gi 23313406 gb AAN19964.1   | Sequence 8 from patent    | ( 125) | 582 | 142.6 | 9.9e-32 |
| gi 111068756 gb EAT89876.1  | hypothetical protein S  | ( 566) | 695 | 169.0 | 4.9e-39 | gi 12808268 gb AAE43488.1   | Sequence 9 from patent    | ( 125) | 582 | 142.6 | 9.9e-32 |
| gi 187979846 gb EDU46472.1  | delta 8-(E)-sphingolip  | ( 570) | 692 | 168.3 | 7.9e-39 | gi 140999045 gb ECO95070.1  | hypothetical protein G    | ( 289) | 575 | 141.2 | 6e-31   |
| gi 167277335 gb ABZ30199.1  | Sequence 4137 from pat  | ( 366) | 687 | 167.1 | 1.2e-38 | gi 139205567 gb ECE13361.1  | hypothetical protein G    | ( 269) | 569 | 139.8 | 1.5e-30 |
| gi 134083492 emb CAK46969.1 | unnamed protein produ   | ( 539) | 686 | 166.9 | 2e-38   | gi 217271830 gb ACK28011.1  | Sequence 45 from paten    | ( 467) | 570 | 140.1 | 2e-30   |
| gi 60499697 gb AAX22051.1   | delta-6-fatty acid desa | ( 459) | 685 | 166.7 | 2e-38   | gi 15823620 dbj BAB69055.1  | delta-6 fatty acid des    | ( 467) | 570 | 140.1 | 2e-30   |
| gi 160814727 emb CAP40208.1 | unnamed protein produ   | ( 459) | 685 | 166.7 | 2e-38   | gi 160814739 emb CAP40214.1 | unnamed protein produ     | ( 467) | 570 | 140.1 | 2e-30   |
| gi 60499699 gb AAX22052.1   | delta-6-fatty acid desa | ( 459) | 685 | 166.7 | 2e-38   | gi 38708284 gb AAR27297.1   | delta-6 desaturase [Amy   | ( 467) | 570 | 140.1 | 2e-30   |
| gi 160814725 emb CAP40207.1 | unnamed protein produ   | ( 459) | 680 | 165.5 | 4.5e-38 | gi 5639724 gb AAD45877.1    | AF139720_1 delta8 fatty a | ( 419) | 554 | 136.4 | 2.3e-29 |
| gi 83027409 gb ABB96724.1   | delta-6 fatty acid desa | ( 459) | 680 | 165.5 | 4.5e-38 | gi 158457283 gb ABW41477.1  | Sequence 6 from patent    | ( 419) | 554 | 136.4 | 2.3e-29 |
| gi 162680220 gb EDQ66658.1  | predicted protein [Phy  | ( 529) | 679 | 165.3 | 5.9e-38 | gi 155291439 gb ABT47043.1  | Sequence 134513 from p    | ( 461) | 549 | 135.3 | 5.6e-29 |
| gi 83775486 dbj BAE65606.1  | unnamed protein produc  | ( 583) | 679 | 165.3 | 6.4e-38 | gi 6434321 emb CAA94233.2   | C. elegans protein W08D   | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 40781930 emb CAF05412.1  | unnamed protein produc  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 126633764 emb CAM55838.1 | unnamed protein produ     | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 126633758 emb CAM55835.1 | unnamed protein produ   | ( 520) | 677 | 164.9 | 8.1e-38 | gi 76059240 emb CAJ30817.1  | unnamed protein produc    | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 12311158 emb CAC22586.1  | unnamed protein produc  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 56664936 gb AAW18133.1   | Sequence 14 from patent   | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 76059234 emb CAJ30814.1  | unnamed protein produc  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 60220740 emb CAI58869.1  | unnamed protein produc    | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 60220734 emb CAI58866.1  | unnamed protein produc  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 9927414 emb CAC04885.1   | unnamed protein product   | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 40781934 emb CAF05414.1  | unnamed protein produc  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 67592977 gb AAY74575.1   | Sequence 2 from patent    | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 160814757 emb CAP40223.1 | unnamed protein produ   | ( 520) | 677 | 164.9 | 8.1e-38 | gi 197038256 gb ACH17686.1  | Sequence 14 from paten    | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 8670979 emb CAB94993.1   | delta 6-fatty acid desa | ( 520) | 677 | 164.9 | 8.1e-38 | gi 67592981 gb AAY74579.1   | Sequence 6 from patent    | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 144976093 gb ABP13188.1  | Sequence 12 from paten  | ( 520) | 677 | 164.9 | 8.1e-38 | gi 3088520 gb AAC15586.1    | delta6-fatty-acid-desatu  | ( 443) | 537 | 132.5 | 3.7e-28 |
| gi 27803034 emb CAD60737.1  | unnamed protein produc  | ( 590) | 675 | 164.4 | 1.2e-37 | gi 157354159 emb CAO46726.1 | unnamed protein produ     | ( 220) | 532 | 131.2 | 4.7e-28 |
| gi 188219276 emb CAP49256.1 | unnamed protein produ   | ( 590) | 675 | 164.4 | 1.2e-37 | gi 56664932 gb AAW18129.1   | Sequence 2 from patent    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 149386657 gb ABN66573.2  | predicted protein [Pic  | ( 573) | 668 | 162.8 | 3.7e-37 | gi 60220722 emb CAI58860.1  | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 116055137 emb CAL57533.1 | S68358 Delta8 sphingo   | ( 473) | 650 | 158.6 | 5.6e-36 | gi 4235626 gb AAD13294.1    | delta5-fatty acid desatu  | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 40781963 emb CAF05424.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 126633738 emb CAM55825.1 | unnamed protein produ     | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 3790209 emb CAA11033.1   | delta6-acyl-lipid desat | ( 525) | 633 | 154.7 | 9.2e-35 | gi 76059230 emb CAJ30812.1  | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 76059238 emb CAJ30816.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 6434326 emb CAB61031.1   | C. elegans protein T13F   | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 12579152 emb CAC27296.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 40781942 emb CAF05418.1  | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 22316697 emb CAD44447.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 126633746 emb CAM55829.1 | unnamed protein produ     | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 55163951 emb CAH68800.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 60220730 emb CAI58864.1  | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 55163940 emb CAH68796.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 4003523 gb AAC95143.1    | delta 5 fatty acid desat  | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 40781936 emb CAF05415.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 50831508 emb CAH05234.1  | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 52748017 emb CAH56933.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 76059222 gb AAY74578.1   | unnamed protein produc    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 22316543 emb CAD44416.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 197038252 gb ACH17682.1  | Sequence 2 from patent    | ( 447) | 534 | 131.8 | 6.1e-28 |
| gi 22316675 emb CAD44440.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 116001263 emb CAL49883.1 | unnamed protein produ     | ( 456) | 531 | 131.1 | 1e-27   |
| gi 40781966 emb CAF05426.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 167279305 gb ABZ32169.1  | Sequence 6107 from pat    | ( 454) | 525 | 129.8 | 2.6e-27 |
| gi 52748006 emb CAH56929.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 67592979 gb AAY74577.1   | Sequence 4 from patent    | ( 443) | 523 | 129.3 | 3.5e-27 |
| gi 22316521 emb CAD44410.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 167279306 gb ABZ32170.1  | Sequence 6108 from pat    | ( 473) | 521 | 128.8 | 5.1e-27 |
| gi 22316540 emb CAD44414.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 40161450 gb AAR67463.1   | Sequence 14 from patent   | ( 453) | 518 | 128.1 | 7.9e-27 |
| gi 60220738 emb CAI58868.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 155709334 gb ABU33983.1  | Sequence 14 from paten    | ( 453) | 518 | 128.1 | 7.9e-27 |
| gi 22316694 emb CAD44445.1  | unnamed protein produc  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 112053839 gb ABH96551.1  | Sequence 14 from paten    | ( 453) | 518 | 128.1 | 7.9e-27 |
| gi 3790207 emb CAA11032.1   | delta6-acyl-lipid desat | ( 525) | 633 | 154.7 | 9.2e-35 | gi 67592980 gb AAY74578.1   | Sequence 5 from patent    | ( 471) | 511 | 126.5 | 2.5e-26 |
| gi 126633762 emb CAM55837.1 | unnamed protein produ   | ( 525) | 633 | 154.7 | 9.2e-35 | gi 22316517 emb CAD44408.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 162684935 gb EDQ71334.1  | predicted protein [Phy  | ( 525) | 633 | 154.7 | 9.2e-35 | gi 19879689 gb AAL92563.1   | delta 6 fatty acid desa   | ( 477) | 510 | 126.3 | 3e-26   |
| gi 197038253 gb ACH17683.1  | Sequence 4 from patent  | ( 421) | 619 | 151.4 | 7.2e-34 | gi 60220736 emb CAI58867.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 56664933 gb AAW18130.1   | Sequence 4 from patent  | ( 421) | 619 | 151.4 | 7.2e-34 | gi 55163965 emb CAH68803.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 158457281 gb ABW41475.1  | Sequence 2 from patent  | ( 421) | 619 | 151.4 | 7.2e-34 | gi 22316671 emb CAD44438.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 158457282 gb ABW41476.1  | Sequence 4 from patent  | ( 421) | 619 | 151.4 | 7.2e-34 | gi 160814745 emb CAP40217.1 | unnamed protein produ     | ( 477) | 510 | 126.3 | 3e-26   |
| gi 158457285 gb ABW41479.1  | Sequence 113 from pate  | ( 422) | 619 | 151.4 | 7.2e-34 | gi 40781932 emb CAF05413.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 60220716 emb CAI58857.1  | unnamed protein produc  | ( 421) | 599 | 146.8 | 1.8e-32 | gi 126633760 emb CAM55836.1 | unnamed protein produ     | ( 477) | 510 | 126.3 | 3e-26   |
| gi 76059216 emb CAJ30805.1  | unnamed protein produc  | ( 421) | 599 | 146.8 | 1.8e-32 | gi 55163963 emb CAH68802.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 50831502 emb CAH05231.1  | unnamed protein produc  | ( 421) | 599 | 146.8 | 1.8e-32 | gi 217271822 gb ACK28003.1  | Sequence 37 from paten    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 148917592 emb CAO00487.1 | unnamed protein produ   | ( 421) | 599 | 146.8 | 1.8e-32 | gi 52748031 emb CAH56936.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 126633732 emb CAM55822.1 | unnamed protein produ   | ( 421) | 599 | 146.8 | 1.8e-32 | gi 52748029 emb CAH56935.1  | unnamed protein produc    | ( 477) | 510 | 126.3 | 3e-26   |
| gi 158457284 gb ABW41478.1  | Sequence 7 from patent  | ( 422) | 591 | 145.0 | 6.4e-32 | gi 145244841 gb ABP49078.1  | delta 6 fatty acid des    | ( 477) | 510 | 126.3 | 3e-26   |

|   |     |       |         |   |     |       |         |
|---|-----|-------|---------|---|-----|-------|---------|
| gi 76059236 emb CAJ30815.1  unnamed protein produc ( 477) | 510 | 126.3 | 3e-26   | gi 160814753 emb CAP40221.1  unnamed protein produ ( 457) | 481 | 119.6 | 3e-24   |
| gi 160814743 emb CAP40216.1  unnamed protein produ ( 458) | 509 | 126.1 | 3.4e-26 | gi 147843618 emb CAN79879.1  hypothetical protein ( 326)  | 475 | 118.1 | 5.8e-24 |
| gi 34221930 dbj BAC82359.1  delta6 fatty acid desa ( 458) | 509 | 126.1 | 3.4e-26 | gi 48596231 gb AAT46029.1  delta-6 fatty acyl desa ( 357) | 463 | 115.4 | 4.3e-23 |
| gi 34221932 dbj BAC82360.1  delta6 fatty acid desa ( 458) | 509 | 126.1 | 3.4e-26 | gi 12007244 gb AAG45093.1 AF307941_1 delta 6-fatty ( 357) | 452 | 112.9 | 2.5e-22 |
| gi 111572541 gb ABH10627.1  delta-6 desaturase [Ph ( 456) | 506 | 125.4 | 5.4e-26 | gi 12007246 gb AAG45094.1 AF307942_1 delta 6-fatty ( 357) | 452 | 112.9 | 2.5e-22 |
| gi 160814755 emb CAP40222.1  unnamed protein produ ( 457) | 503 | 124.7 | 8.8e-26 | gi 134025932 gb AAI34688.1  FADS3 protein [Bos tau ( 443) | 451 | 112.7 | 3.5e-22 |
| gi 11559824 gb AAG38104.1 AF306634_1 delta6-fatty ( 457)  | 503 | 124.7 | 8.8e-26 | gi 98375714 gb ABF58684.1  delta8-desaturase [Perk ( 457) | 448 | 112.0 | 5.8e-22 |
| gi 126013646 gb ABN69091.1  delta-6 fatty acid des ( 457) | 502 | 124.5 | 1e-25   | gi 148917608 emb CAO00495.1  unnamed protein produ ( 457) | 448 | 112.0 | 5.8e-22 |
| gi 160814747 emb CAP40218.1  unnamed protein produ ( 457) | 502 | 124.5 | 1e-25   | gi 160783195 emb CAP40166.1  unnamed protein produ ( 457) | 448 | 112.0 | 5.8e-22 |
| gi 18483177 gb AAL73948.1 AF465282_1 delta 6 fatty ( 457) | 502 | 124.5 | 1e-25   | gi 13436176 gb AAH04901.1  Fatty acid desaturase 3 ( 445) | 444 | 111.1 | 1.1e-21 |
| gi 157677391 emb CAL69819.1  delta6 fatty acid des ( 386) | 501 | 124.2 | 1.1e-25 | gi 29693077 gb AAO93498.1  Sequence 1 from patent ( 445)  | 444 | 111.1 | 1.1e-21 |
| gi 126013644 gb ABN69090.1  delta-6 fatty acid des ( 457) | 501 | 124.2 | 1.2e-25 | gi 119594382 gb EAW73976.1  fatty acid desaturase ( 445)  | 444 | 111.1 | 1.1e-21 |
| gi 34221934 dbj BAC82361.1  delta6 fatty acid desa ( 457) | 501 | 124.2 | 1.2e-25 | gi 119594384 gb EAW73978.1  fatty acid desaturase ( 445)  | 444 | 111.1 | 1.1e-21 |
| gi 160814763 emb CAP40226.1  unnamed protein produ ( 457) | 501 | 124.2 | 1.2e-25 | gi 10798853 gb AAG23122.1 AF084560_1 fatty acid de ( 445) | 444 | 111.1 | 1.1e-21 |
| gi 217271825 gb ACK28006.1  Sequence 40 from paten ( 457) | 501 | 124.2 | 1.2e-25 | gi 4868366 gb AAD31282.1 AF134404_1 delta-6 fatty ( 445)  | 444 | 111.1 | 1.1e-21 |
| gi 6070340 dbj BAA85588.1  delta-6 fatty acid desa ( 457) | 501 | 124.2 | 1.2e-25 | gi 217115831 gb ACJ97546.1  Sequence 524 from pate ( 445) | 444 | 111.1 | 1.1e-21 |
| gi 76059312 emb CAJ30850.1  unnamed protein produc ( 484) | 501 | 124.2 | 1.3e-25 | gi 197722765 gb EDY66673.1  fatty acid desaturase ( 362)  | 441 | 110.3 | 1.5e-21 |
| gi 160814733 emb CAP40211.1  unnamed protein produ ( 484) | 501 | 124.2 | 1.3e-25 | gi 210117575 gb EEA65312.1  hypothetical protein B ( 428) | 433 | 108.5 | 6e-21   |
| gi 60220812 emb CAI58905.1  unnamed protein produc ( 484) | 501 | 124.2 | 1.3e-25 | gi 38490061 gb AAR21624.1  delta-6 fatty acyl desa ( 454) | 428 | 107.4 | 1.4e-20 |
| gi 126633772 emb CAM55842.1  unnamed protein produ ( 484) | 501 | 124.2 | 1.3e-25 | gi 52424053 gb AAU47273.1  delta-6 fatty acyl desa ( 454) | 428 | 107.4 | 1.4e-20 |
| gi 60172984 gb AAX14505.1  delta-6 fatty acid desa ( 484) | 501 | 124.2 | 1.3e-25 | gi 149062366 gb EDM12789.1  fatty acid desaturase ( 449)  | 427 | 107.1 | 1.6e-20 |
| gi 217271824 gb ACK28005.1  Sequence 39 from paten ( 459) | 498 | 123.5 | 2e-25   | gi 21742819 emb CAD38527.1  putative fatty acid de ( 449) | 427 | 107.1 | 1.6e-20 |
| gi 160814751 emb CAP40220.1  unnamed protein produ ( 459) | 498 | 123.5 | 2e-25   | gi 26348537 dbj BAC37908.1  unnamed protein produc ( 449) | 427 | 107.1 | 1.6e-20 |
| gi 16033737 gb AAL13310.1 AF419296_1 delta-6 fatty ( 459) | 498 | 123.5 | 2e-25   | gi 149062365 gb EDM12788.1  fatty acid desaturase ( 449)  | 427 | 107.1 | 1.6e-20 |
| gi 21900891 emb CAD42499.1  unnamed protein produc ( 459) | 498 | 123.5 | 2e-25   | gi 148709391 gb EDL41337.1  fatty acid desaturase ( 449)  | 426 | 106.9 | 1.9e-20 |
| gi 27278518 gb AAN93256.1  Sequence 18 from patent ( 457) | 497 | 123.3 | 2.3e-25 | gi 74192499 dbj BAE43041.1  unnamed protein produc ( 449) | 426 | 106.9 | 1.9e-20 |
| gi 155080898 gb ABS94492.1  Sequence 67 from paten ( 457) | 497 | 123.3 | 2.3e-25 | gi 148709390 gb EDL41336.1  fatty acid desaturase ( 449)  | 426 | 106.9 | 1.9e-20 |
| gi 23313401 gb AAN19959.1  Sequence 2 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 74181920 dbj BAE32659.1  unnamed protein produc ( 469) | 426 | 106.9 | 2e-20   |
| gi 12808262 gb AAE43482.1  Sequence 2 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 7670385 dbj BAA95044.1  unnamed protein product ( 449) | 425 | 106.7 | 2.3e-20 |
| gi 10055430 gb AAE32336.1  Sequence 2 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 26325278 dbj BAC26393.1  unnamed protein produc ( 449) | 424 | 106.5 | 2.6e-20 |
| gi 155070718 gb ABS91063.1  Sequence 43 from paten ( 457) | 497 | 123.3 | 2.3e-25 | gi 51860651 gb AAU11445.1  fatty acid desaturase [ ( 465) | 424 | 106.5 | 2.7e-20 |
| gi 155707464 gb ABU33113.1  Sequence 2 from patent ( 457) | 497 | 123.3 | 2.3e-25 | gi 51860649 gb AAU11444.1  fatty acid desaturase [ ( 465) | 424 | 106.5 | 2.7e-20 |
| gi 12808273 gb AAE43493.1  Sequence 14 from patent ( 457) | 497 | 123.3 | 2.3e-25 | gi 160814731 emb CAP40210.1  unnamed protein produ ( 465) | 424 | 106.5 | 2.7e-20 |
| gi 182916823 gb ACC10858.1  Sequence 2 from patent ( 457) | 497 | 123.3 | 2.3e-25 | gi 16904665 dbj BAB71963.1  putative delata 6-desa ( 452) | 420 | 105.5 | 5e-20   |
| gi 145025091 gb ABP24248.1  Sequence 31 from paten ( 457) | 497 | 123.3 | 2.3e-25 | gi 156617902 gb ABU87822.1  delta5-desaturase-like ( 452) | 417 | 104.8 | 8.1e-20 |
| gi 14477722 gb AAE61285.1  Sequence 2 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 13447755 gb AAK26745.1 AF301910_1 putative delt ( 454) | 416 | 104.6 | 9.8e-18 |
| gi 10056256 gb AAE33162.1  Sequence 4 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 23313403 gb AAN19961.1  Sequence 5 from patent ( 355)  | 404 | 101.8 | 5.3e-19 |
| gi 33757664 gb AAQ51237.1  Sequence 4 from patent ( 457)  | 497 | 123.3 | 2.3e-25 | gi 10055432 gb AAE32338.1  Sequence 5 from patent ( 355)  | 404 | 101.8 | 5.3e-19 |
| gi 160814761 emb CAP40225.1  unnamed protein produ ( 457) | 497 | 123.3 | 2.3e-25 | gi 12808265 gb AAE43485.1  Sequence 6 from patent ( 355)  | 404 | 101.8 | 5.3e-19 |
| gi 6448796 gb AAF08685.1 AF110510_1 delta-6 fatty ( 457)  | 497 | 123.3 | 2.3e-25 | gi 14477724 gb AAE61287.1  Sequence 5 from patent ( 355)  | 404 | 101.8 | 5.3e-19 |
| gi 158475487 gb ABW48563.1  Sequence 24 from paten ( 457) | 497 | 123.3 | 2.3e-25 | gi 61207418 gb AAX40418.1  delta-6-fatty acid desa ( 459) | 403 | 101.6 | 7.7e-19 |
| gi 144998355 gb ABP16928.1  Sequence 17 from paten ( 457) | 497 | 123.3 | 2.3e-25 | gi 72398639 gb AAZ72733.1  delta-6-fatty acid desa ( 459) | 403 | 101.6 | 7.7e-19 |
| gi 40781950 emb CAF05422.1  unnamed protein produc ( 457) | 497 | 123.3 | 2.3e-25 | gi 170937447 emb CAP62105.1  unnamed protein produ ( 573) | 403 | 101.7 | 9.3e-19 |
| gi 118822321 gb ABL20743.1  Sequence 2 from patent ( 457) | 497 | 123.3 | 2.3e-25 | gi 15281354 dbj BAB63440.1  putative delata 6-desa ( 454) | 395 | 99.8  | 2.8e-18 |
| gi 62774622 gb AAY02015.1  Sequence 41 from patent ( 458) | 497 | 123.3 | 2.3e-25 | gi 55846441 gb CAJ62528.1 AF478472_1 delta-5 fatty ( 454) | 395 | 99.8  | 2.8e-18 |
| gi 23329313 gb AAN26147.1  Sequence 44 from patent ( 458) | 497 | 123.3 | 2.3e-25 | gi 157918419 gb ABV99846.1  fatty acid desaturase ( 347)  | 389 | 98.3  | 5.8e-18 |
| gi 62774608 gb AAY02001.1  Sequence 11 from patent ( 458) | 497 | 123.3 | 2.3e-25 | gi 88176241 gb EAQ83709.1  hypothetical protein CH ( 540) | 391 | 98.9  | 6e-18   |
| gi 23329295 gb AAN26129.1  Sequence 10 from patent ( 458) | 497 | 123.3 | 2.3e-25 | gi 111150824 emb CAJ62528.1  putative delta fatty ( 365)  | 388 | 98.1  | 7.1e-18 |
| gi 160814723 emb CAP40206.1  unnamed protein produ ( 459) | 496 | 123.1 | 2.7e-25 | gi 66474461 gb AAY46796.1  delta-6 fatty acyl desa ( 447) | 389 | 98.4  | 7.1e-18 |
| gi 76059402 emb CAJ30866.1  unnamed protein produc ( 459) | 496 | 123.1 | 2.7e-25 | gi 148790756 gb ABR12315.1  delta-6 desaturase [Si ( 445) | 387 | 97.9  | 9.7e-18 |
| gi 160814741 emb CAP40215.1  unnamed protein produ ( 457) | 495 | 122.8 | 3.2e-25 | gi 126633770 emb CAM55841.1  unnamed protein produ ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 46559566 emb CAE53093.1  delta6 fatty acid desa ( 457) | 495 | 122.8 | 3.2e-25 | gi 160814767 emb CAP40228.1  unnamed protein produ ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 210099241 gb EEA47338.1  hypothetical protein B ( 435) | 487 | 121.0 | 1.1e-24 | gi 60220804 emb CAI58901.1  unnamed protein produc ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 217271810 gb ACK27991.1  Sequence 2 from patent ( 359) | 481 | 119.5 | 2.4e-24 | gi 116061047 emb CAL56435.1  delta-6-desaturase (I ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 18483175 gb AAL73947.1 AF465281_1 delta 6 fatty ( 457) | 482 | 119.8 | 2.5e-24 | gi 76059304 emb CAJ30846.1  unnamed protein produc ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 160814749 emb CAP40219.1  unnamed protein produ ( 457) | 482 | 119.8 | 2.5e-24 | gi 58294486 gb AAW70159.1  delta-6-desaturase [Ost ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 18483179 gb AAL73949.1 AF465283_1 delta 6 fatty ( 457) | 481 | 119.6 | 3e-24   | gi 110565253 emb CAL23343.1  unnamed protein produ ( 456) | 387 | 97.9  | 9.9e-18 |
| gi 12007242 gb AAG45092.1 AF307940_1 delta 6-fatty ( 457) | 481 | 119.6 | 3e-24   | gi 190582402 gb EDV22475.1  hypothetical protein T ( 430) | 382 | 96.8  | 2.1e-17 |

|                             |                          |        |     |      |         |                             |                          |        |     |      |         |
|-----------------------------|--------------------------|--------|-----|------|---------|-----------------------------|--------------------------|--------|-----|------|---------|
| gi 14042094 dbj BAB55103.1  | unnamed protein produc   | ( 444) | 382 | 96.8 | 2.2e-17 | gi 23329312 gb AAN26146.1   | Sequence 43 from patent  | ( 444) | 359 | 91.5 | 8.6e-16 |
| gi 40034028 emb CAE90448.1  | unnamed protein produc   | ( 444) | 382 | 96.8 | 2.2e-17 | gi 62774623 gb AAY02016.1   | Sequence 42 from patent  | ( 444) | 359 | 91.5 | 8.6e-16 |
| gi 40037121 emb CAE91519.1  | unnamed protein produc   | ( 444) | 381 | 96.5 | 2.5e-17 | gi 55726256 emb CAH89900.1  | hypothetical protein [   | ( 444) | 357 | 91.0 | 1.2e-15 |
| gi 14042259 dbj BAB55173.1  | unnamed protein produc   | ( 444) | 381 | 96.5 | 2.5e-17 | gi 10798851 gb AAG23121.1   | AF084559_1 fatty acid de | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 39645719 gb AAH63726.1   | MGC68735 protein [Xenop  | ( 446) | 380 | 96.3 | 3e-17   | gi 4406528 gb AAD20018.1    | delta-6 fatty acid desat | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 14043780 gb AAH07846.1   | Fatty acid desaturase 1  | ( 444) | 379 | 96.1 | 3.5e-17 | gi 119594380 gb EAW73974.1  | fatty acid desaturase    | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 6842050 gb AAF29378.1    | delta-5 desaturase [Homo | ( 444) | 379 | 96.1 | 3.5e-17 | gi 45502852 emb CAF86135.1  | unnamed protein produc   | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 23329301 gb AAN26135.1   | Sequence 17 from patent  | ( 323) | 377 | 95.5 | 3.7e-17 | gi 22760712 dbj BAC11305.1  | unnamed protein produc   | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 62774613 gb AAY02006.1   | Sequence 17 from patent  | ( 323) | 377 | 95.5 | 3.7e-17 | gi 217115830 gb ACJ97545.1  | Sequence 522 from pate   | ( 444) | 356 | 90.8 | 1.4e-15 |
| gi 145025095 gb ABP24252.1  | Sequence 41 from paten   | ( 444) | 378 | 95.8 | 4.1e-17 | gi 18381019 gb AAH22139.1   | Fatty acid desaturase 1  | ( 447) | 355 | 90.5 | 1.6e-15 |
| gi 10798849 gb AAG23120.1   | AF084558_1 fatty acid de | ( 444) | 378 | 95.8 | 4.1e-17 | gi 20070924 gb AAH26831.1   | Fatty acid desaturase 1  | ( 447) | 355 | 90.5 | 1.6e-15 |
| gi 189054357 dbj BAG36877.1 | unnamed protein produ    | ( 444) | 378 | 95.8 | 4.1e-17 | gi 148709393 gb EDL41339.1  | fatty acid desaturase    | ( 447) | 354 | 90.3 | 1.9e-15 |
| gi 217115787 gb ACJ97502.1  | Sequence 69 from paten   | ( 444) | 378 | 95.8 | 4.1e-17 | gi 38969781 gb AAH63053.1   | Fatty acid desaturase 1  | ( 447) | 354 | 90.3 | 1.9e-15 |
| gi 3169158 gb AAC23397.1    | BC269730_2 [Homo sapiens | ( 444) | 378 | 95.8 | 4.1e-17 | gi 16151829 dbj BAB69894.1  | delta-5 desaturase [Mu   | ( 447) | 354 | 90.3 | 1.9e-15 |
| gi 12224984 emb CAC21679.1  | hypothetical protein [   | ( 444) | 378 | 95.8 | 4.1e-17 | gi 26350885 gb BAC39079.1   | unnamed protein produc   | ( 447) | 354 | 90.3 | 1.9e-15 |
| gi 158457079 gb ABW41443.1  | Sequence 4 from patent   | ( 473) | 378 | 95.9 | 4.3e-17 | gi 197712992 gb EDY57026.1  | fatty acid desaturase    | ( 354) | 352 | 89.8 | 2.2e-15 |
| gi 119594379 gb EAW73973.1  | fatty acid desaturase    | ( 501) | 378 | 95.9 | 4.5e-17 | gi 51858588 gb AAH81776.1   | Fatty acid desaturase 2  | ( 444) | 353 | 90.1 | 2.2e-15 |
| gi 62897371 dbj BAD96626.1  | fatty acid desaturase    | ( 444) | 377 | 95.6 | 4.8e-17 | gi 149062367 gb EDM12790.1  | fatty acid desaturase    | ( 444) | 353 | 90.1 | 2.2e-15 |
| gi 149022448 gb EDL79342.1  | rCG26407 [Rattus norve   | ( 487) | 377 | 95.6 | 5.2e-17 | gi 4514722 dbj BAA75496.1   | delta-6 fatty acid desa  | ( 444) | 353 | 90.1 | 2.2e-15 |
| gi 145305528 gb ABP56110.1  | fatty acid desaturase    | ( 347) | 374 | 94.9 | 6.3e-17 | gi 20070719 gb AAH26848.1   | Fatty acid desaturase 1  | ( 447) | 353 | 90.1 | 2.2e-15 |
| gi 44502630 emb CAF85923.1  | unnamed protein produc   | ( 501) | 375 | 95.2 | 7.3e-17 | gi 2943693 gb AAH49438.1    | Fatty acid desaturase 2  | ( 444) | 352 | 89.8 | 2.2e-15 |
| gi 22760402 dbj BAC11182.1  | unnamed protein produc   | ( 501) | 375 | 95.2 | 7.3e-17 | gi 74181635 dbj BAE32539.1  | unnamed protein produc   | ( 447) | 352 | 89.8 | 2.6e-15 |
| gi 187438554 gb ACD10793.1  | fatty acid delta-6 des   | ( 445) | 374 | 94.9 | 7.8e-17 | gi 158938657 gb ABW83675.1  | delta-5 fatty acid des   | ( 445) | 344 | 88.0 | 9.4e-15 |
| gi 144962260 gb ABP06289.1  | fatty acid desaturase    | ( 444) | 373 | 94.7 | 9.1e-17 | gi 149062368 gb EDM12791.1  | fatty acid desaturase    | ( 447) | 343 | 87.8 | 1.1e-14 |
| gi 12808266 gb AAE43486.1   | Sequence 7 from patent   | ( 104) | 365 | 92.5 | 1e-16   | gi 15823618 dbj BAB69054.1  | delta-5 fatty acid des   | ( 447) | 343 | 87.8 | 1.1e-14 |
| gi 14477725 gb AAE61288.1   | Sequence 6 from patent   | ( 104) | 365 | 92.5 | 1e-16   | gi 197304192 emb CAQ30479.1 | Acyl-CoA dependent de    | ( 449) | 342 | 87.5 | 1.3e-14 |
| gi 10055433 gb AAE32339.1   | Sequence 6 from patent   | ( 104) | 365 | 92.5 | 1e-16   | gi 137081505 gb EBS10199.1  | hypothetical protein G   | ( 116) | 335 | 85.6 | 1.3e-14 |
| gi 23313404 gb AAN19962.1   | Sequence 6 from patent   | ( 104) | 365 | 92.5 | 1e-16   | gi 62774621 gb AAY02014.1   | Sequence 40 from patent  | ( 347) | 340 | 87.0 | 1.5e-14 |
| gi 169642221 gb AAI60507.1  | LOC100145314 protein [   | ( 429) | 372 | 94.5 | 1e-16   | gi 23329311 gb AAN26145.1   | Sequence 42 from patent  | ( 347) | 340 | 87.0 | 1.5e-14 |
| gi 86577710 gb AAI12949.1   | Fads2 protein [Xenopus   | ( 446) | 372 | 94.5 | 1.1e-16 | gi 11386009 gb AAG35068.1   | AF320509_1 delta-5 desat | ( 447) | 340 | 87.1 | 1.8e-14 |
| gi 50417554 gb AAH77556.1   | Fads2-prov protein [Xen  | ( 446) | 372 | 94.5 | 1.1e-16 | gi 124417974 emb CAR82966.1 | unnamed protein produ    | ( 621) | 341 | 87.4 | 2e-14   |
| gi 33585851 gb AAH55950.1   | Fads3 protein [Mus musc  | ( 404) | 371 | 94.2 | 1.2e-16 | gi 10954035 gb AAG25710.1   | AF309556_1 putative delt | ( 444) | 338 | 86.6 | 2.5e-14 |
| gi 215276658 gb ACJ65149.1  | delta-6 fatty acyl des   | ( 442) | 371 | 94.2 | 1.3e-16 | gi 158457078 gb ABW41442.1  | Sequence 3 from patent   | ( 447) | 337 | 86.4 | 2.9e-14 |
| gi 29693080 gb AAO93499.1   | Sequence 3 from patent   | ( 444) | 371 | 94.2 | 1.3e-16 | gi 62780296 gb AAY05066.1   | Sequence 17 from patent  | ( 114) | 325 | 83.3 | 6.4e-14 |
| gi 44921596 gb AAS49163.1   | delta-6 fatty acyl desa  | ( 445) | 370 | 94.0 | 1.5e-16 | gi 144061162 gb EDI58667.1  | hypothetical protein G   | ( 422) | 331 | 85.0 | 7.2e-14 |
| gi 23428438 gb AAL17639.1   | putative delta 6-desatu  | ( 445) | 370 | 94.0 | 1.5e-16 | gi 137994188 gb EBX17375.1  | hypothetical protein G   | ( 199) | 327 | 83.9 | 7.4e-14 |
| gi 10954037 gb AAG25711.1   | AF309557_1 putative delt | ( 444) | 369 | 93.8 | 1.7e-16 | gi 148763485 gb ABR10503.1  | putative delta fatty a   | ( 365) | 330 | 84.7 | 7.5e-14 |
| gi 62774609 gb AAY02002.1   | Sequence 12 from patent  | ( 444) | 367 | 93.3 | 2.4e-16 | gi 138904171 gb ECC35823.1  | hypothetical protein G   | ( 287) | 321 | 82.6 | 2.6e-13 |
| gi 7861970 gb AAF70457.1    | AF226273_1 delta-5 fatty | ( 444) | 367 | 93.3 | 2.4e-16 | gi 139950162 gb ECS157875.1 | hypothetical protein G   | ( 228) | 318 | 81.8 | 3.5e-13 |
| gi 23329296 gb AAN26130.1   | Sequence 11 from patent  | ( 444) | 367 | 93.3 | 2.4e-16 | gi 124420766 emb CAR85669.1 | unnamed protein produ    | ( 630) | 323 | 83.2 | 3.6e-13 |
| gi 23329314 gb AAN26148.1   | Sequence 45 from patent  | ( 445) | 367 | 93.3 | 2.4e-16 | gi 62774606 gb AAY01999.1   | Sequence 9 from patent   | ( 432) | 319 | 82.2 | 5e-13   |
| gi 23329308 gb AAN26142.1   | Sequence 39 from patent  | ( 445) | 367 | 93.3 | 2.4e-16 | gi 23329294 gb AAN26128.1   | Sequence 9 from patent   | ( 432) | 319 | 82.2 | 5e-13   |
| gi 53954492 gb AAV04489.1   | Sequence 16446 from pat  | ( 177) | 362 | 91.9 | 2.5e-16 | gi 62774619 gb AAY02012.1   | Sequence 38 from patent  | ( 465) | 319 | 82.2 | 5.3e-13 |
| gi 67969447 dbj BAE01074.1  | unnamed protein produc   | ( 444) | 366 | 93.1 | 2.8e-16 | gi 23329309 gb AAN26143.1   | Sequence 40 from patent  | ( 465) | 319 | 82.2 | 5.3e-13 |
| gi 149383938 gb ABR24806.1  | delta-6 fatty acid des   | ( 440) | 365 | 92.8 | 3.3e-16 | gi 142623810 gb ECC40384.1  | hypothetical protein G   | ( 558) | 317 | 81.8 | 8.5e-13 |
| gi 160783196 emb CAP40167.1 | unnamed protein produ    | ( 411) | 364 | 92.6 | 3.6e-16 | gi 142247848 gb ECW69868.1  | hypothetical protein G   | ( 364) | 313 | 80.8 | 1.1e-12 |
| gi 148709392 gb EDL41338.1  | fatty acid desaturase    | ( 444) | 364 | 92.6 | 3.8e-16 | gi 111979089 gb ABH83332.1  | Sequence 69 from paten   | ( 430) | 313 | 80.8 | 1.3e-12 |
| gi 34785344 gb AAH57189.1   | Fatty acid desaturase 2  | ( 444) | 364 | 92.6 | 3.8e-16 | gi 155095521 gb ABS99976.1  | Sequence 69 from paten   | ( 430) | 313 | 80.8 | 1.3e-12 |
| gi 4406526 gb AAD20017.1    | delta-6 fatty acid desat | ( 444) | 364 | 92.6 | 3.8e-16 | gi 155116385 gb ABT11311.1  | Sequence 69 from paten   | ( 430) | 313 | 80.8 | 1.3e-12 |
| gi 74138023 dbj BAE25416.1  | unnamed protein produc   | ( 444) | 364 | 92.6 | 3.8e-16 | gi 155082220 gb ABS94960.1  | Sequence 69 from paten   | ( 430) | 313 | 80.8 | 1.3e-12 |
| gi 111309298 gb AAI20880.1  | 4833423E24Rik protein    | ( 487) | 364 | 92.6 | 4.1e-16 | gi 155116371 gb ABT11297.1  | Sequence 55 from paten   | ( 433) | 313 | 80.8 | 1.3e-12 |
| gi 148695383 gb EDL27330.1  | mCG3008 [Mus musculus]   | ( 487) | 364 | 92.6 | 4.1e-16 | gi 54307110 gb AAV33631.1   | delta-4 desaturase [Iso  | ( 433) | 313 | 80.8 | 1.3e-12 |
| gi 123233825 emb CAM24033.1 | novel protein (483342    | ( 487) | 364 | 92.6 | 4.1e-16 | gi 155082206 gb ABS94946.1  | Sequence 55 from paten   | ( 433) | 313 | 80.8 | 1.3e-12 |
| gi 45502702 emb CAF85988.1  | unnamed protein produc   | ( 501) | 364 | 92.6 | 4.2e-16 | gi 111979075 gb ABH83318.1  | Sequence 55 from paten   | ( 433) | 313 | 80.8 | 1.3e-12 |
| gi 22760516 dbj BAC11229.1  | unnamed protein produc   | ( 501) | 364 | 92.6 | 4.2e-16 | gi 155095507 gb ABS99962.1  | Sequence 55 from paten   | ( 433) | 313 | 80.8 | 1.3e-12 |
| gi 148917598 emb CAO00490.1 | unnamed protein produ    | ( 411) | 362 | 92.1 | 5e-16   | gi 190580163 gb EDV20248.1  | hypothetical protein T   | ( 421) | 310 | 80.1 | 2.1e-12 |
| gi 98375736 gb ABF58685.1   | delta5-desaturase [Perk  | ( 411) | 362 | 92.1 | 5e-16   | gi 74422653 gb ABA06503.1   | delta-6-desaturase [Cun  | ( 466) | 310 | 80.2 | 2.2e-12 |
| gi 133778157 gb AAI23736.1  | FADS2 protein [Bos tau   | ( 444) | 362 | 92.2 | 5.3e-16 | gi 160814729 emb CAP40209.1 | unnamed protein produ    | ( 466) | 310 | 80.2 | 2.2e-12 |

|                             |                                 |     |      |         |
|-----------------------------|---------------------------------|-----|------|---------|
| gi 151362066 gb ABS05069.1  | fatty acid desaturase (357)     | 308 | 79.6 | 2.5e-12 |
| gi 163778616 gb EDQ92231.1  | predicted protein [Mon (419)    | 308 | 79.7 | 2.8e-12 |
| gi 210090975 gb EEA39238.1  | hypothetical protein B (423)    | 308 | 79.7 | 2.9e-12 |
| gi 135458568 gb EBH77415.1  | hypothetical protein G (334)    | 306 | 79.2 | 3.2e-12 |
| gi 199601714 dbj BAG71007.1 | delta5-desaturase [Ob (435)     | 307 | 79.5 | 3.4e-12 |
| gi 112053846 gb ABH96555.1  | Sequence 33 from paten (456)    | 306 | 79.2 | 4.2e-12 |
| gi 136160965 gb EBM29598.1  | hypothetical protein G (362)    | 303 | 78.5 | 5.6e-12 |
| gi 112053847 gb ABH96556.1  | Sequence 35 from paten (442)    | 301 | 78.1 | 9.1e-12 |
| gi 145025100 gb ABP24257.1  | Sequence 56 from paten (442)    | 301 | 78.1 | 9.1e-12 |
| gi 155707474 gb ABU33123.1  | Sequence 119 from pate (442)    | 301 | 78.1 | 9.1e-12 |
| gi 136856060 gb EBQ86244.1  | hypothetical protein G (398)    | 298 | 77.4 | 1.3e-11 |
| gi 136159810 gb EBM28841.1  | hypothetical protein G (363)    | 296 | 76.9 | 1.7e-11 |
| gi 37683439 gb AAQ98793.1   | delta-4 fatty acid desa (445)   | 297 | 77.2 | 1.7e-11 |
| gi 136500512 gb EBQ56762.1  | hypothetical protein G (369)    | 295 | 76.6 | 2e-11   |
| gi 144581309 gb ABO99366.1  | predicted protein [Ost (400)    | 295 | 76.7 | 2.2e-11 |
| gi 151358713 gb ABS01716.1  | fatty acid desaturase (375)     | 293 | 76.2 | 2.9e-11 |
| gi 142070222 gb ECV34327.1  | hypothetical protein G (398)    | 293 | 76.2 | 3e-11   |
| gi 136491773 gb EBQ51081.1  | hypothetical protein G (343)    | 291 | 75.7 | 3.6e-11 |
| gi 160814765 emb CAP40227.1 | unnamed protein produ (439)     | 291 | 75.8 | 4.5e-11 |
| gi 76059226 emb CAJ30810.1  | unnamed protein produc (439)    | 291 | 75.8 | 4.5e-11 |
| gi 126633742 emb CAM55827.1 | unnamed protein produ (439)     | 291 | 75.8 | 4.5e-11 |
| gi 20069123 gb AAM09687.1   | AF489588_1 delta-5 fatty (439)  | 291 | 75.8 | 4.5e-11 |
| gi 40781946 emb CAF05420.1  | unnamed protein produc (439)    | 291 | 75.8 | 4.5e-11 |
| gi 148917604 emb CAO00493.1 | unnamed protein produ (439)     | 291 | 75.8 | 4.5e-11 |
| gi 60220726 emb CAI58862.1  | unnamed protein produc (439)    | 291 | 75.8 | 4.5e-11 |
| gi 21900887 emb CAD42497.1  | unnamed protein produc (439)    | 291 | 75.8 | 4.5e-11 |
| gi 136170160 gb EBM35588.1  | hypothetical protein G (362)    | 290 | 75.5 | 4.5e-11 |
| gi 143039367 gb EDC37030.1  | hypothetical protein G (376)    | 289 | 75.3 | 5.4e-11 |
| gi 166089930 dbj BAG04638.1 | delta 6 acyl-lipid de (364)     | 287 | 74.8 | 7.3e-11 |
| gi 144221401 gb EDJ74889.1  | hypothetical protein G (310)    | 286 | 74.5 | 7.5e-11 |
| gi 88184723 gb EAQ92191.1   | hypothetical protein CH (405)   | 287 | 74.8 | 7.9e-11 |
| gi 187372747 gb ACD03117.1  | delta-5 fatty acid des (439)    | 287 | 74.8 | 8.5e-11 |
| gi 135013953 gb EBE93475.1  | hypothetical protein G (278)    | 284 | 74.0 | 9.4e-11 |
| gi 134368802 gb EBA94147.1  | hypothetical protein G (362)    | 285 | 74.3 | 1e-10   |
| gi 135299436 gb EBG71506.1  | hypothetical protein G (371)    | 284 | 74.1 | 1.2e-10 |
| gi 210118290 gb EEA66022.1  | hypothetical protein B (255)    | 282 | 73.6 | 1.2e-10 |
| gi 142964797 gb EDB84170.1  | hypothetical protein G (342)    | 283 | 73.9 | 1.3e-10 |
| gi 159026904 emb CAO89155.1 | desD [Microcystis aer (364)     | 283 | 73.9 | 1.4e-10 |
| gi 119710109 gb ABL96295.1  | delta-5 desaturase [Pa (425)    | 281 | 73.5 | 2.2e-10 |
| gi 135358824 gb EBH10478.1  | hypothetical protein G (364)    | 280 | 73.2 | 2.2e-10 |
| gi 136109683 gb EBL97756.1  | hypothetical protein G (282)    | 277 | 72.4 | 2.9e-10 |
| gi 135055165 gb EBF20558.1  | hypothetical protein G (354)    | 278 | 72.7 | 3e-10   |
| gi 349563 gb AA27286.1      | delta-6 desaturase (359)        | 277 | 72.5 | 3.6e-10 |
| gi 1653589 dbj BAA18502.1   | delta-6 desaturase [Syn (359)   | 277 | 72.5 | 3.6e-10 |
| gi 158508158 gb ABL96295.1  | Sequence 2 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 167275964 gb ABZ28828.1  | Sequence 2766 from pat (359)    | 277 | 72.5 | 3.6e-10 |
| gi 3999224 gb AAC92656.1    | AR021718 Sequence 2 from (359)  | 277 | 72.5 | 3.6e-10 |
| gi 145009143 gb ABP23375.1  | Sequence 2 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 42689975 gb AAS32274.1   | Sequence 2 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 10056258 gb AAE33164.1   | Sequence 6 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 2096440 gb AAB55272.1    | Sequence 2 from patent U (359)  | 277 | 72.5 | 3.6e-10 |
| gi 12808275 gb AAE43495.1   | Sequence 16 from patent (359)   | 277 | 72.5 | 3.6e-10 |
| gi 20251302 gb AAE96305.1   | Sequence 2 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 33757666 gb AAQ51239.1   | Sequence 6 from patent (359)    | 277 | 72.5 | 3.6e-10 |
| gi 1612522 gb AAB15502.1    | Sequence 2 from patent U (359)  | 277 | 72.5 | 3.6e-10 |
| gi 2490943 gb AAB79079.1    | I63793 Sequence 2 from pa (359) | 277 | 72.5 | 3.6e-10 |
| gi 3012071 gb AAC11519.1    | I75930 Sequence 2 from pa (359) | 277 | 72.5 | 3.6e-10 |
| gi 23329297 gb AAN26131.1   | Sequence 13 from patent (287)   | 274 | 71.7 | 4.8e-10 |

|                             |                                |     |      |         |
|-----------------------------|--------------------------------|-----|------|---------|
| gi 62774610 gb AAY02003.1   | Sequence 14 from patent (287)  | 274 | 71.7 | 4.8e-10 |
| gi 23329300 gb AAN26134.1   | Sequence 16 from patent (288)  | 274 | 71.7 | 4.8e-10 |
| gi 62774611 gb AAY02004.1   | Sequence 15 from patent (288)  | 274 | 71.7 | 4.8e-10 |
| gi 23329302 gb AAN26136.1   | Sequence 18 from patent (288)  | 274 | 71.7 | 4.8e-10 |
| gi 23329298 gb AAN26132.1   | Sequence 14 from patent (288)  | 274 | 71.7 | 4.8e-10 |
| gi 143742490 gb EDG55472.1  | hypothetical protein G (347)   | 274 | 71.8 | 5.6e-10 |
| gi 110282809 gb ABG60995.1  | fatty acid desaturase (356)    | 274 | 71.8 | 5.7e-10 |
| gi 158260127 dbj BAF82241.1 | unnamed protein produ (360)    | 274 | 71.8 | 5.8e-10 |
| gi 193788350 dbj BAG53244.1 | unnamed protein produ (360)    | 274 | 71.8 | 5.8e-10 |
| gi 124389907 gb ABN11122.1  | delta-6 desaturase [Ar (368)   | 274 | 71.8 | 5.9e-10 |
| gi 42565443 gb AAS20991.1   | desaturase [Hyacinthus (82)    | 266 | 69.6 | 6.1e-10 |
| gi 23329310 gb AAN26144.1   | Sequence 41 from patent (360)  | 273 | 71.6 | 6.7e-10 |
| gi 62774620 gb AAY02013.1   | Sequence 39 from patent (360)  | 273 | 71.6 | 6.7e-10 |
| gi 186469986 gb ACC85611.1  | delta 6 desaturase [Ar (368)   | 273 | 71.6 | 6.9e-10 |
| gi 50952212 gb AAT89913.1   | delta fatty acid desatu (416)  | 273 | 71.6 | 7.6e-10 |
| gi 33757667 gb AAQ51240.1   | Sequence 7 from patent (365)   | 272 | 71.3 | 8e-10   |
| gi 12808276 gb AAE43496.1   | Sequence 17 from patent (365)  | 272 | 71.3 | 8e-10   |
| gi 10056259 gb AAE33165.1   | Sequence 7 from patent (365)   | 272 | 71.3 | 8e-10   |
| gi 809110 emb CAA60573.1    | delta 6 desaturase [Arth (368) | 272 | 71.3 | 8.1e-10 |
| gi 158304495 gb ABW26112.1  | linoleoyl-CoA desatura (369)   | 272 | 71.3 | 8.1e-10 |
| gi 134889843 gb EBE10298.1  | hypothetical protein G (356)   | 271 | 71.1 | 9.2e-10 |
| gi 198261491 gb EDY85781.1  | fatty acid desaturase (356)    | 270 | 70.9 | 1.1e-09 |
| gi 56752653 gb AAW24540.1   | SJCHGC05823 protein [Sc (173)  | 266 | 69.8 | 1.1e-09 |
| gi 158938655 gb ABW83674.1  | delta-5 fatty acid des (170)   | 265 | 69.5 | 1.3e-09 |
| gi 138988511 gb ECCT0380.1  | hypothetical protein G (227)   | 266 | 69.8 | 1.4e-09 |
| gi 136779681 gb EBQ35346.1  | hypothetical protein G (372)   | 267 | 70.2 | 1.8e-09 |
| gi 135931467 gb EBK79039.1  | hypothetical protein G (381)   | 267 | 70.2 | 1.8e-09 |
| gi 167780872 gb ABZ99170.1  | Putative fatty acid de (393)   | 267 | 70.2 | 1.9e-09 |
| gi 167777164 gb ABZ95465.1  | Fatty acid desaturase (393)    | 267 | 70.2 | 1.9e-09 |
| gi 169155987 emb CAQ01121.1 | putative fatty acid d (371)    | 266 | 70.0 | 2.1e-09 |
| gi 148917606 emb CAO00494.1 | unnamed protein produ (450)    | 266 | 70.0 | 2.5e-09 |
| gi 142793996 gb EDA62990.1  | hypothetical protein G (326)   | 264 | 69.5 | 2.6e-09 |
| gi 23452396 gb AAN33029.1   | delta 6-desaturase-like (169)  | 260 | 68.4 | 2.9e-09 |
| gi 147830365 emb CAN01300.1 | putative fatty acid d (367)    | 263 | 69.3 | 3.4e-09 |
| gi 217271813 gb ACK27994.1  | Sequence 8 from patent (456)   | 264 | 69.6 | 3.5e-09 |
| gi 217271812 dbj ACK27993.1 | Sequence 6 from patent (466)   | 264 | 69.6 | 3.5e-09 |
| gi 90082433 dbj BAE90398.1  | unnamed protein produc (146)   | 258 | 67.9 | 3.5e-09 |
| gi 217271811 gb ACK27992.1  | Sequence 4 from patent (473)   | 264 | 69.6 | 3.6e-09 |
| gi 136790444 gb EBQ42522.1  | hypothetical protein G (383)   | 262 | 69.0 | 4.1e-09 |
| gi 136611795 gb EBP28193.1  | hypothetical protein G (325)   | 261 | 68.8 | 4.2e-09 |
| gi 85821182 gb EAQ42329.1   | Fatty acid desaturase [ (364)  | 261 | 68.8 | 4.6e-09 |
| gi 162953181 gb ABY22696.1  | putative delta fatty a (385)   | 260 | 68.6 | 5.7e-09 |
| gi 40034123 emb CAE90492.1  | unnamed protein produc (160)   | 255 | 67.2 | 6.2e-09 |
| gi 193786544 dbj BAG51327.1 | unnamed protein produ (160)    | 255 | 67.2 | 6.2e-09 |
| gi 26328979 dbj BAC28228.1  | unnamed protein produc (287)   | 258 | 68.0 | 6.2e-09 |
| gi 29605945 dbj BAC70009.1  | putative fatty acid de (365)   | 259 | 68.3 | 6.4e-09 |
| gi 193784729 dbj BAG53882.1 | unnamed protein produ (168)    | 255 | 67.2 | 6.4e-09 |
| gi 40034682 emb CAE90732.1  | unnamed protein produc (168)   | 255 | 67.2 | 6.4e-09 |
| gi 193786568 dbj BAG51351.1 | unnamed protein produ (168)    | 255 | 67.2 | 6.4e-09 |
| gi 34365279 emb CAE45971.1  | hypothetical protein [ (196)   | 255 | 67.3 | 7.3e-09 |
| gi 45503662 emb CAF86845.1  | unnamed protein produc (210)   | 255 | 67.3 | 7.7e-09 |
| gi 193786708 dbj BAG52031.1 | unnamed protein produ (210)    | 255 | 67.3 | 7.7e-09 |
| gi 134059500 emb CAM41728.1 | fatty acid desaturase (417)    | 257 | 67.9 | 9.8e-09 |
| gi 76875123 emb CAI86344.1  | putative fatty acid de (350)   | 256 | 67.6 | 1e-08   |
| gi 12808271 gb AAE43491.1   | Sequence 12 from patent (143)  | 251 | 66.3 | 1.1e-08 |
| gi 10055438 gb AAE32344.1   | Sequence 11 from patent (143)  | 251 | 66.3 | 1.1e-08 |
| gi 23313409 gb AAN19967.1   | Sequence 11 from patent (143)  | 251 | 66.3 | 1.1e-08 |
| gi 14477730 gb AAE61293.1   | Sequence 11 from patent (143)  | 251 | 66.3 | 1.1e-08 |

gi|45502914|emb|CAF86199.1| unnamed protein produc ( 322) 255 67.4 1.1e-08  
gi|21740255|emb|CAD39138.1| hypothetical protein [ ( 91) 248 65.4 1.2e-08  
gi|62774614|gb|AAY02007.1| Sequence 18 from patent ( 356) 255 67.4 1.2e-08  
gi|23329303|gb|AAN26137.1| Sequence 19 from patent ( 356) 255 67.4 1.2e-08  
gi|120325829|gb|ABM20144.1| fatty acid desaturase ( 357) 255 67.4 1.2e-08  
gi|143139481|gb|EDD10306.1| hypothetical protein G ( 385) 255 67.4 1.3e-08  
gi|10055436|gb|AAE32342.1| Sequence 9 from patent ( 131) 249 65.8 1.4e-08  
gi|12808269|gb|AAE43489.1| Sequence 10 from patent ( 131) 249 65.8 1.4e-08  
gi|14477728|gb|AAE61291.1| Sequence 9 from patent ( 131) 249 65.8 1.4e-08  
gi|23313407|gb|AAN19965.1| Sequence 9 from patent ( 131) 249 65.8 1.4e-08  
gi|119594381|gb|EAW73975.1| fatty acid desaturase ( 422) 255 67.5 1.4e-08  
gi|158261605|dbj|BAF82980.1| unnamed protein produ ( 422) 255 67.5 1.4e-08  
gi|12002125|gb|AAG43192.1|AF108658\_1 p5327 [Homo s ( 422) 255 67.5 1.4e-08  
gi|144580406|gb|ABO98466.1| predicted protein [Ost ( 434) 255 67.5 1.4e-08  
gi|209586126|gb|ACT64811.1| microsomal delta-5 des ( 477) 255 67.5 1.5e-08  
gi|14042244|dbj|BAB55167.1| unnamed protein produc ( 168) 248 65.6 2e-08  
gi|40037090|emb|CAE91508.1| unnamed protein produc ( 168) 248 65.6 2e-08  
gi|111153325|emb|CAJ65077.1| Linoleoyl-CoA desatur ( 381) 252 66.7 2e-08  
gi|144050064|gb|EDI50465.1| hypothetical protein G ( 324) 251 66.5 2.1e-08  
gi|86264104|gb|ABC87787.1| delta-6-desaturase [Cot ( 407) 252 66.8 2.1e-08  
gi|54018085|dbj|BAB59455.1| putative fatty acid de ( 416) 251 66.5 2.6e-08  
gi|4884144|emb|CAB43280.1| hypothetical protein [H ( 311) 249 66.0 2.8e-08  
gi|119947604|gb|ABM06515.1| putative fatty acid de ( 386) 250 66.3 2.8e-08  
gi|210090977|gb|EBA39240.1| hypothetical protein B ( 424) 250 66.3 3.1e-08  
gi|45685163|gb|AAS75335.1| delta-11 fatty acid des ( 477) 250 66.3 3.4e-08  
gi|156211152|gb|EDO32278.1| predicted protein [Nem ( 298) 247 65.5 3.7e-08  
gi|62822747|gb|AAY15136.1| delta-4 desaturase [Pav ( 447) 249 66.1 3.7e-08  
gi|119954878|gb|ABM11883.1| fatty acid desaturase ( 401) 248 65.8 4e-08  
gi|152029615|gb|ABS27383.1| Linoleoyl-CoA desatura ( 426) 248 65.8 4.2e-08  
gi|29605235|dbj|BAC69302.1| putative fatty acid de ( 353) 247 65.6 4.2e-08  
gi|167349333|gb|AB272068.1| fatty acid desaturase ( 342) 246 65.3 4.9e-08  
gi|134898210|gb|EBE15874.1| hypothetical protein G ( 290) 245 65.1 5e-08  
gi|146153926|gb|ABO40780.1| Linoleoyl-CoA desatura ( 365) 245 65.1 6e-08  
gi|149062369|gb|EDM12792.1| fatty acid desaturase ( 146) 240 63.7 6.3e-08  
gi|110589551|gb|ABG77281.1| fatty acid desaturase ( 78) 236 62.6 7.1e-08  
gi|144575966|gb|ABO94035.1| predicted protein [Ost ( 459) 245 65.2 7.2e-08  
gi|196193623|gb|EDX88582.1| Fatty acid desaturase ( 385) 244 64.9 7.4e-08  
gi|136926982|gb|EBR23004.1| hypothetical protein G ( 221) 241 64.1 7.5e-08  
gi|54018084|dbj|BAD59454.1| putative fatty acid de ( 484) 245 65.2 7.6e-08  
gi|169151651|emb|CAP00440.1| putative fatty acid d ( 364) 243 64.7 8.2e-08  
gi|193077962|gb|ABO12876.2| putative fatty acid de ( 364) 243 64.7 8.2e-08  
gi|213986429|gb|ACJ56728.1| Linoleoyl-CoA desatura ( 364) 243 64.7 8.2e-08  
gi|183210578|gb|ACC57976.1| Fatty acid desaturase ( 364) 243 64.7 8.2e-08  
gi|213057331|gb|ACJ42233.1| fatty acid desaturase ( 364) 243 64.7 8.2e-08  
gi|169148090|emb|CAM65683.1| putative fatty acid d ( 364) 243 64.7 8.2e-08  
gi|33702947|gb|AAQ27422.1| Sequence 4394 from pate ( 368) 243 64.7 8.3e-08  
gi|139178176|gb|ECD94220.1| hypothetical protein G ( 188) 239 63.6 9.1e-08  
gi|134067410|emb|CAM65683.1| fatty acid desaturase ( 417) 243 64.7 9.2e-08  
gi|157337268|emb|CAO21614.1| unnamed protein produ ( 98) 235 62.5 1e-07  
gi|110647688|emb|CAL17164.1| conserved hypothetical ( 386) 242 64.4 1e-07  
gi|116610165|gb|ABK02889.1| fatty acid desaturase ( 362) 241 64.2 1.1e-07  
gi|495303373|emb|CAG68085.1| putative fatty acid de ( 364) 241 64.2 1.1e-07  
gi|136729181|gb|EBQ01866.1| hypothetical protein G ( 256) 239 63.6 1.2e-07  
gi|149771057|gb|CAL42524.1| Fatty acid desaturase ( 365) 240 64.0 1.3e-07  
gi|138510180|gb|ECA09251.1| hypothetical protein G ( 276) 238 63.4 1.5e-07  
gi|156232843|gb|ABU57626.1| fatty acid desaturase ( 341) 239 63.7 1.5e-07  
gi|141775249|gb|ECT22616.1| hypothetical protein G ( 283) 238 63.4 1.5e-07  
gi|117578080|emb|CAL66549.1| transmembrane family ( 327) 238 63.5 1.7e-07

gi|139506752|gb|ECF54077.1| hypothetical protein G ( 154) 234 62.4 1.7e-07  
gi|110817945|gb|ABG93229.1| probable linoleoyl-CoA ( 390) 238 63.5 1.9e-07  
gi|141421268|gb|ECRT70990.1| hypothetical protein G ( 233) 235 62.7 2.1e-07  
gi|148569588|gb|ABQ91733.1| fatty acid desaturase ( 346) 237 63.3 2.1e-07  
gi|119951021|gb|ABMO9932.1| putative delta 6 fatty ( 362) 237 63.3 2.1e-07  
gi|142467276|gb|ECY29127.1| hypothetical protein G ( 326) 236 63.0 2.3e-07  
gi|158114110|gb|ABW16307.1| fatty acid desaturase ( 360) 236 63.0 2.5e-07  
gi|183580191|dbj|BAG28662.1| hypothetical protein ( 370) 236 63.0 2.6e-07  
gi|163775730|gb|EDQ89353.1| predicted protein [Mon ( 453) 237 63.3 2.6e-07  
gi|143164003|gb|EDD27862.1| hypothetical protein G ( 384) 236 63.0 2.6e-07  
gi|193075956|gb|ABO10536.2| putative linoleoyl-CoA ( 391) 236 63.1 2.7e-07  
gi|141237040|gb|ECQ57189.1| hypothetical protein G ( 203) 232 62.0 3e-07  
gi|183207976|gb|ACC55374.1| Fatty acid desaturase ( 382) 235 62.8 3.1e-07  
gi|169150862|emb|CAO99465.1| conserved hypothetical ( 382) 235 62.8 3.1e-07  
gi|138069375|gb|EBX56952.1| hypothetical protein G ( 215) 232 62.0 3.1e-07  
gi|33704153|gb|AAQ28628.1| Sequence 5600 from pate ( 390) 235 62.8 3.1e-07  
gi|110818249|gb|ABG93533.1| probable fatty acid de ( 406) 235 62.8 3.2e-07  
gi|160814769|emb|CAP400229.1| unnamed protein produ ( 417) 235 62.8 3.3e-07  
gi|68124314|emb|CAJ07076.1| fatty acid desaturase, ( 417) 235 62.8 3.3e-07  
gi|51493745|gb|AAU04860.1| fatty acid desaturase 2 ( 233) 232 62.0 3.3e-07  
gi|119954888|gb|ABM11893.1| fatty acid desaturase ( 369) 234 62.6 3.5e-07  
gi|213986787|gb|ACJ57086.1| Linoleoyl-CoA desatura ( 382) 234 62.6 3.6e-07  
gi|169150677|emb|CAM88587.1| conserved hypothetical ( 382) 234 62.6 3.6e-07  
gi|119949221|gb|ABMO8132.1| putative delta 6 fatty ( 405) 234 62.6 3.8e-07  
gi|110822828|gb|ABG98112.1| possible fatty acid de ( 418) 234 62.6 3.9e-07  
gi|157422916|gb|AAI53462.1| Fads2 protein [Danio r ( 158) 229 61.2 3.9e-07  
gi|213054610|gb|ACJ39512.1| fatty acid desaturase ( 382) 233 62.4 4.2e-07  
gi|110819865|gb|ABG95149.1| fatty acid desaturase ( 400) 233 62.4 4.4e-07  
gi|60172939|gb|AAAX14503.1| putative desaturase [Th ( 515) 234 62.7 4.6e-07  
gi|15147883|dbj|BAB62850.1| putative delta-6 fatty ( 445) 233 62.4 4.8e-07  
gi|110820966|gb|ABG96250.1| possible linoleoyl-CoA ( 329) 231 61.9 5.2e-07  
gi|141049999|gb|ECP28833.1| hypothetical protein G ( 303) 230 61.6 5.7e-07  
gi|92392651|gb|ABE73926.1| fatty acid desaturase [ ( 448) 232 62.2 5.7e-07  
gi|62774612|gb|AAY02005.1| Sequence 16 from patent ( 315) 230 61.6 5.9e-07  
gi|23329299|gb|AAN26133.1| Sequence 15 from patent ( 315) 230 61.6 5.9e-07  
gi|49529319|emb|ABC67031.1| conserved hypothetical ( 383) 231 61.9 5.9e-07  
gi|47027091|gb|AAT08759.1| desaturase [Hyacinthus ( 81) 223 59.6 5.9e-07  
gi|189830603|gb|ACE19261.1| Sequence 5069 from pat ( 177) 227 60.8 5.9e-07  
gi|5019332|emb|CAB44385.1| putative delta fatty ac ( 345) 230 61.6 6.3e-07  
gi|145218257|gb|ABP47661.1| fatty acid desaturase ( 360) 230 61.6 6.5e-07  
gi|108770960|gb|ABG09682.1| fatty acid desaturase ( 361) 230 61.6 6.5e-07  
gi|119695769|gb|ABL92842.1| fatty acid desaturase ( 361) 230 61.6 6.5e-07  
gi|126235957|gb|ABN99357.1| fatty acid desaturase ( 361) 230 61.6 6.5e-07  
gi|5263169|dbj|BAA81814.1| fatty acid desaturase [ ( 464) 231 61.9 6.9e-07  
gi|85773959|gb|ABC80796.1| Linoleoyl-CoA desaturas ( 364) 229 61.4 7.7e-07  
gi|118174952|gb|ABK75848.1| Fatty acid desaturase ( 382) 229 61.4 8e-07  
gi|162696494|gb|EDQ82832.1| predicted protein [Phy ( 475) 230 61.7 8.2e-07  
gi|144067825|gb|EDI63603.1| hypothetical protein G ( 338) 228 61.2 8.5e-07  
gi|144145826|gb|EDJ19776.1| hypothetical protein G ( 342) 228 61.2 8.6e-07  
gi|160773710|gb|AAI55077.1| Fads2 protein [Danio r ( 421) 229 61.5 8.7e-07  
gi|14290486|gb|AAH09011.1| FADS2 protein [Homo sap ( 386) 228 61.2 9.5e-07  
gi|196113353|gb|ACG67069.1| putative fatty acid de ( 387) 228 61.2 9.5e-07  
gi|197699371|gb|EDY46304.1| delta fatty acid desat ( 350) 227 60.9 1e-06  
gi|143064945|gb|EDC55734.1| hypothetical protein G ( 369) 227 61.0 1.1e-06  
gi|110822829|gb|ABG98113.1| possible fatty acid de ( 412) 226 60.8 1.4e-06  
gi|119692555|gb|ABL89628.1| fatty acid desaturase ( 368) 225 60.5 1.5e-06  
gi|108767801|gb|ABG06523.1| fatty acid desaturase ( 368) 225 60.5 1.5e-06  
gi|9716155|emb|CAC01546.1| putative delta fatty ac ( 347) 224 60.3 1.7e-06

gi|116608872|gb|ABK01596.1| fatty acid desaturase ( 391) 224 60.3 1.8e-06  
gi|145218283|gb|ABP47687.1| fatty acid desaturase ( 382) 223 60.0 2.1e-06  
gi|60220816|emb|CAI58907.1| unnamed protein produc ( 482) 224 60.3 2.2e-06  
gi|126633754|emb|CAM55833.1| unnamed protein produ ( 482) 224 60.3 2.2e-06  
gi|76059316|emb|CAJ30852.1| unnamed protein produc ( 482) 224 60.3 2.2e-06  
gi|178462655|dbj|BAG17175.1| putative delta-6 fatt ( 382) 222 59.8 2.5e-06  
gi|140965018|gb|ECO71441.1| hypothetical protein G ( 269) 220 59.3 2.5e-06  
gi|140965017|gb|ECO71440.1| hypothetical protein G ( 281) 220 59.3 2.6e-06  
gi|145217878|gb|ABP47282.1| fatty acid desaturase ( 345) 221 59.6 2.7e-06  
gi|145218274|gb|ABP47678.1| fatty acid desaturase ( 357) 221 59.6 2.7e-06  
gi|126232803|gb|ABN96203.1| fatty acid desaturase ( 368) 221 59.6 2.8e-06  
gi|540147701|dbj|BAD56140.1| putative fatty acid de ( 382) 221 59.6 2.9e-06  
gi|23329304|gb|AAN26138.1| Sequence 20 from patent ( 219) 218 58.8 3e-06  
gi|62774615|gb|AAY02008.1| Sequence 19 from patent ( 219) 218 58.8 3e-06  
gi|68125348|emb|CAJ03208.1| delta-6 fatty acid des ( 428) 221 59.6 3.2e-06  
gi|140739434|gb|ECN18761.1| hypothetical protein G ( 92) 212 57.1 3.8e-06  
gi|110282811|gb|ABG60997.1| fatty acid desaturase ( 363) 219 59.1 3.8e-06  
gi|167283660|gb|ABZ36524.1| Sequence 10462 from pa ( 366) 219 59.1 3.8e-06  
gi|196171342|gb|ACG72315.1| Linoleoyl-CoA desatura ( 364) 218 58.9 4.5e-06  
gi|134984268|gb|EBE73351.1| hypothetical protein G ( 364) 218 58.9 4.5e-06  
gi|142109188|gb|ECV65610.1| hypothetical protein G ( 243) 215 58.1 5.2e-06  
gi|119693415|gb|ABL90488.1| fatty acid desaturase ( 369) 217 58.7 5.3e-06  
gi|108768649|gb|ABG07371.1| fatty acid desaturase ( 369) 217 58.7 5.3e-06  
gi|141678995|gb|ECS77487.1| hypothetical protein G ( 257) 215 58.1 5.5e-06  
gi|118166446|gb|ABK67343.1| Fatty acid desaturase ( 427) 217 58.7 6e-06  
gi|41398272|gb|AAS05893.1| DesA3\_1 [Mycobacterium ( 427) 217 58.7 6e-06  
gi|118570156|gb|ABL04907.1| linoleoyl-CoA desatura ( 428) 216 58.5 7.1e-06  
gi|157322866|gb|ABV41963.1| fatty acid desaturase ( 361) 215 58.2 7.2e-06  
gi|140816700|gb|ECN71323.1| hypothetical protein G ( 259) 213 57.6 7.6e-06  
gi|138424096|gb|EBZ57519.1| hypothetical protein G ( 100) 208 56.2 7.7e-06  
gi|57228571|gb|AAW45006.1| cytochrome b2, mitochon ( 593) 217 58.8 7.9e-06  
gi|139193582|gb|ECE05189.1| hypothetical protein G ( 195) 211 57.1 8.2e-06  
gi|126348216|emb|CAJ89937.1| putative delta fatty ( 352) 214 58.0 8.3e-06  
gi|183174663|gb|ACC39773.1| linoleoyl-CoA desatura ( 428) 215 58.2 8.3e-06  
gi|140191202|gb|ECK14420.1| hypothetical protein G ( 198) 211 57.1 8.3e-06  
gi|62774616|gb|AAY02009.1| Sequence 20 from patent ( 182) 210 56.9 9.1e-06  
gi|23329305|gb|AAN26139.1| Sequence 21 from patent ( 182) 210 56.9 9.1e-06  
gi|140258005|gb|ECK60243.1| hypothetical protein G ( 137) 208 56.3 1e-05  
gi|119955452|gb|ABM12457.1| fatty acid desaturase ( 377) 213 57.7 1e-05  
gi|190347535|gb|EDK39822.2| hypothetical protein P ( 335) 212 57.5 1.1e-05  
gi|196170643|gb|ACG71616.1| Linoleoyl-CoA desatura ( 364) 212 57.5 1.2e-05  
gi|143901661|gb|EDH45092.1| hypothetical protein G ( 138) 207 56.1 1.2e-05  
gi|119539360|gb|ABL83977.1| fatty acid desaturase ( 409) 212 57.5 1.3e-05  
gi|12808270|gb|AAE43490.1| Sequence 11 from patent ( 87) 204 55.3 1.3e-05  
gi|10055437|gb|ABM32343.1| Sequence 10 from patent ( 87) 204 55.3 1.3e-05  
gi|23313408|gb|AAN19966.1| Sequence 10 from patent ( 87) 204 55.3 1.3e-05  
gi|14477729|gb|AAE61292.1| Sequence 10 from patent ( 87) 204 55.3 1.3e-05  
gi|155241962|gb|ABT18093.1| delta-6 fatty acid des ( 197) 208 56.4 1.3e-05  
gi|137349334|gb|EBT59938.1| hypothetical protein G ( 209) 208 56.4 1.4e-05  
gi|46361702|gb|AAS89346.1| putative delta-6 fatty ( 213) 208 56.4 1.4e-05  
gi|121494767|emb|CAL73248.1| Possible linoleoyl-Co ( 427) 211 57.3 1.6e-05  
gi|38490343|emb|CAE55572.1| POSSIBLE LINOLEOYL-CoA ( 427) 211 57.3 1.6e-05  
gi|148722958|gb|ABR07583.1| hypothetical linoleoyl ( 427) 211 57.3 1.6e-05  
gi|134151369|gb|EBA43414.1| hypothetical linoleoyl ( 427) 211 57.3 1.6e-05  
gi|31620006|emb|CAD95350.1| POSSIBLE LINOLEOYL-CoA ( 427) 211 57.3 1.6e-05  
gi|13883146|gb|AAK47669.1| linoleoyl-CoA desaturas ( 427) 211 57.3 1.6e-05  
gi|124599372|gb|EAY58476.1| hypothetical protein T ( 427) 211 57.3 1.6e-05  
gi|148507244|gb|ABQ75053.1| putative linoleoyl-CoA ( 427) 211 57.3 1.6e-05

gi|121494859|emb|CAL73341.1| Possible linoleoyl-Co ( 427) 211 57.3 1.6e-05  
gi|135102709|gb|EBF50924.1| hypothetical protein G ( 360) 210 57.0 1.6e-05  
gi|49609602|emb|CAG73035.1| putative fatty acid de ( 381) 210 57.1 1.7e-05  
gi|190580110|gb|EDV20196.1| hypothetical protein T ( 464) 211 57.3 1.7e-05  
gi|76059314|emb|CAJ30851.1| unnamed protein produc ( 476) 211 57.3 1.7e-05  
gi|126633752|emb|CAM55832.1| unnamed protein produ ( 476) 211 57.3 1.7e-05  
gi|60220814|emb|CAI58906.1| unnamed protein produc ( 476) 211 57.3 1.7e-05  
gi|136526677|gb|EB073567.1| hypothetical protein G ( 330) 209 56.8 1.7e-05  
gi|169240644|emb|CAM61672.1| Probable fatty acid d ( 403) 210 57.1 1.8e-05  
gi|134068412|emb|CAM66702.1| delta-6 fatty acid de ( 414) 210 57.1 1.8e-05  
gi|60172920|gb|AAX14502.1| delta-8 fatty acid desa ( 476) 210 57.1 2e-05  
gi|10432462|emb|CAC10296.1| putative fatty acid de ( 350) 208 56.6 2.2e-05  
gi|40161452|gb|AAR67465.1| Sequence 29 from patent ( 439) 209 56.9 2.2e-05  
gi|155709336|gb|ABU33985.1| Sequence 29 from paten ( 439) 209 56.9 2.2e-05  
gi|112053843|gb|ABH96553.1| Sequence 29 from paten ( 439) 209 56.9 2.2e-05  
gi|155707475|gb|ABU33124.1| Sequence 123 from pate ( 439) 209 56.9 2.2e-05  
gi|197038258|gb|ACH17688.1| Sequence 16 from paten ( 449) 209 56.9 2.3e-05  
gi|56664938|gb|AAW18135.1| Sequence 16 from patent ( 449) 209 56.9 2.3e-05  
gi|55163952|emb|CAH68801.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|60220720|emb|CAI58859.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|22316698|gb|ABQ44448.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|190888417|gb|ACE95865.1| delta 5 fatty acid des ( 469) 209 56.9 2.3e-05  
gi|52748010|emb|CAH56931.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|22316544|emb|CAD44417.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|145386837|gb|ABP65280.1| delta 5 fatty acid des ( 469) 209 56.9 2.3e-05  
gi|52748018|emb|CAH56934.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|146762533|gb|ABQ45365.1| delta-5-desaturase [Ni ( 469) 209 56.9 2.3e-05  
gi|126633736|emb|CAM55824.1| unnamed protein produ ( 469) 209 56.9 2.3e-05  
gi|40781967|emb|CAF05427.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|40781940|emb|CAF05417.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|22316669|emb|CAD44437.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|76059220|emb|CAJ30807.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|209582581|gb|ACI65202.1| delta 5 fatty acid des ( 469) 209 56.9 2.3e-05  
gi|55163944|emb|CAH68798.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|50831506|emb|CAH05233.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|19879687|gb|EAL92562.1| delta 5 fatty acid desa ( 469) 209 56.9 2.3e-05  
gi|22316515|emb|CAD44407.1| unnamed protein produc ( 469) 209 56.9 2.3e-05  
gi|50882495|gb|AAT85663.1| polyunsaturated fatty a ( 484) 209 56.9 2.4e-05  
gi|212002032|gb|EEB07692.1| cytochrome b5 reductas ( 124) 202 54.9 2.4e-05  
gi|119955585|gb|ABM12590.1| fatty acid desaturase ( 415) 208 56.6 2.5e-05  
gi|167349344|gb|ABZ72079.1| fatty acid desaturase ( 361) 207 56.3 2.6e-05  
gi|207085835|gb|EDZ63119.1| fatty acid desaturase ( 451) 208 56.6 2.6e-05  
gi|83766989|dbj|BAE57129.1| unnamed protein produc ( 474) 208 56.6 2.8e-05  
gi|205277856|gb|ACI01557.1| nitrate reductase [Sol ( 270) 205 55.8 2.8e-05  
gi|88180680|gb|EAG88148.1| hypothetical protein CH ( 502) 208 56.7 2.9e-05  
gi|145217762|gb|ABP47166.1| fatty acid desaturase ( 418) 207 56.4 2.9e-05  
gi|155241942|gb|ABT18092.1| delta-6 fatty acid des ( 197) 203 55.3 3e-05  
gi|205277978|gb|ACI01618.1| nitrate reductase [Sol ( 270) 204 55.6 3.3e-05  
gi|140708236|gb|ECM96873.1| hypothetical protein G ( 277) 204 55.6 3.4e-05  
gi|142123983|gb|ECV76534.1| hypothetical protein G ( 340) 205 55.9 3.4e-05  
gi|38199570|emb|CAE49221.1| Conserved hypothetical ( 426) 206 56.2 3.5e-05  
gi|158603254|gb|EDP39249.1| Delta5 fatty acid desa ( 138) 200 54.5 3.6e-05  
gi|4150956|dbj|BAA37090.1| delta 5 fatty acid desa ( 467) 206 56.2 3.8e-05  
gi|213509839|emb|CAS92469.1| unnamed protein produ ( 573) 207 56.5 3.8e-05  
gi|2748|emb|CAA34183.1| L-lactate:cytochrome c oxi ( 573) 207 56.5 3.8e-05  
gi|110819941|gb|ABG95225.1| probable fatty acid de ( 402) 205 55.9 3.9e-05  
gi|49609603|emb|CAG73036.1| putative fatty acid de ( 363) 204 55.7 4.2e-05  
gi|145303946|gb|ABP54528.1| fatty acid desaturase ( 380) 204 55.7 4.4e-05

|                             |   |     |      |         |                             |   |     |      |         |
|-----------------------------|---|-----|------|---------|-----------------------------|---|-----|------|---------|
| gi 157916653 gb ABV98080.1  | fatty acid desaturase ( 380)                | 204 | 55.7 | 4.4e-05 | gi 205277896 gb ACI01577.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 89287624 gb EAR85613.1   | Cytochrome b5-like Heme ( 214)              | 201 | 54.8 | 4.4e-05 | gi 205277976 gb ACI01617.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 210073804 gb EEA27891.1  | mitochondrial cytochrome b5 ( 495)          | 205 | 56.0 | 4.6e-05 | gi 205277972 gb ACI01615.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 110084610 gb ABG49441.1  | fatty acid desaturase ( 90)                 | 196 | 53.4 | 4.8e-05 | gi 205278008 gb ACI01633.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 118570155 gb ABL04906.1  | linoleoyl-CoA desaturase ( 428)             | 204 | 55.7 | 4.8e-05 | gi 205277852 gb ACI01555.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 126091402 gb ABN66175.1  | outer mitochondrial membrane protein ( 164) | 199 | 54.3 | 4.9e-05 | gi 205277890 gb ACI01574.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 134953667 gb EBE52727.1  | hypothetical protein G ( 136)               | 198 | 54.0 | 4.9e-05 | gi 205277958 gb ACI01608.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 139434429 gb ECF08979.1  | hypothetical protein G ( 137)               | 198 | 54.0 | 4.9e-05 | gi 205277866 gb ACI01562.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 67633944 gb AAY78896.1   | delta-6 fatty acid desaturase ( 140)        | 198 | 54.0 | 5e-05   | gi 205277886 gb ACI01572.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 170946111 emb CAP72912.1 | unnamed protein product ( 460)              | 204 | 55.7 | 5.1e-05 | gi 205277964 gb ACI01611.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 143761571 gb EDG65392.1  | hypothetical protein G ( 212)               | 200 | 54.6 | 5.1e-05 | gi 205277982 gb ACI01620.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 144583100 gb ABP01215.1  | predicted protein [Ost ( 465)               | 204 | 55.7 | 5.2e-05 | gi 205277898 gb ACI01578.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 144581334 gb ABO99391.1  | predicted protein [Ost ( 466)               | 204 | 55.7 | 5.2e-05 | gi 205277900 gb ACI01579.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 137166137 gb EBS57310.1  | hypothetical protein G ( 261)               | 201 | 54.9 | 5.2e-05 | gi 205277950 gb ACI01604.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 144581330 gb ABO99387.1  | predicted protein [Ost ( 587)               | 205 | 56.0 | 5.3e-05 | gi 205277846 gb ACI01552.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 144583104 gb ABP01219.1  | predicted protein [Ost ( 587)               | 205 | 56.0 | 5.3e-05 | gi 205277902 gb ACI01580.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277980 gb ACI01619.1  | nitrate reductase [Sol ( 270)               | 201 | 54.9 | 5.3e-05 | gi 205277960 gb ACI01609.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 70832613 gb EAN78117.1   | delta-6 fatty acid desaturase ( 421)        | 203 | 55.5 | 5.6e-05 | gi 205277928 gb ACI01593.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 145218306 gb ABP47710.1  | fatty acid desaturase ( 464)                | 203 | 55.5 | 6e-05   | gi 205277876 gb ACI01567.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 141112541 gb ECP71320.1  | hypothetical protein G ( 150)               | 197 | 53.8 | 6.2e-05 | gi 205278014 gb ACI01636.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277912 gb ACI01585.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277874 gb ACI01566.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277990 gb ACI01624.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277850 gb ACI01554.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277948 gb ACI01603.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277974 gb ACI01616.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277952 gb ACI01605.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277920 gb ACI01589.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277942 gb ACI01600.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277878 gb ACI01568.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277970 gb ACI01614.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277954 gb ACI01606.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277854 gb ACI01556.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277996 gb ACI01627.1  | nitrate reductase [Sol ( 270)           | 200 | 54.7 | 6.2e-05 |
| gi 205277930 gb ACI01594.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 143284203 gb EDE11570.1  | hypothetical protein G ( 421)           | 202 | 55.2 | 6.5e-05 |
| gi 205277858 gb ACI01558.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 136493923 gb EB052473.1  | hypothetical protein G ( 358)           | 201 | 55.0 | 6.7e-05 |
| gi 205277924 gb ACI01591.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 121888048 gb EAX93542.1  | Cytochrome b5-like Heme ( 94)           | 194 | 53.0 | 6.9e-05 |
| gi 205278000 gb ACI01629.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 197710788 gb EDY54822.1  | fatty acid desaturase ( 372)            | 201 | 55.0 | 6.9e-05 |
| gi 205277916 gb ACI01587.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 197704570 gb EDY50382.1  | fatty acid desaturase ( 381)            | 201 | 55.0 | 7.1e-05 |
| gi 205277994 gb ACI01626.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 194348865 gb ACF51988.1  | fatty acid desaturase ( 382)            | 201 | 55.0 | 7.1e-05 |
| gi 205277848 gb ACI01553.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 190012664 emb CAQ46292.1 | putative transmembrane protein ( 382)   | 201 | 55.0 | 7.1e-05 |
| gi 205277992 gb ACI01625.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 70834807 gb EAN80309.1   | cytochrome b5, putative ( 119)          | 195 | 53.3 | 7.1e-05 |
| gi 205277934 gb ACI01596.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 108878830 gb EAT43055.1  | flavo-hemoprotein B5/b5 ( 478)          | 202 | 55.3 | 7.3e-05 |
| gi 205278016 gb ACI01637.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277884 gb ACI01571.1  | nitrate reductase [Sol ( 270)           | 199 | 54.4 | 7.3e-05 |
| gi 205277870 gb ACI01564.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277944 gb ACI01601.1  | nitrate reductase [Sol ( 270)           | 199 | 54.4 | 7.3e-05 |
| gi 205277888 gb ACI01573.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 517356 emb CAA56696.1    | nitrate reductase (NADH) ( 900)         | 205 | 56.1 | 7.5e-05 |
| gi 205277872 gb ACI01565.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 134060453 emb CAM37621.1 | delta-6 fatty acid desaturase ( 414)    | 201 | 55.0 | 7.6e-05 |
| gi 205277936 gb ACI01597.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 34102956 gb AAQ59320.1   | linoleoyl-CoA desaturase ( 369)         | 200 | 54.7 | 8.1e-05 |
| gi 205277932 gb ACI01595.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 199431473 emb CAR65620.1 | DEHA2D05522p [Debaryo ( 552)            | 202 | 55.3 | 8.2e-05 |
| gi 205277962 gb ACI01610.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 124422628 emb CAK87454.1 | unnamed protein product ( 258)          | 198 | 54.2 | 8.3e-05 |
| gi 205277908 gb ACI01583.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 163777722 gb EDQ91338.1  | predicted protein [Mon ( 384)           | 200 | 54.7 | 8.3e-05 |
| gi 205277860 gb ACI01559.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 143029156 gb EDC29503.1  | hypothetical protein G ( 385)           | 200 | 54.7 | 8.4e-05 |
| gi 205278018 gb ACI01638.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 138505134 gb ECA06792.1  | hypothetical protein G ( 146)           | 195 | 53.3 | 8.4e-05 |
| gi 205277986 gb ACI01622.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205278004 gb ACI01631.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277880 gb ACI01569.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277918 gb ACI01588.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277956 gb ACI01607.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277904 gb ACI01581.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277844 gb ACI01551.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205278002 gb ACI01630.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277894 gb ACI01576.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277914 gb ACI01586.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277984 gb ACI01621.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277906 gb ACI01582.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277940 gb ACI01599.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277998 gb ACI01628.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277946 gb ACI01602.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277910 gb ACI01584.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205278006 gb ACI01632.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277864 gb ACI01561.1  | nitrate reductase [Sol ( 270)           | 198 | 54.2 | 8.6e-05 |
| gi 205277862 gb ACI01560.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 138571936 gb ECA52388.1  | hypothetical protein G ( 239)           | 197 | 53.9 | 9.1e-05 |
| gi 205277938 gb ACI01598.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 197304190 emb CAQ30478.1 | Acyl-CoA dependent dehydrogenase ( 482) | 200 | 54.8 | 0.0001  |
| gi 205277868 gb ACI01563.1  | nitrate reductase [Sol ( 270)               | 200 | 54.7 | 6.2e-05 | gi 205277892 gb ACI01575.1  | nitrate reductase [Sol ( 270)           | 197 | 54.0 | 0.0001  |



|                             |                           |        |     |      |         |                              |                          |        |     |      |         |
|-----------------------------|---------------------------|--------|-----|------|---------|------------------------------|--------------------------|--------|-----|------|---------|
| gi 205277988 gb ACI01623.1  | nitrate reductase [Sol    | ( 270) | 197 | 54.0 | 0.0001  | gi 19068516 emb CAD24984.1   | similarity to HYPOTHET   | ( 94)  | 186 | 51.2 | 0.00025 |
| gi 143992888 gb EDI09679.1  | hypothetical protein G    | ( 270) | 197 | 54.0 | 0.0001  | gi 169117664 gb ACA42970.1   | putative fatty acid de   | ( 387) | 193 | 53.1 | 0.00026 |
| gi 138080494 gb EBX63372.1  | hypothetical protein G    | ( 273) | 197 | 54.0 | 0.0001  | gi 140435196 gb ECL73148.1   | hypothetical protein G   | ( 122) | 187 | 51.5 | 0.00026 |
| gi 116061092 emb CAL56480.1 | Cytochrome b5 (ISS)       | ( 614) | 201 | 55.1 | 0.0001  | gi 3849989 emb CAA11232.1    | nitrate reductase [Pich  | ( 859) | 197 | 54.3 | 0.00026 |
| gi 139427562 gb ECF04173.1  | hypothetical protein G    | ( 142) | 193 | 52.9 | 0.00011 | gi 902626 emb CAA88925.1     | nitrate reductase [Pichi | ( 859) | 197 | 54.3 | 0.00026 |
| gi 124425040 emb CAK89828.1 | unnamed protein produ     | ( 258) | 196 | 53.7 | 0.00011 | gi 49527995 emb CAG61646.1   | unnamed protein produc   | ( 593) | 195 | 53.7 | 0.00027 |
| gi 119538550 gb ABL83167.1  | fatty acid desaturase     | ( 400) | 198 | 54.3 | 0.00012 | gi 213509823 emb CAS92461.1  | unnamed protein produ    | ( 593) | 195 | 53.7 | 0.00027 |
| gi 211589958 emb CAP96113.1 | Pc21g12160 [Penicilli     | ( 488) | 199 | 54.6 | 0.00012 | gi 126233795 gb ABN97195.1   | fatty acid desaturase    | ( 413) | 193 | 53.1 | 0.00027 |
| gi 116060892 emb CAL57370.1 | polyunsaturated fatty     | ( 491) | 199 | 54.6 | 0.00012 | gi 177540045 gb ACB73000.1   | nitrate reductase [Bet   | ( 905) | 197 | 54.3 | 0.00027 |
| gi 150415742 gb EDN11086.1  | cytochrome b2, mitocho    | ( 513) | 199 | 54.6 | 0.00012 | gi 157932108 gb ABW05098.1   | nitrate reductase [Bet   | ( 905) | 197 | 54.3 | 0.00027 |
| gi 183174664 gb ACC39774.1  | linoleoyl-CoA desatura    | ( 428) | 198 | 54.3 | 0.00013 | gi 159124962 gb EDP50079.1   | mitochondrial cytochro   | ( 533) | 194 | 53.4 | 0.00029 |
| gi 139726005 gb ECH04863.1  | hypothetical protein G    | ( 243) | 195 | 53.5 | 0.00013 | gi 159127043 gb EDP52159.1   | cytochrome b5, putativ   | ( 137) | 187 | 51.5 | 0.00029 |
| gi 136389516 gb EBN84143.1  | hypothetical protein G    | ( 243) | 195 | 53.5 | 0.00013 | gi 135882077 gb EBK44848.1   | hypothetical protein G   | ( 114) | 186 | 51.2 | 0.00029 |
| gi 142426436 gb ECX99050.1  | hypothetical protein G    | ( 362) | 197 | 54.0 | 0.00013 | gi 178462727 dbj BAG17247.1  | putative fatty acid d    | ( 372) | 192 | 52.9 | 0.00029 |
| gi 135737182 gb EBJ52948.1  | hypothetical protein G    | ( 304) | 196 | 53.8 | 0.00013 | gi 116000840 emb CAL550520.1 | cytochrome b5 isoform    | ( 127) | 186 | 51.2 | 0.00032 |
| gi 190348942 gb EDK41496.2  | hypothetical protein P    | ( 547) | 199 | 54.6 | 0.00013 | gi 14041825 dbj BAB55002.1   | nitrate reductase [Pru   | ( 906) | 196 | 54.0 | 0.00032 |
| gi 124425583 emb CAK90368.1 | unnamed protein produ     | ( 313) | 196 | 53.8 | 0.00013 | gi 118175254 gb ABK76150.1   | Fatty acid desaturase    | ( 418) | 192 | 52.9 | 0.00032 |
| gi 144580331 gb ABO98391.1  | predicted protein [Ost    | ( 866) | 201 | 55.2 | 0.00014 | gi 190581744 gb EDV21000.1   | expressed hypothetical   | ( 132) | 186 | 51.2 | 0.00033 |
| gi 194339836 gb EDX20802.1  | delta fatty acid desat    | ( 270) | 195 | 53.5 | 0.00014 | gi 134054562 emb CAK43417.1  | unnamed protein produ    | ( 351) | 191 | 52.6 | 0.00033 |
| gi 170945102 emb CAP71213.1 | unnamed protein produ     | ( 498) | 198 | 54.4 | 0.00014 | gi 57223484 gb AAW41527.1    | acyl-CoA dehydrogenase,  | ( 522) | 193 | 53.2 | 0.00033 |
| gi 21165531 dbj EBH93533.1  | nitrate reductase [Sol    | ( 750) | 200 | 54.9 | 0.00014 | gi 138049319 gb EBX46522.1   | hypothetical protein G   | ( 134) | 186 | 51.2 | 0.00033 |
| gi 167499 gb AAA33114.1     | nitrate reductase         | ( 918) | 201 | 55.2 | 0.00015 | gi 41398476 gb AAS06096.1    | DesA3_2 [Mycobacterium   | ( 366) | 191 | 52.7 | 0.00034 |
| gi 114192090 gb EAU33790.1  | conserved hypothetical    | ( 773) | 200 | 54.9 | 0.00015 | gi 62176818 gb AAX70916.1    | hypothetical protein, c  | ( 182) | 187 | 51.6 | 0.00036 |
| gi 140751864 gb ECN27244.1  | hypothetical protein G    | ( 254) | 194 | 53.3 | 0.00016 | gi 70802212 gb AAZ12117.1    | hypothetical protein, c  | ( 182) | 187 | 51.6 | 0.00036 |
| gi 126234693 gb ABN98093.1  | fatty acid desaturase     | ( 464) | 197 | 54.1 | 0.00016 | gi 119399741 gb EAW10167.1   | mitochondrial cytochro   | ( 495) | 192 | 53.0 | 0.00037 |
| gi 119694440 gb ABL91513.1  | fatty acid desaturase     | ( 464) | 197 | 54.1 | 0.00016 | gi 108768749 gb ABG07471.1   | fatty acid desaturase    | ( 413) | 191 | 52.7 | 0.00037 |
| gi 108769654 gb ABG08376.1  | fatty acid desaturase     | ( 464) | 197 | 54.1 | 0.00016 | gi 119693516 gb ABL90589.1   | fatty acid desaturase    | ( 413) | 191 | 52.7 | 0.00037 |
| gi 167863095 gb EDS26478.1  | flavohemoprotein B5/b5    | ( 688) | 199 | 54.7 | 0.00016 | gi 136536686 gb EB079932.1   | hypothetical protein G   | ( 340) | 190 | 52.4 | 0.00037 |
| gi 119538650 gb ABL83267.1  | fatty acid desaturase     | ( 384) | 196 | 53.8 | 0.00016 | gi 470678 gb AAA18377.1      | NADH: nitrate reductase  | ( 640) | 193 | 53.3 | 0.00039 |
| gi 205277926 gb ACI01592.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 142586045 gb ECZ13929.1   | hypothetical protein G   | ( 295) | 189 | 52.1 | 0.00039 |
| gi 205278012 gb ACI01635.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 157335970 emb CA061800.1  | unnamed protein produ    | ( 647) | 193 | 53.3 | 0.00039 |
| gi 205278010 gb ACI01634.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 183173693 gb ACC38803.1   | linoleoyl-CoA desatura   | ( 377) | 190 | 52.4 | 0.00041 |
| gi 205277968 gb ACI01613.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 119407401 gb EAW17350.1   | cytochrome b5, putativ   | ( 97)  | 183 | 50.5 | 0.00041 |
| gi 205277966 gb ACI01612.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 124426835 emb CAK91615.1  | unnamed protein produ    | ( 215) | 187 | 51.6 | 0.00041 |
| gi 205277842 gb ACI01550.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 139747378 gb ECH18288.1   | hypothetical protein G   | ( 180) | 186 | 51.3 | 0.00042 |
| gi 205277882 gb ACI01570.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 144581090 gb ABO99148.1   | predicted protein [Ost   | ( 491) | 191 | 52.7 | 0.00043 |
| gi 205277840 gb ACI01549.1  | nitrate reductase [Sol    | ( 270) | 194 | 53.3 | 0.00016 | gi 90300530 gb EAS30161.1    | hypothetical protein CI  | ( 504) | 191 | 52.7 | 0.00044 |
| gi 205277922 gb ACI01590.1  | nitrate reductase [Sol    | ( 272) | 194 | 53.3 | 0.00016 | gi 118168179 gb ABK69076.1   | Fatty acid desaturase    | ( 366) | 189 | 52.2 | 0.00047 |
| gi 46241490 gb AAS82948.1   | delta-6 fatty acid desa   | ( 153) | 191 | 52.4 | 0.00017 | gi 194344571 gb EDX25537.1   | fatty acid desaturase    | ( 372) | 189 | 52.2 | 0.00047 |
| gi 213509817 emb CAS92457.1 | unnamed protein produ     | ( 501) | 197 | 54.1 | 0.00017 | gi 138345036 gb EBZ09991.1   | hypothetical protein G   | ( 260) | 187 | 51.6 | 0.00048 |
| gi 294114 gb AAA33713.1     | nitrate reductase         | ( 909) | 200 | 55.0 | 0.00017 | gi 83634598 gb ABC30565.1    | Fatty acid desaturase    | ( 388) | 189 | 52.2 | 0.00049 |
| gi 19283 emb CAA32218.1     | nitrate reductase [Solanu | ( 911) | 200 | 55.0 | 0.00017 | gi 210065295 gb EEA19389.1   | cytochrome B2, putativ   | ( 489) | 190 | 52.5 | 0.0005  |
| gi 21165533 dbj BAB93534.1  | nitrate reductase [Sol    | ( 911) | 200 | 55.0 | 0.00017 | gi 119397585 gb EAW08016.1   | mitochondrial cytochro   | ( 495) | 190 | 52.5 | 0.00051 |
| gi 1946812 gb AAB52786.1    | NADH nitrate reductase    | ( 911) | 200 | 55.0 | 0.00017 | gi 143664847 gb EDG15129.1   | hypothetical protein G   | ( 408) | 189 | 52.2 | 0.00051 |
| gi 1673613 gb AAB18985.1    | NADH nitrate reductase    | ( 911) | 200 | 55.0 | 0.00017 | gi 140226880 gb EAP56054.1   | hypothetical protein G   | ( 188) | 185 | 51.1 | 0.00051 |
| gi 484212 gb AAA33712.1     | nitrate reductase apoenzy | ( 915) | 200 | 55.0 | 0.00017 | gi 211969281 gb EEB04477.1   | cytochrome b5, putativ   | ( 233) | 186 | 51.4 | 0.00052 |
| gi 210092261 gb EEA04092.1  | hypothetical protein B    | ( 527) | 197 | 54.1 | 0.00017 | gi 662902 emb CAA58909.1     | nitrate reductase (NADH) | ( 920) | 193 | 53.4 | 0.00052 |
| gi 140236009 gb ECK45013.1  | hypothetical protein G    | ( 309) | 194 | 53.3 | 0.00018 | gi 1402636 dbj BAA13047.1    | nitrate reductase [Spin  | ( 926) | 193 | 53.4 | 0.00053 |
| gi 205278020 gb ACI01639.1  | nitrate reductase [Sol    | ( 270) | 193 | 53.0 | 0.00019 | gi 170119 gb AAA34033.1      | NADH nitrate reductase   | ( 926) | 193 | 53.4 | 0.00053 |
| gi 142677129 gb ECZ78134.1  | hypothetical protein G    | ( 356) | 194 | 53.3 | 0.0002  | gi 137999647 gb EBX20320.1   | hypothetical protein G   | ( 146) | 183 | 50.6 | 0.00057 |
| gi 83772415 dbj BAE62545.1  | unnamed protein produc    | ( 452) | 195 | 53.6 | 0.00021 | gi 159130941 gb EDP56054.1   | mitochondrial cytochro   | ( 471) | 189 | 52.3 | 0.00057 |
| gi 57226795 gb AAW43255.1   | conserved hypothetical    | ( 552) | 196 | 53.9 | 0.00021 | gi 119410655 gb EAW20601.1   | mitochondrial cytochro   | ( 500) | 189 | 52.3 | 0.0006  |
| gi 118174031 gb ABK74927.1  | Fatty acid desaturase     | ( 464) | 195 | 53.6 | 0.00022 | gi 134077581 emb CAK96725.1  | unnamed protein produ    | ( 343) | 187 | 51.7 | 0.00061 |
| gi 89299034 gb ABR97022.1   | Cytochrome b5-like Heme   | ( 697) | 197 | 54.2 | 0.00022 | gi 121886513 gb EAX92092.1   | Cytochrome b5-like Hem   | ( 89)  | 180 | 49.8 | 0.00062 |
| gi 138161750 gb EBY11016.1  | hypothetical protein G    | ( 217) | 191 | 52.5 | 0.00022 | gi 108879915 gb EAT44140.1   | cytochrome b5, putativ   | ( 113) | 181 | 50.0 | 0.00064 |
| gi 210069038 gb EEA23129.1  | mitochondrial cytochro    | ( 498) | 195 | 53.7 | 0.00023 | gi 155707473 gb ABU33122.1   | Sequence 115 from pate   | ( 470) | 188 | 52.0 | 0.00067 |
| gi 164644844 gb EDR09093.1  | predicted protein [Lac    | ( 506) | 195 | 53.7 | 0.00023 | gi 112053841 gb ABH96552.1   | Sequence 20 from paten   | ( 470) | 188 | 52.0 | 0.00067 |
| gi 143152211 gb EDD19579.1  | hypothetical protein G    | ( 356) | 193 | 53.1 | 0.00024 | gi 40161451 gb AAR67464.1    | Sequence 20 from patent  | ( 470) | 188 | 52.0 | 0.00067 |

|                             |                           |        |     |      |         |                             |                           |        |     |      |        |
|-----------------------------|---------------------------|--------|-----|------|---------|-----------------------------|---------------------------|--------|-----|------|--------|
| gi 155709335 gb ABU33984.1  | Sequence 20 from paten    | ( 470) | 188 | 52.0 | 0.00067 | gi 29536058 emb CAD87607.1  | unnamed protein produc    | ( 374) | 183 | 50.8 | 0.0012 |
| gi 68125846 emb CAJ04079.1  | hypothetical protein,     | ( 179) | 183 | 50.6 | 0.00068 | gi 28564443 emb CAD24672.1  | delta 12-acyl-lipid-co    | ( 374) | 183 | 50.8 | 0.0012 |
| gi 162691463 gb EDQ77825.1  | predicted protein [Phy    | ( 150) | 182 | 50.4 | 0.00069 | gi 134059988 emb CAM41946.1 | cytochrome b5, putati     | ( 142) | 178 | 49.4 | 0.0012 |
| gi 135130087 gb EBF68498.1  | hypothetical protein G    | ( 187) | 183 | 50.6 | 0.0007  | gi 2385386 emb CAA04758.1   | L-mandelate dehydrogena   | ( 565) | 185 | 51.4 | 0.0013 |
| gi 392992 gb AAA95940.1     | nitrate reductase         | ( 890) | 191 | 52.9 | 0.0007  | gi 145020433 gb EDK04562.1  | hypothetical protein M    | ( 468) | 184 | 51.1 | 0.0013 |
| gi 209556396 gb EEA06441.1  | cytochrome b5-like hem    | ( 232) | 184 | 50.9 | 0.00071 | gi 29536063 emb CAD87609.1  | unnamed protein produc    | ( 395) | 183 | 50.8 | 0.0013 |
| gi 157322867 gb ABV41964.1  | fatty acid desaturase     | ( 360) | 186 | 51.5 | 0.00074 | gi 213509831 emb CAS92465.1 | unnamed protein produ     | ( 493) | 184 | 51.1 | 0.0013 |
| gi 142975620 gb EDB91603.1  | hypothetical protein G    | ( 137) | 181 | 50.1 | 0.00075 | gi 213509819 emb CAS92459.1 | unnamed protein produ     | ( 494) | 184 | 51.1 | 0.0013 |
| gi 121913911 gb EAY18716.1  | Cytochrome b5-like Hem    | ( 94)  | 179 | 49.5 | 0.00075 | gi 150407977 gb EDN03518.1  | predicted protein [Aje    | ( 337) | 182 | 50.6 | 0.0013 |
| gi 140259971 gb ECK61602.1  | hypothetical protein G    | ( 250) | 184 | 50.9 | 0.00076 | gi 139566716 gb ECF95093.1  | hypothetical protein G    | ( 105) | 176 | 48.9 | 0.0013 |
| gi 143013199 gb EDC18014.1  | hypothetical protein G    | ( 175) | 182 | 50.4 | 0.00078 | gi 160814781 emb CAP40235.1 | unnamed protein produ     | ( 519) | 184 | 51.1 | 0.0014 |
| gi 150411405 gb EDN06793.1  | hypothetical protein H    | ( 565) | 188 | 52.1 | 0.00078 | gi 71842217 gb AAZ43257.1   | delta-4 fatty acid desa   | ( 519) | 184 | 51.1 | 0.0014 |
| gi 76059224 emb CAJ30809.1  | unnamed protein produc    | ( 480) | 187 | 51.8 | 0.0008  | gi 90300343 gb EAS29974.1   | hypothetical protein CI   | ( 631) | 185 | 51.4 | 0.0014 |
| gi 60220724 emb CAI58861.1  | unnamed protein produc    | ( 480) | 187 | 51.8 | 0.0008  | gi 111067352 gb EAT88472.1  | hypothetical protein S    | ( 636) | 185 | 51.4 | 0.0014 |
| gi 162682478 gb EDQ68896.1  | predicted protein [Phy    | ( 480) | 187 | 51.8 | 0.0008  | gi 170942296 emb CAP67948.1 | unnamed protein produ     | ( 524) | 184 | 51.1 | 0.0014 |
| gi 126633740 emb CAM55826.1 | unnamed protein produ     | ( 480) | 187 | 51.8 | 0.0008  | gi 139074519 gb ECD23377.1  | hypothetical protein G    | ( 254) | 180 | 50.0 | 0.0015 |
| gi 83765628 dbj BAE55771.1  | unnamed protein produc    | ( 480) | 187 | 51.8 | 0.0008  | gi 21900889 emb CAD2498.1   | unnamed protein produc    | ( 456) | 183 | 50.9 | 0.0015 |
| gi 930002 emb CAA31787.1    | nitrate reductase NR2     | ( 396) | 186 | 51.5 | 0.0008  | gi 16033740 gb AAL13311.1   | delta-5 fatty acid desa   | ( 456) | 183 | 50.9 | 0.0015 |
| gi 136576492 gb EBP05349.1  | hypothetical protein G    | ( 151) | 181 | 50.1 | 0.00081 | gi 136926981 gb EBR23003.1  | hypothetical protein G    | ( 80)  | 174 | 48.3 | 0.0015 |
| gi 138959575 gb ECC59286.1  | hypothetical protein G    | ( 272) | 184 | 51.0 | 0.00081 | gi 134068897 emb CAM59831.1 | hypothetical protein,     | ( 179) | 178 | 49.5 | 0.0015 |
| gi 136881011 gb EBR02171.1  | hypothetical protein G    | ( 186) | 182 | 50.4 | 0.00082 | gi 197035436 gb ACH16336.1  | Sequence 12 from paten    | ( 395) | 182 | 50.6 | 0.0015 |
| gi 119413109 gb EAW23050.1  | mitochondrial cytochro    | ( 497) | 187 | 51.8 | 0.00082 | gi 28371825 gb AAO37753.1   | fatty acid conjugase [P   | ( 395) | 182 | 50.6 | 0.0015 |
| gi 1762632 gb AAB39555.1    | nitrate reductase         | ( 497) | 187 | 51.8 | 0.00082 | gi 138781865 gb ECB83816.1  | hypothetical protein G    | ( 153) | 177 | 49.2 | 0.0016 |
| gi 134074829 emb CAK38943.1 | unnamed protein produ     | ( 507) | 187 | 51.8 | 0.00084 | gi 150847876 gb EDN23069.1  | hypothetical protein B    | ( 496) | 183 | 50.9 | 0.0016 |
| gi 124403861 emb CAK69321.1 | unnamed protein produ     | ( 513) | 187 | 51.8 | 0.00085 | gi 135413339 gb EBH47135.1  | hypothetical protein G    | ( 337) | 181 | 50.3 | 0.0016 |
| gi 139936283 gb ECI48758.1  | hypothetical protein G    | ( 109) | 179 | 49.6 | 0.00085 | gi 24474446 gb AAN15927.1   | nitrate reductase [Tili   | ( 894) | 186 | 51.7 | 0.0016 |
| gi 9797763 gb AAF98581.1    | AC013427_24 Strong simila | ( 135) | 180 | 49.9 | 0.00087 | gi 296099 emb CAA80270.1    | nitrate reductase [Fusar  | ( 905) | 186 | 51.7 | 0.0016 |
| gi 26450007 dbj BAC42124.1  | putative cytochrome b5    | ( 135) | 180 | 49.9 | 0.00087 | gi 150413720 gb EDN09103.1  | conserved hypothetical    | ( 511) | 183 | 50.9 | 0.0016 |
| gi 12083238 gb AAG48778.1   | AF332415_1 putative cyto  | ( 135) | 180 | 49.9 | 0.00087 | gi 14194133 gb AAK56261.1   | AF367272_1 Atlg37130/F28  | ( 917) | 186 | 51.7 | 0.0016 |
| gi 21536989 gb AAM61330.1   | cytochrome b5 [Arabidop   | ( 135) | 180 | 49.9 | 0.00087 | gi 23296643 gb AAN13137.1   | putative nitrate reduct   | ( 917) | 186 | 51.7 | 0.0016 |
| gi 12321181 gb AAG50683.1   | AC079829_16 cytochrome b  | ( 135) | 180 | 49.9 | 0.00087 | gi 16930703 gb AAL32017.1   | AF436835_1 Atlg37130/F28  | ( 917) | 186 | 51.7 | 0.0016 |
| gi 152028791 gb ABS26559.1  | fatty acid desaturase     | ( 370) | 185 | 51.3 | 0.00089 | gi 166782 gb AAA32830.1     | nitrate reductase (EC 1.6 | ( 917) | 186 | 51.7 | 0.0016 |
| gi 58428663 gb AAW77700.1   | conserved hypothetical    | ( 373) | 185 | 51.3 | 0.0009  | gi 22137030 gb AAM91360.1   | Atlg37130/F28L22_2 [Ara   | ( 917) | 186 | 51.7 | 0.0016 |
| gi 84369783 dbj BAE70941.1  | conserved hypothetical    | ( 373) | 185 | 51.3 | 0.0009  | gi 14532580 gb AAK64018.1   | putative nitrate reduct   | ( 917) | 186 | 51.7 | 0.0016 |
| gi 188519053 gb ACD56998.1  | DesA3_2 [Xanthomonas o    | ( 373) | 185 | 51.3 | 0.0009  | gi 110740277 dbj BAF02035.1 | nitrate reductase [Ar     | ( 917) | 186 | 51.7 | 0.0016 |
| gi 156214583 gb EDO35566.1  | predicted protein [Nem    | ( 65)  | 176 | 48.8 | 0.0009  | gi 14335008 gb AAK59768.1   | Atlg37130/F28L22_2 [Ara   | ( 917) | 186 | 51.7 | 0.0016 |
| gi 62088292 dbj BAD92593.1  | fatty acid desaturase     | ( 315) | 184 | 51.0 | 0.00092 | gi 6623972 gb AAF19225.1    | AC007505_1 nitrate reduct | ( 917) | 186 | 51.7 | 0.0016 |
| gi 210123813 gb EEA71513.1  | hypothetical protein B    | ( 469) | 186 | 51.6 | 0.00092 | gi 110742690 dbj BAE99256.1 | nitrate reductase [Ar     | ( 917) | 186 | 51.7 | 0.0016 |
| gi 141169097 gb ECQ10929.1  | hypothetical protein G    | ( 120) | 179 | 49.6 | 0.00092 | gi 159123640 gb EDP48759.1  | fumarate reductase Osm    | ( 630) | 184 | 51.2 | 0.0016 |
| gi 508315101 emb CAH05235.1 | unnamed protein produc    | ( 480) | 186 | 51.6 | 0.00094 | gi 187985084 gb EDU50572.1  | fumarate reductase [Py    | ( 636) | 184 | 51.2 | 0.0016 |
| gi 142615642 gb ECZ34654.1  | hypothetical protein G    | ( 403) | 185 | 51.3 | 0.00096 | gi 143254709 gb EDD92710.1  | hypothetical protein G    | ( 356) | 181 | 50.3 | 0.0016 |
| gi 55845943 gb AAV66996.1   | nitrate reductase [Phae   | ( 910) | 189 | 52.4 | 0.00098 | gi 156531881 gb ABU76707.1  | hypothetical protein E    | ( 363) | 181 | 50.3 | 0.0017 |
| gi 32307604 gb AAP79207.1   | nitrate reductase [Bige   | ( 160) | 180 | 49.9 | 0.001   | gi 139953648 gb ECI60401.1  | hypothetical protein G    | ( 63)  | 172 | 47.8 | 0.0017 |
| gi 1762628 gb AAB39553.1    | nitrate reductase         | ( 629) | 187 | 51.9 | 0.001   | gi 3038 emb CAA43600.1      | nitrate reductase (NADPH) | ( 982) | 186 | 51.8 | 0.0017 |
| gi 3169157 gb AAC23396.1    | BC269730_1 [Homo sapiens  | ( 352) | 184 | 51.0 | 0.001   | gi 114187560 gb EAU29260.1  | cytochrome b5 [Aspergi    | ( 463) | 182 | 50.6 | 0.0017 |
| gi 150414638 gb EDN10000.1  | predicted protein [Aje    | ( 133) | 179 | 49.6 | 0.001   | gi 139852169 gb ECH91585.1  | hypothetical protein G    | ( 260) | 179 | 49.8 | 0.0017 |
| gi 112053844 gb ABH96554.1  | Sequence 31 from paten    | ( 439) | 185 | 51.3 | 0.001   | gi 29536222 emb CAD87611.1  | unnamed protein produc    | ( 477) | 182 | 50.6 | 0.0018 |
| gi 170181205 gb ACB11556.1  | putative delta-5 fatty    | ( 453) | 185 | 51.3 | 0.0011  | gi 23894018 emb CAD53323.1  | delta 5 fatty acid des    | ( 477) | 182 | 50.6 | 0.0018 |
| gi 142358951 gb ECX50978.1  | hypothetical protein G    | ( 253) | 182 | 50.5 | 0.0011  | gi 211590429 emb CAP96617.1 | Pc21g17200 [Penicilli     | (1048) | 186 | 51.8 | 0.0018 |
| gi 213509833 emb CAS92466.1 | unnamed protein produ     | ( 560) | 186 | 51.6 | 0.0011  | gi 167279701 gb ABZ32565.1  | Sequence 6503 from pat    | ( 103) | 174 | 48.4 | 0.0018 |
| gi 136349935 gb EBN57019.1  | hypothetical protein G    | ( 100) | 177 | 49.1 | 0.0011  | gi 85539725 emb CAJ58492.1  | C. elegans protein D20    | ( 103) | 174 | 48.4 | 0.0018 |
| gi 164644646 gb EDR08895.1  | fumarate reductase [La    | ( 584) | 186 | 51.6 | 0.0011  | gi 139318590 gb ECES1927.1  | hypothetical protein G    | ( 185) | 177 | 49.3 | 0.0018 |
| gi 2385388 emb CAA04759.1   | L-mandelate dehydrogena   | ( 491) | 185 | 51.3 | 0.0011  | gi 134838726 gb EBD76575.1  | hypothetical protein G    | ( 274) | 179 | 49.8 | 0.0018 |
| gi 119713291 gb ABL97356.1  | putative hydrocarbon o    | ( 333) | 183 | 50.8 | 0.0011  | gi 154691545 gb EDN91283.1  | hypothetical protein S    | ( 497) | 182 | 50.7 | 0.0018 |
| gi 119403082 gb EAW13502.1  | mitochondrial cytochro    | ( 500) | 185 | 51.4 | 0.0011  | gi 143290261 gb EDE14484.1  | hypothetical protein G    | ( 337) | 180 | 50.1 | 0.0018 |
| gi 150857509 gb EDN32701.1  | L-lactate ferricytochr    | ( 509) | 185 | 51.4 | 0.0012  | gi 17925 emb CAA38031.1     | nitrate reductase (NADH)  | ( 898) | 185 | 51.5 | 0.0018 |
| gi 141337949 gb ECR14035.1  | hypothetical protein G    | ( 237) | 181 | 50.2 | 0.0012  | gi 169241201 emb CAM66229.1 | Putative linoleoyl-Co     | ( 414) | 181 | 50.4 | 0.0019 |
| gi 118170746 gb ABK71642.1  | Fatty acid desaturase     | ( 363) | 183 | 50.8 | 0.0012  | gi 169990914 dbj BAG12906.1 | nitrate reductase [Fu     | ( 904) | 185 | 51.5 | 0.0019 |

|                             |                           |        |     |      |        |                             |                           |        |     |      |        |
|-----------------------------|---------------------------|--------|-----|------|--------|-----------------------------|---------------------------|--------|-----|------|--------|
| gi 169990912 dbj BAG12905.1 | nitrate reductase [Fu     | ( 904) | 185 | 51.5 | 0.0019 | gi 77799302 dbj BAE46746.1  | nitrate reductase [Nic    | ( 904) | 182 | 50.8 | 0.003  |
| gi 1561580 emb CAA62232.1   | nitrate reductase [Gibb   | ( 907) | 185 | 51.5 | 0.0019 | gi 19891 emb CAA32217.1     | nitrate reductase [Nicoti | ( 904) | 182 | 50.8 | 0.003  |
| gi 140162191 gb ECJ93962.1  | hypothetical protein G    | ( 159) | 176 | 49.0 | 0.0019 | gi 53127692 emb CAG31175.1  | hypothetical protein [    | ( 130) | 172 | 48.0 | 0.003  |
| gi 56204621 emb CAI19905.1  | cytochrome b5 reductas    | ( 109) | 174 | 48.4 | 0.0019 | gi 119404871 gb EAW15233.1  | fumarate reductase Osm    | ( 629) | 180 | 50.3 | 0.0031 |
| gi 56203195 emb CAI22326.1  | cytochrome b5 reductas    | ( 109) | 174 | 48.4 | 0.0019 | gi 134083573 emb CAL00488.1 | unnamed protein produ     | ( 629) | 180 | 50.3 | 0.0031 |
| gi 142094407 gb ECV54250.1  | hypothetical protein G    | ( 355) | 180 | 50.1 | 0.0019 | gi 119410250 gb EAW20197.1  | fumarate reductase Osm    | ( 630) | 180 | 50.3 | 0.0031 |
| gi 145018780 gb EDK03059.1  | hypothetical protein M    | ( 531) | 182 | 50.7 | 0.0019 | gi 158284105 gb EDP09855.1  | fatty acid desaturase     | (1675) | 185 | 51.7 | 0.0031 |
| gi 3342268 gb AAC39508.1    | delta 5 microsomal desat  | ( 446) | 181 | 50.4 | 0.002  | gi 157338493 emb CAO41844.1 | unnamed protein produ     | ( 134) | 172 | 48.0 | 0.0031 |
| gi 929750 emb CAA29497.1    | unnamed protein product   | ( 554) | 182 | 50.7 | 0.002  | gi 134984267 gb EBE73350.1  | hypothetical protein G    | ( 114) | 171 | 47.7 | 0.0032 |
| gi 141151192 gb ECP98183.1  | hypothetical protein G    | ( 142) | 175 | 48.7 | 0.002  | gi 685208 gb AAA96249.1     | nitrate reductase         | ( 95)  | 170 | 47.5 | 0.0032 |
| gi 118571949 gb ABL06700.1  | linoleoyl-CoA desatura    | ( 377) | 180 | 50.1 | 0.002  | gi 685165 gb AAA96246.1     | nitrate reductase         | ( 95)  | 170 | 47.5 | 0.0032 |
| gi 146145929 gb EAR91939.2  | Cytochrome b5-like Hem    | ( 215) | 177 | 49.3 | 0.002  | gi 1217984 emb CAA93814.1   | NADPH-hemoprotein reduc   | ( 147) | 172 | 48.0 | 0.0033 |
| gi 158455068 gb AAI20116.2  | CYB5B protein [Bos tau    | ( 146) | 175 | 48.7 | 0.0021 | gi 136618654 gb EBP32254.1  | hypothetical protein G    | ( 321) | 176 | 49.2 | 0.0033 |
| gi 138664058 gb ECB14808.1  | hypothetical protein G    | ( 329) | 179 | 49.9 | 0.0021 | gi 211584669 emb CAP74195.1 | Pcl4g00540 [Penicilli     | ( 475) | 178 | 49.7 | 0.0033 |
| gi 169242596 emb CAM63624.1 | Putative fatty acid d     | ( 407) | 180 | 50.1 | 0.0021 | gi 47028617 gb AAT09160.1   | delta-5 fatty acid desa   | ( 475) | 178 | 49.7 | 0.0033 |
| gi 119415489 gb EAW25427.1  | mitochondrial cytochro    | ( 495) | 181 | 50.4 | 0.0021 | gi 114197749 gb EAU39449.1  | conserved hypothetical    | ( 477) | 178 | 49.7 | 0.0034 |
| gi 83770938 dbj BAE61071.1  | unnamed protein produc    | ( 498) | 181 | 50.4 | 0.0022 | gi 930001 emb CAA31786.1    | nitrate reductase NR1     | ( 393) | 177 | 49.4 | 0.0034 |
| gi 1119241 gb AAG30576.1    | AF314093_1 nitrate reduc  | ( 914) | 184 | 51.3 | 0.0022 | gi 116056666 emb CAL52955.1 | Fatty acid desaturase     | ( 491) | 178 | 49.7 | 0.0034 |
| gi 124390907 emb CAK56448.1 | unnamed protein produ     | ( 513) | 181 | 50.4 | 0.0022 | gi 114193546 gb EAU35246.1  | cytochrome b2, mitocho    | ( 500) | 178 | 49.7 | 0.0035 |
| gi 114190305 gb EAU32005.1  | hypothetical protein A    | ( 626) | 182 | 50.7 | 0.0022 | gi 135714795 gb EBJ39076.1  | hypothetical protein G    | ( 279) | 175 | 48.9 | 0.0035 |
| gi 210064530 gb EAA261658.1 | fumarate reductase Osm    | ( 627) | 182 | 50.7 | 0.0022 | gi 144576240 gb ABO94309.1  | predicted protein [Ost    | ( 72)  | 168 | 46.9 | 0.0035 |
| gi 119710111 gb ABL96296.1  | delta-8 desaturase [Pa    | ( 427) | 180 | 50.2 | 0.0022 | gi 38567126 emb CAE76421.1  | related to fumarate re    | ( 616) | 179 | 50.0 | 0.0035 |
| gi 41394542 gb AAS02413.1   | hypothetical protein MA   | ( 110) | 173 | 48.2 | 0.0022 | gi 117663207 gb ABK55747.1  | nitrate reductase [Cuc    | ( 130) | 171 | 47.8 | 0.0035 |
| gi 155288785 gb ABT44389.1  | Sequence 131859 from p    | ( 93)  | 172 | 47.9 | 0.0023 | gi 154704002 gb EDO03741.1  | hypothetical protein S    | ( 629) | 179 | 50.0 | 0.0036 |
| gi 9951163 gb AAG08273.1    | AE004902_1 acyl-CoA delta | ( 370) | 179 | 49.9 | 0.0023 | gi 21900885 emb CAD42496.1  | unnamed protein produc    | ( 519) | 178 | 49.7 | 0.0036 |
| gi 115588258 gb ABJ14273.1  | putative fatty acid de    | ( 370) | 179 | 49.9 | 0.0023 | gi 160814779 emb CAP40234.1 | unnamed protein produ     | ( 519) | 178 | 49.7 | 0.0036 |
| gi 126197595 gb EAG261658.1 | conserved hypothetical    | ( 370) | 179 | 49.9 | 0.0023 | gi 20069125 gb AAM09688.1   | AF489589_1 delta-4 fatty  | ( 519) | 178 | 49.7 | 0.0036 |
| gi 126170324 gb EAG25835.1  | conserved hypothetical    | ( 370) | 179 | 49.9 | 0.0023 | gi 160830342 emb CAP40242.1 | unnamed protein produ     | ( 519) | 178 | 49.7 | 0.0036 |
| gi 194150702 gb EDW66386.1  | GJ16001 [Drosophila vi    | ( 117) | 173 | 48.2 | 0.0024 | gi 141255967 gb ECQ70414.1  | hypothetical protein G    | ( 239) | 174 | 48.6 | 0.0036 |
| gi 140353702 gb ECL19512.1  | hypothetical protein G    | ( 266) | 177 | 49.3 | 0.0024 | gi 34979829 gb AAQ83903.1   | flavo-hemoprotein b5/b5R  | ( 435) | 177 | 49.5 | 0.0037 |
| gi 134060943 emb CAM37961.1 | hypothetical protein,     | ( 219) | 176 | 49.1 | 0.0024 | gi 150960739 gb ABR82764.1  | conserved hypothetical    | ( 362) | 176 | 49.2 | 0.0037 |
| gi 196192957 gb EDX87916.1  | Fatty acid desaturase     | ( 399) | 179 | 49.9 | 0.0025 | gi 56679722 gb AAV96388.1   | monooxygenase, putative   | ( 563) | 178 | 49.8 | 0.0039 |
| gi 76154600 gb AA26053.2    | SJCHGC05696 protein [Sc   | ( 223) | 176 | 49.1 | 0.0025 | gi 12007117 gb AAG45053.1   | AF307840_1 hemoflavoprot  | ( 486) | 177 | 49.5 | 0.004  |
| gi 143334463 gb EDE39552.1  | hypothetical protein G    | ( 400) | 179 | 49.9 | 0.0025 | gi 51330724 gb AAH80240.1   | Cytochrome b5 reductase   | ( 486) | 177 | 49.5 | 0.004  |
| gi 134066684 emb CAM44486.1 | delta8 fatty acid des     | ( 400) | 179 | 49.9 | 0.0025 | gi 34979827 gb AAQ83902.1   | flavo-hemoprotein b5/b5R  | ( 486) | 177 | 49.5 | 0.004  |
| gi 46805324 dbj BAD16843.1  | putative nitrate reduc    | ( 889) | 183 | 51.0 | 0.0025 | gi 1762630 gb AAB39554.1    | nitrate reductase         | ( 487) | 177 | 49.5 | 0.004  |
| gi 215717065 dbj BAG95428.1 | unnamed protein produ     | ( 889) | 183 | 51.0 | 0.0025 | gi 2731816 gb AAB93560.1    | nitrate reductase [Glyci  | ( 875) | 180 | 50.3 | 0.004  |
| gi 113537784 dbj BAF10167.1 | Os02g0770800 [Oryza s     | ( 889) | 183 | 51.0 | 0.0025 | gi 149018966 gb EDL77607.1  | cytochrome b5 reductas    | ( 496) | 177 | 49.5 | 0.0041 |
| gi 135205268 gb EBG16172.1  | hypothetical protein G    | ( 127) | 173 | 48.2 | 0.0025 | gi 4389417 gb AAD19790.1    | nitrate reductase [Glyci  | ( 890) | 180 | 50.3 | 0.0041 |
| gi 2894356 emb CAA74005.1   | nitrate reductase (NADP   | ( 891) | 183 | 51.0 | 0.0025 | gi 537627 gb AAA96813.1     | inducible nitrate reducta | ( 890) | 180 | 50.3 | 0.0041 |
| gi 3378500 emb CAA08857.1   | nitrate reductase [Phae   | ( 891) | 183 | 51.0 | 0.0025 | gi 90303484 gb EAS33115.1   | hypothetical protein CI   | ( 504) | 177 | 49.5 | 0.0041 |
| gi 211582852 emb CAP81055.1 | Pc12g14280 [Penicilli     | ( 497) | 180 | 50.2 | 0.0025 | gi 56759130 gb AAW27705.1   | SJCHGC03671 protein [Sc   | ( 129) | 170 | 47.5 | 0.0041 |
| gi 197704680 gb EDY50492.1  | delta fatty acid desat    | ( 338) | 178 | 49.6 | 0.0025 | gi 187985580 gb EDU51068.1  | L-lactate dehydrogenas    | ( 509) | 177 | 49.5 | 0.0042 |
| gi 213509821 emb CAS92460.1 | unnamed protein produ     | ( 502) | 180 | 50.2 | 0.0025 | gi 212512924 gb EEB15590.1  | NADH-cytochrome b5 red    | ( 509) | 177 | 49.5 | 0.0042 |
| gi 19889 emb CAA32216.1     | nitrate reductase [Nicoti | ( 904) | 183 | 51.0 | 0.0026 | gi 14334876 gb AAK59616.1   | putative nitrate reduct   | ( 917) | 180 | 50.4 | 0.0042 |
| gi 237969 gb AAB20155.1     | nitrate reductase heme do | ( 74)  | 170 | 47.4 | 0.0026 | gi 140871229 gb ECO07207.1  | hypothetical protein G    | ( 89)  | 168 | 47.0 | 0.0042 |
| gi 81673810 gb AAI09570.1   | Cytochrome b5 reductase   | ( 520) | 180 | 50.2 | 0.0026 | gi 116000309 emb CAL49989.1 | delta-6 fatty acid de     | ( 237) | 173 | 48.4 | 0.0042 |
| gi 83765492 dbj BAE55635.1  | unnamed protein produc    | ( 633) | 181 | 50.5 | 0.0026 | gi 60220808 emb CAI58903.1  | unnamed protein produc    | ( 237) | 173 | 48.4 | 0.0042 |
| gi 164644197 gb EDR08447.1  | acyl-CoA-dehydrogenase    | ( 522) | 180 | 50.2 | 0.0026 | gi 126633750 emb CAM55831.1 | unnamed protein produ     | ( 237) | 173 | 48.4 | 0.0042 |
| gi 57229321 gb AAW45754.1   | fumarate reductase (NAD   | ( 635) | 181 | 50.5 | 0.0026 | gi 76059308 emb CAJ30848.1  | unnamed protein produc    | ( 237) | 173 | 48.4 | 0.0042 |
| gi 685155 gb AAA96242.1     | nitrate reductase         | ( 91)  | 171 | 47.7 | 0.0026 | gi 110565251 emb CAL23342.1 | unnamed protein produ     | ( 237) | 173 | 48.4 | 0.0042 |
| gi 210122039 gb EAA69748.1  | hypothetical protein B    | (2502) | 188 | 52.5 | 0.0026 | gi 149018965 gb EDL77606.1  | cytochrome b5 reductas    | ( 520) | 177 | 49.5 | 0.0042 |
| gi 161162346 emb CAN93651.1 | putative fatty acid d     | ( 366) | 178 | 49.7 | 0.0027 | gi 190579425 gb EDV19520.1  | hypothetical protein T    | ( 75)  | 167 | 46.7 | 0.0043 |
| gi 136562151 gb EBO96211.1  | hypothetical protein G    | ( 119) | 172 | 48.0 | 0.0028 | gi 145573905 gb ABP83437.1  | fatty acid desaturase     | ( 360) | 175 | 49.0 | 0.0043 |
| gi 134662566 gb EBC68085.1  | hypothetical protein G    | ( 101) | 171 | 47.7 | 0.0029 | gi 118483438 gb ABK93619.1  | unknown [Populus trich    | ( 136) | 170 | 47.6 | 0.0043 |
| gi 6759823 gb AAF28059.1    | AF123281_1 nitrate reduct | ( 870) | 182 | 50.8 | 0.0029 | gi 50844677 gb AAT84460.1   | cytochrome b5 isoform C   | ( 136) | 170 | 47.6 | 0.0043 |
| gi 119407312 gb EAW17262.1  | NADH-cytochrome B5 red    | ( 497) | 179 | 50.0 | 0.003  | gi 118485373 gb ABK94544.1  | unknown [Populus trich    | ( 136) | 170 | 47.6 | 0.0043 |
| gi 109659810 dbj BAE96752.1 | nitrate reductase 2 [     | ( 904) | 182 | 50.8 | 0.003  | gi 119569038 gb EAW48653.1  | hCG401131, isoform CRA    | ( 309) | 174 | 48.7 | 0.0045 |

|   |   |
|---|---|
| gi 49641322 emb CAH02583.1  KLLA0B14795p [Kluyvero ( 556) 177 49.5 0.0045 | gi 74199582 dbj BAE41470.1  unnamed protein produc ( 536) 175 49.1 0.006  |
| gi 143972813 gb EDH95743.1  hypothetical protein G ( 258) 173 48.4 0.0045 | gi 139517562 gb ECF61542.1  hypothetical protein G ( 300) 172 48.2 0.006  |
| gi 108879914 gb EAT44139.1  cytochrome b5, putativ ( 119) 169 47.3 0.0045 | gi 685206 gb AAA96248.1  nitrate reductase ( 94) 166 46.5 0.006           |
| gi 194032857 emb CAQ77148.1  nitrate reductase [Ar ( 845) 179 50.1 0.0046 | gi 59750024 gb AAW98847.1  Sequence 16410 from pat ( 140) 168 47.1 0.0061 |
| gi 210071681 gb EEA25770.1  cytochrome b5 reductas ( 472) 176 49.3 0.0046 | gi 144976091 gb ABP13186.1  Sequence 8 from patent ( 172) 169 47.4 0.0061 |
| gi 58014091 gb AAW63048.1  delta-6 fatty acid desa ( 153) 170 47.6 0.0047 | gi 189860252 gb ACE35658.1  Sequence 2 from patent ( 383) 173 48.5 0.0062 |
| gi 163776521 gb EDQ90140.1  predicted protein [Mon ( 599) 177 49.6 0.0048 | gi 189846875 gb ACE26373.1  Sequence 128 from pate ( 383) 173 48.5 0.0062 |
| gi 213509815 emb CAS92455.1  unnamed protein produ ( 497) 176 49.3 0.0048 | gi 189704782 gb ACE16111.1  Sequence 128 from pate ( 383) 173 48.5 0.0062 |
| gi 134081526 emb CAK41962.1  unnamed protein produ ( 500) 176 49.3 0.0048 | gi 8886726 gb AAF80560.1 AF192486_1 omega-6 fatty ( 383) 173 48.5 0.0062  |
| gi 139399268 gb ECE84652.1  hypothetical protein G ( 192) 171 47.9 0.0049 | gi 59896214 gb AAX11454.1  microsomal oleic acid d ( 383) 173 48.5 0.0062 |
| gi 145010236 gb EDJ94892.1  hypothetical protein M ( 509) 176 49.3 0.0049 | gi 141474689 gb ECS01829.1  hypothetical protein G ( 214) 170 47.7 0.0063 |
| gi 88181913 gb EAQ89381.1  hypothetical protein CH ( 509) 176 49.3 0.0049 | gi 138070317 gb EBX57494.1  hypothetical protein G ( 81) 165 46.3 0.0063  |
| gi 207008942 emb CAR80385.1  unnamed protein produ ( 419) 175 49.0 0.0049 | gi 138737529 gb ECB66494.1  hypothetical protein G ( 262) 171 48.0 0.0063 |
| gi 136950397 gb EBR36166.1  hypothetical protein G ( 242) 172 48.2 0.005  | gi 35210731 dbj BAC88112.1  gl10171 [Gloeobacter v ( 390) 173 48.5 0.0063 |
| gi 148694572 gb EDL26519.1  mCG11884, isoform CRA_ ( 442) 175 49.0 0.0051 | gi 158283021 gb EDP08772.1  flavohemoprotein b5/b5 ( 182) 169 47.4 0.0064 |
| gi 145010043 gb EDJ94699.1  conserved hypothetical ( 540) 176 49.3 0.0051 | gi 189053712 dbj BAG35964.1  unnamed protein produ ( 487) 174 48.8 0.0065 |
| gi 685157 gb AAA96243.1  nitrate reductase ( 94) 167 46.8 0.0051          | gi 155082042 gb ABS94877.1  Sequence 16 from paten ( 487) 174 48.8 0.0065 |
| gi 34979825 gb AAQ83901.1  flavohemoprotein b5/b5R ( 451) 175 49.0 0.0052 | gi 6166392 gb AAF04812.1 AF169803_1 flavohemoprote ( 487) 174 48.8 0.0065 |
| gi 685159 gb AAA96250.1  nitrate reductase ( 95) 167 46.8 0.0052          | gi 119569037 gb EAW48652.1  hCG401131, isoform CRA ( 487) 174 48.8 0.0065 |
| gi 685163 gb AAA96245.1  nitrate reductase ( 95) 167 46.8 0.0052          | gi 67588749 gb AAY73180.1  Sequence 16 from patent ( 487) 174 48.8 0.0065 |
| gi 685167 gb AAA96247.1  nitrate reductase ( 95) 167 46.8 0.0052          | gi 108868602 gb EAT32827.1  cytochrome b5, putativ ( 103) 166 46.6 0.0065 |
| gi 685161 gb AAA96244.1  nitrate reductase ( 95) 167 46.8 0.0052          | gi 134991760 gb EBE78443.1  hypothetical protein G ( 333) 172 48.2 0.0065 |
| gi 134067939 emb CAM66221.1  cytochrome b5, putati ( 142) 169 47.3 0.0052 | gi 44890326 gb AAH66748.1  Cytochrome b5 type B [D ( 153) 168 47.1 0.0065 |
| gi 68124823 gb CAJ02657.1  cytochrome b5, putativ ( 142) 169 47.3 0.0052  | gi 108873820 gb EAT38045.1  cytochrome B5 (cytb5) ( 104) 166 46.6 0.0066  |
| gi 194160147 gb EDW75048.1  GK19965 [Drosophila wi ( 118) 168 47.1 0.0053 | gi 24030478 gb AAN41389.1  putative nitrate reduct ( 917) 177 49.7 0.0067 |
| gi 60392574 gb AAX19393.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053 | gi 22757 emb CAA79494.1  nitrate reductase [Arabid ( 917) 177 49.7 0.0067 |
| gi 60392576 gb AAX19394.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053 | gi 15983499 gb AAL11617.1 AF424624_1 Atlg77760/T32 ( 917) 177 49.7 0.0067 |
| gi 60392578 gb AAX19395.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053 | gi 12323295 gb AAG51627.1 AC012193_9 nitrate reduc ( 917) 177 49.7 0.0067 |
| gi 18418651 gb AAL68982.1 AF251843_1 delta-12 olea ( 383) 174 48.7 0.0053 | gi 20259345 gb AAM13997.1  putative nitrate reduct ( 917) 177 49.7 0.0067 |
| gi 60392572 gb AAX19392.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053 | gi 142125111 gb ECV77356.1  hypothetical protein G ( 89) 165 46.3 0.0068  |
| gi 60392580 gb AAX19396.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053 | gi 164640618 gb EDR04882.1  acyl-CoA-dehydrogenase ( 514) 174 48.8 0.0068 |
| gi 134055511 emb CAK37158.1  unnamed protein produ ( 475) 175 49.0 0.0054 | gi 148878755 emb CAD91715.2  C. elegans protein Y5 ( 516) 174 48.8 0.0068 |
| gi 74195406 dbj BAE39522.1  unnamed protein produc ( 477) 175 49.0 0.0054 | gi 14530946 gb AAK63186.1  probable acyl-CoA dehyd ( 520) 174 48.8 0.0068 |
| gi 3633 emb CAA26959.1  unnamed protein product [S ( 591) 176 49.3 0.0055 | gi 119569035 gb EAW48650.1  hCG401131, isoform CRA ( 521) 174 48.8 0.0068 |
| gi 213509813 emb CAS92454.1  unnamed protein produ ( 591) 176 49.3 0.0055 | gi 123246238 emb CAI19904.2  cytochrome b5 reducta ( 521) 174 48.8 0.0068 |
| gi 190408190 gb EDV11455.1  L-lactate cytochrome c ( 591) 176 49.3 0.0055 | gi 71052101 gb AAH25380.2  Cytochrome b5 reductase ( 521) 174 48.8 0.0068 |
| gi 577142 emb CAA86721.1  cytochrome b2 precursor ( 591) 176 49.3 0.0055  | gi 123231684 emb CAI22325.2  cytochrome b5 reducta ( 521) 174 48.8 0.0068 |
| gi 66968234 gb AAY59538.1  nitrate reductase [Cyli ( 873) 178 49.9 0.0055 | gi 167882814 gb ACA06109.1  cytochrome b5 reductas ( 521) 174 48.8 0.0068 |
| gi 90307490 gb EAS37121.1  hypothetical protein CI ( 492) 175 49.0 0.0056 | gi 89267449 emb CAJ83762.1  novel protein similar ( 523) 174 48.8 0.0069  |
| gi 148694571 gb EDL26518.1  mCG11884, isoform CRA_ ( 493) 175 49.0 0.0056 | gi 194162158 gb EDW77059.1  GK22167 [Drosophila wi ( 528) 174 48.8 0.0069 |
| gi 12802901 gb AAK08116.1 AF338818_1 flavohemoprot ( 494) 175 49.0 0.0056 | gi 116059990 emb CAL56049.1  Nia, nitrate reductas ( 952) 177 49.7 0.007  |
| gi 26354983 dbj BAC41118.1  unnamed protein produc ( 494) 175 49.0 0.0056 | gi 44984185 gb AAS53151.1  AFL223Wp [Ashbya gossyp ( 165) 168 47.1 0.007  |
| gi 111069742 gb EAT90862.1  hypothetical protein S ( 496) 175 49.0 0.0056 | gi 39545945 gb AAR28035.1  delta-5 desaturase [Mor ( 446) 173 48.6 0.0071 |
| gi 159122277 gb EDP47399.1  mitochondrial cytochro ( 500) 175 49.0 0.0056 | gi 137074039 gb EBS06013.1  hypothetical protein G ( 207) 169 47.4 0.0071 |
| gi 34979823 gb AAQ83900.1  flavohemoprotein b5/b5R ( 502) 175 49.0 0.0057 | gi 148878754 gb AAQ71721.2  C. elegans protein Y5 ( 552) 174 48.8 0.0072  |
| gi 74178803 dbj BAE34044.1  unnamed protein produc ( 502) 175 49.0 0.0057 | gi 138028652 gb EBX35101.1  hypothetical protein G ( 258) 170 47.7 0.0073 |
| gi 74186235 dbj BAE42908.1  unnamed protein produc ( 502) 175 49.0 0.0057 | gi 6118361 gb AAF04094.1 AF188264_1 delta-12 oleat ( 383) 172 48.3 0.0073 |
| gi 19343569 gb AAH25438.1  Cyb5r4 protein [Mus mus ( 502) 175 49.0 0.0057 | gi 6118359 gb AAF04093.1 AF188263_1 delta-12 oleat ( 383) 172 48.3 0.0073 |
| gi 144577191 gb ABO95258.1  predicted protein [Ost ( 417) 174 48.8 0.0057 | gi 136543878 gb EBO84500.1  hypothetical protein G ( 180) 168 47.2 0.0075 |
| gi 210093325 gb EEA41530.1  hypothetical protein B ( 283) 172 48.2 0.0057 | gi 49642320 emb CAH00282.1  KLLA0D02640p [Kluyvero ( 589) 174 48.9 0.0076 |
| gi 136152096 gb EBM23834.1  hypothetical protein G ( 284) 172 48.2 0.0057 | gi 213509825 emb CAS92462.1  unnamed protein produ ( 589) 174 48.9 0.0076 |
| gi 100811423 dbj BAE94683.1  cytochrome b5 [Physar ( 132) 168 47.1 0.0058 | gi 1262166 gb AAA96727.1  nitrate reductase ( 886) 176 49.4 0.0077        |
| gi 148694573 gb EDL26520.1  mCG11884, isoform CRA_ ( 521) 175 49.1 0.0058 | gi 211592741 emb CAP99107.1  Pc22g18190 [Penicilli ( 494) 173 48.6 0.0077 |
| gi 148694570 gb EDL26517.1  mCG11884, isoform CRA_ ( 521) 175 49.1 0.0058 | gi 143689120 gb EDG29192.1  hypothetical protein G ( 337) 171 48.0 0.0077 |
| gi 50844679 gb AAT84461.1  cytochrome b5 isoform C ( 134) 168 47.1 0.0059 | gi 190346046 gb EDK38044.2  hypothetical protein P ( 156) 167 46.9 0.0078 |
| gi 139956548 gb ECI62451.1  hypothetical protein G ( 111) 167 46.8 0.0059 | gi 136608109 gb EBP25642.1  hypothetical protein G ( 129) 166 46.6 0.0078 |
| gi 148694574 gb EDL26521.1  mCG11884, isoform CRA_ ( 530) 175 49.1 0.0059 | gi 145011655 gb EDJ96311.1  hypothetical protein M ( 911) 176 49.4 0.0079 |
| gi 148694569 gb EDL26516.1  mCG11884, isoform CRA_ ( 536) 175 49.1 0.006  | gi 143292923 gb EDE15893.1  hypothetical protein G ( 284) 170 47.7 0.0079 |

|                             |                           |        |     |      |        |                             |                           |        |     |      |       |
|-----------------------------|---------------------------|--------|-----|------|--------|-----------------------------|---------------------------|--------|-----|------|-------|
| gi 3264765 gb AAC24586.1    | omega-6 fatty acid desat  | ( 346) | 171 | 48.0 | 0.0079 | gi 141175753 gb ECQ15498.1  | hypothetical protein G    | ( 277) | 168 | 47.3 | 0.011 |
| gi 146450057 gb EDK44313.1  | hypothetical protein L    | ( 160) | 167 | 46.9 | 0.008  | gi 210065776 gb EEA19870.1  | mitochondrial cytochro    | ( 497) | 171 | 48.1 | 0.011 |
| gi 147818083 emb CAN78289.1 | hypothetical protein      | ( 133) | 166 | 46.6 | 0.008  | gi 158596083 gb EDP34488.1  | Cytochrome b5-like Hem    | ( 414) | 170 | 47.8 | 0.011 |
| gi 157353583 emb CAO46100.1 | unnamed protein produ     | ( 133) | 166 | 46.6 | 0.008  | gi 88185681 gb EAQ93149.1   | conserved hypothetical    | ( 615) | 172 | 48.4 | 0.011 |
| gi 124422313 emb CAK87150.1 | unnamed protein produ     | ( 358) | 171 | 48.0 | 0.0081 | gi 30090027 gb AAO17707.1   | cytochrome b5 [Sorghum    | ( 133) | 164 | 46.2 | 0.011 |
| gi 116782813 gb ABK22670.1  | unknown [Picea sitchen    | ( 136) | 166 | 46.6 | 0.0082 | gi 190621368 gb EDV36892.1  | GF13182 [Drosophila an    | ( 134) | 164 | 46.2 | 0.011 |
| gi 210124132 gb EEA71830.1  | hypothetical protein B    | (3128) | 182 | 51.1 | 0.0083 | gi 144998358 gb ABP16931.1  | Sequence 25 from paten    | ( 446) | 170 | 47.9 | 0.011 |
| gi 135652066 gb EBJ00330.1  | hypothetical protein G    | ( 304) | 170 | 47.8 | 0.0083 | gi 126633744 emb CAM55828.1 | unnamed protein produ     | ( 446) | 170 | 47.9 | 0.011 |
| gi 154702325 gb EDO02064.1  | hypothetical protein S    | ( 452) | 172 | 48.3 | 0.0084 | gi 27278517 gb AAN93255.1   | Sequence 12 from patent   | ( 446) | 170 | 47.9 | 0.011 |
| gi 57228742 gb AAW45177.1   | L-mandelate dehydrogena   | ( 555) | 173 | 48.6 | 0.0085 | gi 3859488 gb AAC72755.1    | delta-5 fatty acid desat  | ( 446) | 170 | 47.9 | 0.011 |
| gi 190629074 gb EDV44491.1  | GF20301 [Drosophila an    | ( 117) | 165 | 46.4 | 0.0085 | gi 145025094 gb ABP24251.1  | Sequence 39 from paten    | ( 446) | 170 | 47.9 | 0.011 |
| gi 58013373 gb AAW63040.1   | microsomal delta-12 ole   | ( 381) | 171 | 48.1 | 0.0086 | gi 157393820 emb CAP07471.1 | unnamed protein produ     | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392523 gb AAX19368.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 60220728 emb CAI58863.1  | unnamed protein produc    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392517 gb AAX19365.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 42683654 gb AAS29215.1   | Sequence 30 from patent   | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392533 gb AAX19373.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 155070721 gb ABS91066.1  | Sequence 51 from paten    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392535 gb AAX19374.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 75183352 gb ABA13323.1   | Sequence 29 from patent   | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392525 gb AAX19369.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 23310238 gb AAN18904.1   | Sequence 23 from patent   | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392521 gb AAX19367.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 76059228 emb CAJ30811.1  | unnamed protein produc    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392519 gb AAX19366.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 112060964 gb ABH98583.1  | Sequence 27 from paten    | ( 446) | 170 | 47.9 | 0.011 |
| gi 18418653 gb AAL68983.1   | AF251844_1 delta-12 olea  | ( 382) | 171 | 48.1 | 0.0086 | gi 33757662 gb AAQ51235.1   | Sequence 2 from patent    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392537 gb AAX19375.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 155707465 gb ABU33114.1  | Sequence 4 from patent    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392531 gb AAX19372.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 12808264 gb AAE43484.1   | Sequence 5 from patent    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392527 gb AAX19370.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 189868191 gb ACE40437.1  | Sequence 30 from paten    | ( 446) | 170 | 47.9 | 0.011 |
| gi 60392529 gb AAX19371.1   | delta-12 oleate desatur   | ( 382) | 171 | 48.1 | 0.0086 | gi 10056254 gb AAE33160.1   | Sequence 2 from patent    | ( 446) | 170 | 47.9 | 0.011 |
| gi 215510977 gb EEC20430.1  | cytochrome b5, putativ    | ( 145) | 166 | 46.7 | 0.0086 | gi 138183810 gb EBY26414.1  | hypothetical protein G    | ( 205) | 166 | 46.7 | 0.011 |
| gi 194339835 gb EDX20801.1  | delta fatty acid desat    | ( 100) | 164 | 46.1 | 0.0087 | gi 23329315 gb AAN26149.1   | Sequence 46 from patent   | ( 447) | 170 | 47.9 | 0.011 |
| gi 53955894 gb AAV05891.1   | Sequence 17848 from pat   | ( 219) | 168 | 47.2 | 0.0088 | gi 62774607 gb AAO2000.1    | Sequence 10 from patent   | ( 447) | 170 | 47.9 | 0.011 |
| gi 146451121 gb EDK45377.1  | cytochrome b2, mitocho    | ( 582) | 173 | 48.6 | 0.0088 | gi 125603712 gb EZA43037.1  | hypothetical protein O    | ( 660) | 172 | 48.4 | 0.011 |
| gi 21019 emb CAA37672.1     | nitrate reductase [Phaseo | ( 881) | 175 | 49.2 | 0.009  | gi 57230918 gb AAW47227.1   | cytoplasm protein, puta   | ( 305) | 168 | 47.3 | 0.012 |
| gi 59956948 dbj BAD89863.1  | microsomal omega-6 fat    | ( 337) | 170 | 47.8 | 0.0091 | gi 136797655 gb EBQ47335.1  | hypothetical protein G    | ( 140) | 164 | 46.2 | 0.012 |
| gi 211592111 emb CAP98435.1 | Pc22g11470 [Penicilli     | ( 502) | 172 | 48.4 | 0.0091 | gi 61402002 gb AAH92017.1   | MGC85036 protein [Xenop   | ( 141) | 164 | 46.2 | 0.012 |
| gi 194717283 gb ACF93242.1  | nitrate reductase [Bra    | ( 910) | 175 | 49.2 | 0.0092 | gi 193907545 gb EDW06412.1  | GI21528 [Drosophila mo    | ( 117) | 163 | 45.9 | 0.012 |
| gi 540485 dbj BAA07394.1    | nitrate reductase [Brass  | ( 911) | 175 | 49.2 | 0.0092 | gi 77369196 gb ABA66944.1   | Sequence 2586 from pate   | ( 261) | 167 | 47.0 | 0.012 |
| gi 145009796 gb EDJ94452.1  | conserved hypothetical    | ( 619) | 173 | 48.6 | 0.0093 | gi 136436694 gb EB015454.1  | hypothetical protein G    | ( 99)  | 162 | 45.6 | 0.012 |
| gi 59803125 gb AAX07713.1   | FAD-dependent oxidoredu   | ( 619) | 173 | 48.6 | 0.0093 | gi 159128112 gb EDP53227.1  | cytochrome b5 reductas    | ( 479) | 170 | 47.9 | 0.012 |
| gi 142958067 gb EDB79503.1  | hypothetical protein G    | ( 348) | 170 | 47.8 | 0.0093 | gi 19065 emb CAA42739.1     | nitrate reductase (NAD(P) | ( 891) | 173 | 48.7 | 0.012 |
| gi 57230302 gb AAW46703.1   | conserved hypothetical    | ( 514) | 172 | 48.4 | 0.0093 | gi 168517 gb AAA33483.1     | nitrate reductase         | ( 501) | 170 | 47.9 | 0.013 |
| gi 164644433 gb EDR08683.1  | acyl-CoA-dehydrogenase    | ( 519) | 172 | 48.4 | 0.0094 | gi 10834811 gb AAG23835.1   | AF290427_1 cytochrome b5  | ( 131) | 163 | 45.9 | 0.013 |
| gi 126633798 emb CAM55855.1 | unnamed protein produ     | ( 536) | 172 | 48.4 | 0.0097 | gi 158420737 gb ABW37749.1  | cytochrome b5 [Drosoph    | ( 134) | 163 | 45.9 | 0.013 |
| gi 60220810 emb CAI58904.1  | unnamed protein produc    | ( 536) | 172 | 48.4 | 0.0097 | gi 21645586 gb AAF59233.3   | CG2140-PB, isoform B [D   | ( 134) | 163 | 45.9 | 0.013 |
| gi 76059310 emb CAJ30849.1  | unnamed protein produc    | ( 536) | 172 | 48.4 | 0.0097 | gi 28557605 gb AAO45208.1   | RE66521p [Drosophila me   | ( 134) | 163 | 45.9 | 0.013 |
| gi 116001279 emb CAL49891.1 | unnamed protein produ     | ( 536) | 172 | 48.4 | 0.0097 | gi 51092023 gb AAT94425.1   | RE73695p [Drosophila me   | ( 134) | 163 | 45.9 | 0.013 |
| gi 110565247 emb CAL23340.1 | unnamed protein produ     | ( 536) | 172 | 48.4 | 0.0097 | gi 194124733 gb EDW46776.1  | GM20961 [Drosophila se    | ( 134) | 163 | 45.9 | 0.013 |
| gi 125540509 gb EAY86904.1  | hypothetical protein O    | ( 138) | 165 | 46.4 | 0.0097 | gi 194175589 gb EDW89200.1  | GE19131 [Drosophila ya    | ( 134) | 163 | 45.9 | 0.013 |
| gi 125683074 gb EZA224005.1 | hypothetical protein O    | ( 138) | 165 | 46.4 | 0.0097 | gi 194192455 gb EDX06031.1  | GD10488 [Drosophila si    | ( 134) | 163 | 45.9 | 0.013 |
| gi 113537116 dbj BAF09499.1 | Os02g0649800 [Oryza s     | ( 138) | 165 | 46.4 | 0.0097 | gi 190662478 gb EDV59670.1  | GG23285 [Drosophila er    | ( 134) | 163 | 45.9 | 0.013 |
| gi 49387865 dbj BAD26552.1  | putative cytochrome b5    | ( 138) | 165 | 46.4 | 0.0097 | gi 193903202 gb EDW02069.1  | HG20101 [Drosophila gr    | ( 134) | 163 | 45.9 | 0.013 |
| gi 215694965 dbj BAG90156.1 | unnamed protein produ     | ( 138) | 165 | 46.4 | 0.0097 | gi 63102503 gb AAH95683.1   | Zgc:112177 [Danio rerio   | ( 527) | 170 | 47.9 | 0.013 |
| gi 49388452 dbj BAD25582.1  | putative cytochrome b5    | ( 138) | 165 | 46.4 | 0.0097 | gi 108464299 gb ABF89484.1  | fatty acid desaturase     | ( 383) | 168 | 47.4 | 0.014 |
| gi 126091469 gb ABN66242.1  | NADPH cytochrome B5 ox    | ( 139) | 165 | 46.4 | 0.0098 | gi 3646444 emb CAA20908.1   | NADPH-hemoprotein reduc   | ( 145) | 163 | 46.0 | 0.014 |
| gi 2564237 emb CAA71199.1   | omega-6 desaturase [Gos   | ( 383) | 170 | 47.8 | 0.01   | gi 22137120 gb AAM91405.1   | Atlg60660/F8A5_18 [Arab   | ( 121) | 162 | 45.7 | 0.014 |
| gi 91125664 gb ABE12612.1   | Sequence 6 from patent    | ( 383) | 170 | 47.8 | 0.01   | gi 15146312 gb AAK83639.1   | Atlg60660/F8A5_18 [Arab   | ( 121) | 162 | 45.7 | 0.014 |
| gi 5994481 gb AAE19894.1    | Sequence 4 from patent U  | ( 384) | 170 | 47.8 | 0.01   | gi 2462759 gb AAB71978.1    | Putative Cytochrome B5 [  | ( 121) | 162 | 45.7 | 0.014 |
| gi 1661518 gb AAX51386.1    | delta-5 fatty acid desa   | ( 476) | 171 | 48.1 | 0.01   | gi 90299640 gb EAS29271.1   | hypothetical protein CI   | (1044) | 173 | 48.8 | 0.014 |
| gi 211962233 gb EEA97428.1  | cytochrome b5-like hem    | (1579) | 177 | 49.8 | 0.011  | gi 119594383 gb EAW73977.1  | fatty acid desaturase     | ( 325) | 167 | 47.1 | 0.014 |
| gi 76573515 dbj BAE4599.1   | hypothetical protein [    | ( 126) | 164 | 46.2 | 0.011  | gi 213509837 emb CAS92468.1 | unnamed protein produ     | ( 585) | 170 | 47.9 | 0.014 |
| gi 49650093 emb CAG79819.1  | YAL10E21307p [Yarrowia    | ( 493) | 171 | 48.1 | 0.011  | gi 5262950 emb CAB45871.1   | cytochrome b2 [Kluyvero   | ( 585) | 170 | 47.9 | 0.014 |
| gi 213509829 emb CAS92464.1 | unnamed protein produ     | ( 493) | 171 | 48.1 | 0.011  | gi 68130365 emb CAJ09677.1  | delta8 fatty acid desa    | ( 400) | 168 | 47.4 | 0.014 |

|                             |                                 |     |      |       |                             |                                  |     |      |       |
|-----------------------------|---------------------------------|-----|------|-------|-----------------------------|----------------------------------|-----|------|-------|
| gi 210071626 gb EEA25715.1  | nitrate reductase NiaD ( 883)   | 172 | 48.5 | 0.015 | gi 111979069 gb ABH83312.1  | Sequence 20 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 156219664 gb EDO40543.1  | predicted protein [Nem ( 87)    | 160 | 45.1 | 0.015 | gi 155082199 gb ABS94939.1  | Sequence 19 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 136496996 gb EBO54490.1  | hypothetical protein G ( 231)   | 165 | 46.5 | 0.015 | gi 155082221 gb ABS94961.1  | Sequence 70 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 540487 dbj BAA07395.1    | nitrate reductase [Brass ( 911) | 172 | 48.5 | 0.015 | gi 155095502 gb ABS99957.1  | Sequence 21 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 113623975 dbj BAF23920.1 | Os08g0468100 [Oryza s ( 916)    | 172 | 48.5 | 0.015 | gi 155116364 gb ABT11290.1  | Sequence 19 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 424074001 dbj BAD09558.1 | nitrate reductase apoe ( 916)   | 172 | 48.5 | 0.015 | gi 155116386 gb ABT11312.1  | Sequence 70 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 113623978 dbj BAF23923.1 | Os08g0468700 [Oryza s ( 916)    | 172 | 48.5 | 0.015 | gi 60220756 emb CAI58877.1  | unnamed protein produc ( 515)    | 168 | 47.4 | 0.018 |
| gi 27527625 emb CAA33817.2  | nitrate reductase apoe ( 916)   | 172 | 48.5 | 0.015 | gi 160814787 emb CAP40238.1 | unnamed protein produ ( 515)     | 168 | 47.4 | 0.018 |
| gi 125603710 gb EZA243035.1 | hypothetical protein O ( 916)   | 172 | 48.5 | 0.015 | gi 160830340 emb CAP40241.1 | unnamed protein produ ( 515)     | 168 | 47.4 | 0.018 |
| gi 42407404 dbj BAD09562.1  | putative nitrate reduc ( 916)   | 172 | 48.5 | 0.015 | gi 155095499 gb ABS99954.1  | Sequence 18 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 150858368 gb EDN33560.1  | hypothetical protein B ( 423)   | 168 | 47.4 | 0.015 | gi 155116366 gb ABT11292.1  | Sequence 21 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 140669635 gb ECM69837.1  | hypothetical protein G ( 238)   | 165 | 46.5 | 0.015 | gi 160814789 emb CAP40239.1 | unnamed protein produ ( 515)     | 168 | 47.4 | 0.018 |
| gi 2695711 emb CAA04703.1   | cytochrome b5 [Olea euro ( 134) | 162 | 45.7 | 0.015 | gi 25956290 gb AAN75708.1   | AF391544_1 delta 4-desat ( 515)  | 168 | 47.4 | 0.018 |
| gi 158273950 gb EDO99735.1  | cytochrome b5 protein ( 112)    | 161 | 45.4 | 0.015 | gi 76059256 emb CAJ30825.1  | unnamed protein produc ( 515)    | 168 | 47.4 | 0.018 |
| gi 602208061 emb CAI58902.1 | unnamed protein produc ( 201)   | 164 | 46.3 | 0.016 | gi 155102609 gb ABT03232.1  | Sequence 29 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 126633748 emb CAM55830.1 | unnamed protein produ ( 201)    | 164 | 46.3 | 0.016 | gi 155116365 gb ABT11291.1  | Sequence 20 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 76059306 emb CAJ30847.1  | unnamed protein produc ( 201)   | 164 | 46.3 | 0.016 | gi 155095501 gb ABS99956.1  | Sequence 20 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 110565249 emb CAL23341.1 | unnamed protein produ ( 201)    | 164 | 46.3 | 0.016 | gi 111979070 gb ABH83313.1  | Sequence 21 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 156219508 gb EDO40389.1  | predicted protein [Nem ( 361)   | 167 | 47.1 | 0.016 | gi 111979090 gb ABH83333.1  | Sequence 70 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 210095508 gb EEA43670.1  | hypothetical protein B ( 361)   | 167 | 47.1 | 0.016 | gi 155082201 gb ABS94941.1  | Sequence 21 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 211582522 emb CAP80710.1 | Pc12g10830 [Penicilli ( 137)    | 162 | 45.7 | 0.016 | gi 155095500 gb ABS99955.1  | Sequence 19 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 60220754 emb CAI58876.1  | unnamed protein produc ( 541)   | 169 | 47.7 | 0.016 | gi 25956288 gb AAN75707.1   | AF391543_1 delta 4-desat ( 515)  | 168 | 47.4 | 0.018 |
| gi 126633794 emb CAM55853.1 | unnamed protein produ ( 541)    | 169 | 47.7 | 0.016 | gi 111979067 gb ABH83310.1  | Sequence 18 from paten ( 515)    | 168 | 47.4 | 0.018 |
| gi 76059254 emb CAJ30824.1  | unnamed protein produc ( 541)   | 169 | 47.7 | 0.016 | gi 215506991 gb EEC16485.1  | cytochrome B5, putativ ( 134)    | 161 | 45.5 | 0.018 |
| gi 160814785 emb CAP40237.1 | unnamed protein produ ( 541)    | 169 | 47.7 | 0.016 | gi 51011616 gb AAT92217.1   | cytochrome b5 [Ixodes p ( 134)   | 161 | 45.5 | 0.018 |
| gi 33466346 gb AAQ19605.1   | delta-4 fatty acid desa ( 541)  | 169 | 47.7 | 0.016 | gi 34103762 gb AAQ60123.1   | probable linoleoyl-CoA ( 357)    | 166 | 46.9 | 0.018 |
| gi 116001283 emb CAL49893.1 | unnamed protein produ ( 541)    | 169 | 47.7 | 0.016 | gi 195652285 gb ACG45610.1  | cytochrome b5 [Zea may ( 135)    | 161 | 45.5 | 0.018 |
| gi 55467928 emb CAH69570.1  | unnamed protein produc ( 541)   | 169 | 47.7 | 0.016 | gi 195623138 gb ACG33399.1  | cytochrome b5 [Zea may ( 135)    | 161 | 45.5 | 0.018 |
| gi 141417734 gb ECR68442.1  | hypothetical protein G ( 250)   | 165 | 46.6 | 0.016 | gi 162667052 gb EDQ53691.1  | predicted protein [Phy ( 77)     | 158 | 44.6 | 0.018 |
| gi 140106319 gb ECJ57827.1  | hypothetical protein G ( 78)    | 159 | 44.9 | 0.016 | gi 146449222 gb EDK43478.1  | conserved hypothetical ( 248)    | 164 | 46.3 | 0.018 |
| gi 190650077 gb EDV47355.1  | GG17685 [Drosophila er ( 117)   | 161 | 45.4 | 0.016 | gi 199429801 emb CAG85354.2 | DEHA2B09196p [Debaryo ( 170)     | 162 | 45.8 | 0.019 |
| gi 23428547 gb AAL23676.1   | delta-12 fatty acid des ( 382)  | 167 | 47.1 | 0.016 | gi 141122012 gb ECP77867.1  | hypothetical protein G ( 307)    | 165 | 46.6 | 0.019 |
| gi 156227910 gb EDO48711.1  | predicted protein [Nem ( 315)   | 166 | 46.9 | 0.016 | gi 49645443 emb CAG99015.1  | KLLA0F27577p [Kluyvero ( 172)    | 162 | 45.8 | 0.019 |
| gi 76059404 emb CAJ30867.1  | unnamed protein produc ( 383)   | 167 | 47.1 | 0.016 | gi 134067698 emb CAM65978.1 | cytochrome b5-like, p ( 117)     | 160 | 45.2 | 0.019 |
| gi 13447102 gb AAK26633.1   | AF343065_1 delta-12 fatt ( 383) | 167 | 47.1 | 0.016 | gi 136563461 gb EBO97051.1  | hypothetical protein G ( 143)    | 161 | 45.5 | 0.019 |
| gi 17382283 emb CAD13056.1  | unnamed protein produc ( 383)   | 167 | 47.1 | 0.016 | gi 167876111 gb EDS39494.1  | cytochrome b5 [Culex q ( 121)    | 160 | 45.2 | 0.019 |
| gi 83702515 gb ABC41578.1   | endoplasmic reticulum 1 ( 388)  | 167 | 47.1 | 0.016 | gi 198261777 gb EDY86063.1  | linoleoyl-coa desatura ( 392)    | 166 | 46.9 | 0.019 |
| gi 83775528 dbj BAE65648.1  | unnamed protein produc ( 101)   | 160 | 45.2 | 0.017 | gi 134900714 gb EBE17538.1  | hypothetical protein G ( 150)    | 161 | 45.5 | 0.02  |
| gi 138183035 gb EBY25878.1  | hypothetical protein G ( 269)   | 165 | 46.6 | 0.017 | gi 138148757 gb EBY01924.1  | hypothetical protein G ( 187)    | 162 | 45.8 | 0.02  |
| gi 156203103 gb EDO27494.1  | predicted protein [Nem ( 327)   | 166 | 46.9 | 0.017 | gi 140893949 gb ECO22325.1  | hypothetical protein G ( 155)    | 161 | 45.5 | 0.02  |
| gi 211582756 emb CAP80956.1 | Pc12g13290 [Penicilli ( 488)    | 168 | 47.4 | 0.017 | gi 111069636 gb EAT90756.1  | hypothetical protein S ( 502)    | 167 | 47.2 | 0.02  |
| gi 137712075 gb EBV59302.1  | hypothetical protein G ( 332)   | 166 | 46.9 | 0.017 | gi 29469883 gb AAO73962.1   | cytochrome b5 [Candida ( 129)    | 160 | 45.2 | 0.02  |
| gi 140226881 gb ECK38746.1  | hypothetical protein G ( 186)   | 163 | 46.0 | 0.017 | gi 29703119 gb AAO96611.1   | Sequence 2 from patent ( 129)    | 160 | 45.2 | 0.02  |
| gi 83769244 dbj BAE59381.1  | unnamed protein produc ( 495)   | 168 | 47.4 | 0.017 | gi 42677386 gb AAS26339.1   | Sequence 5 from patent ( 129)    | 160 | 45.2 | 0.02  |
| gi 676850 gb AAA62316.1     | nitrate reductase ( 889)        | 171 | 48.3 | 0.017 | gi 56611998 gb AAW04235.1   | Sequence 5 from patent ( 129)    | 160 | 45.2 | 0.02  |
| gi 144097145 gb EDT84470.1  | hypothetical protein G ( 277)   | 165 | 46.6 | 0.017 | gi 150855546 gb EDN30738.1  | hypothetical protein B ( 907)    | 170 | 48.0 | 0.02  |
| gi 2342599 emb CAA04554.1   | Nitrate reductase [Meta ( 892)  | 171 | 48.3 | 0.017 | gi 6224515 emb CAB60010.1   | nitrate reductase [Hebe ( 908)   | 170 | 48.0 | 0.02  |
| gi 141122011 gb ECP77866.1  | hypothetical protein G ( 280)   | 165 | 46.6 | 0.017 | gi 154697219 gb EDN96957.1  | hypothetical protein S ( 910)    | 170 | 48.0 | 0.021 |
| gi 155095522 gb ABS99977.1  | Sequence 70 from paten ( 515)   | 168 | 47.4 | 0.018 | gi 5020385 gb AAD38068.1    | AF153448_1 nitrate reduct ( 910) | 170 | 48.0 | 0.021 |
| gi 25956294 gb AAN75710.1   | AF391546_1 delta 4-desat ( 515) | 168 | 47.4 | 0.018 | gi 138729976 gb ECB61117.1  | hypothetical protein G ( 283)    | 164 | 46.4 | 0.021 |
| gi 111979068 gb ABH83311.1  | Sequence 19 from paten ( 515)   | 168 | 47.4 | 0.018 | gi 138192263 gb EBY31848.1  | hypothetical protein G ( 233)    | 163 | 46.1 | 0.021 |
| gi 160814992 emb CAP40240.1 | unnamed protein produ ( 515)    | 168 | 47.4 | 0.018 | gi 19045 emb CAA40975.1     | nitrate reductase [Hordeu ( 912) | 170 | 48.0 | 0.021 |
| gi 116001281 emb CAL49892.1 | unnamed protein produ ( 515)    | 168 | 47.4 | 0.018 | gi 18994 emb CAA40976.1     | nitrate reductase [Hordeu ( 915) | 170 | 48.0 | 0.021 |
| gi 155082200 gb ABS94940.1  | Sequence 20 from paten ( 515)   | 168 | 47.4 | 0.018 | gi 118481960 gb ABK92912.1  | unknown [Populus trich ( 134)    | 160 | 45.2 | 0.021 |
| gi 25956292 gb AAN75709.1   | AF391545_1 delta 4-desat ( 515) | 168 | 47.4 | 0.018 | gi 118483464 gb ABK93631.1  | unknown [Populus trich ( 134)    | 160 | 45.2 | 0.021 |
| gi 155116363 gb ABT11289.1  | Sequence 18 from paten ( 515)   | 168 | 47.4 | 0.018 | gi 118489280 gb ABK96445.1  | unknown [Populus trich ( 134)    | 160 | 45.2 | 0.021 |
| gi 155082198 gb ABS94938.1  | Sequence 18 from paten ( 515)   | 168 | 47.4 | 0.018 | gi 194112989 gb EDW35032.1  | GL20014 [Drosophila pe ( 135)    | 160 | 45.2 | 0.021 |
| gi 126633796 emb CAM55854.1 | unnamed protein produ ( 515)    | 168 | 47.4 | 0.018 | gi 198136706 gb EAL25975.2  | GA15264 [Drosophila ps ( 135)    | 160 | 45.2 | 0.021 |

|                             |                          |         |     |      |       |
|-----------------------------|--------------------------|---------|-----|------|-------|
| gi 194145667 gb EDW62063.1  | GJ19962 [Drosophila vi   | ( 135)  | 160 | 45.2 | 0.021 |
| gi 195659495 gb ACG49215.1  | cytochrome b5 [Zea may   | ( 135)  | 160 | 45.2 | 0.021 |
| gi 170944233 emb CAP70343.1 | unnamed protein produ    | ( 952)  | 170 | 48.1 | 0.021 |
| gi 119408251 gb EAW18200.1  | cytochrome b5, putativ   | ( 136)  | 160 | 45.3 | 0.021 |
| gi 194194233 gb EDX07809.1  | GD11452 [Drosophila si   | ( 535)  | 167 | 47.2 | 0.021 |
| gi 194126550 gb EDW48593.1  | GM21957 [Drosophila se   | ( 535)  | 167 | 47.2 | 0.021 |
| gi 125550542 gb EAY96251.1  | hypothetical protein O   | ( 137)  | 160 | 45.3 | 0.021 |
| gi 14719320 gb AAK73138.1   | AC079022_11 cytochrome B | ( 137)  | 160 | 45.3 | 0.021 |
| gi 113577985 dbj BAF16348.1 | Os05g0108800 [Oryza s    | ( 137)  | 160 | 45.3 | 0.021 |
| gi 125592545 gb EAZ32604.1  | hypothetical protein O   | ( 137)  | 160 | 45.3 | 0.021 |
| gi 215694024 dbj BAG89223.1 | unnamed protein produ    | ( 137)  | 160 | 45.3 | 0.021 |
| gi 414705 emb CAA53366.1    | cytochrome b5 [Oryza sa  | ( 137)  | 160 | 45.3 | 0.021 |
| gi 52353573 gb AAU44139.1   | cytochrome b5 [Oryza sa  | ( 137)  | 160 | 45.3 | 0.021 |
| gi 54635516 gb EAL24919.1   | GA10870 [Drosophila pse  | ( 536)  | 167 | 47.2 | 0.021 |
| gi 194109647 gb EDW31690.1  | GL10825 [Drosophila pe   | ( 536)  | 167 | 47.2 | 0.021 |
| gi 194144162 gb EDW60558.1  | GJ20792 [Drosophila vi   | ( 539)  | 167 | 47.2 | 0.022 |
| gi 296386 emb CAA50575.1    | cytochrome b5 [Nicotiana | ( 139)  | 160 | 45.3 | 0.022 |
| gi 28202143 gb AAO34680.1   | reductase [Gibberella z  | ( 452)  | 166 | 46.9 | 0.022 |
| gi 68124617 emb CAJ03111.1  | cytochrome b5-like, pu   | ( 117)  | 159 | 45.0 | 0.022 |
| gi 144976090 gb ABP13185.1  | Sequence 6 from patent   | ( 173)  | 161 | 45.5 | 0.022 |
| gi 154423266 gb ABS81534.1  | ortho-nitrophenol 2-mo   | ( 558)  | 167 | 47.2 | 0.022 |
| gi 136615850 gb EBP30589.1  | hypothetical protein G   | ( 258)  | 163 | 46.1 | 0.022 |
| gi 134718411 gb EBD00780.1  | hypothetical protein G   | ( 258)  | 163 | 46.1 | 0.022 |
| gi 5994480 gb AAE19893.1    | Sequence 2 from patent U | ( 382)  | 165 | 46.7 | 0.022 |
| gi 140396654 gb ECL49154.1  | hypothetical protein G   | ( 259)  | 163 | 46.1 | 0.022 |
| gi 32451979 gb AAH54749.1   | Cytochrome b5 type B [M  | ( 146)  | 160 | 45.3 | 0.023 |
| gi 148679454 gb EDL11401.1  | cytochrome b5 type B [   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 12841545 dbj BAB25251.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 38566255 gb AAH62980.1   | Cytochrome b5 type B [M  | ( 146)  | 160 | 45.3 | 0.023 |
| gi 74225098 dbj BAE38245.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 37590501 gb AAH58812.1   | Cytochrome b5 type B [M  | ( 146)  | 160 | 45.3 | 0.023 |
| gi 74214155 dbj BAE40334.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 12859383 dbj BAB31635.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 12833936 dbj BAB27221.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 26354094 dbj BAC40677.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 26342999 dbj BAC35156.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 12834709 dbj BAB23012.1  | unnamed protein produc   | ( 146)  | 160 | 45.3 | 0.023 |
| gi 141086034 gb ECP52629.1  | hypothetical protein G   | ( 264)  | 163 | 46.1 | 0.023 |
| gi 119407800 gb EAW17749.1  | nitrate reductase, put   | ( 1032) | 170 | 48.1 | 0.023 |
| gi 4007804 emb CAA22444.1   | cytochrome b5 (predicte  | ( 124)  | 159 | 45.0 | 0.023 |
| gi 164650801 gb EDR15041.1  | predicted protein [Lac   | ( 485)  | 166 | 47.0 | 0.023 |
| gi 142471021 gb ECY31970.1  | hypothetical protein G   | ( 333)  | 164 | 46.4 | 0.023 |
| gi 111062588 gb EAT83708.1  | hypothetical protein S   | ( 498)  | 166 | 47.0 | 0.024 |
| gi 170948370 emb CAP60534.1 | unnamed protein produ    | ( 607)  | 167 | 47.3 | 0.024 |
| gi 168519 gb AAA03202.1     | NADH:nitrate reductase   | ( 618)  | 167 | 47.3 | 0.024 |
| gi 45446820 gb AAS65265.1   | CG3566-PC, isoform C [D  | ( 89)   | 157 | 44.4 | 0.024 |
| gi 17946653 gb AAL49357.1   | RH45308p [Drosophila me  | ( 89)   | 157 | 44.4 | 0.024 |
| gi 136515691 gb EBO66540.1  | hypothetical protein G   | ( 132)  | 159 | 45.0 | 0.024 |
| gi 144579309 gb ABO97371.1  | predicted protein [Ost   | ( 517)  | 166 | 47.0 | 0.024 |
| gi 139943757 gb ECI54134.1  | hypothetical protein G   | ( 240)  | 162 | 45.9 | 0.025 |
| gi 50844675 gb AAT84459.1   | cytochrome b5 isoform C  | ( 134)  | 159 | 45.0 | 0.025 |
| gi 139996105 gb ECI90046.1  | hypothetical protein G   | ( 111)  | 158 | 44.7 | 0.025 |
| gi 767811501 gb ABA5490.1   | cytochrome b5 type 11 [  | ( 136)  | 159 | 45.0 | 0.025 |
| gi 198138222 gb EDY70015.1  | GA25795 [Drosophila ps   | ( 440)  | 165 | 46.7 | 0.025 |
| gi 7302484 gb AAF57568.1    | CG11257-PA [Drosophila m | ( 535)  | 166 | 47.0 | 0.025 |
| gi 66771089 gb AAY54856.1   | IP11715p [Drosophila me  | ( 535)  | 166 | 47.0 | 0.025 |
| gi 190345236 gb EDK37091.2  | hypothetical protein P   | ( 453)  | 165 | 46.7 | 0.026 |
| gi 116787072 gb ABK24364.1  | unknown [Picea sitchen   | ( 375)  | 164 | 46.4 | 0.026 |

|                             |                           |        |     |      |       |
|-----------------------------|---------------------------|--------|-----|------|-------|
| gi 60392566 gb AAAX19389.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 69061718 gb AAY99777.1   | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 60418974 gb AAAX19894.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 60392570 gb AAAX19391.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 69061719 gb AAY99778.1   | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 134284837 gb ABO69520.1  | microsomal oleate desa    | ( 378) | 164 | 46.4 | 0.026 |
| gi 60392568 gb AAAX19390.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 33766657 gb AAQ52860.1   | Sequence 14 from patent   | ( 378) | 164 | 46.4 | 0.026 |
| gi 60418976 gb AAAX19895.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 2290404 gb AAB65146.1    | delta-12 oleate desatura  | ( 378) | 164 | 46.4 | 0.026 |
| gi 18418649 gb AAL68981.1   | AF251842_1 delta-12 olea  | ( 378) | 164 | 46.4 | 0.026 |
| gi 209967428 gb ACJ02341.1  | seed-specific oleoyl-p    | ( 378) | 164 | 46.4 | 0.026 |
| gi 60392564 gb AAAX19388.1  | delta-12 oleate desatur   | ( 378) | 164 | 46.4 | 0.026 |
| gi 134284835 gb ABO69519.1  | microsomal oleate desa    | ( 378) | 164 | 46.4 | 0.026 |
| gi 155689134 gb ABU29144.1  | Sequence 14 from paten    | ( 378) | 164 | 46.4 | 0.026 |
| gi 145046502 gb ABP33181.1  | nitrate reductase [Dek    | ( 379) | 164 | 46.4 | 0.026 |
| gi 198146999 gb EAL32156.2  | GA17524 [Drosophila ps    | ( 118) | 158 | 44.8 | 0.026 |
| gi 149038111 gb EDL92471.1  | cytochrome b5 type B,     | ( 146) | 159 | 45.0 | 0.027 |
| gi 48735409 gb AAH72535.1   | Cytochrome b5 type B [R   | ( 146) | 159 | 45.0 | 0.027 |
| gi 2253161 emb CAA73117.1   | cytochrome b5, mitochon   | ( 146) | 159 | 45.0 | 0.027 |
| gi 159129010 gb EDP54124.1  | cytochrome b5, putativ    | ( 217) | 161 | 45.6 | 0.027 |
| gi 89301602 gb EAR99590.1   | Fatty acid desaturase f   | ( 399) | 164 | 46.5 | 0.027 |
| gi 116061100 emb CAL56488.1 | Linoleoyl-CoA desatur     | ( 487) | 165 | 46.7 | 0.027 |
| gi 134062959 gb CAM39407.1  | hypothetical protein,     | ( 488) | 165 | 46.7 | 0.027 |
| gi 156114680 gb EDO16188.1  | hypothetical protein K    | ( 596) | 166 | 47.0 | 0.027 |
| gi 215508350 gb EEC17804.1  | flavohemoprotein B5/b5    | ( 492) | 165 | 46.7 | 0.028 |
| gi 119610528 gb EAW90122.1  | cytochrome b5 domain c    | ( 157) | 159 | 45.1 | 0.028 |
| gi 91131655 gb ABE15393.1   | Sequence 2926 from pate   | ( 157) | 159 | 45.1 | 0.028 |
| gi 16552638 dbj BAB71357.1  | unnamed protein produc    | ( 157) | 159 | 45.1 | 0.028 |
| gi 28850428 gb AAO53192.1   | similar to Homo sapiens   | ( 158) | 159 | 45.1 | 0.028 |
| gi 76781148 gb ABA54489.1   | cytochrome b5 type 06 [   | ( 131) | 158 | 44.8 | 0.028 |
| gi 89296735 gb EAR94723.1   | Cytochrome b5-like Heme   | ( 109) | 157 | 44.5 | 0.029 |
| gi 23197754 gb AAN15404.1   | putative cytochrome b5    | ( 134) | 158 | 44.8 | 0.029 |
| gi 22136052 gb AAM91608.1   | putative cytochrome b5    | ( 134) | 158 | 44.8 | 0.029 |
| gi 2914701 gb AAC04491.1    | putative cytochrome b5 [  | ( 134) | 158 | 44.8 | 0.029 |
| gi 110743053 dbj BAE99419.1 | putative cytochrome b     | ( 134) | 158 | 44.8 | 0.029 |
| gi 194106690 gb EDW28733.1  | GL18786 [Drosophila pe    | ( 440) | 164 | 46.5 | 0.029 |
| gi 190657990 gb EDV55203.1  | GG21968 [Drosophila er    | ( 535) | 165 | 46.8 | 0.03  |
| gi 190659447 gb EDV56606.1  | GG22772 [Drosophila er    | ( 441) | 164 | 46.5 | 0.03  |
| gi 146451117 gb EDK45373.1  | hypothetical protein L    | ( 655) | 166 | 47.0 | 0.03  |
| gi 16945429 emb CAB91687.2  | probable cytochrome b5    | ( 139) | 158 | 44.8 | 0.03  |
| gi 135195289 gb EBG10299.1  | hypothetical protein G    | ( 170) | 159 | 45.1 | 0.03  |
| gi 27924030 gb AAO27755.1   | reductase [Fusarium spo   | ( 452) | 164 | 46.5 | 0.03  |
| gi 190584960 gb EDV25029.1  | hypothetical protein T    | ( 551) | 165 | 46.8 | 0.03  |
| gi 45446819 gb AAN09163.3   | CG3566-PB, isoform B [D   | ( 117) | 157 | 44.5 | 0.03  |
| gi 194115856 gb EDW37899.1  | GL21352 [Drosophila pe    | ( 118) | 157 | 44.5 | 0.031 |
| gi 146156749 gb ABQ07603.1  | fatty acid desaturase     | ( 386) | 163 | 46.2 | 0.031 |
| gi 162471891 gb ABX99726.1  | Sequence 2 from patent    | ( 120) | 157 | 44.5 | 0.031 |
| gi 431762 gb AAA67468.1     | cytochrome b5 [Saccharomy | ( 120) | 157 | 44.5 | 0.031 |
| gi 22316532 emb CAD44473.1  | unnamed protein produc    | ( 216) | 160 | 45.4 | 0.031 |
| gi 22316686 emb CAD44443.1  | unnamed protein produc    | ( 216) | 160 | 45.4 | 0.031 |
| gi 134925723 gb EBE34119.1  | hypothetical protein G    | ( 324) | 162 | 45.9 | 0.032 |
| gi 28828102 gb AAO50785.1   | similar to cytochrome b   | ( 149) | 158 | 44.8 | 0.032 |
| gi 126095722 gb ABN65544.1  | cytochrome b5 [Pichia     | ( 124) | 157 | 44.5 | 0.032 |
| gi 136207959 gb EBM60653.1  | hypothetical protein G    | ( 489) | 164 | 46.5 | 0.032 |
| gi 138293221 gb EBY83808.1  | hypothetical protein G    | ( 127) | 157 | 44.5 | 0.033 |
| gi 55733155 emb CAH93261.1  | hypothetical protein [    | ( 228) | 160 | 45.4 | 0.033 |
| gi 138408697 gb EBZ46713.1  | hypothetical protein G    | ( 156) | 158 | 44.8 | 0.033 |

|                             |                                 |     |      |       |                             |                                 |     |      |       |
|-----------------------------|---------------------------------|-----|------|-------|-----------------------------|---------------------------------|-----|------|-------|
| gi 154702550 gb ED002289.1  | hypothetical protein S ( 509)   | 164 | 46.5 | 0.033 | gi 155265493 gb ABT21097.1  | Sequence 108567 from p ( 142)   | 156 | 44.3 | 0.042 |
| gi 211581814 emb CAP79936.1 | Pcl2g03090 [Penicilli ( 622)    | 165 | 46.8 | 0.033 | gi 155324281 gb ABT79885.1  | Sequence 167355 from p ( 142)   | 156 | 44.3 | 0.042 |
| gi 2647949 emb CAA04702.1   | cytochrome b5 [Olea eur ( 132)  | 157 | 44.6 | 0.034 | gi 8980835 gb AAF82295.1    | microsomal oleate desatu ( 379) | 161 | 45.7 | 0.042 |
| gi 51968520 dbj BAD42952.1  | putative cytochrome b5 ( 132)   | 157 | 44.6 | 0.034 | gi 8980833 gb AAF82294.1    | microsomal oleate desatu ( 379) | 161 | 45.7 | 0.042 |
| gi 98961069 gb ABF59018.1   | At2g46650 [Arabidopsis ( 132)   | 157 | 44.6 | 0.034 | gi 67090583 gb AAAY67653.1  | oleate desaturase [Arac ( 379)  | 161 | 45.7 | 0.042 |
| gi 21593247 gb IAM65196.1   | putative cytochrome b5 ( 132)   | 157 | 44.6 | 0.034 | gi 211587273 emb CAP79467.1 | Pcl19g00510 [Penicilli ( 469)   | 162 | 46.0 | 0.043 |
| gi 3831439 gb AAC69922.1    | putative cytochrome b5 [ ( 132) | 157 | 44.6 | 0.034 | gi 83767338 dbj BAE57477.1  | unnamed protein produc ( 573)   | 163 | 46.3 | 0.043 |
| gi 20197779 gb AAM15242.1   | putative cytochrome b5 ( 132)   | 157 | 44.6 | 0.034 | gi 136648940 gb EBP50174.1  | hypothetical protein G ( 320)   | 160 | 45.5 | 0.043 |
| gi 2062405 gb AAC49701.1    | cytochrome b5 [Borago of ( 132) | 157 | 44.6 | 0.034 | gi 139643374 gb ECG46848.1  | hypothetical protein G ( 268)   | 159 | 45.2 | 0.044 |
| gi 24899389 gb AAN64993.1   | nitrate reductase [Tube ( 929)  | 167 | 47.4 | 0.034 | gi 121905115 gb EAY10049.1  | Cytochrome b5-like Hem ( 102)   | 154 | 43.8 | 0.044 |
| gi 193808522 emb CAQ39225.1 | Heme binding protein, ( 162)    | 158 | 44.8 | 0.034 | gi 90299699 gb EAS29330.1   | hypothetical protein CI ( 337)  | 160 | 45.5 | 0.045 |
| gi 30090033 gb AAO86521.1   | cytochrome B5 [Triticum ( 135)  | 157 | 44.6 | 0.034 | gi 155265491 gb ABT21095.1  | Sequence 108565 from p ( 158)   | 156 | 44.4 | 0.046 |
| gi 195644840 gb ACG41888.1  | cytochrome b5 [Zea may ( 135)   | 157 | 44.6 | 0.034 | gi 155116369 gb ABT11295.1  | Sequence 37 from paten ( 509)   | 162 | 46.1 | 0.046 |
| gi 114192094 gb EAU33794.1  | cytochrome b5 [Aspergi ( 137)   | 157 | 44.6 | 0.035 | gi 155095505 gb ABS99960.1  | Sequence 37 from paten ( 509)   | 162 | 46.1 | 0.046 |
| gi 51969026 dbj BAM43205.1  | putative cytochrome b5 ( 140)   | 157 | 44.6 | 0.035 | gi 155082204 gb ABS94944.1  | Sequence 37 from paten ( 509)   | 162 | 46.1 | 0.046 |
| gi 134059770 emb CAM41893.1 | cytochrome b5-like, p ( 117)    | 156 | 44.3 | 0.036 | gi 111979073 gb ABH83316.1  | Sequence 37 from paten ( 509)   | 162 | 46.1 | 0.046 |
| gi 19853 emb CAA8240.1      | cytochrome b5 [Nicotiana ( 97)  | 155 | 44.0 | 0.036 | gi 68127215 emb CAJ05265.1  | hypothetical protein, (1126)    | 166 | 47.2 | 0.046 |
| gi 1054843 emb CAA63432.1   | D12 oleate desaturase [ ( 383)  | 162 | 46.0 | 0.036 | gi 140257004 gb ECK59579.1  | hypothetical protein G ( 161)   | 156 | 44.4 | 0.046 |
| gi 34600650 gb AAQ78507.1   | Sequence 12 from patent ( 383)  | 162 | 46.0 | 0.036 | gi 134070521 emb CAM68864.1 | hypothetical protein, (1148)    | 166 | 47.2 | 0.047 |
| gi 17225582 gb AAL37484.1   | AF331163_1 delta-12 fatt ( 384) | 162 | 46.0 | 0.036 | gi 158594261 gb EDP32845.1  | Cytochrome b5-like Hem ( 111)   | 154 | 43.8 | 0.047 |
| gi 19040908 gb EDV12363.1   | cytochrome b5 [Sacchar ( 120)   | 156 | 44.3 | 0.036 | gi 170940958 emb CAP66608.1 | unnamed protein produ ( 136)    | 155 | 44.1 | 0.047 |
| gi 167275173 gb ABZ28037.1  | Sequence 1975 from pat ( 120)   | 156 | 44.3 | 0.036 | gi 157350710 emb CAO40801.1 | unnamed protein produ ( 166)    | 156 | 44.4 | 0.048 |
| gi 51013663 gb AAT93125.1   | YNL111C [Saccharomyces ( 120)   | 156 | 44.3 | 0.036 | gi 195608042 gb ACG25851.1  | cytochrome b5 [Zea may ( 139)   | 155 | 44.1 | 0.048 |
| gi 1302032 emb CAA95990.1   | CYB5 [Saccharomyces cer ( 120)  | 156 | 44.3 | 0.036 | gi 195608192 gb ACG25926.1  | cytochrome b5 [Zea may ( 139)   | 155 | 44.1 | 0.048 |
| gi 1183962 emb CAA93396.1   | Cytochrome B5 [Saccharo ( 120)  | 156 | 44.3 | 0.036 | gi 195615256 gb ACG29458.1  | cytochrome b5 [Zea may ( 139)   | 155 | 44.1 | 0.048 |
| gi 18478404 dbj BAB84515.1  | nitrate reductase [Mon ( 873)   | 166 | 47.1 | 0.038 | gi 194187409 gb EDX00993.1  | GE16473 [Drosophila ya ( 117)   | 154 | 43.8 | 0.049 |
| gi 138746826 gb ECB72846.1  | hypothetical protein G ( 125)   | 156 | 44.3 | 0.038 | gi 8980831 gb AAF82293.1    | microsomal oleate desatu ( 379) | 160 | 45.5 | 0.049 |
| gi 144005727 gb EDI19070.1  | hypothetical protein G ( 153)   | 157 | 44.6 | 0.038 | gi 66734339 gb AAV53559.1   | oleate desaturase [Arac ( 379)  | 160 | 45.5 | 0.049 |
| gi 140913054 gb ECO34721.1  | hypothetical protein G ( 153)   | 157 | 44.6 | 0.038 | gi 121104181 gb ABM47430.1  | delta-12 fatty acid de ( 379)   | 160 | 45.5 | 0.049 |
| gi 146452690 gb EDK46946.1  | cytochrome b5 [Loddero ( 127)   | 156 | 44.3 | 0.038 | gi 121104183 gb ABM47431.1  | delta-12 fatty acid de ( 379)   | 160 | 45.5 | 0.049 |
| gi 38174502 gb AAH60779.1   | Cytochrome b5 domain co ( 228)  | 159 | 45.2 | 0.038 | gi 14572857 gb AAK67829.1   | delta-12 fatty acid des ( 379)  | 160 | 45.5 | 0.049 |
| gi 119610525 gb EAW90119.1  | cytochrome b5 domain c ( 228)   | 159 | 45.2 | 0.038 | gi 71064149 gb AAZ22543.1   | oleate desaturase [Arac ( 379)  | 160 | 45.5 | 0.049 |
| gi 119610527 gb EAW90121.1  | cytochrome b5 domain c ( 228)   | 159 | 45.2 | 0.038 | gi 49647598 emb CAG82041.1  | YALI0C11627p [Yarrowia ( 257)   | 158 | 45.0 | 0.05  |
| gi 158260063 dbj BAF82209.1 | unnamed protein produ ( 228)    | 159 | 45.2 | 0.038 | gi 126233687 gb ABN97087.1  | fatty acid desaturase ( 380)    | 160 | 45.5 | 0.05  |
| gi 136563033 gb EBO96777.1  | hypothetical protein G ( 188)   | 158 | 44.9 | 0.038 | gi 162694677 gb EDQ81024.1  | predicted protein [Phy ( 144)   | 155 | 44.1 | 0.05  |
| gi 187979816 gb EDU46442.1  | L-lactate dehydrogenas ( 508)   | 163 | 46.3 | 0.039 | gi 160703451 gb EAT80428.2  | hypothetical protein S ( 471)   | 161 | 45.8 | 0.05  |
| gi 163777626 gb EDQ91242.1  | predicted protein [Mon ( 130)   | 156 | 44.3 | 0.039 | gi 138092570 gb EBX70193.1  | hypothetical protein G ( 147)   | 155 | 44.1 | 0.051 |
| gi 66968448 gb AAV59603.1   | fatty acid desaturase [ ( 159)  | 157 | 44.6 | 0.039 | gi 190348933 gb EDK41487.2  | hypothetical protein P ( 151)   | 155 | 44.1 | 0.052 |
| gi 197713706 gb EDY57740.1  | fatty acid desaturase ( 235)    | 159 | 45.2 | 0.039 | gi 27868666 gb AAO24766.1   | cytochrome b5 [Anophele ( 128)  | 154 | 43.9 | 0.053 |
| gi 111979074 gb ABH83317.1  | Sequence 46 from paten ( 513)   | 163 | 46.3 | 0.039 | gi 119855481 gb ABM01874.1  | cytochrome b5 [Anophel ( 128)   | 154 | 43.9 | 0.053 |
| gi 155095506 gb ABS99961.1  | Sequence 46 from paten ( 513)   | 163 | 46.3 | 0.039 | gi 134076459 emb CAK45099.1 | unnamed protein produ ( 901)    | 164 | 46.7 | 0.053 |
| gi 155082205 gb ABS94945.1  | Sequence 46 from paten ( 513)   | 163 | 46.3 | 0.039 | gi 140473492 gb ECL94361.1  | hypothetical protein G ( 72)    | 151 | 43.0 | 0.053 |
| gi 155116370 gb ABT11296.1  | Sequence 46 from paten ( 513)   | 163 | 46.3 | 0.039 | gi 144118082 gb EDI99440.1  | hypothetical protein G ( 344)   | 159 | 45.3 | 0.054 |
| gi 134609363 gb EBC36463.1  | hypothetical protein G ( 288)   | 160 | 45.4 | 0.039 | gi 57997557 emb CAI46070.1  | hypothetical protein [ ( 107)   | 153 | 43.6 | 0.054 |
| gi 194157067 gb EDW10604.1  | GK10686 [Drosophila wi ( 133)   | 156 | 44.3 | 0.04  | gi 116060798 emb CAL57276.1 | Cytochrome b5 (ISS) [ ( 921)    | 164 | 46.7 | 0.054 |
| gi 53956025 gb AAV06022.1   | Sequence 17979 from pat ( 241)  | 159 | 45.2 | 0.04  | gi 139918077 gb ECI36068.1  | hypothetical protein G ( 289)   | 158 | 45.0 | 0.055 |
| gi 135410697 gb EBH45357.1  | hypothetical protein G ( 356)   | 161 | 45.7 | 0.04  | gi 9759195 dbj BAB09732.1   | cytochrome b5 [Arabidop ( 134)  | 154 | 43.9 | 0.055 |
| gi 53954683 gb AAV04680.1   | Sequence 16637 from pat ( 434)  | 162 | 46.0 | 0.04  | gi 21592682 gb AAM64631.1   | cytochrome b5 (dbj BAA7 ( 134)  | 154 | 43.9 | 0.055 |
| gi 193910639 gb EDW09506.1  | GI18997 [Drosophila mo ( 135)   | 156 | 44.3 | 0.04  | gi 4240120 dbj BAA74839.1   | cytochrome b5 [Arabidop ( 134)  | 154 | 43.9 | 0.055 |
| gi 450585 gb AAA62621.1     | cytochrome b5 ( 135)            | 156 | 44.3 | 0.04  | gi 21281008 gb AAM45093.1   | putative cytochrome b5 ( 134)   | 154 | 43.9 | 0.055 |
| gi 193911737 gb EDW10604.1  | GI21190 [Drosophila mo ( 528)   | 163 | 46.3 | 0.04  | gi 19423894 gb AAL87348.1   | putative cytochrome b5 ( 134)   | 154 | 43.9 | 0.055 |
| gi 194176616 gb EDW90227.1  | GE12766 [Drosophila ya ( 441)   | 162 | 46.0 | 0.041 | gi 138331574 gb EBZ01581.1  | hypothetical protein G ( 243)   | 157 | 44.7 | 0.055 |
| gi 134071272 emb CAM69957.1 | nitrate reductase, pu ( 537)    | 163 | 46.3 | 0.041 | gi 190620188 gb EDV35712.1  | GF12339 [Drosophila an ( 534)   | 161 | 45.8 | 0.056 |
| gi 194177892 gb EDW91503.1  | GE12047 [Drosophila ya ( 537)   | 163 | 46.3 | 0.041 | gi 136449013 gb EBQ23435.1  | hypothetical protein G ( 64)    | 150 | 42.7 | 0.057 |
| gi 162678763 gb EDQ65218.1  | predicted protein [Phy ( 138)   | 156 | 44.3 | 0.041 | gi 118486433 gb ABK95056.1  | unknown [Populus trich ( 140)   | 154 | 43.9 | 0.057 |
| gi 167881581 gb EDS44964.1  | conserved hypothetical ( 444)   | 162 | 46.0 | 0.041 | gi 115879980 gb ABJ46912.1  | Sequence 7651 from pat ( 79)    | 151 | 43.0 | 0.058 |
| gi 114192719 gb EAU34419.1  | hypothetical protein A ( 541)   | 163 | 46.3 | 0.041 | gi 40046146 emb CAF01849.1  | unnamed protein produc ( 79)    | 151 | 43.0 | 0.058 |
| gi 193899317 gb EDV98183.1  | GH22815 [Drosophila gr ( 547)   | 163 | 46.3 | 0.041 | gi 77454024 gb ABA85719.1   | Sequence 7651 from pate ( 79)   | 151 | 43.0 | 0.058 |



|                             |                          |        |     |      |       |                             |                           |        |     |      |       |
|-----------------------------|--------------------------|--------|-----|------|-------|-----------------------------|---------------------------|--------|-----|------|-------|
| gi 60117056 gb AAX14399.1   | oleate desaturase [Arac  | ( 379) | 159 | 45.3 | 0.058 | gi 192910754 gb ACF06485.1  | cytochrome b5 [Elaeis     | ( 135) | 152 | 43.4 | 0.076 |
| gi 110623234 emb CAL24257.1 | unnamed protein produ    | ( 387) | 159 | 45.3 | 0.059 | gi 136475405 gb EBO040494.1 | hypothetical protein G    | ( 297) | 156 | 44.5 | 0.077 |
| gi 110623232 emb CAL24256.1 | unnamed protein produ    | ( 387) | 159 | 45.3 | 0.059 | gi 83767336 dbj BAE57475.1  | unnamed protein produc    | ( 137) | 152 | 43.4 | 0.077 |
| gi 134058839 emb CAM41406.1 | cytochrome b-domain p    | ( 218) | 156 | 44.4 | 0.06  | gi 212513236 gb EEB15854.1  | cytochrome B5, putativ    | ( 455) | 158 | 45.1 | 0.079 |
| gi 139086057 gb ECD31462.1  | hypothetical protein G   | ( 83)  | 151 | 43.0 | 0.06  | gi 213509827 emb CAS92463.1 | unnamed protein produ     | ( 558) | 159 | 45.4 | 0.08  |
| gi 55726804 emb CAH90162.1  | hypothetical protein [   | ( 150) | 154 | 43.9 | 0.06  | gi 114188382 gb EAU30082.1  | conserved hypothetical    | ( 460) | 158 | 45.1 | 0.08  |
| gi 141266737 gb ECQ77935.1  | hypothetical protein G   | ( 125) | 153 | 43.6 | 0.061 | gi 33766655 gb AAQ52858.1   | Sequence 11 from patent   | ( 380) | 157 | 44.8 | 0.08  |
| gi 142121294 gb ECV74577.1  | hypothetical protein G   | ( 333) | 158 | 45.0 | 0.061 | gi 45643653 gb AAS72902.1   | trans-delta12 oleic aci   | ( 380) | 157 | 44.8 | 0.08  |
| gi 155095520 gb ABS99975.1  | Sequence 68 from paten   | ( 335) | 158 | 45.0 | 0.062 | gi 155689132 gb ABU29142.1  | Sequence 11 from paten    | ( 380) | 157 | 44.8 | 0.08  |
| gi 155082219 gb ABS94959.1  | Sequence 68 from paten   | ( 335) | 158 | 45.0 | 0.062 | gi 155349158 gb ABU04763.1  | Sequence 192232 from p    | ( 82)  | 149 | 42.6 | 0.082 |
| gi 155116384 gb ABT11310.1  | Sequence 68 from paten   | ( 335) | 158 | 45.0 | 0.062 | gi 56199450 gb AAV84214.1   | cytochrome B5 [Culicoid   | ( 149) | 152 | 43.4 | 0.083 |
| gi 111979088 gb ABH83331.1  | Sequence 68 from paten   | ( 335) | 158 | 45.0 | 0.062 | gi 134076460 emb CAK45100.1 | unnamed protein produ     | (1048) | 162 | 46.2 | 0.083 |
| gi 187981254 gb EDU47880.1  | nitrate reductase [Pyr   | ( 605) | 161 | 45.9 | 0.062 | gi 142648604 gb ECZ57889.1  | hypothetical protein G    | ( 331) | 156 | 44.6 | 0.084 |
| gi 134058564 emb CAK96451.1 | unnamed protein produ    | ( 503) | 160 | 45.6 | 0.062 | gi 114187902 gb EAU29602.1  | conserved hypothetical    | ( 490) | 158 | 45.1 | 0.084 |
| gi 167881026 gb EDS44409.1  | cytochrome B5 [Culex q   | ( 129) | 153 | 43.6 | 0.063 | gi 140473491 gb ECL94360.1  | hypothetical protein G    | ( 225) | 154 | 44.0 | 0.084 |
| gi 145386893 gb ABP65296.1  | omega-6 fatty desatura   | ( 350) | 158 | 45.0 | 0.064 | gi 124402256 emb CAK67729.1 | unnamed protein produ     | ( 279) | 155 | 44.3 | 0.086 |
| gi 5919159 gb AAD56233.1    | cytochrome b558 [Ectothi | ( 90)  | 151 | 43.1 | 0.064 | gi 164648448 gb EDR12691.1  | predicted protein [Lac    | ( 129) | 151 | 43.2 | 0.086 |
| gi 143054273 gb EDC47947.1  | hypothetical protein G   | ( 242) | 156 | 44.5 | 0.065 | gi 199432414 emb CAK87560.2 | DEHA2E00836p [Debaryo     | ( 615) | 159 | 45.4 | 0.086 |
| gi 187984054 gb EDU49542.1  | microsomal cytochrome    | ( 135) | 153 | 43.6 | 0.065 | gi 57228635 gb AAW45070.1   | cytochrome b5, putative   | ( 158) | 152 | 43.4 | 0.087 |
| gi 154698802 gb EDN98540.1  | hypothetical protein S   | ( 137) | 153 | 43.6 | 0.066 | gi 11177032 dbj BAB17854.1  | cytochrome b5 [Ciona s    | ( 132) | 151 | 43.2 | 0.088 |
| gi 21555150 gb AAM63789.1   | cytochrome b5 (dbj BAA7  | ( 140) | 153 | 43.6 | 0.067 | gi 125545758 gb EAY91897.1  | hypothetical protein O    | ( 196) | 153 | 43.7 | 0.088 |
| gi 4240122 dbj BAA74840.1   | cytochrome b5 [Arabidop  | ( 140) | 153 | 43.6 | 0.067 | gi 125587957 gb EAZ28621.1  | hypothetical protein O    | ( 196) | 153 | 43.7 | 0.088 |
| gi 17104717 gb AAL34247.1   | putative cytochrome b5   | ( 140) | 153 | 43.6 | 0.067 | gi 195622790 gb ACG33225.1  | cytochrome b5 [Zea may    | ( 133) | 151 | 43.2 | 0.088 |
| gi 9758880 dbj BAB09434.1   | cytochrome b5 [Arabidop  | ( 140) | 153 | 43.6 | 0.067 | gi 195651237 gb ACG45086.1  | cytochrome b5 [Zea may    | ( 133) | 151 | 43.2 | 0.088 |
| gi 13877987 gb AAK44071.1   | AF370256_1 putative cyto | ( 140) | 153 | 43.6 | 0.067 | gi 195627196 gb ACG35428.1  | cytochrome b5 [Zea may    | ( 133) | 151 | 43.2 | 0.088 |
| gi 157337660 emb CAO22006.1 | unnamed protein produ    | ( 376) | 158 | 45.1 | 0.068 | gi 13786468 gb AAK39593.1   | AC025296_28 putative cyt  | ( 134) | 151 | 43.2 | 0.089 |
| gi 147858117 emb CAN79670.1 | hypothetical protein     | ( 376) | 158 | 45.1 | 0.068 | gi 600524 gb AAA56985.1     | cytochrome b5 [Musca dome | ( 134) | 151 | 43.2 | 0.089 |
| gi 116057571 emb CAL53774.1 | delta8 fatty acid des    | ( 461) | 159 | 45.3 | 0.068 | gi 31433081 gb AAP54641.1   | Cytochrome b5, putative   | ( 134) | 151 | 43.2 | 0.089 |
| gi 168014138 gb ACA14460.1  | oleate desaturase [Car   | ( 380) | 158 | 45.1 | 0.068 | gi 116785377 gb ABK23699.1  | unknown [Picea sitchen    | ( 134) | 151 | 43.2 | 0.089 |
| gi 124400724 emb CAK66208.1 | unnamed protein produ    | ( 259) | 156 | 44.5 | 0.069 | gi 194699934 gb ACF84051.1  | unknown [Zea mays]        | ( 135) | 151 | 43.2 | 0.089 |
| gi 116057908 emb CAL54111.1 | Cytochrome b5 (ISS) [    | ( 145) | 153 | 43.7 | 0.069 | gi 195605698 gb ACG24679.1  | cytochrome b5 [Zea may    | ( 135) | 151 | 43.2 | 0.089 |
| gi 27261183 gb AAN87574.1   | delta 12 fatty acid con  | ( 386) | 158 | 45.1 | 0.069 | gi 195627462 gb ACG35561.1  | cytochrome b5 [Zea may    | ( 135) | 151 | 43.2 | 0.089 |
| gi 211589285 emb CAP95425.1 | Pc21g05280 [Penicilli    | ( 469) | 159 | 45.3 | 0.069 | gi 190615928 gb EDV31452.1  | GF15361 [Drosophila an    | ( 440) | 157 | 44.9 | 0.09  |
| gi 37514836 gb AAH14431.2   | Cytochrome b5 type B (o  | ( 146) | 153 | 43.7 | 0.069 | gi 119415338 gb EAW25276.1  | acyl-CoA dehydrogenase    | ( 541) | 158 | 45.1 | 0.091 |
| gi 13325120 gb AAH04373.1   | Cytochrome b5 type B (o  | ( 146) | 153 | 43.7 | 0.069 | gi 159125110 gb EDP50227.1  | acyl-CoA dehydrogenase    | ( 541) | 158 | 45.1 | 0.091 |
| gi 158256584 dbj BAF84265.1 | unnamed protein produ    | ( 146) | 153 | 43.7 | 0.069 | gi 143580935 gb EDF74097.1  | hypothetical protein G    | ( 305) | 155 | 44.3 | 0.092 |
| gi 2662291 dbj BAA23735.1   | cytochrome b5 [Homo sap  | ( 146) | 153 | 43.7 | 0.069 | gi 124408857 emb CAK74210.1 | unnamed protein produ     | ( 253) | 154 | 44.0 | 0.093 |
| gi 110623228 emb CAL24254.1 | unnamed protein produ    | ( 387) | 158 | 45.1 | 0.069 | gi 150844218 gb EDN19411.1  | acyl-CoA dehydrogenase    | ( 554) | 158 | 45.2 | 0.093 |
| gi 110623230 emb CAL24255.1 | unnamed protein produ    | ( 387) | 158 | 45.1 | 0.069 | gi 162684231 gb EDQ70635.1  | predicted protein [Phy    | ( 143) | 151 | 43.2 | 0.094 |
| gi 146391238 gb EDK39396.1  | hypothetical protein P   | ( 122) | 152 | 43.4 | 0.07  | gi 53136458 emb CAG32558.1  | hypothetical protein [    | ( 144) | 151 | 43.2 | 0.094 |
| gi 155278884 gb ABT34488.1  | Sequence 121958 from p   | ( 123) | 152 | 43.4 | 0.071 | gi 157348500 emb CAO23392.1 | unnamed protein produ     | ( 382) | 156 | 44.6 | 0.094 |
| gi 142213441 gb ECW44286.1  | hypothetical protein G   | ( 123) | 152 | 43.4 | 0.071 | gi 51556906 gb AAT72296.2   | microsomal omega-6-desa   | ( 383) | 156 | 44.6 | 0.095 |
| gi 90084591 dbj BAE91137.1  | unnamed protein produc   | ( 150) | 153 | 43.7 | 0.071 | gi 76257461 gb ABA41034.1   | delta12-fatty acid desa   | ( 383) | 156 | 44.6 | 0.095 |
| gi 119603681 gb EAW83275.1  | cytochrome b5 type B (   | ( 150) | 153 | 43.7 | 0.071 | gi 124429694 emb CAK94485.1 | unnamed protein produ     | ( 214) | 153 | 43.8 | 0.095 |
| gi 119603682 gb EAW83276.1  | cytochrome b5 type B (   | ( 150) | 153 | 43.7 | 0.071 | gi 33358364 gb AAQ16653.1   | delta-12 fatty acid des   | ( 384) | 156 | 44.6 | 0.095 |
| gi 142104369 gb ECV62134.1  | hypothetical protein G   | ( 330) | 157 | 44.8 | 0.071 | gi 33358366 gb AAQ16654.1   | delta-12 fatty acid des   | ( 384) | 156 | 44.6 | 0.095 |
| gi 156226481 gb EDO47290.1  | predicted protein [Nem   | ( 333) | 157 | 44.8 | 0.072 | gi 159126666 gb EDP51782.1  | nitrate reductase, put    | (1026) | 161 | 46.0 | 0.096 |
| gi 139286247 gb ECE45492.1  | hypothetical protein G   | ( 154) | 153 | 43.7 | 0.072 | gi 7331156 gb AAF60299.1    | AF233640_1 cytochrome b5  | ( 149) | 151 | 43.2 | 0.097 |
| gi 137563224 gb EBU77215.1  | hypothetical protein G   | ( 277) | 156 | 44.5 | 0.072 | gi 49645271 emb CAG98843.1  | KLLAOF23672p [Kluyvero    | ( 123) | 150 | 42.9 | 0.097 |
| gi 5977400 gb AAE14810.1    | Sequence 1 from patent U | ( 155) | 153 | 43.7 | 0.073 | gi 155284665 gb ABT40269.1  | Sequence 127739 from p    | ( 150) | 151 | 43.2 | 0.097 |
| gi 12813432 gb AAE44732.1   | Sequence 1 from patent   | ( 155) | 153 | 43.7 | 0.073 | gi 140877332 gb EC011367.1  | hypothetical protein G    | ( 227) | 153 | 43.8 | 0.099 |
| gi 14536586 emb CAC42651.1  | unnamed protein produc   | ( 105) | 151 | 43.1 | 0.073 | gi 142972052 gb EDB89098.1  | hypothetical protein G    | ( 345) | 155 | 44.3 | 0.1   |
| gi 5748690 emb CAB53082.1   | cytochrome b5 (predicte  | ( 129) | 152 | 43.4 | 0.073 | gi 138164275 gb EBY12800.1  | hypothetical protein G    | ( 285) | 154 | 44.1 | 0.1   |
| gi 124422542 emb CAK87368.1 | unnamed protein produ    | ( 417) | 158 | 45.1 | 0.074 | gi 89272063 emb CAJ82840.1  | cytochrome b-5 [Xenopu    | ( 132) | 150 | 42.9 | 0.1   |
| gi 155280300 gb ABT35904.1  | Sequence 123374 from p   | ( 134) | 152 | 43.4 | 0.076 | gi 163915979 gb AAI57168.1  | Hypothetical protein L    | ( 132) | 150 | 42.9 | 0.1   |
| gi 167140 gb AAA32990.1     | cytochrome b-5           | ( 134) | 152 | 43.4 | 0.076 | gi 118485108 gb ABK94417.1  | unknown [Populus trich    | ( 134) | 150 | 42.9 | 0.1   |
| gi 25044825 gb AAM28288.1   | cytochrome b5 [Ananas c  | ( 134) | 152 | 43.4 | 0.076 | gi 195609184 gb ACG26422.1  | cytochrome b5 [Zea may    | ( 134) | 150 | 42.9 | 0.1   |
| gi 155280299 gb ABT35903.1  | Sequence 123373 from p   | ( 134) | 152 | 43.4 | 0.076 | gi 195650059 gb ACG44497.1  | cytochrome b5 [Zea may    | ( 134) | 150 | 42.9 | 0.1   |

|                             |                          |        |     |      |      |                             |                           |        |     |      |      |
|-----------------------------|--------------------------|--------|-----|------|------|-----------------------------|---------------------------|--------|-----|------|------|
| gi 195636578 gb ACG37757.1  | cytochrome b5 [Zea may   | ( 134) | 150 | 42.9 | 0.1  | gi 145280641 gb ABP49577.1  | oleate desaturase [Car    | ( 383) | 154 | 44.1 | 0.13 |
| gi 116784877 gb ABK23501.1  | unknown [Picea sitchen   | ( 134) | 150 | 42.9 | 0.1  | gi 136362143 gb EBN65335.1  | hypothetical protein G    | ( 121) | 148 | 42.5 | 0.13 |
| gi 195657733 gb ACG48334.1  | cytochrome b5 [Zea may   | ( 134) | 150 | 42.9 | 0.1  | gi 145009425 gb EDJ94117.1  | hypothetical protein M    | ( 480) | 155 | 44.4 | 0.13 |
| gi 155270908 gb ABT26512.1  | Sequence 113982 from p   | ( 134) | 150 | 42.9 | 0.1  | gi 116059112 emb CAL54819.1 | Medium-chain acyl-CoA     | (1048) | 159 | 45.5 | 0.13 |
| gi 195649129 gb ACG44032.1  | cytochrome b5 [Zea may   | ( 134) | 150 | 42.9 | 0.1  | gi 143986234 gb EDI04801.1  | hypothetical protein G    | ( 273) | 152 | 43.6 | 0.14 |
| gi 157355224 emb CAO48600.1 | unnamed protein produ    | ( 134) | 150 | 42.9 | 0.1  | gi 199431479 emb CAG86857.2 | DEHA2D05720p [Debaryo     | ( 153) | 149 | 42.7 | 0.14 |
| gi 142611604 gb ECZ31808.1  | hypothetical protein G   | ( 355) | 155 | 44.3 | 0.1  | gi 187975410 gb EDU42036.1  | L-lactate dehydrogenas    | ( 500) | 155 | 44.4 | 0.14 |
| gi 137113171 gb EBS27626.1  | hypothetical protein G   | ( 294) | 154 | 44.1 | 0.1  | gi 161162329 emb CAN93634.1 | hypothetical protein      | ( 413) | 154 | 44.2 | 0.14 |
| gi 149391361 gb ABR25698.1  | cytochrome b5 [Oryza s   | ( 135) | 150 | 42.9 | 0.1  | gi 167870179 gb EDS33562.1  | conserved hypothetical    | ( 157) | 149 | 42.8 | 0.14 |
| gi 125573473 gb EAZ14988.1  | hypothetical protein O   | ( 135) | 150 | 42.9 | 0.1  | gi 194697072 gb ACF82620.1  | unknown [Zea mays]        | ( 135) | 148 | 42.5 | 0.14 |
| gi 510539 emb CAA56318.1    | cytochrome b5 [Nicotiana | ( 135) | 150 | 42.9 | 0.1  | gi 195621176 gb ACG32418.1  | cytochrome b5 [Zea may    | ( 135) | 148 | 42.5 | 0.14 |
| gi 215767969 dbj BAH00198.1 | unnamed protein produ    | ( 135) | 150 | 42.9 | 0.1  | gi 136753758 gb EBQ17986.1  | hypothetical protein G    | ( 243) | 151 | 43.3 | 0.14 |
| gi 125529283 gb EAY77397.1  | hypothetical protein O   | ( 135) | 150 | 42.9 | 0.1  | gi 119400878 gb EAW11302.1  | cytochrome b5, putativ    | ( 136) | 148 | 42.5 | 0.15 |
| gi 15289978 dbj BAB63673.1  | putative cytochrome b5   | ( 135) | 150 | 42.9 | 0.1  | gi 114192897 gb EAU34597.1  | hypothetical protein A    | ( 536) | 155 | 44.5 | 0.15 |
| gi 113535065 dbj BAF07448.1 | Os01g0971500 [Oryza s    | ( 135) | 150 | 42.9 | 0.1  | gi 210125472 gb EEA73163.1  | hypothetical protein B    | ( 138) | 148 | 42.5 | 0.15 |
| gi 149392595 gb ABR26100.1  | cytochrome b5 [Oryza s   | ( 135) | 150 | 42.9 | 0.1  | gi 124416107 emb CAK81155.1 | unnamed protein produ     | ( 207) | 150 | 43.1 | 0.15 |
| gi 76781154 gb ABA54492.1   | cytochrome b5 type 56 [  | ( 136) | 150 | 42.9 | 0.11 | gi 116060159 emb CAL56218.1 | Delta 6-fatty acid de     | ( 309) | 152 | 43.6 | 0.15 |
| gi 143350724 gb EDE49728.1  | hypothetical protein G   | ( 244) | 153 | 43.8 | 0.11 | gi 83272395 gb ABC00771.1   | delta-12 fatty acid des   | ( 377) | 153 | 43.9 | 0.15 |
| gi 210068794 gb EEA22885.1  | heme/steroid binding p   | ( 297) | 154 | 44.1 | 0.11 | gi 84626279 gb ABC59684.1   | delta-12 fatty acid ace   | ( 377) | 153 | 43.9 | 0.15 |
| gi 142149054 gb ECV95134.1  | hypothetical protein G   | ( 137) | 150 | 42.9 | 0.11 | gi 146389168 gb EDK37326.1  | hypothetical protein P    | ( 378) | 153 | 43.9 | 0.15 |
| gi 155298102 gb ABT53706.1  | Sequence 141176 from p   | ( 138) | 150 | 42.9 | 0.11 | gi 60594769 gb AAX29989.1   | microsomal omega-6-desa   | ( 379) | 153 | 43.9 | 0.15 |
| gi 62484905 dbj BAD95486.1  | delta5 fatty acid desa   | ( 446) | 156 | 44.6 | 0.11 | gi 21507257 gb AAM57793.1   | Sequence 6 from patent    | ( 379) | 153 | 43.9 | 0.15 |
| gi 156207805 gb EDO29550.1  | predicted protein [Nem   | ( 378) | 155 | 44.4 | 0.11 | gi 75205882 gb ABA17986.1   | Sequence 6 from patent    | ( 379) | 153 | 43.9 | 0.15 |
| gi 2613051 gb AAB84262.1    | omega-6 desaturase [Arac | ( 379) | 155 | 44.4 | 0.11 | gi 62789094 gb AAY07977.1   | Sequence 6 from patent    | ( 379) | 153 | 43.9 | 0.15 |
| gi 2501790 gb AAB80696.1    | omega-6 fatty acid desat | ( 382) | 155 | 44.4 | 0.11 | gi 115833234 gb ABJ40712.1  | Sequence 6 from patent    | ( 379) | 153 | 43.9 | 0.15 |
| gi 49528253 emb CAG61910.1  | unnamed protein produc   | ( 121) | 149 | 42.7 | 0.11 | gi 139750378 gb ECH20331.1  | hypothetical protein G    | ( 314) | 152 | 43.6 | 0.15 |
| gi 136596108 gb EBP17865.1  | hypothetical protein G   | ( 101) | 148 | 42.4 | 0.11 | gi 33766650 gb AAQ52853.1   | Sequence 5 from patent    | ( 387) | 153 | 43.9 | 0.15 |
| gi 156114730 gb EDO16237.1  | hypothetical protein K   | ( 123) | 149 | 42.7 | 0.11 | gi 34600651 gb AAQ78508.1   | Sequence 13 from patent   | ( 387) | 153 | 43.9 | 0.15 |
| gi 49652236 emb CAG84528.1  | DEHA2A05742p [Debaryom   | ( 123) | 149 | 42.7 | 0.11 | gi 155713301 gb ABU35457.1  | Sequence 5 from patent    | ( 387) | 153 | 43.9 | 0.15 |
| gi 208498920 gb ACT29313.1  | NADPH nitrate reductas   | ( 864) | 159 | 45.5 | 0.11 | gi 91125672 gb ABE12620.1   | Sequence 33 from patent   | ( 387) | 153 | 43.9 | 0.15 |
| gi 30039221 gb AAP12556.1   | nitrate reductase [Peni  | ( 864) | 159 | 45.5 | 0.11 | gi 9041521 gb AAB00859.1    | microsomal omega-6 desatu | ( 387) | 153 | 43.9 | 0.15 |
| gi 134077192 emb CAK45533.1 | nitrate reductase (NA    | ( 867) | 159 | 45.5 | 0.11 | gi 59956942 dbj BAD89860.1  | microsomal omega-6 fat    | ( 387) | 153 | 43.9 | 0.15 |
| gi 141275093 gb ECQ83658.1  | hypothetical protein G   | ( 222) | 152 | 43.5 | 0.11 | gi 5994482 gb AAE19895.1    | Sequence 5 from patent U  | ( 387) | 153 | 43.9 | 0.15 |
| gi 195641908 gb ACG40422.1  | cytochrome b5 [Zea may   | ( 185) | 151 | 43.3 | 0.12 | gi 155689127 gb ABU29137.1  | Sequence 5 from patent    | ( 387) | 153 | 43.9 | 0.15 |
| gi 187979172 gb EDU45798.1  | acyl-CoA dehydrogenase   | ( 511) | 156 | 44.7 | 0.12 | gi 155278641 gb ABT34245.1  | Sequence 121715 from p    | ( 149) | 148 | 42.5 | 0.16 |
| gi 189016254 gb ACD70298.1  | delta-6 fatty acid des   | ( 159) | 150 | 43.0 | 0.12 | gi 138540123 gb EAC29874.1  | hypothetical protein G    | ( 270) | 151 | 43.4 | 0.16 |
| gi 189303970 gb ACD85900.1  | nitrate reductase [Hyp   | ( 235) | 152 | 43.5 | 0.12 | gi 143250156 gb EDD89444.1  | hypothetical protein G    | ( 273) | 151 | 43.4 | 0.16 |
| gi 99109681 gb ABF67509.1   | cytochrome b5 [Haliotis  | ( 133) | 149 | 42.7 | 0.12 | gi 139505981 gb ECF53542.1  | hypothetical protein G    | ( 86)  | 145 | 41.7 | 0.16 |
| gi 118484567 gb ABK94157.1  | unknown [Populus trich   | ( 134) | 149 | 42.7 | 0.12 | gi 134916704 gb EBE28096.1  | hypothetical protein G    | ( 337) | 152 | 43.6 | 0.16 |
| gi 195655973 gb ACG47454.1  | cytochrome b5 [Zea may   | ( 134) | 149 | 42.7 | 0.12 | gi 124403949 emb CAK69408.1 | unnamed protein produ     | ( 280) | 151 | 43.4 | 0.16 |
| gi 143101975 gb EDC82888.1  | hypothetical protein G   | ( 355) | 154 | 44.1 | 0.12 | gi 136137059 gb EBM15398.1  | hypothetical protein G    | ( 159) | 148 | 42.5 | 0.17 |
| gi 11177030 dbj BAB17853.1  | cytochrome b5 [Polyand   | ( 135) | 149 | 42.7 | 0.12 | gi 49527670 emb CAG61319.1  | unnamed protein produc    | ( 194) | 149 | 42.8 | 0.17 |
| gi 215264539 emb CAS08906.1 | predicted protein [Es    | ( 363) | 154 | 44.1 | 0.12 | gi 50416385 gb AAH77334.1   | MGC80327 protein [Xenop   | ( 132) | 147 | 42.2 | 0.17 |
| gi 134064027 emb CAM40218.1 | nitrate reductase, pu    | ( 537) | 156 | 44.7 | 0.12 | gi 138336124 gb EBZ03923.1  | hypothetical protein G    | ( 74)  | 144 | 41.4 | 0.17 |
| gi 119399890 gb EAW10316.1  | acyl-CoA dehydrogenase   | ( 542) | 156 | 44.7 | 0.13 | gi 124423282 emb CAK88077.1 | unnamed protein produ     | ( 358) | 152 | 43.7 | 0.17 |
| gi 57870222 gb AAH89049.1   | LOC100036773 protein [X  | ( 140) | 149 | 42.7 | 0.13 | gi 199425292 emb CAG82239.2 | YALI0C16797p [Yarrowi     | ( 530) | 154 | 44.2 | 0.17 |
| gi 160703651 gb EAT80311.2  | hypothetical protein S   | ( 140) | 149 | 42.7 | 0.13 | gi 143330688 gb EDE37222.1  | hypothetical protein G    | ( 296) | 151 | 43.4 | 0.17 |
| gi 55774572 gb AAV64871.1   | cytochrome b5 [Xenopus   | ( 141) | 149 | 42.7 | 0.13 | gi 211587064 emb CAP94727.1 | Pc18g05030 [Penicilli     | ( 361) | 152 | 43.7 | 0.17 |
| gi 77748376 gb AAI06221.1   | Unknown (protein for MG  | ( 141) | 149 | 42.7 | 0.13 | gi 139049367 gb ECD05908.1  | hypothetical protein G    | ( 93)  | 145 | 41.7 | 0.17 |
| gi 197127610 gb ACH44108.1  | putative cytochrome b5   | ( 141) | 149 | 42.7 | 0.13 | gi 150851185 gb EDN26378.1  | cytochrome b5 [Botryot    | ( 139) | 147 | 42.3 | 0.17 |
| gi 217071298 gb ACJ84009.1  | unknown [Medicago trun   | ( 142) | 149 | 42.7 | 0.13 | gi 158274018 gb EDO99803.1  | cytochrome b5 protein     | ( 139) | 147 | 42.3 | 0.17 |
| gi 217071624 gb ACJ84172.1  | unknown [Medicago trun   | ( 142) | 149 | 42.7 | 0.13 | gi 14456133 emb CAC41650.1  | putative nitrate reduc    | ( 983) | 157 | 45.1 | 0.17 |
| gi 189846878 gb ACE26376.1  | Sequence 136 from pate   | ( 378) | 154 | 44.1 | 0.13 | gi 195657819 gb ACG48377.1  | cytochrome b5 [Zea may    | ( 117) | 146 | 42.0 | 0.18 |
| gi 38564776 gb AAW23815.1   | delta 12 fatty acid epo  | ( 378) | 154 | 44.1 | 0.13 | gi 31322135 gb AAO38032.1   | delta12-fatty acid acet   | ( 377) | 152 | 43.7 | 0.18 |
| gi 189702340 gb ACE14957.1  | Sequence 2 from patent   | ( 378) | 154 | 44.1 | 0.13 | gi 114190157 gb EAU31857.1  | conserved hypothetical    | ( 999) | 157 | 45.1 | 0.18 |
| gi 193893371 gb EDV92237.1  | GH24801 [Drosophila gr   | ( 118) | 148 | 42.4 | 0.13 | gi 3135020 emb CAA76157.1   | delta 12 fatty acid des   | ( 379) | 152 | 43.7 | 0.18 |
| gi 49642276 emb CAH00238.1  | KLLA0D01639p [Kluyvero   | ( 381) | 154 | 44.1 | 0.13 | gi 56759060 gb AAW26760.1   | SJCHGC00480 protein [Sc   | ( 118) | 146 | 42.0 | 0.18 |
| gi 141194560 gb ECQ27436.1  | hypothetical protein G   | ( 175) | 150 | 43.0 | 0.13 | gi 135612136 gb EBI75574.1  | hypothetical protein G    | ( 314) | 151 | 43.4 | 0.18 |

|                             |                           |        |     |      |      |                             |                           |        |     |      |      |
|-----------------------------|---------------------------|--------|-----|------|------|-----------------------------|---------------------------|--------|-----|------|------|
| gi 438451 gb AAA32782.1     | delta-12 desaturase       | ( 383) | 152 | 43.7 | 0.18 | gi 40737984 gb AAR89457.1   | cytochrome B5 [Petunia    | ( 149) | 146 | 42.0 | 0.22 |
| gi 76007349 gb ABA38263.1   | Sequence 6 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 10183662 emb CAC08830.1  | unnamed protein produc    | ( 149) | 146 | 42.0 | 0.22 |
| gi 110623200 emb CAL24240.1 | unnamed protein produ     | ( 383) | 152 | 43.7 | 0.18 | gi 194699154 gb ACF83661.1  | unknown [Zea mays]        | ( 186) | 147 | 42.3 | 0.22 |
| gi 91125671 gb ABE12619.1   | Sequence 32 from patent   | ( 383) | 152 | 43.7 | 0.18 | gi 119402848 gb EAW13269.1  | cytochrome b5, putativ    | ( 105) | 144 | 41.5 | 0.22 |
| gi 56666937 gb AAW18476.1   | Sequence 4 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 212003383 gb EEB09043.1  | cytochrome b5 [Schizos    | ( 128) | 145 | 41.8 | 0.22 |
| gi 62789092 gb AAE82559.1   | Sequence 2 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 89299416 gb EAR97404.1   | Fatty acid desaturase f   | ( 413) | 151 | 43.5 | 0.22 |
| gi 14517474 gb AAK62627.1   | AT3g12120/T21B14_107 [A   | ( 383) | 152 | 43.7 | 0.18 | gi 138455028 gb EBZ79017.1  | hypothetical protein G    | ( 280) | 149 | 42.9 | 0.22 |
| gi 75205880 gb ABA17984.1   | Sequence 2 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 135549142 gb EBI35878.1  | hypothetical protein G    | ( 344) | 150 | 43.2 | 0.23 |
| gi 17909752 gb AAE82559.1   | Sequence 6 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 160705808 gb EAT76132.2  | hypothetical protein S    | ( 619) | 153 | 44.0 | 0.23 |
| gi 34600647 gb AAQ78504.1   | Sequence 9 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 154691737 gb EDN91475.1  | hypothetical protein S    | ( 512) | 152 | 43.7 | 0.23 |
| gi 189846872 gb ACE26370.1  | Sequence 125 from pate    | ( 383) | 152 | 43.7 | 0.18 | gi 136527749 gb EBO74245.1  | hypothetical protein G    | ( 239) | 148 | 42.6 | 0.23 |
| gi 92941109 dbj BAB01960.1  | omega-6 fatty acid desa   | ( 383) | 152 | 43.7 | 0.18 | gi 143299135 gb EDE19043.1  | hypothetical protein G    | ( 198) | 147 | 42.3 | 0.23 |
| gi 17918535 gb AAE85969.1   | Sequence 6 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 119404606 gb EAW14982.1  | cytochrome b5-like Hem    | ( 163) | 146 | 42.1 | 0.23 |
| gi 189704779 gb ACE16108.1  | Sequence 125 from pate    | ( 383) | 152 | 43.7 | 0.18 | gi 143089206 gb EDC73513.1  | hypothetical protein G    | ( 297) | 149 | 42.9 | 0.24 |
| gi 68164987 gb AAY87459.1   | omega-6 fatty acid desa   | ( 383) | 152 | 43.7 | 0.18 | gi 31419550 gb AAH53263.1   | Cytochrome b5 type A (m   | ( 137) | 145 | 41.8 | 0.24 |
| gi 12322004 gb AAG51042.1   | AC069473_4 omega-6 fatty  | ( 383) | 152 | 43.7 | 0.18 | gi 159156005 gb AAI54825.1  | Cyb5a protein [Danio r    | ( 137) | 145 | 41.8 | 0.24 |
| gi 5955846 gb AAE07502.1    | Sequence 41 from patent   | ( 383) | 152 | 43.7 | 0.18 | gi 134079114 emb CAK04669.1 | unnamed protein produ     | ( 138) | 145 | 41.8 | 0.24 |
| gi 58013375 gb AAW63041.1   | microsomal delta-12 ole   | ( 383) | 152 | 43.7 | 0.18 | gi 210125476 gb EEA73167.1  | cytochrome b5 [Branchi    | ( 138) | 145 | 41.8 | 0.24 |
| gi 71057275 emb CAJ18799.1  | unnamed protein produc    | ( 383) | 152 | 43.7 | 0.18 | gi 89294120 gb EAR92108.1   | Cytochrome b5-like Heme   | ( 114) | 144 | 41.5 | 0.24 |
| gi 110623202 emb CAL24241.1 | unnamed protein produ     | ( 383) | 152 | 43.7 | 0.18 | gi 135869837 gb EBK36254.1  | hypothetical protein G    | ( 303) | 149 | 42.9 | 0.24 |
| gi 2492223 gb AAB80359.1    | I66170 Sequence 41 from p | ( 383) | 152 | 43.7 | 0.18 | gi 142975618 gb EDB19601.1  | hypothetical protein G    | ( 251) | 148 | 42.6 | 0.24 |
| gi 22655458 gb AAM98321.1   | At3g12120/T21B14_107 [A   | ( 383) | 152 | 43.7 | 0.18 | gi 136600981 gb EBP20985.1  | hypothetical protein G    | ( 307) | 149 | 42.9 | 0.24 |
| gi 21536781 gb AAM61113.1   | omega-6 fatty acid desa   | ( 383) | 152 | 43.7 | 0.18 | gi 144578041 gb ABO96106.1  | predicted protein [Ost    | ( 141) | 145 | 41.8 | 0.24 |
| gi 115833232 gb ABJ40710.1  | Sequence 2 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 40644254 emb CAD22050.1  | cytochrome b5 [Oryza s    | ( 143) | 145 | 41.8 | 0.24 |
| gi 21507255 gb AAM57791.1   | Sequence 2 from patent    | ( 383) | 152 | 43.7 | 0.18 | gi 108878535 gb EAT42760.1  | conserved hypothetical    | ( 462) | 151 | 43.5 | 0.25 |
| gi 150408849 gb EDN04305.1  | hypothetical protein H    | ( 177) | 148 | 42.6 | 0.18 | gi 45272283 gb AAS57577.1   | delta12-oleic acid desa   | ( 382) | 150 | 43.2 | 0.25 |
| gi 194153330 gb EDW68514.1  | GJ12661 [Drosophila vi    | ( 120) | 146 | 42.0 | 0.18 | gi 113623677 dbj BAF23622.1 | Os08g0386300 [Oryza s     | ( 119) | 144 | 41.5 | 0.25 |
| gi 28371827 gb AAO37754.1   | delta-12 oleate desatur   | ( 387) | 152 | 43.7 | 0.18 | gi 40253472 dbj BAD05422.1  | cytochrome b5-like [Or    | ( 119) | 144 | 41.5 | 0.25 |
| gi 160706885 gb EAT87086.2  | hypothetical protein S    | ( 697) | 155 | 44.5 | 0.18 | gi 91125663 gb ABE12611.1   | Sequence 4 from patent    | ( 385) | 150 | 43.2 | 0.25 |
| gi 135277729 gb EBG58802.1  | hypothetical protein G    | ( 267) | 150 | 43.1 | 0.18 | gi 2578033 emb CAA65744.1   | omega-6 desaturase [Gos   | ( 385) | 150 | 43.2 | 0.25 |
| gi 119395856 gb EAW06288.1  | cytochrome b5, putativ    | ( 83)  | 144 | 41.4 | 0.18 | gi 194700608 gb ACF84388.1  | unknown [Zea mays]        | ( 216) | 147 | 42.4 | 0.25 |
| gi 149015873 gb EDL75180.1  | cytochrome b-5, isofor    | ( 83)  | 144 | 41.4 | 0.18 | gi 194708396 gb ACF88282.1  | unknown [Zea mays]        | ( 216) | 147 | 42.4 | 0.25 |
| gi 142847889 gb EDB03384.1  | hypothetical protein G    | ( 331) | 151 | 43.4 | 0.19 | gi 195619472 gb ACG31566.1  | cytoplasm protein [Zea    | ( 216) | 147 | 42.4 | 0.25 |
| gi 124427005 emb CAK91785.1 | unnamed protein produ     | ( 417) | 152 | 43.7 | 0.19 | gi 8373451 gb AAB32285.1    | peditoxin, pedin=cytochro | ( 82)  | 142 | 41.0 | 0.25 |
| gi 125536127 gb EAY82615.1  | hypothetical protein O    | ( 159) | 147 | 42.3 | 0.19 | gi 139435639 gb ECF09823.1  | hypothetical protein G    | ( 83)  | 142 | 41.0 | 0.25 |
| gi 144104790 gb EDI89877.1  | hypothetical protein G    | ( 353) | 151 | 43.4 | 0.2  | gi 211584179 emb CAP92210.1 | nitrate reductase (NA     | ( 864) | 154 | 44.3 | 0.25 |
| gi 119400947 gb EAW11371.1  | heme/steroid binding p    | ( 362) | 151 | 43.4 | 0.2  | gi 1431858 gb AAB03900.1    | nitrate reductase         | ( 864) | 154 | 44.3 | 0.25 |
| gi 68127721 emb CAJ05968.1  | nitrate reductase, put    | ( 536) | 153 | 44.0 | 0.2  | gi 140353714 gb ECL19515.1  | hypothetical protein G    | ( 152) | 145 | 41.8 | 0.26 |
| gi 194374511 dbj BAG57151.1 | unnamed protein produ     | ( 204) | 148 | 42.6 | 0.2  | gi 135411199 gb EBH45692.1  | hypothetical protein G    | ( 337) | 149 | 42.9 | 0.26 |
| gi 170939457 emb CAP64685.1 | unnamed protein produ     | ( 544) | 153 | 44.0 | 0.2  | gi 31322226 gb AAO63560.1   | nitrate reductase [Vert   | ( 893) | 154 | 44.4 | 0.26 |
| gi 156531882 gb ABU76708.1  | hypothetical protein E    | ( 369) | 151 | 43.4 | 0.2  | gi 155102616 gb ABT03239.1  | Sequence 48 from paten    | ( 412) | 150 | 43.2 | 0.26 |
| gi 134058611 emb CAK38595.1 | unnamed protein produ     | ( 545) | 153 | 44.0 | 0.2  | gi 136510696 gb EBO63349.1  | hypothetical protein G    | ( 281) | 148 | 42.7 | 0.26 |
| gi 137947269 gb EBW91038.1  | hypothetical protein G    | ( 78)  | 143 | 41.2 | 0.2  | gi 134080434 emb CAK41183.1 | unnamed protein produ     | ( 508) | 151 | 43.5 | 0.27 |
| gi 90300461 gb EAS30092.1   | hypothetical protein CI   | ( 547) | 153 | 44.0 | 0.2  | gi 139123905 gb ECD57816.1  | hypothetical protein G    | ( 130) | 144 | 41.5 | 0.27 |
| gi 189704774 gb ACE16103.1  | Sequence 38 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 28950126 gb ABZ28586.1   | related to ACYL-COA DE    | ( 519) | 151 | 43.5 | 0.27 |
| gi 189846871 gb ACE26369.1  | Sequence 42 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 70834124 gb EAN79626.1   | cytochrome b5, putative   | ( 133) | 144 | 41.6 | 0.27 |
| gi 189704772 gb ACE16101.1  | Sequence 36 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 139794221 gb ECH50961.1  | hypothetical protein G    | ( 164) | 145 | 41.8 | 0.27 |
| gi 189704778 gb ACE16107.1  | Sequence 42 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 119408175 gb EAW18124.1  | heme/steroid binding p    | ( 358) | 149 | 43.0 | 0.27 |
| gi 189846865 gb ACE26363.1  | Sequence 36 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 143665744 gb EDG15555.1  | hypothetical protein G    | ( 296) | 148 | 42.7 | 0.28 |
| gi 189846867 gb ACE26365.1  | Sequence 38 from paten    | ( 377) | 151 | 43.4 | 0.21 | gi 1483145 dbj BAA10888.1   | Cytochrome b5 [Ascaris    | ( 112) | 143 | 41.3 | 0.28 |
| gi 124403690 emb CAK69152.1 | unnamed protein produ     | ( 258) | 149 | 42.9 | 0.21 | gi 167275722 gb ABZ28586.1  | Sequence 2524 from pat    | ( 201) | 146 | 42.1 | 0.28 |
| gi 137164908 gb EBS56599.1  | hypothetical protein G    | ( 213) | 148 | 42.6 | 0.21 | gi 88177673 gb EAQ85141.1   | cytochrome b5, putative   | ( 137) | 144 | 41.6 | 0.28 |
| gi 143332594 gb EDE38331.1  | hypothetical protein G    | ( 259) | 149 | 42.9 | 0.21 | gi 186467605 gb ACC83406.1  | fatty acid desaturase     | ( 366) | 149 | 43.0 | 0.28 |
| gi 159126631 gb EDP51747.1  | cytochrome b5 reductas    | ( 471) | 152 | 43.7 | 0.21 | gi 25989476 gb AAL93620.1   | fatty acid desaturase 2   | ( 383) | 149 | 43.0 | 0.29 |
| gi 157335617 emb CAO61447.1 | unnamed protein produ     | ( 147) | 146 | 42.0 | 0.21 | gi 55509203 gb AAV52834.1   | delta-12 fatty acid des   | ( 383) | 149 | 43.0 | 0.29 |
| gi 147838440 emb CAN63256.1 | hypothetical protein      | ( 147) | 146 | 42.0 | 0.21 | gi 181392 gb AAA52165.1     | cytochrome b-5            | ( 98)  | 142 | 41.0 | 0.29 |
| gi 85700983 gb ABC74800.1   | cytochrome B5 [Petunia    | ( 149) | 146 | 42.0 | 0.22 | gi 119586949 gb EAW66545.1  | cytochrome b5 type A (    | ( 98)  | 142 | 41.0 | 0.29 |
| gi 4204575 gb AAD10774.1    | cytochrome b5 DIF-F [Pet  | ( 149) | 146 | 42.0 | 0.22 | gi 135042934 gb EBF12759.1  | hypothetical protein G    | ( 176) | 145 | 41.9 | 0.29 |

|                             |                          |        |     |      |      |
|-----------------------------|--------------------------|--------|-----|------|------|
| gi 1212781 emb CAA62578.1   | oleate desaturase [Bras  | ( 384) | 149 | 43.0 | 0.29 |
| gi 34600648 gb AAQ78505.1   | Sequence 10 from patent  | ( 384) | 149 | 43.0 | 0.29 |
| gi 930010 emb CAA40090.1    | nitrate reductase (NADH) | ( 318) | 148 | 42.7 | 0.29 |
| gi 119407840 gb EAW17789.1  | cytochrome b5 reductas   | ( 470) | 150 | 43.3 | 0.29 |
| gi 193918587 gb EDW17454.1  | GI12677 [Drosophila mo   | ( 121) | 143 | 41.3 | 0.29 |
| gi 38175775 dbj BAC55856.2  | flavoheomoprotein b5/b5  | ( 218) | 146 | 42.1 | 0.29 |
| gi 113610774 dbj BAF21152.1 | Os07g0232200 [Oryza s    | ( 218) | 146 | 42.1 | 0.29 |
| gi 195635929 gb ACG37433.1  | omega-6 fatty acid des   | ( 394) | 149 | 43.0 | 0.3  |
| gi 119397119 gb EAW07550.1  | nitrate reductase NiaD   | ( 868) | 153 | 44.1 | 0.3  |
| gi 154694855 gb EDN94593.1  | hypothetical protein S   | ( 124) | 143 | 41.3 | 0.3  |
| gi 135256356 gb EBG46227.1  | hypothetical protein G   | ( 271) | 147 | 42.4 | 0.3  |
| gi 138277015 gb EBY75438.1  | hypothetical protein G   | ( 271) | 147 | 42.4 | 0.3  |
| gi 146150662 gb ABP97095.1  | nitrate reductase [Chl   | ( 877) | 153 | 44.1 | 0.3  |
| gi 197701160 gb ABJ91208.4  | nitrate reductase [Chl   | ( 877) | 153 | 44.1 | 0.3  |
| gi 136567798 gb EBQ99802.1  | hypothetical protein G   | ( 334) | 148 | 42.7 | 0.3  |
| gi 144189797 gb EDJ52342.1  | hypothetical protein G   | ( 71)  | 140 | 40.5 | 0.31 |
| gi 135095505 gb EBF46310.1  | hypothetical protein G   | ( 71)  | 140 | 40.5 | 0.31 |
| gi 4530972 emb CAA03836.1   | DELTA-12 DESATURASE [Co  | ( 338) | 148 | 42.7 | 0.31 |
| gi 212508562 gb EEB12210.1  | Cytochrome b5, putativ   | ( 156) | 144 | 41.6 | 0.31 |
| gi 126633772 emb CAM55852.1 | unnamed protein produ    | ( 503) | 150 | 43.3 | 0.31 |
| gi 116001277 emb CAL49890.1 | unnamed protein produ    | ( 503) | 150 | 43.3 | 0.31 |
| gi 60220818 emb CAI58908.1  | unnamed protein produc   | ( 503) | 150 | 43.3 | 0.31 |
| gi 76059318 emb CAJ30853.1  | unnamed protein produc   | ( 503) | 150 | 43.3 | 0.31 |
| gi 83766286 dbj BAE56429.1  | unnamed protein produc   | ( 419) | 149 | 43.0 | 0.31 |
| gi 145011783 gb EDJ96439.1  | conserved hypothetical   | ( 513) | 150 | 43.3 | 0.31 |
| gi 23505081 emb CAD51863.1  | heme binding protein,    | ( 162) | 144 | 41.6 | 0.32 |
| gi 136436696 gb EB015456.1  | hypothetical protein G   | ( 242) | 146 | 42.2 | 0.32 |
| gi 159128931 gb EDP54045.1  | heme/steroid binding p   | ( 358) | 148 | 42.7 | 0.32 |
| gi 190657614 gb EDV54827.1  | GG21732 [Drosophila er   | ( 137) | 143 | 41.3 | 0.33 |
| gi 26107962 gb AAN80162.1   | AE016760_21 Hypothetical | ( 363) | 148 | 42.7 | 0.33 |
| gi 54645384 gb EAL34124.1   | GA19919 [Drosophila pse  | ( 138) | 143 | 41.3 | 0.33 |
| gi 194117726 gb EDW39769.1  | GL15857 [Drosophila pe   | ( 138) | 143 | 41.3 | 0.33 |
| gi 140367568 gb ECL28905.1  | hypothetical protein G   | ( 169) | 144 | 41.6 | 0.33 |
| gi 162471892 gb ABX99727.1  | Sequence 5 from patent   | ( 115) | 142 | 41.1 | 0.33 |
| gi 160814783 emb CAP40236.1 | unnamed protein produ    | ( 550) | 150 | 43.3 | 0.33 |
| gi 60173017 gb AAI14506.1   | delta-4 fatty acid desa  | ( 550) | 150 | 43.3 | 0.33 |
| gi 115878494 gb ABJ45510.1  | Sequence 6249 from pat   | ( 116) | 142 | 41.1 | 0.33 |
| gi 40043342 emb CAF00447.1  | unnamed protein produc   | ( 116) | 142 | 41.1 | 0.33 |
| gi 77452622 gb ABA84317.1   | Sequence 6249 from pate  | ( 116) | 142 | 41.1 | 0.33 |
| gi 194346322 gb ACF49507.1  | omega-6 desaturase [Li   | ( 382) | 148 | 42.7 | 0.34 |
| gi 194702722 gb ACF85445.1  | unknown [Zea mays]       | ( 382) | 148 | 42.7 | 0.34 |
| gi 4530970 emb CAA03835.1   | DELTA-12 DESATURASE [Co  | ( 382) | 148 | 42.7 | 0.34 |
| gi 119655554 gb ABL86147.1  | delta-12 oleic acid de   | ( 383) | 148 | 42.7 | 0.34 |
| gi 1372997 gb AAC14455.1    | cytochrome b-5 [Bos taur | ( 98)  | 141 | 40.8 | 0.34 |
| gi 471150 dbj BAA01712.1    | soluble cytochrome b5 [O | ( 98)  | 141 | 40.8 | 0.34 |
| gi 14536614 emb CAC42665.1  | unnamed protein produc   | ( 469) | 149 | 43.0 | 0.34 |
| gi 162667805 gb EDQ54426.1  | predicted protein [Phy   | ( 469) | 149 | 43.0 | 0.34 |
| gi 197111722 gb ACH43025.1  | omega-6 fatty acid des   | ( 387) | 148 | 42.8 | 0.34 |
| gi 155295235 gb ABT50839.1  | Sequence 138309 from p   | ( 387) | 148 | 42.8 | 0.34 |
| gi 150415386 gb EDN10739.1  | hypothetical protein H   | (1049) | 153 | 44.2 | 0.35 |
| gi 19171683 gb AAL85636.1   | AF336236_1 nitrate reduc | ( 869) | 152 | 43.9 | 0.35 |
| gi 137453581 gb EBU18923.1  | hypothetical protein G   | ( 223) | 145 | 41.9 | 0.35 |
| gi 168062 gb AAA33314.1     | nitrate reductase        | ( 873) | 152 | 43.9 | 0.35 |
| gi 164638088 gb EDR02368.1  | nitrate reductase [Lac   | ( 880) | 152 | 43.9 | 0.36 |
| gi 134956202 gb EBE54415.1  | hypothetical protein G   | ( 333) | 147 | 42.5 | 0.36 |
| gi 108868763 gb EAT32988.1  | conserved hypothetical   | ( 154) | 143 | 41.4 | 0.36 |
| gi 108875378 gb EAT39603.1  | conserved hypothetical   | ( 154) | 143 | 41.4 | 0.36 |
| gi 190589801 gb EDV29823.1  | expressed hypothetical   | ( 127) | 142 | 41.1 | 0.36 |

|                             |                          |        |     |      |      |
|-----------------------------|--------------------------|--------|-----|------|------|
| gi 71979795 dbj BAE17053.1  | nitrate reductase [Phy   | ( 892) | 152 | 43.9 | 0.36 |
| gi 162683005 gb EDQ69419.1  | predicted protein [Phy   | ( 892) | 152 | 43.9 | 0.36 |
| gi 73486691 dbj BAE19755.1  | nitrate reductase [Phy   | ( 892) | 152 | 43.9 | 0.36 |
| gi 68532865 dbj BAE06057.1  | pyridine nucleotide-de   | ( 892) | 152 | 43.9 | 0.36 |
| gi 541566 gb AAA50579.1     | nitrate reductase        | ( 893) | 152 | 43.9 | 0.36 |
| gi 217072516 gb ACJ84618.1  | unknown [Medicago trun   | ( 411) | 148 | 42.8 | 0.36 |
| gi 211590769 emb CAP96968.1 | Pc2lg20710 [Penicilli    | ( 513) | 149 | 43.1 | 0.37 |
| gi 62088814 dbj BAD92854.1  | cytochrome b-5 isoform   | ( 132) | 142 | 41.1 | 0.37 |
| gi 144581901 gb ABO99956.1  | predicted protein [Ost   | ( 74)  | 139 | 40.2 | 0.37 |
| gi 23329307 gb AAN26141.1   | Sequence 23 from patent  | ( 133) | 142 | 41.1 | 0.37 |
| gi 62774618 gb AAY02011.1   | Sequence 22 from patent  | ( 133) | 142 | 41.1 | 0.37 |
| gi 181227 gb AAA35729.1     | cytochrome b5            | ( 134) | 142 | 41.1 | 0.37 |
| gi 15929506 gb AAH15182.1   | Cytochrome b5 type A (m  | ( 134) | 142 | 41.1 | 0.37 |
| gi 12822034 gb AAE48475.1   | Sequence 1 from patent   | ( 134) | 142 | 41.1 | 0.37 |
| gi 48146097 emb CAG33271.1  | CYB5 [Homo sapiens]      | ( 134) | 142 | 41.1 | 0.37 |
| gi 2642486 gb AAC48779.1    | cytochrome b5 [Sus scrof | ( 134) | 142 | 41.1 | 0.37 |
| gi 119586948 gb EAW66544.1  | cytochrome b5 type A (   | ( 134) | 142 | 41.1 | 0.37 |
| gi 139669063 gb ECG64984.1  | hypothetical protein G   | ( 91)  | 140 | 40.5 | 0.38 |
| gi 139179798 gb ECD95369.1  | hypothetical protein G   | ( 294) | 146 | 42.2 | 0.38 |
| gi 162471890 gb ABX99725.1  | Sequence 1 from patent   | ( 135) | 142 | 41.1 | 0.38 |
| gi 210074133 gb EEA28220.1  | cytochrome b5, putativ   | ( 135) | 142 | 41.1 | 0.38 |
| gi 194176547 gb EDW90158.1  | GE13120 [Drosophila ya   | ( 137) | 142 | 41.1 | 0.38 |
| gi 138071748 gb EBX58336.1  | hypothetical protein G   | ( 113) | 141 | 40.8 | 0.38 |
| gi 91685106 gb ABE41408.1   | cytochrome b5 [Rhodopse  | ( 115) | 141 | 40.8 | 0.39 |
| gi 703083 gb AAA63169.1     | cytochrome b5            | ( 142) | 142 | 41.1 | 0.39 |
| gi 12813433 gb AAE44733.1   | Sequence 3 from patent   | ( 142) | 142 | 41.1 | 0.39 |
| gi 5977401 gb AAE14811.1    | Sequence 3 from patent U | ( 142) | 142 | 41.1 | 0.39 |
| gi 149053047 gb EDM04864.1  | similar to novel prote   | ( 97)  | 140 | 40.5 | 0.4  |
| gi 195621540 gb ACG32600.1  | cytochrome b5 [Zea may   | ( 118) | 141 | 40.8 | 0.4  |
| gi 197111724 gb ACH43026.1  | omega-6 fatty acid des   | ( 387) | 147 | 42.5 | 0.4  |
| gi 59956944 dbj BAD89861.1  | microsomal omega-6 fat   | ( 387) | 147 | 42.5 | 0.4  |
| gi 21507259 gb AAM57794.1   | Sequence 8 from patent   | ( 387) | 147 | 42.5 | 0.4  |
| gi 194688628 gb ACF78398.1  | unknown [Zea mays]       | ( 387) | 147 | 42.5 | 0.4  |
| gi 62789095 gb AAY07978.1   | Sequence 8 from patent   | ( 387) | 147 | 42.5 | 0.4  |
| gi 115833235 gb ABJ40713.1  | Sequence 8 from patent   | ( 387) | 147 | 42.5 | 0.4  |
| gi 75205883 gb ABA17987.1   | Sequence 8 from patent   | ( 387) | 147 | 42.5 | 0.4  |
| gi 70799836 gb AAZ10014.1   | cytochrome b-domain pro  | ( 218) | 144 | 41.7 | 0.41 |
| gi 70801860 gb AAZ11766.1   | nitrate reductase, puta  | ( 394) | 147 | 42.5 | 0.41 |
| gi 62360424 gb AAJ80838.1   | nitrate reductase, puta  | ( 394) | 147 | 42.5 | 0.41 |
| gi 134380916 gb EBB02366.1  | hypothetical protein G   | ( 221) | 144 | 41.7 | 0.41 |
| gi 113648928 dbj BAF29440.1 | Os12g0223300 [Oryza s    | ( 150) | 142 | 41.1 | 0.41 |
| gi 215765640 dbj BAG87337.1 | unnamed protein produ    | ( 150) | 142 | 41.1 | 0.41 |
| gi 77553981 gb ABA96777.1   | Cytochrome b5-like Heme  | ( 150) | 142 | 41.1 | 0.41 |
| gi 77553982 gb ABA96778.1   | Cytochrome b5-like Heme  | ( 150) | 142 | 41.1 | 0.41 |
| gi 125578858 gb EAD220004.1 | hypothetical protein O   | ( 150) | 142 | 41.1 | 0.41 |
| gi 119412643 gb EAW22584.1  | nitrate reductase NiaD   | ( 869) | 151 | 43.7 | 0.41 |
| gi 42820686 emb CAF31999.1  | nitrate reductase, put   | ( 869) | 151 | 43.7 | 0.41 |
| gi 159131406 gb EDP56519.1  | nitrate reductase NiaD   | ( 869) | 151 | 43.7 | 0.41 |
| gi 162670060 gb EDQ56636.1  | predicted protein [Phy   | ( 124) | 141 | 40.8 | 0.41 |
| gi 144578118 gb ABO96183.1  | predicted protein [Ost   | ( 485) | 148 | 42.8 | 0.41 |
| gi 111069428 gb EAT90548.1  | hypothetical protein S   | (1062) | 152 | 43.9 | 0.41 |
| gi 135719112 gb EBJ41763.1  | hypothetical protein G   | ( 272) | 145 | 42.0 | 0.41 |
| gi 139933428 gb ECI46694.1  | hypothetical protein G   | ( 272) | 145 | 42.0 | 0.41 |
| gi 155325093 gb ABT60697.1  | Sequence 168167 from p   | ( 224) | 144 | 41.7 | 0.41 |
| gi 44982549 gb AAS51835.1   | ADL085Cp [Ashbya gossyp  | ( 273) | 145 | 42.0 | 0.42 |
| gi 90655562 gb ABD96399.1   | fatty acid desaturase [  | ( 185) | 143 | 41.4 | 0.42 |
| gi 145016037 gb EDK00527.1  | hypothetical protein M   | (1586) | 154 | 44.5 | 0.42 |
| gi 134922019 gb EBE31653.1  | hypothetical protein G   | ( 338) | 146 | 42.3 | 0.42 |

|                             |                                    |     |      |      |
|-----------------------------|------------------------------------|-----|------|------|
| gi 143513831 gb EDF39707.1  | hypothetical protein G ( 344)      | 146 | 42.3 | 0.43 |
| gi 210065986 gb EEA20079.1  | acyl-CoA dehydrogenase ( 512)      | 148 | 42.8 | 0.43 |
| gi 134055198 emb CAK43785.1 | unnamed protein produ ( 350)       | 146 | 42.3 | 0.43 |
| gi 50844673 gb AAT84458.1   | cytochrome b5 isoform C ( 133)     | 141 | 40.9 | 0.44 |
| gi 135224456 gb EBG27440.1  | hypothetical protein G ( 353)      | 146 | 42.3 | 0.44 |
| gi 5977402 gb AAE14812.1    | Sequence 4 from patent U ( 134)    | 141 | 40.9 | 0.44 |
| gi 146230092 gb ABQ12619.1  | cytochrome b5 [Capra h ( 134)      | 141 | 40.9 | 0.44 |
| gi 79160196 gb AAI08114.1   | CYB5 protein [Bos tauru ( 134)     | 141 | 40.9 | 0.44 |
| gi 164785 gb AAB03878.1     | cytochrome b-5 ( 134)              | 141 | 40.9 | 0.44 |
| gi 12813434 gb AAE44734.1   | Sequence 4 from patent ( 134)      | 141 | 40.9 | 0.44 |
| gi 298 emb CAA31949.1       | unnamed protein product [Bo ( 134) | 141 | 40.9 | 0.44 |
| gi 211707 gb AAA48740.1     | cytochrome b5 ( 138)               | 141 | 40.9 | 0.45 |
| gi 211693 gb AAA48733.1     | cytochrome b5 ( 138)               | 141 | 40.9 | 0.45 |
| gi 126633152 emb CAM55541.1 | unnamed protein produ ( 446)       | 147 | 42.6 | 0.45 |
| gi 138861632 gb ECC19277.1  | hypothetical protein G ( 208)      | 143 | 41.4 | 0.46 |
| gi 89271352 emb CAJ83457.1  | cyb5-m [Xenopus tropic ( 141)      | 141 | 40.9 | 0.46 |
| gi 140512248 gb ECM07288.1  | hypothetical protein G ( 253)      | 144 | 41.7 | 0.46 |
| gi 135114892 gb EBF58711.1  | hypothetical protein G ( 253)      | 144 | 41.7 | 0.46 |
| gi 51968362 dbj BAD42873.1  | unknown protein [Arabi ( 211)      | 143 | 41.4 | 0.46 |
| gi 34146794 gb AAQ62405.1   | At5g09680 [Arabidopsis ( 211)      | 143 | 41.4 | 0.46 |
| gi 51969432 dbj BAD43408.1  | unknown protein [Arabi ( 211)      | 143 | 41.4 | 0.46 |
| gi 7671421 emb CAB89362.1   | putative protein [Arabi ( 211)     | 143 | 41.4 | 0.46 |
| gi 147776501 emb CAN71892.1 | hypothetical protein ( 382)        | 146 | 42.3 | 0.47 |
| gi 33766658 gb AAQ52861.1   | Sequence 15 from patent ( 383)     | 146 | 42.3 | 0.47 |
| gi 155689135 gb ABU29145.1  | Sequence 15 from paten ( 383)      | 146 | 42.3 | 0.47 |
| gi 3417601 gb AAC31698.1    | delta-12 fatty acid desa ( 383)    | 146 | 42.3 | 0.47 |
| gi 42541363 gb AAS19533.1   | omega-6 fatty acid desa ( 383)     | 146 | 42.3 | 0.47 |
| gi 34600649 gb AAQ78506.1   | Sequence 11 from patent ( 383)     | 146 | 42.3 | 0.47 |
| gi 904154 gb AAB00860.1     | microsomal omega-6 desatu ( 383)   | 146 | 42.3 | 0.47 |
| gi 189846874 gb ACE26372.1  | Sequence 127 from pate ( 383)      | 146 | 42.3 | 0.47 |
| gi 189704781 gb ACE16110.1  | Sequence 127 from pate ( 383)      | 146 | 42.3 | 0.47 |
| gi 91125670 gb ABE12618.1   | Sequence 31 from patent ( 383)     | 146 | 42.3 | 0.47 |
| gi 110623206 emb CAL24243.1 | unnamed protein produ ( 387)       | 146 | 42.3 | 0.47 |
| gi 92380879 dbj BAE93382.1  | delta-12 fatty acid de ( 387)      | 146 | 42.3 | 0.47 |
| gi 29536061 emb CAD87608.1  | unnamed protein produc ( 387)      | 146 | 42.3 | 0.47 |
| gi 94982471 gb ABF50053.1   | FAD2 [Zea mays] ( 387)             | 146 | 42.3 | 0.47 |
| gi 28564441 emb CAD24671.1  | delta 12-acyl-lipid-de ( 387)      | 146 | 42.3 | 0.47 |
| gi 110623204 emb CAL24242.1 | unnamed protein produ ( 387)       | 146 | 42.3 | 0.47 |
| gi 139863303 gb ECH99135.1  | hypothetical protein G ( 216)      | 143 | 41.4 | 0.47 |
| gi 156113331 gb ED014908.1  | hypothetical protein K ( 217)      | 143 | 41.4 | 0.47 |
| gi 62774617 gb AAY02010.1   | Sequence 21 from patent ( 179)     | 142 | 41.2 | 0.48 |
| gi 23329306 gb AAN26140.1   | Sequence 22 from patent ( 179)     | 142 | 41.2 | 0.48 |
| gi 170941385 emb CAP67035.1 | unnamed protein produ (1541)       | 153 | 44.3 | 0.48 |
| gi 119408444 gb EAW18393.1  | cytochrome b5, putativ ( 84)       | 138 | 40.1 | 0.48 |
| gi 114190581 gb EAU32281.1  | conserved hypothetical ( 84)       | 138 | 40.1 | 0.48 |
| gi 211583576 emb CAP91591.1 | Pcl3g05220 [Penicilli ( 84)        | 138 | 40.1 | 0.48 |
| gi 1113863 gb AAC49460.1    | nitrate reductase ( 877)           | 150 | 43.4 | 0.49 |
| gi 1113861 gb AAC49459.1    | nitrate reductase ( 877)           | 150 | 43.4 | 0.49 |
| gi 139082605 gb ECD29132.1  | hypothetical protein G ( 273)      | 144 | 41.7 | 0.49 |
| gi 125583832 gb EAE24763.1  | hypothetical protein O ( 890)      | 150 | 43.4 | 0.49 |
| gi 144160439 gb EDJ30569.1  | hypothetical protein G ( 413)      | 146 | 42.3 | 0.5  |
| gi 124392166 emb CAK57700.1 | unnamed protein produ ( 342)       | 145 | 42.0 | 0.5  |
| gi 1197523 gb AAC02633.1    | nitrate reductase [Botry ( 907)    | 150 | 43.4 | 0.5  |
| gi 134532838 gb EBB90647.1  | hypothetical protein G ( 282)      | 144 | 41.7 | 0.5  |
| gi 5478307 dbj BAA82441.1   | cytochrome b5 [Mortiere ( 130)     | 140 | 40.6 | 0.5  |
| gi 5478287 dbj BAA82440.1   | cytochrome b5 [Mortiere ( 130)     | 140 | 40.6 | 0.5  |
| gi 170947135 emb CAP73940.1 | unnamed protein produ ( 520)       | 147 | 42.6 | 0.51 |
| gi 190659446 gb EDV56659.1  | GG20107 [Drosophila er ( 436)      | 146 | 42.3 | 0.52 |

|                             |                                |     |      |      |
|-----------------------------|--------------------------------|-----|------|------|
| gi 152022930 gb ABS20700.1  | fatty acid desaturase ( 360)   | 145 | 42.0 | 0.52 |
| gi 160705089 gb EAT77467.2  | hypothetical protein S (1713)  | 153 | 44.3 | 0.52 |
| gi 145016063 gb EDK00553.1  | hypothetical protein M ( 139)  | 140 | 40.6 | 0.53 |
| gi 162471893 gb ABX99728.1  | Sequence 7 from patent ( 115)  | 139 | 40.4 | 0.53 |
| gi 52138991 gb AAH82722.1   | Hypothetical LOC496418 ( 141)  | 140 | 40.6 | 0.54 |
| gi 167278288 gb ABZ31152.1  | Sequence 5090 from pat ( 141)  | 140 | 40.6 | 0.54 |
| gi 13384553 gb AAK21480.1   | Hypothetical protein W0 ( 141) | 140 | 40.6 | 0.54 |
| gi 136222416 gb EBM70431.1  | hypothetical protein G ( 141)  | 140 | 40.6 | 0.54 |
| gi 155264893 gb ABT20497.1  | Sequence 107967 from p ( 118)  | 139 | 40.4 | 0.55 |
| gi 212559737 gb ACJ32792.1  | Fatty acid desaturase ( 380)   | 145 | 42.1 | 0.55 |
| gi 139259149 gb ECE38644.1  | hypothetical protein G ( 258)  | 143 | 41.5 | 0.55 |
| gi 146141441 gb ABQ01458.1  | oleate 12-hydroxylase ( 383)   | 145 | 42.1 | 0.55 |
| gi 117957296 gb ABK59093.1  | oleate desaturase [Ric ( 383)  | 145 | 42.1 | 0.55 |
| gi 27261181 gb AAN87573.1   | delta 12 oleic acid des ( 383) | 145 | 42.1 | 0.55 |
| gi 110623210 emb CAL24245.1 | unnamed protein produ ( 383)   | 145 | 42.1 | 0.55 |
| gi 110623208 emb CAL24244.1 | unnamed protein produ ( 383)   | 145 | 42.1 | 0.55 |
| gi 158307010 gb ABW28627.1  | beta-carotene hydroxyl ( 316)  | 144 | 41.8 | 0.55 |
| gi 119402466 gb EAW12887.1  | cytochrome b5 reductas ( 472)  | 146 | 42.3 | 0.56 |
| gi 148677409 gb EDL09356.1  | cytochrome b-5, isofo ( 122)   | 139 | 40.4 | 0.56 |
| gi 18376390 emb CAD21279.1  | probable cytochrome b5 ( 83)   | 137 | 39.8 | 0.56 |
| gi 31322143 gb AAO38036.1   | delta12-fatty acid acet ( 326) | 144 | 41.8 | 0.56 |
| gi 161611934 gb AAI55726.1  | Zgc:112008 protein [Da ( 69)   | 136 | 39.5 | 0.57 |
| gi 139014560 gb ECC81442.1  | hypothetical protein G ( 270)  | 143 | 41.5 | 0.57 |
| gi 155297801 gb ABT53405.1  | Sequence 140875 from p ( 84)   | 137 | 39.8 | 0.57 |
| gi 156105864 gb ABU49297.1  | cytochrome b5 domain-c ( 152)  | 140 | 40.7 | 0.57 |
| gi 156105858 gb ABU49294.1  | cytochrome b5 domain-c ( 152)  | 140 | 40.7 | 0.57 |
| gi 156105860 gb ABU49295.1  | cytochrome b5 domain-c ( 152)  | 140 | 40.7 | 0.57 |
| gi 156105862 gb ABU49296.1  | cytochrome b5 domain-c ( 152)  | 140 | 40.7 | 0.57 |
| gi 156105856 gb ABU49293.1  | cytochrome b5 domain-c ( 152)  | 140 | 40.7 | 0.57 |
| gi 134365592 gb EBA92006.1  | hypothetical protein G ( 273)  | 143 | 41.5 | 0.57 |
| gi 135391117 gb EBH32165.1  | hypothetical protein G ( 85)   | 137 | 39.8 | 0.57 |
| gi 143298767 gb EDE18862.1  | hypothetical protein G ( 85)   | 137 | 39.8 | 0.57 |
| gi 78168019 gb ABB25116.1   | fatty acid desaturase [ ( 333) | 144 | 41.8 | 0.57 |
| gi 136112719 gb EBL99839.1  | hypothetical protein G ( 333)  | 144 | 41.8 | 0.57 |
| gi 9758996 dbj BAB09523.1   | unnamed protein product ( 275) | 143 | 41.5 | 0.58 |
| gi 62358441 gb AAJ78904.1   | fatty acid desaturase, ( 408)  | 145 | 42.1 | 0.58 |
| gi 34551088 gb AAQ74969.1   | oleate desaturase [Tryp ( 408) | 145 | 42.1 | 0.58 |
| gi 33348439 gb AAQ15765.1   | fatty acid desaturase, ( 408)  | 145 | 42.1 | 0.58 |
| gi 115878493 gb ABJ45509.1  | Sequence 6248 from pat ( 128)  | 139 | 40.4 | 0.58 |
| gi 77452621 gb ABA84316.1   | Sequence 6248 from pate ( 128) | 139 | 40.4 | 0.58 |
| gi 40043340 emb CAF00446.1  | unnamed protein produc ( 128)  | 139 | 40.4 | 0.58 |
| gi 143305952 gb EDE22864.1  | hypothetical protein G ( 88)   | 137 | 39.8 | 0.59 |
| gi 136345216 gb EBN53791.1  | hypothetical protein G ( 193)  | 141 | 41.0 | 0.59 |
| gi 136676011 gb EBP67037.1  | hypothetical protein G ( 73)   | 136 | 39.6 | 0.59 |
| gi 114187625 gb EAU29325.1  | hypothetical protein A ( 512)  | 146 | 42.4 | 0.59 |
| gi 159124543 gb EDP49661.1  | acyl-CoA dehydrogenase ( 512)  | 146 | 42.4 | 0.59 |
| gi 119406364 gb EAW16315.1  | acyl-CoA dehydrogenase ( 512)  | 146 | 42.4 | 0.59 |
| gi 83773777 dbj BAE63902.1  | unnamed protein produc ( 513)  | 146 | 42.4 | 0.59 |
| gi 135134683 gb EBF71466.1  | hypothetical protein G ( 194)  | 141 | 41.0 | 0.6  |
| gi 193810810 emb CAQ42708.1 | heme/steroid binding ( 292)    | 143 | 41.5 | 0.61 |
| gi 143300860 gb EDE19878.1  | hypothetical protein G ( 169)  | 140 | 40.7 | 0.62 |
| gi 28371823 gb AAO37752.1   | delta-12 oleate desatur ( 369) | 144 | 41.8 | 0.62 |
| gi 90302444 gb EAS32075.1   | hypothetical protein CI ( 372) | 144 | 41.8 | 0.63 |
| gi 116055625 emb CAL58293.1 | P0434E03.7 gene produ ( 116)   | 138 | 40.1 | 0.63 |
| gi 135130262 gb EBF68611.1  | hypothetical protein G ( 211)  | 141 | 41.0 | 0.64 |
| gi 144163625 gb EDJ32950.1  | hypothetical protein G ( 211)  | 141 | 41.0 | 0.64 |
| gi 135084318 gb EBF39138.1  | hypothetical protein G ( 211)  | 141 | 41.0 | 0.64 |
| gi 90655389 gb ABD96230.1   | possible fatty acid des ( 379) | 144 | 41.8 | 0.64 |

|                             |                          |        |     |      |      |
|-----------------------------|--------------------------|--------|-----|------|------|
| gi 143358107 gb EDE53793.1  | hypothetical protein G   | ( 200) | 139 | 40.5 | 0.84 |
| gi 155324337 gb ABT79941.1  | Sequence 167411 from p   | ( 165) | 138 | 40.2 | 0.84 |
| gi 155295412 gb ABT51016.1  | Sequence 138486 from p   | ( 138) | 137 | 39.9 | 0.85 |
| gi 56266266 emb CAE75863.1  | cytochrome b5 [Corypha   | ( 138) | 137 | 39.9 | 0.85 |
| gi 167280184 gb ABZ33048.1  | Sequence 6986 from pat   | ( 138) | 137 | 39.9 | 0.85 |
| gi 141006880 gb ECP00377.1  | hypothetical protein G   | ( 94)  | 135 | 39.4 | 0.86 |
| gi 143902618 gb EDH45751.1  | hypothetical protein G   | ( 205) | 139 | 40.5 | 0.86 |
| gi 149015875 gb EDL75182.1  | cytochrome b-5, isofo    | ( 139) | 137 | 40.0 | 0.86 |
| gi 193905261 gb EDW04128.1  | GH10148 [Drosophila gr   | ( 140) | 137 | 40.0 | 0.86 |
| gi 68124282 emb CAJ07044.1  | flavoprotein subunit-1   | ( 670) | 145 | 42.2 | 0.87 |
| gi 145033461 gb ABP27586.1  | Sequence 2601 from pat   | ( 374) | 142 | 41.4 | 0.87 |
| gi 12753467 dbj BAC04349.1  | unnamed protein produc   | ( 374) | 142 | 41.4 | 0.87 |
| gi 145013323 gb EDJ97964.1  | hypothetical protein M   | ( 379) | 142 | 41.4 | 0.88 |
| gi 190624514 gb EDV40038.1  | GF10319 [Drosophila an   | ( 119) | 136 | 39.7 | 0.89 |
| gi 141685248 gb ECS80491.1  | hypothetical protein G   | ( 81)  | 134 | 39.1 | 0.89 |
| gi 138746127 gb ECB72386.1  | hypothetical protein G   | ( 147) | 137 | 40.0 | 0.9  |
| gi 138158275 gb EBY08621.1  | hypothetical protein G   | ( 269) | 140 | 40.8 | 0.91 |
| gi 134075051 emb CAK44850.1 | unnamed protein produ    | ( 84)  | 134 | 39.1 | 0.92 |
| gi 30526321 gb AAP32278.1   | nitrate reductase [Chl   | ( 898) | 146 | 42.5 | 0.94 |
| gi 124429770 emb CAK94560.1 | unnamed protein produ    | ( 342) | 141 | 41.1 | 0.95 |
| gi 119396333 gb EAW06765.1  | acyl-CoA dehydrogenase   | ( 512) | 143 | 41.7 | 0.96 |
| gi 84619354 emb CAD92095.1  | cytochrome b5 [Crassos   | ( 131) | 136 | 39.7 | 0.96 |
| gi 137768481 gb EBV89098.1  | hypothetical protein G   | ( 289) | 140 | 40.8 | 0.97 |
| gi 16197801 gb AAL13516.1   | GH03691p [Drosophila me  | ( 436) | 142 | 41.4 | 0.99 |
| gi 72983391 gb AAF53567.1   | CG13279-PA [Drosophila m | ( 436) | 142 | 41.4 | 0.99 |
| gi 33634986 emb CAE20972.1  | Fatty acid desaturase,   | ( 361) | 141 | 41.1 | 0.99 |
| gi 48431267 gb AAT44123.1   | microsomal omega-6-desa  | ( 362) | 141 | 41.1 | 0.99 |
| gi 155295428 gb ABT51032.1  | Sequence 138502 from p   | ( 137) | 136 | 39.7 |      |

|        |  | 10  | 20    | 30    | 40    | 50    |
|--------|--|---|-------|-------|-------|-------|
| del_6  |  | MTKTIYITSSSELEKHNKPGDLWISIHGQYVDVSSWAALHPGGIAPLLALAGHDVTD     |       |       |       |       |
|        |  | ...   | ..... | ..    | ..... | ..... |
| gi 151 |  | MANKSQGTGYITSSSELETHNKAGDLWISIHGQYVDVSSWAGLHPGGTAPLLALAGHDVTD |       |       |       |       |
|        |  | 10  | 20    | 30    | 40    | 50    |
|        |  | 60  | 70    | 80    | 90    | 100   |
| del_6  |  | FLAYHPPSTRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYATFVI   |       |       |       |       |
|        |  | .....   | ..... | ..... | ..... | ..... |
| gi 151 |  | FLAYHPPSTARLLPPLSTHLLQHQHSVPTSSDYRSLLDNFHKLGLFRAGHTAYATFVI    |       |       |       |       |
|        |  | 70  | 80    | 90    | 100   | 110   |
|        |  | 120   | 130   | 140   | 150   | 160   |
| del_6  |  | MILMLVSVSTGVLCSENPWWHLVCGAAMGFAWIIQCGWIGHDSGHYRIMTDRKWNRFQIL  |       |       |       |       |
|        |  | ..  | ..... | ..... | ..... | ..... |
| gi 151 |  | MIAMFLASVTGVLCSDKAWVHLASGGAMGFAWIIQCGWIGHDSGHYRIMSGEKWNRFQIL  |       |       |       |       |
|        |  | 130   | 140   | 150   | 160   | 170   |
|        |  | 180   | 190   | 200   | 210   | 220   |
| del_6  |  | SSNCLOGISIGWWWNNHNAHHIACNSLEYDPLQYIPLLVSVPKFFNSLTSRFYDKKLN    |       |       |       |       |
|        |  | .....   | ..... | ..... | ..... | ..... |
| gi 151 |  | STNCLOGISIGWWWNNHNAHHIACNSLDYDPLQYIPLLVSVPKFFNSLTSRFYDKKLN    |       |       |       |       |

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190      200      210      220      230      240
del_6    240      250      260      270      280      290
DGVSRFLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLL
gi|151   DGVSRFLVQYQHWSFYPMCVARLNMLAQSFIMLFSSREVAQRVQGI FGLAVFWVWFPLL
250      260      270      280      290      300

300      310      320      330      340      350
del_6    LSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTLNISC
gi|151   LSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTLNISC
310      320      330      340      350      360

360      370      380      390      400      410
del_6    PAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLE
gi|151   PAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLM
370      380      390      400      410      420

420      430      440
del_6    TLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi|151   TLRNTAIEARDLSNPIPKNMVWEAVQTLG
430      440

>>gi|118627908|emb|CAL85354.1| unnamed protein product [ (453 aa)
initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

10      20      30      40      50
del_6    MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi|118   MANKSPPNPKTYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
10      20      30      40      50      60

60      70      80      90      100      110
del_6    VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
gi|118   VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLDNFHKHGLFRAGHTAYA
70      80      90      100      110      120

120      130      140      150      160      170
del_6    TFVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCWGIGHDSGHYRIMTDRKWNRF
gi|118   TFVFMIAMFLMSVTGVLCSDSA WVLASGGAMGFAWIQCWGIGHDSGHYRIMSDRKWNWF
130      140      150      160      170      180

180      190      200      210      220      230
del_6    AQILSSNCLQGIGISIGWWKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDK
gi|118   AQILSTNCLQGIGISIGWWKWNHNAHHIACNSLDYDPDLQYIPLLVSPKFFNSLTSRFYDK
190      200      210      220      230      240

240      250      260      270      280      290
del_6    KLNFDGVSRLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW

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gi|118   KLNFDGVSRLVQYQHWSFYPMCVARLNMLAQSFITLFSREVCRAQEVFGLAVFWWW
250      260      270      280      290      300

300      310      320      330      340      350
del_6    FPLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
gi|118   FPLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
310      320      330      340      350      360

360      370      380      390      400      410
del_6    NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
gi|118   NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
370      380      390      400      410      420

420      430      440
del_6    LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi|118   FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
430      440      450

>>gi|126633766|emb|CAM55839.1| unnamed protein product [ (453 aa)
initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

10      20      30      40      50
del_6    MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi|126   MANKSPPNPKTYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
10      20      30      40      50      60

60      70      80      90      100      110
del_6    VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
gi|126   VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLDNFHKHGLFRAGHTAYA
70      80      90      100      110      120

120      130      140      150      160      170
del_6    TFVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCWGIGHDSGHYRIMTDRKWNRF
gi|126   TFVFMIAMFLMSVTGVLCSDSA WVLASGGAMGFAWIQCWGIGHDSGHYRIMSDRKWNWF
130      140      150      160      170      180

180      190      200      210      220      230
del_6    AQILSSNCLQGIGISIGWWKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDK
gi|126   AQILSTNCLQGIGISIGWWKWNHNAHHIACNSLDYDPDLQYIPLLVSPKFFNSLTSRFYDK
190      200      210      220      230      240

240      250      260      270      280      290
del_6    KLNFDGVSRLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
gi|126   KLNFDGVSRLVQYQHWSFYPMCVARLNMLAQSFITLFSREVCRAQEVFGLAVFWWW
250      260      270      280      290      300

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      300      310      320      330      340      350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL
      .....
gi|126  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      .....
gi|126  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420

      420      430      440
del_6  LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|126  FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|39750753|emb|CAE84827.1| unnamed protein product [P (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
  Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi|397  MANKSPPNPKTGYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100     110
del_6  VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYA
      .....
gi|397  VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLDNFHKHGLFRAGHTAYA
      70      80      90      100     110     120

      120     130     140     150     160     170
del_6  TFVIMILMLVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      .....
gi|397  TFVFMIAMFLMSVTGVLCSNDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130     140     150     160     170     180

      180     190     200     210     220     230
del_6  AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPDLQYIPLLVSPPKFFNSLTSRFYDK
      .....
gi|397  AQILSTNCLQGIGISIGWKKWNHNAHHIACNSLDYDPDLQYIPLLVSPPKFFNSLTSRFYDK
      190     200     210     220     230     240

      240     250     260     270     280     290
del_6  KLNFDGVSRLFVQYQHWSFYPMVCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      .....
gi|397  KLNFDGVSRLFVQYQHWSFYPMVCVARLNMLAQSFITLFSREVCHRAQEVFGLAVFWVW
      250     260     270     280     290     300

      300     310     320     330     340     350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL
      .....
gi|397  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL

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      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      .....
gi|397  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420

      420      430      440
del_6  LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|397  FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|60220786|emb|CAI58892.1| unnamed protein product [P (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
  Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi|602  MANKSPPNPKTGYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100     110
del_6  VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYA
      .....
gi|602  VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLDNFHKHGLFRAGHTAYA
      70      80      90      100     110     120

      120     130     140     150     160     170
del_6  TFVIMILMLVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      .....
gi|602  TFVFMIAMFLMSVTGVLCSNDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130     140     150     160     170     180

      180     190     200     210     220     230
del_6  AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPDLQYIPLLVSPPKFFNSLTSRFYDK
      .....
gi|602  AQILSTNCLQGIGISIGWKKWNHNAHHIACNSLDYDPDLQYIPLLVSPPKFFNSLTSRFYDK
      190     200     210     220     230     240

      240     250     260     270     280     290
del_6  KLNFDGVSRLFVQYQHWSFYPMVCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      .....
gi|602  KLNFDGVSRLFVQYQHWSFYPMVCVARLNMLAQSFITLFSREVCHRAQEVFGLAVFWVW
      250     260     270     280     290     300

      300     310     320     330     340     350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL
      .....
gi|602  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFKKQTAGTL
      310     320     330     340     350     360

      360     370     380     390     400     410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV

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gi|602 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTPYNIASF TKANV
      370      380      390      400      410      420

del_6      420      430      440
L TLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
.....

gi|602 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|30350277|gb|AAP23034.1| fatty acid delta-6 desatura (453 aa)
initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

del_6      10      20      30      40      50
M T K T I Y I T S S E L E K H N K P G D L W I S I H G Q V Y D V S S W A A L H P G G I A P L L A G H D
:: .....

gi|303 MANKSPPNPKTG YITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

del_6      60      70      80      90      100      110
V T D A F L A Y H P P S T S R L L P P F S T N L L L E K H S V S E T S S D Y R K L L D S F H K M G M F R A R G H T A Y A
.....

gi|303 V T D A F L A Y H P P S T A R L L P P L S T N L L L Q N H S V S P T S S D Y R K L L D N F H K H G L F R A R G H T A Y A
      70      80      90      100      110      120

del_6      120      130      140      150      160      170
T F V I M I L M L V S S V T G V L C S E N P W V H L V C G A A M G F A W I Q C G W I G H D S G H Y R I M T D R K W N R F
.....

gi|303 T F V F M I A M F L M S V T G V L C S D S A W V H L A S G G A M G F A W I Q C G W I G H D S G H Y R I M S D R K W N W F
      130      140      150      160      170      180

del_6      180      190      200      210      220      230
A Q I L S S N C L Q G I S I G W W K W N H N A H H I A C N S L E Y D P D L Q Y I P L L V V S P K F F N S L T S R F Y D K
.....

gi|303 A Q I L S T N C L Q G I S I G W W K W N H N A H H I A C N S L D Y D P D L Q Y I P L L V V S P K F F N S L T S R F Y D K
      190      200      210      220      230      240

del_6      240      250      260      270      280      290
K L N F D G V S R F L V Q Y Q H W S F Y P V M C V A R L N M L A Q S F I L L F S R R E V A N R V Q E I L G L A V F W L W
.....

gi|303 K L N F D G V S R F L V C Y Q H W T F Y P V M C V A R L N M L A Q S F I T L F S S R E V C H R A Q E V F G L A V F W V W
      250      260      270      280      290      300

del_6      300      310      320      330      340      350
F P L L L S C L P N W G E R I M F L L A S Y S V T G I Q H V Q F S L N H F S S D V Y V G P P V G N D W F K K Q T A G T L
.....

gi|303 F P L L L S C L P N W G E R I M F L L A S Y S V T G I Q H V Q F S L N H F S S D V Y V G P P V G N D W F K K Q T A G T L
      310      320      330      340      350      360

del_6      360      370      380      390      400      410
N I S C P A W M D W F H G G L Q F Q V E H H L F P R M P R G Q F R K I S P F V R D L C K K H N L T Y N I A S F T K A N V
.....

gi|303 N I S C P A W M D W F H G G L Q F Q V E H H L F P R M P R G Q F R K I S P F V R D L C K K H N L P Y N I A S F T K A N V
      370      380      390      400      410      420

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del_6      420      430      440
L TLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
.....

gi|303 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|76059286|emb|CAJ30837.1| unnamed protein product [P (453 aa)
initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

del_6      10      20      30      40      50
M T K T I Y I T S S E L E K H N K P G D L W I S I H G Q V Y D V S S W A A L H P G G I A P L L A G H D
:: .....

gi|760 MANKSPPNPKTG YITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

del_6      60      70      80      90      100      110
V T D A F L A Y H P P S T S R L L P P F S T N L L L E K H S V S E T S S D Y R K L L D S F H K M G M F R A R G H T A Y A
.....

gi|760 V T D A F L A Y H P P S T A R L L P P L S T N L L L Q N H S V S P T S S D Y R K L L D N F H K H G L F R A R G H T A Y A
      70      80      90      100      110      120

del_6      120      130      140      150      160      170
T F V I M I L M L V S S V T G V L C S E N P W V H L V C G A A M G F A W I Q C G W I G H D S G H Y R I M T D R K W N R F
.....

gi|760 T F V F M I A M F L M S V T G V L C S D S A W V H L A S G G A M G F A W I Q C G W I G H D S G H Y R I M S D R K W N W F
      130      140      150      160      170      180

del_6      180      190      200      210      220      230
A Q I L S S N C L Q G I S I G W W K W N H N A H H I A C N S L E Y D P D L Q Y I P L L V V S P K F F N S L T S R F Y D K
.....

gi|760 A Q I L S T N C L Q G I S I G W W K W N H N A H H I A C N S L D Y D P D L Q Y I P L L V V S P K F F N S L T S R F Y D K
      190      200      210      220      230      240

del_6      240      250      260      270      280      290
K L N F D G V S R F L V Q Y Q H W S F Y P V M C V A R L N M L A Q S F I L L F S R R E V A N R V Q E I L G L A V F W L W
.....

gi|760 K L N F D G V S R F L V C Y Q H W T F Y P V M C V A R L N M L A Q S F I T L F S S R E V C H R A Q E V F G L A V F W V W
      250      260      270      280      290      300

del_6      300      310      320      330      340      350
F P L L L S C L P N W G E R I M F L L A S Y S V T G I Q H V Q F S L N H F S S D V Y V G P P V G N D W F K K Q T A G T L
.....

gi|760 F P L L L S C L P N W G E R I M F L L A S Y S V T G I Q H V Q F S L N H F S S D V Y V G P P V G N D W F K K Q T A G T L
      310      320      330      340      350      360

del_6      360      370      380      390      400      410
N I S C P A W M D W F H G G L Q F Q V E H H L F P R M P R G Q F R K I S P F V R D L C K K H N L T Y N I A S F T K A N V
.....

gi|760 N I S C P A W M D W F H G G L Q F Q V E H H L F P R M P R G Q F R K I S P F V R D L C K K H N L P Y N I A S F T K A N V
      370      380      390      400      410      420

del_6      420      430      440
L TLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
.....

gi|760 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG

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430      440      450
>>gi|118627910|emb|CAL85355.1| unnamed protein product [ (453 aa)
  initn: 2853 initl: 2821 opt: 2821 Z-score: 3513.9 bits: 659.4 E(): 9.5e-
  187
  Smith-Waterman score: 2821; 89.189% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6      MTKTIYITSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: ::::: . ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      MANKSPPNPKTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10      20      30      40      50      60
del_6      60      70      80      90      100      110
      VTDAFLAYHPPSTARLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLHNFHKIGMFARAGHTAYA
      70      80      90      100      110      120
del_6      120      130      140      150      160      170
      TFVIMILMLVSSVTGVLCSNPWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      TFVIMIVMFLTSVTGVLCSDSA WVHLASGAAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180
del_6      180      190      200      210      220      230
      AQILSSNCLQGIGISIGWWKWNHNAHHIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      AQVLSTNCLQGIGISIGWWKWNHNAHHIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
      190      200      210      220      230      240
del_6      240      250      260      270      280      290
      KLNFDGVSRLVQYQHWSFYFVMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      KLNFDGVSRLVQYQHWSFYFVMCVARLNMLAQSFITLFSREVGHRAQEIFGLAVFWVW
      250      260      270      280      290      300
del_6      300      310      320      330      340      350
      FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTL
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTL
      310      320      330      340      350      360
del_6      360      370      380      390      400      410
      NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420
del_6      420      430      440
      LTLETLRNTAIEARDLSNPPIKNNMVWEAVKNVG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|118      LTLKTLRNTAIEARDLSNPPIKNNMVWEAVHTHG
      430      440      450
>>gi|39750755|emb|CAE84828.1| unnamed protein product [P (453 aa)

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  initn: 2853 initl: 2821 opt: 2821 Z-score: 3513.9 bits: 659.4 E(): 9.5e-
  187
  Smith-Waterman score: 2821; 89.189% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6      MTKTIYITSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: ::::: . ::::: ::::: ::::: ::::: ::::: :::::
gi|397      MANKSPPNPKTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10      20      30      40      50      60
del_6      60      70      80      90      100      110
      VTDAFLAYHPPSTARLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLHNFHKIGMFARAGHTAYA
      70      80      90      100      110      120
del_6      120      130      140      150      160      170
      TFVIMILMLVSSVTGVLCSNPWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      TFVIMIVMFLTSVTGVLCSDSA WVHLASGAAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180
del_6      180      190      200      210      220      230
      AQILSSNCLQGIGISIGWWKWNHNAHHIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      AQVLSTNCLQGIGISIGWWKWNHNAHHIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
      190      200      210      220      230      240
del_6      240      250      260      270      280      290
      KLNFDGVSRLVQYQHWSFYFVMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      KLNFDGVSRLVQYQHWSFYFVMCVARLNMLAQSFITLFSREVGHRAQEIFGLAVFWVW
      250      260      270      280      290      300
del_6      300      310      320      330      340      350
      FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTL
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTL
      310      320      330      340      350      360
del_6      360      370      380      390      400      410
      NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420
del_6      420      430      440
      LTLETLRNTAIEARDLSNPPIKNNMVWEAVKNVG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|397      LTLKTLRNTAIEARDLSNPPIKNNMVWEAVHTHG
      430      440      450
>>gi|126633768|emb|CAM55840.1| unnamed protein product [ (453 aa)
  initn: 2845 initl: 2813 opt: 2813 Z-score: 3503.9 bits: 657.5 E(): 3.4e-
  186
  Smith-Waterman score: 2813; 88.964% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

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del_6      10      20      30      40      50
      MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 MANKSPPNPKTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10      20      30      40      50      60

del_6      60      70      80      90      100     110
      VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLHNFHKIGMFRAGHTAYA
      70      80      90      100     110     120

del_6      120     130     140     150     160     170
      TFMIMILMLVSSVTGVLCSENPFWHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRF
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 TFMIMIVMFLTSTGVLCSDSA WVLASGAAMGFAWICQGWIGHDSGHYRIMSDRKWNWF
      130     140     150     160     170     180

del_6      180     190     200     210     220     230
      AQILSSNCLQGIGISIGWKNHNAHHIACNSLEYDQYIPLLVSPKFFNSLTSRFYDK
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 AQVLSNCLQGIGISIGWKNHNAHHIACNSLDYDQYIPLLVSPKFFNSLTSRFYDK
      190     200     210     220     230     240

del_6      240     250     260     270     280     290
      KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFITLFSREVGHRAQEIFGLAVFWVW
      250     260     270     280     290     300

del_6      300     310     320     330     340     350
      FPLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 FPLLSCLPNWSERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVANDWFKKQTAGTL
      310     320     330     340     350     360

del_6      360     370     380     390     400     410
      NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTEKANV
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTPYNIASFTEKANV
      370     380     390     400     410     420

del_6      420     430     440
      LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|126 LTLKTLRNTAIEARDLSNPTPKNMVWEAVHTHG
      430     440     450

>>gi|30350281|gb|AAP23036.1| fatty acid delta-6 desatura (453 aa)
      initn: 2845 initl: 2813 opt: 2813 Z-score: 3503.9 bits: 657.5 E(): 3.4e-
      186
      Smith-Waterman score: 2813; 88.964% identity (96.622% similar) in 444 aa
      overlap (3-446:10-453)

del_6      10      20      30      40      50
      MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: ..... : : ..... : : ..... : : ..... : : ..... :

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gi|303 MANKSPPNPKTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10      20      30      40      50      60

del_6      60      70      80      90      100     110
      VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYA
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 VTDAFLAYHPPSTARLLPPLSTNLLQNHSVSPTSSDYRKLLHNFHKIGMFRAGHTAYA
      70      80      90      100     110     120

del_6      120     130     140     150     160     170
      TFMIMILMLVSSVTGVLCSENPFWHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRF
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 TFMIMIVMFLTSTGVLCSDSA WVLASGAAMGFAWICQGWIGHDSGHYRIMSDRKWNWF
      130     140     150     160     170     180

del_6      180     190     200     210     220     230
      AQILSSNCLQGIGISIGWKNHNAHHIACNSLEYDQYIPLLVSPKFFNSLTSRFYDK
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 AQVLSNCLQGIGISIGWKNHNAHHIACNSLDYDQYIPLLVSPKFFNSLTSRFYDK
      190     200     210     220     230     240

del_6      240     250     260     270     280     290
      KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFITLFSREVGHRAQEIFGLAVFWVW
      250     260     270     280     290     300

del_6      300     310     320     330     340     350
      FPLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 FPLLSCLPNWSERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVANDWFKKQTAGTL
      310     320     330     340     350     360

del_6      360     370     380     390     400     410
      NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTEKANV
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 NISCPAWMDWFHGGQLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTPYNIASFTEKANV
      370     380     390     400     410     420

del_6      420     430     440
      LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      ..... : : ..... : : ..... : : ..... : : ..... :
gi|303 LTLKTLRNTAIEARDLSNPTPKNMVWEAVHTHG
      430     440     450

>>gi|60220788|emb|CAI58893.1| unnamed protein product [P (453 aa)
      initn: 2845 initl: 2813 opt: 2813 Z-score: 3503.9 bits: 657.5 E(): 3.4e-
      186
      Smith-Waterman score: 2813; 88.964% identity (96.622% similar) in 444 aa
      overlap (3-446:10-453)

del_6      10      20      30      40      50
      MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: ..... : : ..... : : ..... : : ..... : : ..... :
gi|602 MANKSPPNPKTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10      20      30      40      50      60

del_6      60      70      80      90      100     110

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      240      250      260      270      280      290
del_6  VSRFLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLLS
      .....
gi|129  FTRFLVSNQHWTFYPMCLARINLFAQSFIILLSSKKNVPYRVQELLGVVAFWIWYPLLVS
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6  CLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTLNISCPA
      .....
gi|129  CLPNWGERIMFVLASFVTGTGIQHVQFCLNHFSSDIYVAPPKGNDWFEKQTGGSLDISCPS
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  WMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLET
      .....
gi|129  WMDWFYGGGLQFQIEHHLFPRLPRLPRQVSPFVKDLCKKHGLPYNCASFYMANALTISTL
      370      380      390      400      410      420

      420      430      440
del_6  RNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|129  RTAALQARDLTKPVPKNLVWEAVNTHG
      430      440

>>gi|144583293|gb|ABP01349.1| D8-sphingolipid desaturase (447 aa)
  initn: 2175 initl: 2175 opt: 2175 Z-score: 2708.6 bits: 510.4 E(): 6.8e-
  142
Smith-Waterman score: 2175; 65.760% identity (87.528% similar) in 441 aa
overlap (6-446:7-447)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD AFL
      .. .....
gi|144  MADSKKYISEEELKHKTKSGDLWISIQGKVYNVTGWTKDHPGGELPLLHLSGQDVTD AFV
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6  AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYATFVIMI
      ....
gi|144  AYHPGTAWQYLDKFFTGYLLKDHVSVEVSKDYRKLLAEFTKMGLFEKKGHVTLVTL CVVA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6  LMLVSSVTGVLCSENPWVHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRF AQILSS
      ...
gi|144  MLLSFSIYGILCSDSTWVHLLSGGLIGFLWIQSGWIGHDSGHYQVMTSPKINRLVQIL TG
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6  NCLQGIGISGWKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDKKLNFDG
      ...
gi|144  NCLAGISIAWKKWNHNTHHIACNSLEFDPDLQHMPFFAVSSKLFSSLSYFYERKMNFDS
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6  VSRFLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLLS
      : .....

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gi|144  VCRFLVSYQHWTFYPMCFARLNLFQAQSFLLLLSKRRVPNRGQEILGLVLFWIWYPLLVS
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6  CLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTLNISCPA
      .....
gi|144  CLPNWGERVMFVLASFAVTGTGIQHVQFCLNHFSSNVYVGLPSGNDWFEKQTKGTLNINCSS
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  WMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLET
      .....
gi|144  WMDWFHGGGLQFQIEHHLFPRLPRLPRCQLRKISPFVKELCKKHHLPYDSASFWKANVMTIRTL
      370      380      390      400      410      420

      420      430      440
del_6  RNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|144  SAAALQARDLANPVPKNLVWEAVNTHG
      430      440

>>gi|157339279|emb|CAO43820.1| unnamed protein product [ (447 aa)
  initn: 2191 initl: 2166 opt: 2166 Z-score: 2697.4 bits: 508.3 E(): 2.9e-
  141
Smith-Waterman score: 2166; 65.986% identity (87.302% similar) in 441 aa
overlap (6-446:7-447)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD AFL
      ...
gi|157  MAETKRYISKEELKTHSRDGLWISIQGKVYNVSDWAKVHPGGSAPLLSLAGQDATDAFV
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6  AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARAGHTAYATFVIMI
      ....
gi|157  AYHPGVLWSRLDDFFTGFHLEDYAVSEASRDYRRLVYEFTKMGLFEKKGHVTVTL CAMA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6  LMLVSSVTGVLCSENPWVHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRF AQILSS
      ...
gi|157  VMFSACIYGVLGSDNTWVHLASGALMGLFWIQSGWIGHDSGHYQVMMNRRLNRFVQVLSG
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6  NCLQGIGISGWKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDKKLNFDG
      ...
gi|157  NCLAGISIAWKKWNHNAHHIACNSLDFDPDLQHMPVFAVSSKLFSSLTSYFYERKMNFDC
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6  VSRFLVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLLS
      .....
gi|157  VARFLVSYQHWTFYPMCVARLNLFQAQSWSLLSKRRVRYRAQEILGLLVFWIWIWYPLLVS
      250      260      270      280      290      300

      300      310      320      330      340      350

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gi|377 SWVDWFHGGGLQFQIEHHLPRLPRSQLRKVSPFVRELCKKHNLPHYDTASFWKANALTVRT
      370      380      390      400      410      420

      420      430      440
del_6 LRNTAIEARDLSNPPIKPNMVWEAVKNVG
      ..... :
gi|377 LRNAALQARDVANPVQKNLVWEAVNTHG
      430      440

>>gi|4102021|gb|AAD01410.1| delta 6-desaturase [Borago o (448 aa)
      initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-
      138
      Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa
      overlap (6-446:8-448)

      10      20      30      40      50
del_6 MTKTIYITSSSELEKHKNKPGDLWISIHQVYDVSSWAALHPGGIAPLLALAGHDVTDFAF
      ..... :
gi|410 MAAQIKKYITSDCLKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDFAF
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6 LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARGHTAYATFVIM
      ..... :
gi|410 VAFHPASTWKNLDKFFTGYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFI
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6 ILMLVSSVTGVLCSNPFWHLVCGAAMGFAWICGWIHDSGHYRIMTDRKWNRFQILS
      ..... :
gi|410 AMLFAMSVMVGLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRNLKFMGIFA
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6 SNCLQGIGISGWWKWNHNAHHIACNSLEYDPDLQYIPLLVVSPKFFNSLTSRFYDKKLNFD
      ..... :
gi|410 ANCLSGISGWWKWNHNAHHIACNSLEYDPDLQYIPLLVSSKFFGSLTSHFYEKRLTFD
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6 GVSRLFVQYQHWSFYPMCMVARLNMLAQSFILLFSRREANRVQEILGLAVFWLWFPLLL
      ..... :
gi|410 SLSRFFVSYQHWTFFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLL
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6 SCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTLNISC
      ..... :
gi|410 SCLPNWGERIMFVIASLSVTGMQVQFSLNHFSSSVYVGPVGNDFWFEKQTDGTLDISC
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6 AWMDFHGGGLQFQVEHHLPFRMPRGQFRKISPFVRDLCKKHNLTYNIASFETKANVLTLET
      ..... :
gi|410 PWNDWFHGGGLQFQIEHHLPKMPRCNLRKISPYVIELCKKHNLPTYNYASFETKANEMTLRT
      370      380      390      400      410      420

      420      430      440

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del_6 LRNTAIEARDLSNPPIKPNMVWEAVKNVG
      ..... :
gi|410 LRNTALQARDITKPLPKNLVWEALHTHG
      430      440

>>gi|126633756|emb|CAM55834.1| unnamed protein product [ (448 aa)
      initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-
      138
      Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa
      overlap (6-446:8-448)

      10      20      30      40      50
del_6 MTKTIYITSSSELEKHKNKPGDLWISIHQVYDVSSWAALHPGGIAPLLALAGHDVTDFAF
      ..... :
gi|126 MAAQIKKYITSDCLKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDFAF
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6 LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARGHTAYATFVIM
      ..... :
gi|126 VAFHPASTWKNLDKFFTGYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFI
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6 ILMLVSSVTGVLCSNPFWHLVCGAAMGFAWICGWIHDSGHYRIMTDRKWNRFQILS
      ..... :
gi|126 AMLFAMSVMVGLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRNLKFMGIFA
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6 SNCLQGIGISGWWKWNHNAHHIACNSLEYDPDLQYIPLLVVSPKFFNSLTSRFYDKKLNFD
      ..... :
gi|126 ANCLSGISGWWKWNHNAHHIACNSLEYDPDLQYIPLLVSSKFFGSLTSHFYEKRLTFD
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6 GVSRLFVQYQHWSFYPMCMVARLNMLAQSFILLFSRREANRVQEILGLAVFWLWFPLLL
      ..... :
gi|126 SLSRFFVSYQHWTFFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLL
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6 SCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKQTAGTLNISC
      ..... :
gi|126 SCLPNWGERIMFVIASLSVTGMQVQFSLNHFSSSVYVGPVGNDFWFEKQTDGTLDISC
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6 AWMDFHGGGLQFQVEHHLPFRMPRGQFRKISPFVRDLCKKHNLTYNIASFETKANVLTLET
      ..... :
gi|126 PWNDWFHGGGLQFQIEHHLPKMPRCNLRKISPYVIELCKKHNLPTYNYASFETKANEMTLRT
      370      380      390      400      410      420

      420      430      440
del_6 LRNTAIEARDLSNPPIKPNMVWEAVKNVG
      ..... :
gi|126 LRNTALQARDITKPLPKNLVWEALHTHG
      430      440

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>>gi|70795233|gb|AAZ08559.1| delta-6 desaturase [Echium (448 aa)  
initn: 2120 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138  
Smith-Waterman score: 2120; 65.079% identity (87.982% similar) in 441 aa  
overlap (6-446:8-448)

```

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTDAF
      :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|707  MANAIKKYITAEELKKHKAGDLWISIQGKIYDVSDWLKDHPPGNFLLSLAGQEVTDFAF
      10      20      30      40      50      60
```

```

      60      70      80      90     100     110
del_6  LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYATFVIM
      .::: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|707  VAFHSGTTWKLLKFFFTGYLKDYSVSEVSKDYRKLVFEFNKMGFLDKKGHIVLVTVLFIF
      70      80      90     100     110     120
```

```

     120     130     140     150     160     170
del_6  ILMLVSSVTGVLCSNPVWHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRFQILS
      ... : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  AMLFGMSVYGVLFCEGVLVHLLAGGLMGFVWIQSGWIGHDAGHYIVMPDARLNKIMGIVA
      130     140     150     160     170     180
```

```

     180     190     200     210     220     230
del_6  SNCLQGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFYDKKLNFD
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  ANCLSGISIGWKKWNHNAHHIACNSLDYDPLQYIPFLVSSKLFSSLTSHFYEKRLTFD
      190     200     210     220     230     240
```

```

     240     250     260     270     280     290
del_6  GVSRLFVQYQHSFYFVPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLL
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  SLSRFFVSHQHTFYFVPMCMARVNMVFVQSLIMLLTKRNVFYRSQELLGLVVFVIWYPLLV
      250     260     270     280     290     300
```

```

     300     310     320     330     340     350
del_6  SCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTLNISC
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  SCLPNWGERVMFVVASLSVTGMQQVQFSLNHFSSSVYVGQPKGNDWFEKQTCGTLDISCP
      310     320     330     340     350     360
```

```

     360     370     380     390     400     410
del_6  AWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFSTKANVLTLET
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  SWMDWFHGGGLQFQVEHHLFPKLPRCHLRKISPFVMECLCKKHNLSYNCASFSEANNMTLRT
      370     380     390     400     410     420
```

```

     420     430     440
del_6  LRNTAIEARDLSNPIPKNMVWEAVKNVG
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|707  LRDTALQARDLTKPLPKNLVWEALNTHG
      430     440
```

>>gi|76059232|emb|CAJ30813.1| unnamed protein product [B (448 aa)  
initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138

Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa  
overlap (6-446:8-448)

```

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTDFAF
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  MAAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDFAF
      10      20      30      40      50      60
```

```

      60      70      80      90     100     110
del_6  LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFRRAGHTAYATFVIM
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  VAFHPASTWKNLDKFFTGYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFI
      70      80      90     100     110     120
```

```

     120     130     140     150     160     170
del_6  ILMLVSSVTGVLCSNPVWHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRFQILS
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  AMLFAMSVMYGVLFCEGVLVHLLFSGCLMGFLWVQSGWIGHDAGHYMVVDSRLNKFMGIFA
      130     140     150     160     170     180
```

```

     180     190     200     210     220     230
del_6  SNCLQGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFYDKKLNFD
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  ANCLSGISIGWKKWNHNAHHIACNSLEYDPLQYIPFLVSSKFFGSLTSHFYEKRLTFD
      190     200     210     220     230     240
```

```

     240     250     260     270     280     290
del_6  GVSRLFVQYQHSFYFVPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLL
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  SLSRFFVSYQHWTFYFIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWIYPLLV
      250     260     270     280     290     300
```

```

     300     310     320     330     340     350
del_6  SCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTLNISC
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  SCLPNWGERIMFVIALSVTGMQQVQFSLNHFSSSVYVGPKGNWFEKQTDGTLDISCP
      310     320     330     340     350     360
```

```

     360     370     380     390     400     410
del_6  AWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFSTKANVLTLET
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  PWMDWFHGGGLQFQIEHHLFPKMPCNLRKISPYVIELCKKHNLTPYNYASFSEKANEMTLRT
      370     380     390     400     410     420
```

```

     420     430     440
del_6  LRNTAIEARDLSNPIPKNMVWEAVKNVG
      .: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|760  LRNTALQARDITKPLPKNLVWEALHTHG
      430     440
```

>>gi|156141045|gb|ABU51607.1| delta 6-desaturase [Borago (448 aa)  
initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138  
Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa  
overlap (6-446:8-448)

```

      10      20      30      40      50
```

```

del_6      MTKTIYITTSSELEKHNKPGDLWISIHQVYDVSSWAALHPGGIAPLLALAGHDVTDADF
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     MAAQIKKIYITSDCLKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDADF
          10          20          30          40          50          60

          60          70          80          90          100         110
del_6      LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMGMFARGHTAYATFVIM
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     VAFHPASTWKNLDKFFTGYLLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFI
          70          80          90          100         110         120

          120         130         140         150         160         170
del_6      ILMLVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRFQILS
          .... ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     AMLFAMSVYGVLFCEGLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFA
          130         140         150         160         170         180

          180         190         200         210         220         230
del_6      SNCLQGISIGWKKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDKKLNFD
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     ANCLSGISIGWKKWNHNAHHIACNSLEYDPDLQYIPLLVSPKFFNSLTSRFYDKKLNFD
          190         200         210         220         230         240

          240         250         260         270         280         290
del_6      GVSRLFVQYQHSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFPLLL
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     SLSRFFVSQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLV
          250         260         270         280         290         300

          300         310         320         330         340         350
del_6      SCLPNWGERIMFLLASYSVTGIQHVFSLNHFSSDVYVGGPVGNDWFKKQTAGTLNISCP
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     SCLPNWGERIMFVIAISLVTGMQQVQFSLNHFSSSVYVGGPKGNWFEKQTDGTLDISCP
          310         320         330         340         350         360

          360         370         380         390         400         410
del_6      AWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVVDLCKKHNLTYNIASTKANVLTLET
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     PWMDWFHGGGLQFQIEHHLFPMKPRCNLRKISPYVIELCKKHNLPYNYASFSEKANEMLT
          370         380         390         400         410         420

          420         430         440
del_6      LRNTAIEARDLSNPIPKNMVWEAVKNVG
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|156     LRNTALQARDITKPLPKNLVWEALHTHG
          430         440

446 residues in 1 query sequences
3787527556 residues in 14717352 library sequences
Scomplib [34t26]
start: Tue Oct 20 14:14:09 2009 done: Tue Oct 20 14:41:28 2009
Total Scan time: 1580.300 Total Display time: 21.500

Function used was FASTA [version 3.4t26 July 7, 2006]

```

## Appendix 2. Bioinformatic analysis of NcΔ15D (polypeptide del\_15)

```

>del_15
MAVTRSHKAAAATEPEVVSTGVDAVSAAPSSSSSSSSQKSAEPIEYDPIKTIRDAIPDHCFRPRVWISMAYFIRD
FAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFAFSRHTWFNNVMGWIGHSFLLVPYF
SWKFSHRRHRRFTGHMEKDMAFVPATEADNRQKRLANLYMDKETAEMFEDVPVQLVKLIAHQLAGWQMYLLFNVS
GKGSQWETGKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYILYQAAQVVGWQMVGLLYFQQYFVWHHW
LVAITYLHHTHEEVHHFDADSWTFVKGALATVDRDFGFIGKHLFHNIDHHVHHLFPRIPIFYAAEATNSIRPMLG
PLYHRDRSRFMSGQLWYNFTCKWVVPDPQVPGALIWAHTVQS

```

---

Sliding 8 amino acid window search  
Database searched = AD\_2009  
Query = del\_15

Start time: Tue Oct 20 14:41:32 CDT 2009 Finish time: Tue Oct 20 14:41:33 CDT 2009

|             |    |          |    |
|-------------|----|----------|----|
| gi-66840994 | 76 | SSSSSSSS | 83 |
| Query       | 32 | SSSSSSSS | 39 |

|             |    |          |    |
|-------------|----|----------|----|
| gi-66840994 | 77 | SSSSSSSS | 84 |
| Query       | 32 | SSSSSSSS | 39 |

gi-66840994 emb CAI64396.1 serine carboxypeptidase II [Triticum aestivum]

---

```

# fasta34 del_15.pep /home/andre/db/AD_2009 -Q -E 1 -O del_15.pep_ad.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006

```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

del\_15, 427 aa  
vs /home/andre/db/AD\_2009 library

|      | opt | E()        |                                      |
|------|-----|------------|--------------------------------------|
| < 20 | 3   | 0:=        |                                      |
| 22   | 0   | 0:         | one = represents 3 library sequences |
| 24   | 0   | 0:         |                                      |
| 26   | 0   | 0:         |                                      |
| 28   | 1   | 0:=        |                                      |
| 30   | 0   | 2:*        |                                      |
| 32   | 7   | 7:==*      |                                      |
| 34   | 26  | 20:=====*  |                                      |
| 36   | 44  | 41:=====*  |                                      |
| 38   | 46  | 68:=====*  | *                                    |
| 40   | 86  | 95:=====*  | *                                    |
| 42   | 112 | 116:=====* | *                                    |
| 44   | 110 | 128:=====* | *                                    |
| 46   | 141 | 130:=====* | *                                    |
| 48   | 88  | 125:=====* | *                                    |
| 50   | 101 | 114:=====* | *                                    |

```

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
  join: 37, opt: 25, open/ext: -10/-2, width: 16
The best scores are:
                                     opt bits E(1386)
gi|30794292|ref|NP_851341.1| lactotransferrin [Bos ( 708) 92 30.6 0.25
gi|66845476|gb|EAL85811.1| allergen Asp F3 [Asperg ( 168) 81 27.9 0.39
gi|2769700|gb|AAB95638.1| peroxisomal-like protein ( 168) 81 27.9 0.39

>>gi|30794292|ref|NP_851341.1| lactotransferrin [Bos tau (708 aa)
  initn: 69 initl: 69 opt: 92 Z-score: 112.6 bits: 30.6 E(): 0.25
Smith-Waterman score: 92; 25.225% identity (45.946% similar) in 111 aa
overlap (49-159:51-160)

          20          30          40          50          60          70
del_15 VSTGVDVAVSAAPSSSSSSSSQKSAEPIEYPDIKTIRDAIPDHCFRPRVWISMA YFIRDF
                                     :: :: :: :: :: :: :: ::
gi|307 PRKNVRWCTISOPEWFKRRWOWRMKKLGAP SITCVRRFALECI RIAEKKKDAVTLDG

```

---

Characterization Center  
9-520
Page 51 of 80

```
427 residues in 1 query sequences
307888 residues in 1386 library sequences
Scomplib [34t26]
start: Tue Oct 20 14:41:31 2009 done: Tue Oct 20 14:41:31 2009
Total Scan time: 0.160 Total Display time: 0.010
```

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 del_15.pep /home/andre/db/TOX_2009 -Q -E 1 -O del_15.pep_tx.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

del\_15, 427 aa

vs /home/andre/db/TOX\_2009 library

```
opt      E()
< 20    59    0:=====
22      0      0:
24      0      0:
26      1      0:=
28      18     2:*=
30      12     11:*
32      27     41:==*
34     105    110:=====*
36     247    227:=====*=
38     342    375:===== *
40     602    523:=====*=
42     555    639:===== *
44     551    705:===== *
46     711    718:=====*=
48     539    688:===== *
50     709    627:=====*=
52     669    552:=====*=
54     417    471:===== *
56     328    394:===== *
58     297    323:===== *
60     307    262:=====*=
62     111    210:===== *
64      92    167:===== *
66     123    132:=====*
68     134    104:=====*=
70     156     81:=====*=
72     108     64:=====*=
74      35     50:===== *
76      83     39:=====*=
78      22     30:=====*
80     185     23:=====*=
82      14     18:=====*
84      35     14:=====*=
```

```
86      14     11:*=
88      15     8:*=
90       8      7:*
92       5      5:*
94       7      4:*
96       2      3:*
98       0      2:*
100      0      2:*
102      0      1:*
104      0      1:*
106      0      1:*
108      0      1:*
110      0      1:*
112      0      0:
114      1      0:=
116      0      0:
118      0      0:
>120     0      0:
1891534 residues in 7651 sequences
Expectation_n fit: rho(ln(x))= 5.43590.000716; mu= 7.4762 0.036
mean_var=58.033113.609, 0's: 59 Z-trim: 59 B-trim: 768 in 2/60
Lambda= 0.168359
Kolmogorov-Smirnov statistic: 0.0544 (N=29) at 66
```

```
FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
!! No sequences with E() < 1.000000
```

```
427 residues in 1 query sequences
1891534 residues in 7651 library sequences
Scomplib [34t26]
start: Tue Oct 20 14:41:33 2009 done: Tue Oct 20 14:41:34 2009
Total Scan time: 0.700 Total Display time: 0.000
```

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 del_15.pep /home/andre/db/PRT_2009 -Q -E 1 -O del_15.pep_prt.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

del\_15, 427 aa

vs /home/andre/db/PRT\_2009 library

```
opt      E()
< 20 221653 0:=====
22   126      0:=
24   426     14:*
26   985    309:*
28  3808   3336:*
30 18208  20267:*
32 67668  78364:=====*
34 179719 212513:===== *
36 379640 436452:===== *
```

```

38 663309 721292:===== *
40 948566 1006139:===== *
42 1158604 1229883:===== *
44 1308167
1356675:===== *
46 1354903
1381807:===== *
48 1328241
1322921:===== *
50 1191316 1207171:===== *
52 1076496 1061305:===== *
54 899846 906540:===== *
56 772898 757239:===== *
58 635312 621679:===== *
60 505671 503596:===== *
62 413251 403735:===== *
64 331577 321088:===== *
66 268151 253778:===== *
68 214438 199617:===== *
70 165894 156431:===== *
72 137283 122236:===== *
74 108787 95303:===== *
76 80277 74177:===== *
78 63324 57657:===== *
80 49705 44769:===== *
82 37718 34248:===== *
84 29315 27128:===== *
86 22297 20991:===== *
88 16817 16241:===== *
90 13286 12567:===== *
92 10447 9723:===== *
94 7631 7523:===== *
96 5880 5821:===== *
98 4384 4504:===== *
100 3359 3485:===== *
102 2937 2697:===== *
104 1997 2086:===== *
106 1495 1614:===== *
108 1196 1249:===== *
110 934 967:===== *
112 835 748:===== *
114 657 579:===== *
116 463 448:===== *
118 385 346:===== *
>120 4136 268:===== *
3787527556 residues in 14717352 library sequences
statistics sampled from 60000 to 14710445 sequences
Expectation_n fit: rho(ln(x))= 5.27860.000191; mu= 9.7049 0.010
mean_var=65.615013.206, 0's: 854 Z-trim: 868 B-trim: 0 in 0/62
Lambda= 0.158333
Kolmogorov-Smirnov statistic: 0.0258 (N=29) at 50

```

```

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
The best scores are:
E(14717352)
gi|88181398|gb|EQA88866.1| hypothetical protein CH ( 400) 1886 439.6 1.2e-120
gi|170940419|emb|CAP65646.1| unnamed protein produ ( 399) 1884 439.1 1.6e-120

```

```

gi|167276960|gb|ABZ29824.1| Sequence 3762 from pat ( 429) 1871 436.2 1.3e-119
gi|145012308|gb|EDJ96964.1| hypothetical protein M ( 394) 1674 391.2 4.4e-106
gi|158467921|gb|ABW45178.1| Sequence 58 from paten ( 402) 1658 387.5 5.6e-105
gi|217312880|gb|ACK35371.1| Sequence 94 from paten ( 402) 1658 387.5 5.6e-105
gi|82658705|gb|ABB88516.1| bifunctional D12/D15 fa ( 402) 1658 387.5 5.6e-105
gi|114188648|gb|EAU30348.1| conserved hypothetical ( 394) 1369 321.5 4.1e-85
gi|134082006|emb|CAK46691.1| unnamed protein produ ( 398) 1349 316.9 9.9e-84
gi|83776412|dbj|BAE66531.1| unnamed protein produc ( 392) 1337 314.2 6.5e-83
gi|119405648|gb|EAW15599.1| oleate delta-12 desatu ( 395) 1321 310.5 8.3e-82
gi|159122555|gb|EDP47676.1| oleate delta-12 desatu ( 396) 1318 309.8 1.3e-81
gi|211593378|emb|CAP99761.1| Pc22g24730 [Penicilli ( 395) 1306 307.1 8.9e-81
gi|119398366|gb|EAW08796.1| oleate delta-12 desatu ( 391) 1305 306.9 1e-80
gi|160707460|gb|EAT91011.2| hypothetical protein S ( 979) 1238 291.8 9e-76
gi|150408460|gb|EDN04001.1| hypothetical protein H ( 472) 1174 277.0 1.2e-71
gi|90301761|gb|EAS31392.1| hypothetical protein CI ( 445) 1165 274.9 4.9e-71
gi|159131376|gb|EDP56489.1| oleate delta-12 desatu ( 469) 1143 269.9 1.7e-69
gi|145025092|gb|ABP24249.1| Sequence 34 from paten ( 477) 1141 269.5 2.3e-69
gi|82658703|gb|ABB8515.1| delta-12 fatty acid des ( 477) 1141 269.5 2.3e-69
gi|144998356|gb|ABP16929.1| Sequence 20 from paten ( 477) 1141 269.5 2.3e-69
gi|158475488|gb|ABW48564.1| Sequence 27 from paten ( 477) 1141 269.5 2.3e-69
gi|155080899|gb|ABS94493.1| Sequence 69 from paten ( 477) 1141 269.5 2.3e-69
gi|155070719|gb|ABS91064.1| Sequence 46 from paten ( 477) 1141 269.5 2.3e-69
gi|119412672|gb|EAW22613.1| oleate delta-12 desatu ( 469) 1140 269.2 2.7e-69
gi|151935301|gb|ABS18716.1| delta12 fatty acid des ( 476) 1132 267.4 9.6e-69
gi|41581329|emb|CAE47978.1| oleate delta-12 desatu ( 424) 1131 267.1 1e-68
gi|145012848|gb|EDJ97489.1| hypothetical protein M ( 487) 1131 267.2 1.1e-68
gi|211584351|emb|CAP92386.1| Pc13g13170 [Penicilli ( 468) 1129 266.7 1.5e-68
gi|167277069|gb|ABZ29933.1| Sequence 3871 from pat ( 413) 1116 263.7 1.1e-67
gi|210071661|gb|EEA25750.1| oleate delta-12 desatu ( 470) 1112 262.8 2.3e-67
gi|30385622|gb|AAP23194.1| oleate delta-12 desatur ( 466) 1108 261.9 4.2e-67
gi|114197390|gb|EAU39090.1| hypothetical protein A ( 467) 1108 261.9 4.2e-67
gi|30721845|gb|AAP33789.1| oleate delta-12 desatur ( 466) 1106 261.4 5.8e-67
gi|83766627|dbj|BAE56767.1| unnamed protein produc ( 466) 1106 261.4 5.8e-67
gi|194400325|gb|ACF61036.1| delta-12 desaturase is ( 483) 1104 261.0 8.2e-67
gi|151935303|gb|ABS18717.1| fatty acid desaturase ( 477) 1101 260.3 1.3e-66
gi|194477488|gb|ACF74838.1| putative delta-12 desa ( 483) 1101 260.3 1.3e-66
gi|39652599|dbj|BAD04850.1| oleate delta12 desatur ( 466) 1098 259.6 2.1e-66
gi|134077147|emb|CAK45488.1| unnamed protein produ ( 466) 1097 259.4 2.4e-66
gi|187979836|gb|EDU46462.1| delta(12) fatty acid d ( 447) 1096 259.2 2.7e-66
gi|159906226|gb|ABI96224.2| putative delta-12 desa ( 480) 1094 258.7 4e-66
gi|119397150|gb|EAW07581.1| oleate delta-12 desatu ( 469) 1093 258.5 4.6e-66
gi|11527199|gb|AAG36933.1| AF262955_1 oleate delta- ( 420) 1088 257.3 9.2e-66
gi|111070000|gb|EAT91120.1| hypothetical protein S ( 494) 1088 257.4 1.1e-65
gi|194271138|gb|ACF37070.1| fatty acid hydroxylase ( 477) 1081 255.7 3.1e-65
gi|167286028|gb|ABZ38892.1| Sequence 12830 from pa ( 419) 1080 255.5 3.2e-65
gi|150845063|gb|EDN20256.1| hypothetical protein B ( 481) 1071 253.5 1.5e-64
gi|154699086|gb|EDN98824.1| hypothetical protein S ( 481) 1069 253.0 2.1e-64
gi|211999443|gb|EEB05103.1| Delta(12) fatty acid d ( 449) 1062 251.4 6e-64
gi|211581853|emb|CAP79976.1| Pc12g03490 [Penicilli ( 453) 943 224.2 9.1e-56
gi|23313402|gb|AAN19960.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|12808263|gb|AAE43483.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|14477723|gb|AAE61286.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|6448794|gb|AAF08684.1| AF110509_1 delta-12 fatty ( 399) 935 222.4 2.9e-55
gi|27278519|gb|AAN93257.1| Sequence 20 from patent ( 399) 935 222.4 2.9e-55
gi|10055431|gb|AAE32337.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|5257239|dbj|BAA81754.1| delta-12 fatty acid des ( 400) 931 221.4 5.5e-55
gi|16033618|gb|AAL13300.1| AF417244_1 delta 12 fatt ( 400) 929 221.0 7.6e-55
gi|16033621|gb|AAL13301.1| AF417245_1 delta 12 fatt ( 400) 929 221.0 7.6e-55

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|                             |                         |        |     |       |         |                             |                          |        |     |       |         |
|-----------------------------|-------------------------|--------|-----|-------|---------|-----------------------------|--------------------------|--------|-----|-------|---------|
| gi 145025099 gb ABP24256.1  | Sequence 54 from paten  | ( 400) | 929 | 221.0 | 7.6e-55 | gi 15823622 dbj BAB69056.1  | delta-12 fatty acid de   | ( 396) | 518 | 127.1 | 1.4e-26 |
| gi 157677395 emb CAL69821.1 | delta12 fatty acid de   | ( 354) | 848 | 202.5 | 2.5e-49 | gi 68124764 emb CAJ03117.1  | fatty acid desaturase,   | ( 394) | 513 | 126.0 | 3e-26   |
| gi 45861536 gb AAS78627.1   | delta-12 fatty acid des | ( 446) | 827 | 197.7 | 8.5e-48 | gi 68124625 emb CAJ02312.1  | fatty acid desaturase,   | ( 394) | 513 | 126.0 | 3e-26   |
| gi 51873230 gb AAU12575.1   | delta-12 fatty acid des | ( 446) | 827 | 197.7 | 8.5e-48 | gi 134059778 emb CAM37203.1 | fatty acid desaturase    | ( 394) | 511 | 125.5 | 4.1e-26 |
| gi 3724332 dbj BAA33772.1   | fatty acid desaturase [ | ( 193) | 800 | 191.3 | 3e-46   | gi 17402593 dbj BAB78716.1  | delta12 fatty acid des   | ( 376) | 510 | 125.3 | 4.7e-26 |
| gi 88175663 gb EAQ83131.1   | hypothetical protein CH | ( 348) | 799 | 191.3 | 5.8e-46 | gi 68129162 emb CAJ06920.1  | fatty acid desaturase,   | ( 394) | 510 | 125.3 | 4.8e-26 |
| gi 62084356 dbj BAD91495.1  | omega3 desaturase [Mor  | ( 403) | 779 | 186.7 | 1.6e-44 | gi 134059919 emb CAM37348.1 | fatty acid desaturase    | ( 394) | 509 | 125.0 | 5.7e-26 |
| gi 57226459 gb AAW42919.1   | Delta-12 fatty acid des | ( 448) | 775 | 185.8 | 3.2e-44 | gi 154702189 gb EDO01928.1  | hypothetical protein S   | ( 337) | 507 | 124.5 | 6.8e-26 |
| gi 57226460 gb AAW42920.1   | Delta-12 fatty acid des | ( 448) | 775 | 185.8 | 3.2e-44 | gi 160812279 emb CAP40201.1 | unnamed protein produ    | ( 384) | 506 | 124.3 | 8.9e-26 |
| gi 155322974 gb ABT78578.1  | Sequence 166048 from p  | ( 282) | 768 | 184.1 | 6.6e-44 | gi 162771694 emb CAP58838.1 | unnamed protein produ    | ( 384) | 506 | 124.3 | 8.9e-26 |
| gi 167286479 gb ABZ39343.1  | Sequence 13281 from pa  | ( 251) | 765 | 183.4 | 9.7e-44 | gi 134072754 emb CAM71471.1 | fatty acid desaturase    | ( 394) | 503 | 123.7 | 1.5e-25 |
| gi 22316679 emb CAD44482.1  | unnamed protein produc  | ( 436) | 765 | 183.5 | 1.5e-43 | gi 134067875 emb CAM66157.1 | fatty acid desaturase    | ( 394) | 502 | 123.4 | 1.7e-25 |
| gi 22316525 emb CAD44412.1  | unnamed protein produc  | ( 436) | 765 | 183.5 | 1.5e-43 | gi 157361224 gb ABV44669.1  | fatty acid desaturase-   | ( 390) | 501 | 123.2 | 2e-25   |
| gi 27883909 gb AAO23564.1   | delta 12 fatty acid des | ( 436) | 765 | 183.5 | 1.5e-43 | gi 102230628 gb ABF70295.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 209582989 gb ACI65609.1  | delta 12 fatty acid de  | ( 436) | 765 | 183.5 | 1.5e-43 | gi 102230633 gb ABF70297.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 76059324 emb CAJ30856.1  | unnamed protein produc  | ( 434) | 746 | 179.2 | 3.1e-42 | gi 102230621 gb ABF70292.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 126633858 emb CAM55885.1 | unnamed protein produ   | ( 434) | 746 | 179.2 | 3.1e-42 | gi 102230625 gb ABF70294.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 60220824 emb CAI5811.1   | unnamed protein produc  | ( 434) | 746 | 179.2 | 3.1e-42 | gi 102230639 gb ABF70299.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 170939665 emb CAP64892.1 | unnamed protein produ   | ( 343) | 687 | 165.7 | 2.9e-38 | gi 102230631 gb ABF70296.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 190347297 gb EDK39542.2  | hypothetical protein P  | ( 417) | 665 | 160.7 | 1.1e-36 | gi 102230623 gb ABF70293.1  | delta-12 desaturase [B   | ( 261) | 498 | 122.4 | 2.3e-25 |
| gi 49655606 emb CAD44482.1  | DEHA2E14542p [Debaryom  | ( 435) | 648 | 156.8 | 1.7e-35 | gi 46399191 gb AAS92240.1   | delta-12 oleate desatur  | ( 384) | 500 | 123.0 | 2.3e-25 |
| gi 146447730 gb EDK42118.1  | hypothetical protein L  | ( 432) | 641 | 155.2 | 5.1e-35 | gi 1212781 emb CAA62578.1   | oleate desaturase [Bras  | ( 384) | 500 | 123.0 | 2.3e-25 |
| gi 22316519 emb CAD44409.1  | unnamed protein produc  | ( 495) | 638 | 154.6 | 9.2e-35 | gi 34600648 gb AAQ78505.1   | Sequence 10 from patent  | ( 384) | 500 | 123.0 | 2.3e-25 |
| gi 22316673 emb CAD44439.1  | unnamed protein produc  | ( 495) | 638 | 154.6 | 9.2e-35 | gi 102230701 gb ABF70327.1  | delta-12 desaturase [R   | ( 261) | 497 | 122.2 | 2.7e-25 |
| gi 27883911 gb AAO23565.1   | delta 12 fatty acid des | ( 495) | 638 | 154.6 | 9.2e-35 | gi 160812277 emb CAP40200.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 52546174 dbj BAD51484.1  | delta 12-fatty acid de  | ( 435) | 635 | 153.8 | 1.3e-34 | gi 5997736 gb AAE21283.1    | Sequence 2 from patent U | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 41529188 dbj BAD08375.1  | delta 12-fatty acid de  | ( 416) | 627 | 152.0 | 4.6e-34 | gi 46518253 emb CAG26981.1  | fatty acid desaturase    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 146452188 gb EDK46444.1  | hypothetical protein L  | ( 428) | 620 | 150.4 | 1.4e-33 | gi 40193151 gb AAR78123.1   | Sequence 8 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 164649561 gb EDR13803.1  | delta-12 fatty acid de  | ( 440) | 618 | 150.0 | 2e-33   | gi 20230154 gb AAE91297.1   | Sequence 6 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 49644538 emb CAG98110.1  | KLLA0F07095p [Kluyvero  | ( 410) | 601 | 146.1 | 2.8e-32 | gi 210028785 emb CAR94993.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 134056016 emb CAK37451.1 | unnamed protein produ   | ( 393) | 598 | 145.4 | 4.3e-32 | gi 83349266 gb ABC14919.1   | Sequence 14 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 49657448 emb CAG90237.1  | DEHA2G05346p [Debaryom  | ( 416) | 589 | 143.3 | 1.9e-31 | gi 189846873 gb ACE26371.1  | Sequence 126 from pate   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 126091907 gb ABN66656.1  | oleate delta-12 desatu  | ( 418) | 586 | 142.6 | 3e-31   | gi 20230159 gb AAE91302.1   | Sequence 16 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 150856710 gb EDN31902.1  | hypothetical protein B  | ( 389) | 577 | 140.6 | 1.2e-30 | gi 210028783 emb CAR94992.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 60459908 gb AAX20125.1   | delta 12-fatty acid des | ( 420) | 576 | 140.4 | 1.5e-30 | gi 213508651 emb CAS91773.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 190346683 gb EDK38830.2  | hypothetical protein P  | ( 417) | 571 | 139.2 | 3.2e-30 | gi 83349268 gb ABC14921.1   | Sequence 18 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 49646573 emb CAG82952.1  | YALI0B10153p [Yarrowia  | ( 419) | 569 | 138.8 | 4.5e-30 | gi 21507256 gb AAM57792.1   | Sequence 4 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 53952284 gb AAV02281.1   | Sequence 14238 from pat | ( 441) | 569 | 138.8 | 4.7e-30 | gi 83349263 gb ABC14916.1   | Sequence 8 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 150843820 gb EDN19013.1  | hypothetical protein B  | ( 221) | 558 | 136.1 | 1.5e-29 | gi 33749919 gb AAQ46759.1   | Sequence 6 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 145025098 gb ABP24255.1  | Sequence 51 from paten  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 40193152 gb AAR78124.1   | Sequence 10 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 158475490 gb ABW48566.1  | Sequence 49 from paten  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 162771688 emb CAP58835.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 89254947 emb CAJ81209.1  | unnamed protein produc  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 40193155 gb AAR78127.1   | Sequence 16 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 155070723 gb ABS91068.1  | Sequence 59 from paten  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 20520624 emb CAD30827.1  | fatty acid desaturase    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 158457287 gb ABW41481.1  | Sequence 147 from pate  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 115833233 gb ABJ40711.1  | Sequence 4 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 144998363 emb CAH01943.1 | Sequence 33 from paten  | ( 419) | 560 | 136.7 | 1.9e-29 | gi 160812273 gb AAE91301.1  | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 148915386 emb CAO00418.1 | unnamed protein produ   | ( 419) | 560 | 136.7 | 1.9e-29 | gi 210028787 emb CAR94994.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 55469813 gb AAV52631.1   | delta-12-fatty acid des | ( 389) | 559 | 136.5 | 2e-29   | gi 62789093 gb AAV07976.1   | Sequence 4 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 44885796 dbj BAD11952.1  | omega-3 fatty acid des  | ( 419) | 557 | 136.0 | 3e-29   | gi 20230160 gb AAE91303.1   | Sequence 18 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 48994801 gb AAT48093.1   | delta-12 fatty acid des | ( 389) | 555 | 135.5 | 3.9e-29 | gi 189704780 gb ACE16109.1  | Sequence 126 from pate   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 49246463 gb AAT58363.1   | delta-12-fatty acid des | ( 389) | 555 | 135.5 | 3.9e-29 | gi 8705229 gb AAF78778.1    | delta-12 oleate desatura | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 49640683 emb CAH01944.1  | KLLA0B00473p [Kluyvero  | ( 415) | 551 | 134.6 | 7.7e-29 | gi 20230158 gb AAE91301.1   | Sequence 14 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 119352252 gb ABL63813.1  | delta 15-fatty acid de  | ( 415) | 548 | 134.0 | 1.2e-28 | gi 40193156 gb AAR78128.1   | Sequence 18 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 44985182 gb AAS53960.1   | AFR589Cp [Ashbya gossyp | ( 413) | 545 | 133.3 | 2e-28   | gi 20230156 gb AAE91299.1   | Sequence 10 from patent  | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 123720728 dbj BAF45335.1 | fatty acid desaturase   | ( 441) | 540 | 132.1 | 4.6e-28 | gi 213508653 emb CAS91774.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 24298827 dbj BAC22091.1  | delta-12 desaturase [S  | ( 382) | 528 | 129.4 | 2.7e-27 | gi 75205881 gb ABA17985.1   | Sequence 4 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 134065453 emb CAM40887.1 | fatty acid desaturase   | ( 394) | 524 | 128.5 | 5.3e-27 | gi 162771692 emb CAP58837.1 | unnamed protein produ    | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 125599973 gb EAZ39549.1  | hypothetical protein O  | ( 362) | 521 | 127.8 | 7.9e-27 | gi 83349262 gb ABC14915.1   | Sequence 6 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |
| gi 125558094 gb EAZ03630.1  | hypothetical protein O  | ( 390) | 518 | 127.1 | 1.4e-26 | gi 158473902 gb ABW47802.1  | Sequence 8 from patent   | ( 384) | 499 | 122.7 | 2.7e-25 |

|                             |                          |       |     |       |         |                             |                           |       |     |       |         |
|-----------------------------|--------------------------|-------|-----|-------|---------|-----------------------------|---------------------------|-------|-----|-------|---------|
| gi 210028775 emb CAR94988.1 | unnamed protein produ    | (384) | 499 | 122.7 | 2.7e-25 | gi 118901300 gb ABL51015.1  | Sequence 2 from patent    | (384) | 489 | 120.5 | 1.3e-24 |
| gi 83349264 gb ABC14917.1   | Sequence 10 from patent  | (384) | 499 | 122.7 | 2.7e-25 | gi 102230697 gb ABF70326.1  | delta-12 desaturase [R    | (260) | 486 | 119.7 | 1.5e-24 |
| gi 210028773 emb CAR94987.1 | unnamed protein produ    | (384) | 499 | 122.7 | 2.7e-25 | gi 102230655 gb ABF70307.1  | delta-12 desaturase [E    | (260) | 486 | 119.7 | 1.5e-24 |
| gi 118901302 gb ABL51017.1  | Sequence 6 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 102230658 gb ABF70308.1  | delta-12 desaturase [E    | (260) | 486 | 119.7 | 1.5e-24 |
| gi 118901303 gb ABL51018.1  | Sequence 8 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 56666937 gb AAW18476.1   | Sequence 4 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 6778901 emb CAB70436.1   | unnamed protein product  | (384) | 499 | 122.7 | 2.7e-25 | gi 17909752 gb AAE82559.1   | Sequence 6 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 40193150 gb AAR78122.1   | Sequence 6 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 12322004 gb AAG51042.1   | AC069473_4 omega-6 fatty  | (383) | 488 | 120.2 | 1.5e-24 |
| gi 217272163 gb ACK28081.1  | Sequence 2 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 14517474 gb AAK62627.1   | AT3g12120/T21B14_107 [A   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 23334555 gb AAN27913.1   | Sequence 6 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 21536781 gb AAM61113.1   | omega-6 fatty acid desa   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 20230155 gb AAE91298.1   | Sequence 8 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 5955846 gb AAE07502.1    | Sequence 41 from patent   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 40193154 gb AAR78126.1   | Sequence 14 from patent  | (384) | 499 | 122.7 | 2.7e-25 | gi 22655458 gb AAM98321.1   | At3g12120/T21B14_107 [A   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 158473901 gb ABW47801.1  | Sequence 6 from patent   | (384) | 499 | 122.7 | 2.7e-25 | gi 189704779 gb ACE16108.1  | Sequence 125 from pate    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 83349267 gb ABC14920.1   | Sequence 16 from patent  | (384) | 499 | 122.7 | 2.7e-25 | gi 189846872 gb ACE26370.1  | Sequence 125 from pate    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 91148810 gb ABE23044.1   | Sequence 3 from patent   | (392) | 499 | 122.8 | 2.7e-25 | gi 115833232 gb ABJ40710.1  | Sequence 2 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 12330616 gb ABF70290.1   | delta-12 desaturase [B   | (260) | 496 | 122.0 | 3.1e-25 | gi 34600647 gb AAQ78504.1   | Sequence 9 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 102230614 gb ABF70289.1  | delta-12 desaturase [B   | (261) | 496 | 122.0 | 3.1e-25 | gi 438451 gb AAA32782.1     | delta-12 desaturase       | (383) | 488 | 120.2 | 1.5e-24 |
| gi 149395006 gb ABR27357.1  | fatty acid desaturase    | (384) | 498 | 122.5 | 3.2e-25 | gi 110623202 emb CAL24241.1 | unnamed protein produ     | (383) | 488 | 120.2 | 1.5e-24 |
| gi 115833233 gb ABJ40713.1  | Sequence 8 from patent   | (387) | 498 | 122.5 | 3.2e-25 | gi 62789092 gb AAY07975.1   | Sequence 2 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 194688628 gb ACF78398.1  | unknown [Zea mays]       | (387) | 498 | 122.5 | 3.2e-25 | gi 2492223 gb AAB80359.1    | I66170 Sequence 41 from p | (383) | 488 | 120.2 | 1.5e-24 |
| gi 21507259 gb AAM57794.1   | Sequence 8 from patent   | (387) | 498 | 122.5 | 3.2e-25 | gi 21507255 gb AAM57791.1   | Sequence 2 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 62789095 gb AAY07978.1   | Sequence 8 from patent   | (387) | 498 | 122.5 | 3.2e-25 | gi 75205880 gb ABA17984.1   | Sequence 2 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 75205883 gb ABA17987.1   | Sequence 8 from patent   | (387) | 498 | 122.5 | 3.2e-25 | gi 110623200 emb CAL24240.1 | unnamed protein produ     | (383) | 488 | 120.2 | 1.5e-24 |
| gi 126633152 emb CAM55541.1 | unnamed protein produ    | (446) | 498 | 122.6 | 3.6e-25 | gi 9294109 dbj BAB01960.1   | omega-6 fatty acid desa   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 4378875 gb AAD19742.1    | delta-12 desaturase [Bra | (446) | 497 | 122.3 | 3.7e-25 | gi 17918535 gb AAE85969.1   | Sequence 6 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 46849977 gb AAT02411.1   | delta-12 oleate desatur  | (384) | 497 | 122.3 | 3.7e-25 | gi 91125671 gb ABE12619.1   | Sequence 32 from patent   | (383) | 488 | 120.2 | 1.5e-24 |
| gi 102230693 gb ABF70324.1  | delta-12 desaturase [O   | (260) | 494 | 121.5 | 4.3e-25 | gi 71057275 emb CAJ18799.1  | unnamed protein produc    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 195631540 gb ACG36665.1  | omega-6 fatty acid des   | (392) | 495 | 121.8 | 5.2e-25 | gi 76007349 gb ABA38263.1   | Sequence 6 from patent    | (383) | 488 | 120.2 | 1.5e-24 |
| gi 110623218 emb CAL24249.1 | unnamed protein produ    | (392) | 495 | 121.8 | 5.2e-25 | gi 125661169 gb ABN49520.1  | fatty acid desaturase     | (385) | 488 | 120.2 | 1.5e-24 |
| gi 195624882 gb ACG34271.1  | omega-6 fatty acid des   | (392) | 495 | 121.8 | 5.2e-25 | gi 92380879 dbj BAE93382.1  | delta-12 fatty acid de    | (387) | 488 | 120.2 | 1.6e-24 |
| gi 110623216 emb CAL24248.1 | unnamed protein produ    | (392) | 495 | 121.8 | 5.2e-25 | gi 94982471 gb ABF50053.1   | FAD2 [Zea mays]           | (387) | 488 | 120.2 | 1.6e-24 |
| gi 126633352 emb CAM55641.1 | unnamed protein produ    | (452) | 495 | 121.9 | 5.8e-25 | gi 195635929 gb ACG37433.1  | omega-6 fatty acid des    | (394) | 488 | 120.2 | 1.6e-24 |
| gi 102230612 gb ABF70288.1  | delta-12 desaturase [B   | (261) | 492 | 121.1 | 5.9e-25 | gi 102230682 gb ABF70319.1  | delta-12 desaturase [I    | (260) | 485 | 119.5 | 1.8e-24 |
| gi 40193153 gb AAR78125.1   | Sequence 12 from patent  | (384) | 494 | 121.6 | 6e-25   | gi 102230669 gb ABF70313.1  | delta-12 desaturase [C    | (260) | 485 | 119.5 | 1.8e-24 |
| gi 20230157 gb AAE91300.1   | Sequence 12 from patent  | (384) | 494 | 121.6 | 6e-25   | gi 5997738 gb AAE21285.1    | Sequence 6 from patent U  | (384) | 487 | 120.0 | 1.8e-24 |
| gi 83349265 gb ABC14918.1   | Sequence 12 from patent  | (384) | 494 | 121.6 | 6e-25   | gi 168805244 gb ACA28704.1  | fatty acid desaturase     | (387) | 487 | 120.0 | 1.8e-24 |
| gi 217272164 gb ACK28082.1  | Sequence 4 from patent   | (384) | 494 | 121.6 | 6e-25   | gi 102230703 gb ABF70328.1  | delta-12 desaturase [S    | (262) | 483 | 119.0 | 2.5e-24 |
| gi 102230671 gb ABF70314.1  | delta-12 desaturase [C   | (261) | 491 | 120.8 | 6.9e-25 | gi 189846864 gb ACE26362.1  | Sequence 35 from paten    | (383) | 485 | 119.6 | 2.5e-24 |
| gi 210028777 emb CAR94989.1 | unnamed protein produ    | (384) | 492 | 121.1 | 8.2e-25 | gi 189704771 gb ACE16100.1  | Sequence 35 from paten    | (383) | 485 | 119.6 | 2.5e-24 |
| gi 102230695 gb ABF70325.1  | delta-12 desaturase [R   | (260) | 489 | 120.4 | 9.5e-25 | gi 189704767 gb ACE16096.1  | Sequence 22 from paten    | (384) | 485 | 119.6 | 2.5e-24 |
| gi 217272165 gb ACK28083.1  | Sequence 6 from patent   | (384) | 491 | 120.9 | 9.6e-25 | gi 189846860 gb ACE26358.1  | Sequence 22 from paten    | (384) | 485 | 119.6 | 2.5e-24 |
| gi 217272166 gb ACK28084.1  | Sequence 8 from patent   | (384) | 491 | 120.9 | 9.6e-25 | gi 3135020 emb CAA76157.1   | delta 12 fatty acid des   | (379) | 484 | 119.3 | 2.9e-24 |
| gi 102230665 gb ABF70311.1  | delta-12 desaturase [C   | (260) | 488 | 120.1 | 1.1e-24 | gi 102230641 gb ABF70300.1  | delta-12 desaturase [B    | (260) | 482 | 118.8 | 2.9e-24 |
| gi 102230684 gb ABF70320.1  | delta-12 desaturase [I   | (260) | 488 | 120.1 | 1.1e-24 | gi 102230649 gb ABF70304.1  | delta-12 desaturase [C    | (260) | 482 | 118.8 | 2.9e-24 |
| gi 102230667 gb ABF70312.1  | delta-12 desaturase [C   | (260) | 488 | 120.1 | 1.1e-24 | gi 102230647 gb ABF70303.1  | delta-12 desaturase [C    | (260) | 482 | 118.8 | 2.9e-24 |
| gi 102230686 gb ABF70321.1  | delta-12 desaturase [I   | (260) | 488 | 120.1 | 1.1e-24 | gi 102230643 gb ABF70301.1  | delta-12 desaturase [B    | (260) | 482 | 118.8 | 2.9e-24 |
| gi 102230610 gb ABF70287.1  | delta-12 desaturase [A   | (260) | 488 | 120.1 | 1.1e-24 | gi 33749918 gb AAQ46758.1   | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 102230660 gb ABF70309.1  | delta-12 desaturase [C   | (261) | 488 | 120.1 | 1.1e-24 | gi 83349261 gb ABC14914.1   | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 189704761 gb ACE16090.1  | Sequence 16 from paten   | (384) | 490 | 120.7 | 1.1e-24 | gi 23334554 gb AAN27912.1   | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 189846854 gb ACE26352.1  | Sequence 16 from paten   | (384) | 490 | 120.7 | 1.1e-24 | gi 158473900 gb ABW47800.1  | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 17909753 gb AAE82560.1   | Sequence 7 from patent   | (383) | 489 | 120.5 | 1.3e-24 | gi 40193149 gb AAR78121.1   | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 20230152 gb AAE91295.1   | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 118901301 gb ABL51016.1  | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 158473899 gb ABW47799.1  | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 20230153 gb AAE91296.1   | Sequence 4 from patent    | (384) | 484 | 119.3 | 2.9e-24 |
| gi 23334553 gb AAN27911.1   | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 217072516 gb ACJ84618.1  | unknown [Medicago trun    | (411) | 484 | 119.3 | 3.1e-24 |
| gi 40193148 gb ACE16120.1   | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 102230688 gb ABF70322.1  | delta-12 desaturase [P    | (259) | 480 | 118.3 | 3.9e-24 |
| gi 83349260 gb ABC14913.1   | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 102230677 gb ABF70317.1  | delta-12 desaturase [E    | (260) | 480 | 118.3 | 3.9e-24 |
| gi 17918536 gb AAE85970.1   | Sequence 7 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 102230645 gb ABF70302.1  | delta-12 desaturase [C    | (260) | 480 | 118.3 | 3.9e-24 |
| gi 33749917 gb AAQ46757.1   | Sequence 2 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 102230635 gb ABF70298.1  | delta-12 desaturase [B    | (261) | 480 | 118.3 | 4e-24   |
| gi 76007350 gb ABA38264.1   | Sequence 7 from patent   | (384) | 489 | 120.5 | 1.3e-24 | gi 5997737 gb AAE21284.1    | Sequence 4 from patent U  | (384) | 482 | 118.9 | 4e-24   |

|                             |                           |        |     |       |         |                             |                           |        |     |       |         |
|-----------------------------|---------------------------|--------|-----|-------|---------|-----------------------------|---------------------------|--------|-----|-------|---------|
| gi 102230662 gb ABF70310.1  | delta-12 desaturase [C    | ( 260) | 479 | 118.1 | 4.6e-24 | gi 28371827 gb AAO37754.1   | delta-12 oleate desatur   | ( 387) | 467 | 115.4 | 4.3e-23 |
| gi 23428547 gb AAL23676.1   | delta-12 fatty acid des   | ( 382) | 480 | 118.4 | 5.4e-24 | gi 110623226 emb CAL24253.1 | unnamed protein produ     | ( 341) | 466 | 115.2 | 4.5e-23 |
| gi 102230705 gb ABF70329.1  | delta-12 desaturase [T    | ( 260) | 477 | 117.6 | 6.3e-24 | gi 110623224 emb CAL24252.1 | unnamed protein produ     | ( 341) | 466 | 115.2 | 4.5e-23 |
| gi 6118361 gb AAF04094.1    | AF188264_1 delta-12 oleat | ( 383) | 479 | 118.2 | 6.4e-24 | gi 60392519 gb AAX19366.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 102230651 gb ABF70305.1  | delta-12 desaturase [C    | ( 260) | 476 | 117.4 | 7.4e-24 | gi 60392517 gb AAX19365.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 102230653 gb ABF70306.1  | delta-12 desaturase [C    | ( 260) | 476 | 117.4 | 7.4e-24 | gi 18418653 gb AAL68983.1   | AF251844_1 delta-12 olea  | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 147776501 emb CAN71892.1 | hypothetical protein      | ( 382) | 478 | 118.0 | 7.5e-24 | gi 60392525 gb AAX19369.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 157348500 emb CAO23392.1 | unnamed protein produ     | ( 382) | 478 | 118.0 | 7.5e-24 | gi 60392531 gb AAX19372.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 17918533 gb AAE85967.1   | Sequence 4 from patent    | ( 384) | 478 | 118.0 | 7.5e-24 | gi 60392523 gb AAX19368.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 17909750 gb AAE82557.1   | Sequence 4 from patent    | ( 384) | 478 | 118.0 | 7.5e-24 | gi 60392527 gb AAX19370.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 3452129 gb AAC32755.1    | bifunctional oleate 12-h  | ( 384) | 478 | 118.0 | 7.5e-24 | gi 60392529 gb AAX19371.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 76007347 gb ABA38261.1   | Sequence 4 from patent    | ( 384) | 478 | 118.0 | 7.5e-24 | gi 60392537 gb AAX19375.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 193290416 gb ACF17571.1  | mutant bifunctional ol    | ( 355) | 476 | 117.5 | 9.7e-24 | gi 60392533 gb AAX19373.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 189704759 gb ACE16088.1  | Sequence 14 from paten    | ( 384) | 476 | 117.5 | 1e-23   | gi 60392535 gb AAX19374.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 189846852 gb ACE26350.1  | Sequence 14 from paten    | ( 384) | 476 | 117.5 | 1e-23   | gi 60392521 gb AAX19367.1   | delta-12 oleate desatur   | ( 382) | 464 | 114.8 | 6.9e-23 |
| gi 154813798 gb ABS86964.1  | delta-12 fatty acid de    | ( 383) | 475 | 117.3 | 1.2e-23 | gi 140421522 gb ECL64495.1  | hypothetical protein G    | ( 284) | 462 | 114.2 | 7.3e-23 |
| gi 189860252 gb ACE35658.1  | Sequence 2 from patent    | ( 383) | 474 | 117.0 | 1.4e-23 | gi 60392578 gb AAX19395.1   | delta-12 oleate desatur   | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 8886726 gb AAF80560.1    | AF192486_1 omega-6 fatty  | ( 383) | 474 | 117.0 | 1.4e-23 | gi 18418651 gb AAL68982.1   | AF251843_1 delta-12 olea  | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 189704782 gb ACE16111.1  | Sequence 128 from pate    | ( 383) | 474 | 117.0 | 1.4e-23 | gi 60392580 gb AAX19396.1   | delta-12 oleate desatur   | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 189846875 gb ACE26373.1  | Sequence 128 from pate    | ( 383) | 474 | 117.0 | 1.4e-23 | gi 60392574 gb AAX19393.1   | delta-12 oleate desatur   | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 59896214 gb AAX11454.1   | microsomal oleic acid d   | ( 383) | 474 | 117.0 | 1.4e-23 | gi 60392572 gb AAX19392.1   | delta-12 oleate desatur   | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 189846855 gb ACE26353.1  | Sequence 17 from paten    | ( 384) | 474 | 117.0 | 1.4e-23 | gi 60392576 gb AAX19394.1   | delta-12 oleate desatur   | ( 383) | 463 | 114.5 | 8.1e-23 |
| gi 189704776 gb ACE16105.1  | Sequence 40 from paten    | ( 384) | 474 | 117.0 | 1.4e-23 | gi 29536061 emb CAD87608.1  | unnamed protein produc    | ( 387) | 463 | 114.5 | 8.1e-23 |
| gi 189846869 gb ACE26367.1  | Sequence 40 from paten    | ( 384) | 474 | 117.0 | 1.4e-23 | gi 28564441 emb CAD24671.1  | delta 12-acyl-lipid-de    | ( 387) | 463 | 114.5 | 8.1e-23 |
| gi 189704762 gb ACE16091.1  | Sequence 17 from paten    | ( 384) | 474 | 117.0 | 1.4e-23 | gi 116001287 emb CAL49895.1 | unnamed protein produ     | ( 398) | 463 | 114.5 | 8.3e-23 |
| gi 189846880 gb ACE26378.1  | Sequence 138 from pate    | ( 384) | 474 | 117.0 | 1.4e-23 | gi 77920892 gb ABB05230.1   | delta 12 desaturase [Li   | ( 378) | 462 | 114.3 | 9.3e-23 |
| gi 2501790 gb AAB80696.1    | omega-6 fatty acid desat  | ( 382) | 473 | 116.8 | 1.6e-23 | gi 42541363 gb AAS19533.1   | omega-6 fatty acid desa   | ( 383) | 462 | 114.3 | 9.4e-23 |
| gi 76059404 emb CAJ30867.1  | unnamed protein produc    | ( 383) | 473 | 116.8 | 1.7e-23 | gi 194346324 gb ACF49508.1  | omega-6 desaturase [Li    | ( 378) | 461 | 114.1 | 1.1e-22 |
| gi 2501792 gb AAB80697.1    | funga elicitor-induced    | ( 383) | 473 | 116.8 | 1.7e-23 | gi 33358366 gb AAQ16654.1   | delta-12 fatty acid des   | ( 384) | 461 | 114.1 | 1.1e-22 |
| gi 6118359 gb AAF04093.1    | AF188263_1 delta-12 oleat | ( 383) | 473 | 116.8 | 1.7e-23 | gi 33358364 gb AAQ16653.1   | delta-12 fatty acid des   | ( 384) | 461 | 114.1 | 1.1e-22 |
| gi 17382283 emb CAD13056.1  | unnamed protein produc    | ( 383) | 473 | 116.8 | 1.7e-23 | gi 189846870 gb ACE26368.1  | Sequence 41 from paten    | ( 374) | 460 | 113.8 | 1.3e-22 |
| gi 13447102 gb AAK26633.1   | AF343065_1 delta-12 fatt  | ( 383) | 473 | 116.8 | 1.7e-23 | gi 189704777 gb ACE16106.1  | Sequence 41 from paten    | ( 374) | 460 | 113.8 | 1.3e-22 |
| gi 189846877 gb ACE26375.1  | Sequence 135 from pate    | ( 374) | 472 | 116.6 | 1.9e-23 | gi 84626279 gb ABC59684.1   | delta-12 fatty acid ace   | ( 377) | 460 | 113.8 | 1.3e-22 |
| gi 102230675 gb ABF70316.1  | delta-12 desaturase [C    | ( 260) | 470 | 116.0 | 1.9e-23 | gi 102230691 gb ABF70323.1  | delta-12 desaturase [L    | ( 260) | 458 | 113.3 | 1.3e-22 |
| gi 58013373 gb AAW63040.1   | microsomal delta-12 ole   | ( 381) | 471 | 116.4 | 2.3e-23 | gi 17225582 gb AAL37484.1   | AF331163_1 delta-12 fatt  | ( 384) | 460 | 113.8 | 1.3e-22 |
| gi 189704766 gb ACE16095.1  | Sequence 21 from paten    | ( 383) | 471 | 116.4 | 2.3e-23 | gi 31322135 gb AAO38032.1   | delta12-fatty acid acet   | ( 377) | 459 | 113.6 | 1.5e-22 |
| gi 189846859 gb ACE26357.1  | Sequence 21 from paten    | ( 383) | 471 | 116.4 | 2.3e-23 | gi 102230673 gb ABF70315.1  | delta-12 desaturase [C    | ( 260) | 457 | 113.1 | 1.5e-22 |
| gi 102230679 gb ABF70318.1  | delta-12 desaturase [E    | ( 260) | 468 | 115.6 | 2.6e-23 | gi 10863190 gb AAG23929.1   | AF239833_1 ELI7.8 [Petro  | ( 382) | 459 | 113.6 | 1.5e-22 |
| gi 189846862 gb ACE26360.1  | Sequence 24 from paten    | ( 380) | 470 | 116.1 | 2.6e-23 | gi 58013375 gb AAW63041.1   | microsomal delta-12 ole   | ( 383) | 459 | 113.6 | 1.5e-22 |
| gi 189704769 gb ACE16098.1  | Sequence 24 from paten    | ( 380) | 470 | 116.1 | 2.6e-23 | gi 68146846 emb CAI48076.2  | omega-6 desaturase [Ca    | ( 306) | 457 | 113.1 | 1.7e-22 |
| gi 146141441 gb ABQ01458.1  | oleate 12-hydroxylase     | ( 383) | 470 | 116.1 | 2.7e-23 | gi 22532409 gb AAM97924.1   | delta-12 desaturase [Mu   | ( 396) | 458 | 113.4 | 1.8e-22 |
| gi 59956946 dbj BAD89862.1  | microsomal omega-6 fat    | ( 383) | 470 | 116.1 | 2.7e-23 | gi 3264765 gb AAC24586.1    | omega-6 fatty acid desat  | ( 346) | 457 | 113.1 | 1.9e-22 |
| gi 110623210 emb CAL24245.1 | unnamed protein produ     | ( 383) | 470 | 116.1 | 2.7e-23 | gi 145280641 gb ABP49577.1  | oleate desaturase [Car    | ( 383) | 457 | 113.2 | 2.1e-22 |
| gi 76257461 gb ABA41034.1   | delta12-fatty acid desa   | ( 383) | 470 | 116.1 | 2.7e-23 | gi 10863182 gb AAG23925.1   | AF239829_1 ELI7.4 [Petro  | ( 384) | 457 | 113.2 | 2.1e-22 |
| gi 107785184 gb ABF84063.1  | microsomal oleate desa    | ( 383) | 470 | 116.1 | 2.7e-23 | gi 102230619 gb ABF70291.1  | delta-12 desaturase [B    | ( 265) | 455 | 112.6 | 2.1e-22 |
| gi 110623208 emb CAL24244.1 | unnamed protein produ     | ( 383) | 470 | 116.1 | 2.7e-23 | gi 5917670 gb AAD55982.1    | delta-12 desaturase [Muc  | ( 396) | 457 | 113.2 | 2.1e-22 |
| gi 10278514 emb CAC09644.1  | unnamed protein produc    | ( 374) | 469 | 115.9 | 3.1e-23 | gi 17909756 gb AAE82563.1   | Sequence 10 from patent   | ( 371) | 456 | 112.9 | 2.4e-22 |
| gi 3135018 emb CAA76156.1   | delta 12 fatty acid epo   | ( 374) | 469 | 115.9 | 3.1e-23 | gi 17918539 gb AAE85973.1   | Sequence 10 from patent   | ( 372) | 456 | 112.9 | 2.4e-22 |
| gi 34600643 gb AAQ78500.1   | Sequence 2 from patent    | ( 374) | 469 | 115.9 | 3.1e-23 | gi 76007353 gb ABA38267.1   | Sequence 10 from patent   | ( 372) | 456 | 112.9 | 2.4e-22 |
| gi 189846853 gb ACE26351.1  | Sequence 15 from paten    | ( 383) | 469 | 115.9 | 3.1e-23 | gi 189704763 gb ACE16092.1  | Sequence 18 from paten    | ( 374) | 456 | 112.9 | 2.4e-22 |
| gi 189704760 gb ACE16089.1  | Sequence 15 from paten    | ( 383) | 469 | 115.9 | 3.1e-23 | gi 189846856 gb ACE26354.1  | Sequence 18 from paten    | ( 374) | 456 | 112.9 | 2.4e-22 |
| gi 189704765 gb ACE16094.1  | Sequence 20 from paten    | ( 384) | 469 | 115.9 | 3.1e-23 | gi 13560785 gb AAK30206.1   | AF349965_1 fatty acid de  | ( 383) | 456 | 112.9 | 2.4e-22 |
| gi 189846858 gb ACE26356.1  | Sequence 20 from paten    | ( 384) | 469 | 115.9 | 3.1e-23 | gi 25989476 gb AAL93620.1   | fatty acid desaturase 2   | ( 383) | 456 | 112.9 | 2.4e-22 |
| gi 189846879 gb ACE26377.1  | Sequence 137 from pate    | ( 374) | 468 | 115.7 | 3.6e-23 | gi 1161568 emb CAA64414.1   | lipid desaturase-like p   | ( 333) | 455 | 112.7 | 2.5e-22 |
| gi 194346322 gb ACF49507.1  | omega-6 desaturase [Li    | ( 382) | 467 | 115.4 | 4.3e-23 | gi 904154 gb AAB00860.1     | microsomal omega-6 desatu | ( 383) | 455 | 112.7 | 2.9e-22 |
| gi 117957296 gb ABK59093.1  | oleate desaturase [Ric    | ( 383) | 467 | 115.4 | 4.3e-23 | gi 189704781 gb ACE16110.1  | Sequence 127 from pate    | ( 383) | 455 | 112.7 | 2.9e-22 |
| gi 189846861 gb ACE26359.1  | Sequence 23 from paten    | ( 384) | 467 | 115.4 | 4.3e-23 | gi 68164987 gb AAY87459.1   | omega-6 fatty acid desa   | ( 383) | 455 | 112.7 | 2.9e-22 |
| gi 189704768 gb ACE16097.1  | Sequence 23 from paten    | ( 384) | 467 | 115.4 | 4.3e-23 | gi 10863178 gb AAG23923.1   | AF239827_1 ELI7.1 [Petro  | ( 383) | 455 | 112.7 | 2.9e-22 |



|                             |                          |       |     |       |         |                             |                          |       |     |       |         |
|-----------------------------|--------------------------|-------|-----|-------|---------|-----------------------------|--------------------------|-------|-----|-------|---------|
| gi 91125670 gb ABE12618.1   | Sequence 31 from patent  | (383) | 455 | 112.7 | 2.9e-22 | gi 2564237 emb CAA71199.1   | omega-6 desaturase [Gos  | (383) | 444 | 110.2 | 1.6e-21 |
| gi 34600649 gb AAQ78506.1   | Sequence 11 from patent  | (383) | 455 | 112.7 | 2.9e-22 | gi 155713304 gb ABU35460.1  | Sequence 24 from paten   | (387) | 444 | 110.2 | 1.6e-21 |
| gi 189846874 gb ACE26372.1  | Sequence 127 from pate   | (383) | 455 | 112.7 | 2.9e-22 | gi 165882019 gb ABY71269.1  | delta-12 fatty acid de   | (234) | 441 | 109.4 | 1.7e-21 |
| gi 10863188 gb AAG23928.1   | AF239832_1 ELI7.7 [Petro | (384) | 455 | 112.7 | 2.9e-22 | gi 33766648 gb AAQ52851.1   | Sequence 2 from patent   | (374) | 443 | 110.0 | 1.9e-21 |
| gi 10863186 gb AAG23927.1   | AF239831_1 ELI7.6 [Petro | (384) | 455 | 112.7 | 2.9e-22 | gi 17382281 emb CAD13055.1  | unnamed protein produc   | (374) | 443 | 110.0 | 1.9e-21 |
| gi 154701225 gb ED000964.1  | hypothetical protein S   | (221) | 452 | 111.9 | 2.9e-22 | gi 155689125 gb ABU29135.1  | Sequence 2 from patent   | (374) | 443 | 110.0 | 1.9e-21 |
| gi 10863180 gb AAG23924.1   | AF239828_1 ELI7.2 [Petro | (383) | 454 | 112.5 | 3.3e-22 | gi 11991241 gb AAG42259.1   | AF310155_1 FadX-1 [Calen | (374) | 443 | 110.0 | 1.9e-21 |
| gi 155295241 gb ABT50845.1  | Sequence 138315 from p   | (185) | 450 | 111.4 | 3.4e-22 | gi 134471100 gb AAK26632.1  | AF343064_1 fatty acid co | (374) | 443 | 110.0 | 1.9e-21 |
| gi 33766658 gb AAQ52861.1   | Sequence 15 from patent  | (383) | 453 | 112.2 | 3.9e-22 | gi 13275554 emb CAC34032.1  | unnamed protein produc   | (374) | 443 | 110.0 | 1.9e-21 |
| gi 155689135 gb ABU29145.1  | Sequence 15 from paten   | (383) | 453 | 112.2 | 3.9e-22 | gi 189704764 gb ACE16093.1  | Sequence 19 from paten   | (383) | 443 | 110.0 | 1.9e-21 |
| gi 3417601 gb AAC31698.1    | delta-12 fatty acid desa | (383) | 453 | 112.2 | 3.9e-22 | gi 189846857 gb ACE26355.1  | Sequence 19 from paten   | (383) | 443 | 110.0 | 1.9e-21 |
| gi 215697837 dbj BAG92030.1 | unnamed protein produ    | (390) | 453 | 112.2 | 4e-22   | gi 110623214 emb CAL24247.1 | unnamed protein produ    | (218) | 440 | 109.1 | 1.9e-21 |
| gi 113611002 dbj BAF21380.1 | Os07g0416900 [Oryza s    | (390) | 453 | 112.2 | 4e-22   | gi 110623212 emb CAL24246.1 | unnamed protein produ    | (218) | 440 | 109.1 | 1.9e-21 |
| gi 27261056 dbj BAC45170.1  | putative delta 12 olei   | (390) | 453 | 112.2 | 4e-22   | gi 155713303 gb ABU35459.1  | Sequence 20 from paten   | (387) | 443 | 110.0 | 1.9e-21 |
| gi 34600644 gb AAQ78501.1   | Sequence 4 from patent   | (374) | 452 | 112.0 | 4.5e-22 | gi 155689131 gb ABU29141.1  | Sequence 9 from patent   | (387) | 443 | 110.0 | 1.9e-21 |
| gi 10278516 emb CAC09645.1  | unnamed protein produc   | (374) | 452 | 112.0 | 4.5e-22 | gi 33766654 gb AAQ52857.1   | Sequence 9 from patent   | (387) | 443 | 110.0 | 1.9e-21 |
| gi 10863192 gb AAG23930.1   | AF239834_1 ELI7.9 [Petro | (376) | 452 | 112.0 | 4.5e-22 | gi 198444772 gb ACH88346.1  | omega-6 fatty acid des   | (173) | 438 | 108.6 | 2.2e-21 |
| gi 115392237 gb ABT96919.1  | delta-12 fatty acid de   | (381) | 452 | 112.0 | 4.6e-22 | gi 83702515 gb ABC41578.1   | endoplasmic reticulum 1  | (388) | 442 | 109.7 | 2.3e-21 |
| gi 55509203 gb AAV52834.1   | delta-12 fatty acid des  | (383) | 452 | 112.0 | 4.6e-22 | gi 31322141 gb AAO38035.1   | deltal2-fatty acid acet  | (326) | 441 | 109.5 | 2.3e-21 |
| gi 51556906 gb AAT72296.2   | microsomal omega-6-des   | (383) | 452 | 112.0 | 4.6e-22 | gi 107785182 gb ABF84062.1  | microsomal oleate desa   | (387) | 441 | 109.5 | 2.6e-21 |
| gi 10863184 gb AAG23926.1   | AF239830_1 ELI7.5 [Petro | (384) | 452 | 112.0 | 4.6e-22 | gi 31322137 gb AAO38033.1   | deltal2-fatty acid acet  | (324) | 440 | 109.2 | 2.7e-21 |
| gi 110623234 emb CAL24257.1 | unnamed protein produ    | (387) | 450 | 111.6 | 6.4e-22 | gi 148917610 emb CAO00496.1 | unnamed protein produ    | (407) | 441 | 109.5 | 2.8e-21 |
| gi 110623232 emb CAL24256.1 | unnamed protein produ    | (387) | 450 | 111.6 | 6.4e-22 | gi 148917612 emb CAO00497.1 | unnamed protein produ    | (407) | 441 | 109.5 | 2.8e-21 |
| gi 147819968 emb CAN73788.1 | hypothetical protein     | (366) | 449 | 111.3 | 7.1e-22 | gi 116672830 gb ABK15557.1  | bi-functional microsom   | (407) | 441 | 109.5 | 2.8e-21 |
| gi 147858117 emb CAN79670.1 | hypothetical protein     | (376) | 449 | 111.3 | 7.3e-22 | gi 189704770 gb ACE16099.1  | Sequence 34 from paten   | (383) | 440 | 109.3 | 3.1e-21 |
| gi 157337660 emb CAO22006.1 | unnamed protein produ    | (376) | 449 | 111.3 | 7.3e-22 | gi 27261181 gb AAN87573.1   | delta 12 oleic acid des  | (383) | 440 | 109.3 | 3.1e-21 |
| gi 34600650 gb AAQ78507.1   | Sequence 12 from patent  | (383) | 448 | 111.1 | 8.7e-22 | gi 189846863 gb ACE26361.1  | Sequence 34 from paten   | (383) | 440 | 109.3 | 3.1e-21 |
| gi 1054843 emb CAA63432.1   | D12 oleate desaturase [  | (383) | 448 | 111.1 | 8.7e-22 | gi 155295235 gb ABT50839.1  | Sequence 138309 from p   | (387) | 440 | 109.3 | 3.1e-21 |
| gi 48431267 gb AAT44123.1   | microsomal omega-6-des   | (362) | 447 | 110.9 | 9.7e-22 | gi 148917614 emb CAO00498.1 | unnamed protein produ    | (417) | 440 | 109.3 | 3.3e-21 |
| gi 10945375 gb AAG24521.1   | AF239835_1 fatty acid de | (383) | 447 | 110.9 | 1e-21   | gi 11991243 gb AAG42260.1   | AF310156_1 FadX-2 [Calen | (372) | 439 | 109.0 | 3.5e-21 |
| gi 110623228 emb CAL24254.1 | unnamed protein produ    | (387) | 447 | 110.9 | 1e-21   | gi 155689126 gb ABU29136.1  | Sequence 4 from patent   | (372) | 439 | 109.0 | 3.5e-21 |
| gi 59956944 dbj BAD89861.1  | microsomal omega-6 fat   | (387) | 447 | 110.9 | 1e-21   | gi 13275556 emb CAC34033.1  | unnamed protein produc   | (372) | 439 | 109.0 | 3.5e-21 |
| gi 110623230 emb CAL24255.1 | unnamed protein produ    | (387) | 447 | 110.9 | 1e-21   | gi 33766649 gb AAQ52852.1   | Sequence 4 from patent   | (372) | 439 | 109.0 | 3.5e-21 |
| gi 110623206 emb CAL24243.1 | unnamed protein produ    | (387) | 447 | 110.9 | 1e-21   | gi 83272391 gb ABC00769.1   | delta-12 fatty acid ace  | (375) | 439 | 109.0 | 3.5e-21 |
| gi 110623204 emb CAL24242.1 | unnamed protein produ    | (387) | 447 | 110.9 | 1e-21   | gi 11991460 emb CAA76158.2  | delta 12 fatty acid ac   | (375) | 439 | 109.0 | 3.5e-21 |
| gi 197111724 gb ACH43026.1  | omega-6 fatty acid des   | (387) | 447 | 110.9 | 1e-21   | gi 83272395 gb ABC00771.1   | delta-12 fatty acid des  | (377) | 439 | 109.0 | 3.6e-21 |
| gi 62358441 gb AAX78904.1   | fatty acid desaturase,   | (408) | 447 | 110.9 | 1.1e-21 | gi 2578033 emb CAA65744.1   | omega-6 desaturase [Gos  | (385) | 439 | 109.0 | 3.6e-21 |
| gi 33348439 gb AAQ15765.1   | fatty acid desaturase,   | (408) | 447 | 110.9 | 1.1e-21 | gi 91125663 gb ABE12611.1   | Sequence 4 from patent   | (385) | 439 | 109.0 | 3.6e-21 |
| gi 34551088 gb AAQ74969.1   | oleate desaturase [Tryp  | (408) | 447 | 110.9 | 1.1e-21 | gi 31322139 gb AAO38034.1   | deltal2-fatty acid acet  | (324) | 438 | 108.8 | 3.7e-21 |
| gi 29536058 emb CAD87607.1  | unnamed protein produc   | (374) | 445 | 110.4 | 1.4e-21 | gi 155102616 gb ABT03239.1  | Sequence 48 from paten   | (412) | 439 | 109.1 | 3.8e-21 |
| gi 28564443 emb CAD24672.1  | delta 12-acyl-lipid-co   | (374) | 445 | 110.4 | 1.4e-21 | gi 69061719 gb AAY99778.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 5994481 gb AAE19894.1    | Sequence 4 from patent U | (384) | 445 | 110.4 | 1.4e-21 | gi 134284835 gb ABO69519.1  | microsomal oleate desa   | (378) | 438 | 108.8 | 4.2e-21 |
| gi 45735853 dbj BAD12887.1  | putative delta-12 olea   | (388) | 445 | 110.4 | 1.4e-21 | gi 134284837 gb ABO69520.1  | microsomal oleate desa   | (378) | 438 | 108.8 | 4.2e-21 |
| gi 110623220 emb CAL24250.1 | unnamed protein produ    | (388) | 445 | 110.4 | 1.4e-21 | gi 60392566 gb AAX19389.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 42408040 dbj BAD09176.1  | putative delta-12 olea   | (388) | 445 | 110.4 | 1.4e-21 | gi 155689134 gb ABU29144.1  | Sequence 14 from paten   | (378) | 438 | 108.8 | 4.2e-21 |
| gi 113537458 dbj BAF09841.1 | Os02g0716500 [Oryza s    | (388) | 445 | 110.4 | 1.4e-21 | gi 60418976 gb AAX19895.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 125540897 gb EAY87292.1  | hypothetical protein O   | (388) | 445 | 110.4 | 1.4e-21 | gi 2290404 gb AAB65146.1    | delta-12 oleate desatura | (378) | 438 | 108.8 | 4.2e-21 |
| gi 125583461 gb EAF224392.1 | hypothetical protein O   | (388) | 445 | 110.4 | 1.4e-21 | gi 60418974 gb AAX19894.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 110623222 emb CAL24251.1 | unnamed protein produ    | (388) | 445 | 110.4 | 1.4e-21 | gi 33766657 gb AAQ52860.1   | Sequence 14 from patent  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 29536063 emb CAD87609.1  | unnamed protein produc   | (395) | 445 | 110.4 | 1.4e-21 | gi 60392568 gb AAX19390.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 28371825 gb AAO37753.1   | fatty acid conjugase [P  | (395) | 445 | 110.4 | 1.4e-21 | gi 69061718 gb AAY99777.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 197035436 gb ACH16336.1  | Sequence 12 from paten   | (395) | 445 | 110.4 | 1.4e-21 | gi 60392564 gb AAX19388.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 155356845 gb ABU12450.1  | Sequence 199919 from p   | (174) | 440 | 109.1 | 1.6e-21 | gi 18418649 gb AAL68981.1   | AF251842_1 delta-12 olea | (378) | 438 | 108.8 | 4.2e-21 |
| gi 194702722 gb ACF85445.1  | unknown [Zea mays]       | (382) | 444 | 110.2 | 1.6e-21 | gi 209967428 gb ACJ02341.1  | seed-specific oleoyl-p   | (378) | 438 | 108.8 | 4.2e-21 |
| gi 5994480 gb AAE19893.1    | Sequence 2 from patent U | (382) | 444 | 110.2 | 1.6e-21 | gi 60392570 gb AAX19391.1   | delta-12 oleate desatur  | (378) | 438 | 108.8 | 4.2e-21 |
| gi 31322133 gb AAO38031.1   | deltal2-fatty acid acet  | (382) | 444 | 110.2 | 1.6e-21 | gi 197111722 gb ACH43025.1  | omega-6 fatty acid des   | (387) | 438 | 108.8 | 4.3e-21 |
| gi 91125664 gb ABE12612.1   | Sequence 6 from patent   | (383) | 444 | 110.2 | 1.6e-21 | gi 168014166 gb ACA14461.1  | oleate desaturase [Car   | (283) | 436 | 108.3 | 4.5e-21 |
| gi 119655554 gb ABL86147.1  | delta-12 oleic acid de   | (383) | 444 | 110.2 | 1.6e-21 | gi 125558079 gb EAO33615.1  | hypothetical protein O   | (362) | 436 | 108.3 | 5.5e-21 |

|  |     |       |         |   |     |       |         |
|--|-----|-------|---------|---|-----|-------|---------|
| gi 113611003 dbj BAF21381.1  Os07g0417200 [Oryza s ( 362)  | 436 | 108.3 | 5.5e-21 | gi 91125594 gb ABE12594.1  Sequence 2 from patent ( 387)  | 427 | 106.3 | 2.4e-20 |
| gi 125599974 gb EA239550.1  hypothetical protein O ( 362)  | 436 | 108.3 | 5.5e-21 | gi 189846851 gb ACE26349.1  Sequence 13 from paten ( 387) | 427 | 106.3 | 2.4e-20 |
| gi 27261059 dbj BAC45173.1  putative delta 12 olei ( 362)  | 436 | 108.3 | 5.5e-21 | gi 155713302 gb ABU35458.1  Sequence 6 from patent ( 387) | 427 | 106.3 | 2.4e-20 |
| gi 18252115 gb AAL61826.1  putative delta12 acid d ( 255)  | 434 | 107.8 | 5.7e-21 | gi 189846876 gb ACE26374.1  Sequence 134 from pate ( 399) | 427 | 106.3 | 2.5e-20 |
| gi 155713305 gb ABU35446.1  Sequence 28 from paten ( 255)  | 434 | 107.8 | 5.7e-21 | gi 28371823 gb AAO37752.1  delta-12 oleate desatur ( 369) | 425 | 105.8 | 3.2e-20 |
| gi 168014138 gb ACA14460.1  oleate desaturase [Car ( 380)  | 436 | 108.4 | 5.8e-21 | gi 13443733 emb CAC34898.1  unnamed protein produc ( 377) | 425 | 105.8 | 3.3e-20 |
| gi 4530970 emb CAA03835.1  DELTA-12 DESATURASE [Co ( 382)  | 436 | 108.4 | 5.8e-21 | gi 6634080 emb CAB64256.1  (8,11)-linoleoyl desatu ( 377) | 425 | 105.8 | 3.3e-20 |
| gi 17225559 gb AAL37475.1 AF329635_1 delta-12 fatt ( 182)  | 432 | 107.3 | 5.9e-21 | gi 123201159 gb ABM72767.1  fatty acid desaturase, ( 375) | 423 | 105.4 | 4.5e-20 |
| gi 45272283 gb AAS57577.1  delta12-oleic acid desa ( 382)  | 435 | 108.1 | 6.8e-21 | gi 8980833 gb AAF82294.1  microsomal oleate desatu ( 379) | 422 | 105.2 | 5.3e-20 |
| gi 31322145 gb AAO38037.1  delta12-fatty acid acet ( 326)  | 434 | 107.9 | 6.9e-21 | gi 67090583 gb AAY67653.1  oleate desaturase [Arac ( 379) | 422 | 105.2 | 5.3e-20 |
| gi 60594769 gb AAX29989.1  microsomal omega-6-desa ( 379)  | 434 | 107.9 | 7.9e-21 | gi 75205885 gb ABA17989.1  Sequence 12 from patent ( 387) | 422 | 105.2 | 5.4e-20 |
| gi 115833234 gb ABJ480712.1  Sequence 6 from patent ( 379) | 434 | 107.9 | 7.9e-21 | gi 62789097 gb AAY07980.1  Sequence 12 from patent ( 387) | 422 | 105.2 | 5.4e-20 |
| gi 62789094 gb AAY07977.1  Sequence 6 from patent ( 379)   | 434 | 107.9 | 7.9e-21 | gi 21507261 gb AAM57796.1  Sequence 12 from patent ( 387) | 422 | 105.2 | 5.4e-20 |
| gi 21507257 gb AAM57793.1  Sequence 6 from patent ( 379)   | 434 | 107.9 | 7.9e-21 | gi 115833238 gb ABJ40715.1  Sequence 12 from paten ( 387) | 422 | 105.2 | 5.4e-20 |
| gi 75205882 gb ABA17986.1  Sequence 6 from patent ( 379)   | 434 | 107.9 | 7.9e-21 | gi 143073531 gb EDC62056.1  hypothetical protein G ( 271) | 419 | 104.4 | 6.4e-20 |
| gi 91125672 gb ABE12620.1  Sequence 33 from patent ( 387)  | 434 | 107.9 | 8e-21   | gi 8980835 gb AAF82295.1  microsomal oleate desatu ( 379) | 419 | 104.5 | 8.5e-20 |
| gi 155689127 gb ABU29137.1  Sequence 5 from patent ( 387)  | 434 | 107.9 | 8e-21   | gi 123960857 gb ABM75640.1  Fatty acid desaturase ( 405)  | 419 | 104.5 | 9e-20   |
| gi 34600651 gb AAQ87508.1  Sequence 13 from patent ( 387)  | 434 | 107.9 | 8e-21   | gi 31322143 gb AAC38036.1  delta12-fatty acid acet ( 326) | 417 | 104.0 | 1e-19   |
| gi 155713301 gb ABU35457.1  Sequence 5 from patent ( 387)  | 434 | 107.9 | 8e-21   | gi 27261183 gb AAN87574.1  delta 12 fatty acid con ( 386) | 417 | 104.0 | 1.2e-19 |
| gi 33766650 gb AAQ52853.1  Sequence 5 from patent ( 387)   | 434 | 107.9 | 8e-21   | gi 58578276 emb CAI48074.1  omega-6 fatty acid des ( 304) | 415 | 103.5 | 1.3e-19 |
| gi 59956942 dbj BAD89860.1  mocosomal omega-6 fat ( 387)   | 434 | 107.9 | 8e-21   | gi 189704778 gb ACE16107.1  Sequence 42 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 5994482 gb AAE19895.1  Sequence 5 from patent U ( 387)  | 434 | 107.9 | 8e-21   | gi 189704772 gb ACE16101.1  Sequence 36 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 904152 gb AAB00859.1  microsomal omega-6 desatu ( 387)  | 434 | 107.9 | 8e-21   | gi 189846871 gb ACE26369.1  Sequence 42 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 6063030 gb AAF03100.1 AF162199_1 oleate 12-hydr ( 189)  | 430 | 106.8 | 8.3e-21 | gi 189846865 gb ACE26363.1  Sequence 36 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 33766653 gb AAQ52856.1  Sequence 8 from patent ( 399)   | 430 | 107.0 | 1.5e-20 | gi 189704774 gb ACE16103.1  Sequence 38 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 155689130 gb ABU29140.1  Sequence 8 from patent ( 399)  | 430 | 107.0 | 1.5e-20 | gi 189846867 gb ACE26365.1  Sequence 38 from paten ( 377) | 416 | 103.8 | 1.4e-19 |
| gi 155713300 gb ABU35456.1  Sequence 4 from patent ( 399)  | 430 | 107.0 | 1.5e-20 | gi 2613051 gb AAB84262.1  omega-6 desaturase [Arac ( 379) | 416 | 103.8 | 1.4e-19 |
| gi 6224716 gb AAF05916.1 AF182521_1 delta-12 oleic ( 399)  | 430 | 107.0 | 1.5e-20 | gi 4092879 gb AAC99622.1  delta-12 desaturase [Bra ( 312) | 413 | 103.1 | 1.9e-19 |
| gi 60117056 gb AAX14399.1  oleate desaturase [Arac ( 379)  | 428 | 106.5 | 2e-20   | gi 137103080 gb EBS21930.1  hypothetical protein G ( 288) | 412 | 102.8 | 2e-19   |
| gi 121104181 gb ABM47430.1  delta-12 fatty acid de ( 379)  | 428 | 106.5 | 2e-20   | gi 143934227 gb EDH68469.1  hypothetical protein G ( 302) | 412 | 102.8 | 2.1e-19 |
| gi 71064149 gb AAZ22543.1  oleate desaturase [Arac ( 379)  | 428 | 106.5 | 2e-20   | gi 46392790 gb AAS91160.1  delta-12 desaturase-lik ( 121) | 406 | 101.2 | 2.6e-19 |
| gi 14572857 gb AAK67829.1  delta-12 fatty acid des ( 379)  | 428 | 106.5 | 2e-20   | gi 66734339 gb AAY53559.1  oleate desaturase [Arac ( 379) | 412 | 102.9 | 2.6e-19 |
| gi 121104183 gb ABM47431.1  delta-12 fatty acid de ( 379)  | 428 | 106.5 | 2e-20   | gi 83286879 gb ABC00770.1  delta-12 fatty acid des ( 382) | 412 | 102.9 | 2.6e-19 |
| gi 8980831 gb AAF82293.1  microsomal oleate desatu ( 379)  | 428 | 106.5 | 2e-20   | gi 78713359 gb ABB50536.1  Delta(12)-fatty acid de ( 391) | 410 | 102.4 | 3.6e-19 |
| gi 189846868 gb ACE26366.1  Sequence 39 from paten ( 387)  | 428 | 106.5 | 2.1e-20 | gi 157087398 gb ABV21586.1  fatty acid desaturase ( 385)  | 409 | 102.2 | 4.2e-19 |
| gi 189704773 gb ACE16102.1  Sequence 37 from paten ( 387)  | 428 | 106.5 | 2.1e-20 | gi 164636954 gb EDR01244.1  delta-12 fatty acid de ( 394) | 408 | 102.0 | 5e-19   |
| gi 189846866 gb ACE26364.1  Sequence 37 from paten ( 387)  | 428 | 106.5 | 2.1e-20 | gi 89305244 gb EAS03232.1  Fatty acid desaturase f ( 387) | 407 | 101.7 | 5.8e-19 |
| gi 189704775 gb ACE16104.1  Sequence 39 from paten ( 387)  | 428 | 106.5 | 2.1e-20 | gi 141832428 gb ECT55938.1  hypothetical protein G ( 283) | 405 | 101.2 | 6.1e-19 |
| gi 38426731 gb AAR20443.1  delta-12 desaturase [Sa ( 393)  | 428 | 106.5 | 2.1e-20 | gi 164638120 gb EDR02400.1  delta-12 fatty acid de ( 425) | 407 | 101.8 | 6.2e-19 |
| gi 155102610 gb ABT03233.1  Sequence 42 from paten ( 393)  | 428 | 106.5 | 2.1e-20 | gi 18252113 gb AAL61825.1  putative delta12 oleic ( 255)  | 404 | 101.0 | 6.5e-19 |
| gi 155102611 gb ABT03234.1  Sequence 43 from paten ( 393)  | 428 | 106.5 | 2.1e-20 | gi 155713306 gb ABU35462.1  Sequence 30 from paten ( 255) | 404 | 101.0 | 6.5e-19 |
| gi 72002083 gb AAZ57885.1  delta(12)-fatty acid de ( 405)  | 428 | 106.5 | 2.2e-20 | gi 78197948 gb ABB35713.1  Delta(12)-fatty acid de ( 381) | 406 | 101.5 | 6.7e-19 |
| gi 189702340 gb ACE14957.1  Sequence 2 from patent ( 378)  | 427 | 106.3 | 2.4e-20 | gi 14572859 gb AAK67830.1 AF248740_1 truncated del ( 164) | 401 | 100.2 | 7.3e-19 |
| gi 189846878 gb ACE26376.1  Sequence 136 from pate ( 378)  | 427 | 106.3 | 2.4e-20 | gi 197944847 gb ACH79976.1  truncated delta-12 fat ( 164) | 401 | 100.2 | 7.3e-19 |
| gi 38564776 gb AAR23815.1  delta 12 fatty acid epo ( 378)  | 427 | 106.3 | 2.4e-20 | gi 155689129 gb ABU35455.1  Sequence 7 from patent ( 383) | 404 | 101.0 | 9.2e-19 |
| gi 5994483 gb AAE19896.1  Sequence 6 from patent U ( 387)  | 427 | 106.3 | 2.4e-20 | gi 6224714 gb AAF05915.1  delta-12 oleic acid desa ( 383) | 404 | 101.0 | 9.2e-19 |
| gi 5955847 gb AAE07503.1  Sequence 42 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 155707470 gb ABU33119.1  Sequence 57 from paten ( 383) | 404 | 101.0 | 9.2e-19 |
| gi 2492222 gb AAB80358.1 I66169 Sequence 40 from p ( 387)  | 427 | 106.3 | 2.4e-20 | gi 155713299 gb ABU35455.1  Sequence 2 from patent ( 383) | 404 | 101.0 | 9.2e-19 |
| gi 5955845 gb AAE07501.1  Sequence 40 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 33766652 gb AAQ52855.1  Sequence 7 from patent ( 383)  | 404 | 101.0 | 9.2e-19 |
| gi 17909751 gb AAE82558.1  Sequence 5 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 155707469 gb ABU33118.1  Sequence 53 from paten ( 383) | 404 | 101.0 | 9.2e-19 |
| gi 189704758 gb AAZ57887.1  Sequence 13 from paten ( 387)  | 427 | 106.3 | 2.4e-20 | gi 143173998 gb EDD34949.1  hypothetical protein G ( 403) | 404 | 101.1 | 9.6e-19 |
| gi 722351 gb AAC49010.1  oleate 12-hydroxylase ( 387)      | 427 | 106.3 | 2.4e-20 | gi 138284618 gb EBY79340.1  hypothetical protein G ( 256) | 400 | 100.0 | 1.2e-18 |
| gi 155689128 gb ABU29138.1  Sequence 6 from patent ( 387)  | 427 | 106.3 | 2.4e-20 | gi 197035435 gb ACH16335.1  Sequence 1 from patent ( 387) | 402 | 100.6 | 1.3e-18 |
| gi 33766651 gb AAQ52854.1  Sequence 6 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 28371821 gb AAO37751.1  fatty acid conjugase [T ( 387) | 402 | 100.6 | 1.3e-18 |
| gi 34600652 gb AAQ78509.1  Sequence 14 from patent ( 387)  | 427 | 106.3 | 2.4e-20 | gi 86769314 gb ABD15171.1  truncated delta-12 fatt ( 135) | 396 | 99.0  | 1.4e-18 |
| gi 2492224 gb AAB80360.1 I66171 Sequence 42 from p ( 387)  | 427 | 106.3 | 2.4e-20 | gi 137357188 gb EBT64399.1  hypothetical protein G ( 289) | 400 | 100.1 | 1.4e-18 |
| gi 17918534 gb AAE85968.1  Sequence 5 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 139693867 gb ECG82230.1  hypothetical protein G ( 276) | 399 | 99.8  | 1.5e-18 |
| gi 76007348 gb ABA38262.1  Sequence 5 from patent ( 387)   | 427 | 106.3 | 2.4e-20 | gi 4530972 emb CAA03836.1  DELTA-12 DESATURASE [Co ( 338) | 399 | 99.9  | 1.8e-18 |

gi|135637216|gb|EBI91132.1| hypothetical protein G ( 350) 399 99.9 1.9e-18  
gi|336403061|emb|CAB19841.1| fatty acid desaturase, ( 392) 399 99.9 2.1e-18  
gi|332381921|gb|AAQ00259.1| Fatty acid desaturase [ ( 368) 397 99.4 2.7e-18  
gi|162690784|gb|EDQ77149.1| predicted protein [Phy ( 375) 397 99.4 2.7e-18  
gi|143761874|gb|EDG65538.1| hypothetical protein G ( 406) 397 99.5 2.9e-18  
gi|140346041|gb|ECL14042.1| hypothetical protein G ( 286) 395 98.9 3e-18  
gi|140706595|gb|ECM95975.1| hypothetical protein G ( 243) 394 98.7 3.1e-18  
gi|143151544|gb|EDD19097.1| hypothetical protein G ( 407) 396 99.2 3.4e-18  
gi|123199234|gb|ABM70875.1| fatty acid desaturase, ( 344) 395 99.0 3.5e-18  
gi|137847989|gb|EBW34483.1| hypothetical protein G ( 237) 393 98.4 3.5e-18  
gi|148524113|gb|ABQ81921.1| FAD2 [Brassica napus] ( 142) 390 97.6 3.7e-18  
gi|126543957|gb|ABO18199.1| fatty acid desaturase, ( 388) 395 99.0 3.9e-18  
gi|163772970|gb|EDQ86615.1| predicted protein [Mon ( 592) 397 99.6 4e-18  
gi|139197177|gb|ECE07780.1| hypothetical protein G ( 295) 393 98.5 4.2e-18  
gi|134995018|gb|EBE80676.1| hypothetical protein G ( 369) 394 98.8 4.3e-18  
gi|134976357|gb|EBE67982.1| hypothetical protein G ( 313) 393 98.5 4.4e-18  
gi|157388526|gb|ABV51231.1| fatty acid desaturase, ( 388) 394 98.8 4.5e-18  
gi|162692736|gb|EDQ79092.1| predicted protein [Phy ( 375) 393 98.5 5.2e-18  
gi|135754439|gb|EBJ63635.1| hypothetical protein G ( 324) 392 98.3 5.3e-18  
gi|155102615|gb|ABT03238.1| Sequence 47 from paten ( 333) 392 98.3 5.5e-18  
gi|135621037|gb|EBT81141.1| hypothetical protein G ( 362) 392 98.3 5.9e-18  
gi|158279015|gb|EDP04777.1| fatty acid desaturase, ( 383) 391 98.1 7.2e-18  
gi|136351801|gb|EBN58294.1| hypothetical protein G ( 263) 389 97.5 7.2e-18  
gi|142677465|gb|ECZ78385.1| hypothetical protein G ( 388) 391 98.1 7.3e-18  
gi|135681213|gb|EBJ18314.1| hypothetical protein G ( 271) 388 97.3 8.7e-18  
gi|143848454|gb|EDH06493.1| hypothetical protein G ( 401) 390 97.9 8.8e-18  
gi|138318032|gb|EBY94335.1| hypothetical protein G ( 275) 388 97.3 8.8e-18  
gi|136250130|gb|EBM89171.1| hypothetical protein G ( 406) 390 97.9 8.9e-18  
gi|33327237|gb|AAQ08982.1| delta-12 fatty acid des ( 233) 387 97.0 8.9e-18  
gi|143821886|gb|EDG87315.1| hypothetical protein G ( 237) 387 97.1 9.1e-18  
gi|145386893|gb|ABP65296.1| omega-6 fatty desatura ( 350) 389 97.6 9.2e-18  
gi|140859315|gb|ECN98726.1| hypothetical protein G ( 255) 386 96.8 1.1e-17  
gi|116787072|gb|ABK24364.1| unknown [Picea sitchen ( 375) 388 97.4 1.1e-17  
gi|17064784|gb|AAL32546.1| temperature-sensitive o ( 435) 388 97.4 1.3e-17  
gi|20259912|gb|AAM13303.1| temperature-sensitive o ( 435) 388 97.4 1.3e-17  
gi|143419214|gb|EDE85479.1| hypothetical protein G ( 406) 387 97.2 1.4e-17  
gi|137278133|gb|EBT20260.1| hypothetical protein G ( 250) 384 96.4 1.5e-17  
gi|143165925|gb|EDD29220.1| hypothetical protein G ( 327) 385 96.7 1.6e-17  
gi|59956948|dbj|BAD89863.1| microsomal omega-6 fat ( 337) 384 96.4 2e-17  
gi|144160439|gb|EDJ30569.1| hypothetical protein G ( 413) 385 96.7 2e-17  
gi|137689128|gb|EBV46724.1| hypothetical protein G ( 246) 382 95.9 2.1e-17  
gi|143784241|gb|EDG76662.1| hypothetical protein G ( 407) 384 96.5 2.3e-17  
gi|134798877|gb|EBD51227.1| hypothetical protein G ( 410) 383 96.3 2.7e-17  
gi|137783082|gb|EBV97124.1| hypothetical protein G ( 293) 381 95.7 2.8e-17  
gi|144165642|gb|EBL15614.1| hypothetical protein G ( 445) 383 96.3 2.9e-17  
gi|136361108|gb|EBN64632.1| hypothetical protein G ( 389) 382 96.0 3e-17  
gi|141897758|gb|ECU01814.1| hypothetical protein G ( 208) 378 95.0 3.4e-17  
gi|135985651|gb|EBL15614.1| hypothetical protein G ( 401) 381 95.8 3.6e-17  
gi|136755838|gb|EBJ19318.1| hypothetical protein G ( 402) 381 95.8 3.6e-17  
gi|143629305|gb|EDF94875.1| hypothetical protein G ( 406) 381 95.8 3.7e-17  
gi|45643653|gb|AAS72902.1| trans-delta12 oleic aci ( 380) 380 95.6 4.1e-17  
gi|33766655|gb|AAQ52858.1| Sequence 11 from patent ( 380) 380 95.6 4.1e-17  
gi|155689132|gb|ABU29142.1| Sequence 11 from paten ( 380) 380 95.6 4.1e-17  
gi|471093|dbj|BAA04504.1| plastid fatty acid desat ( 435) 380 95.6 4.6e-17  
gi|10178135|dbj|BAB11547.1| temperature-sensitive ( 435) 380 95.6 4.6e-17  
gi|516045|gb|AAA65621.1| omega-3 fatty acid desatu ( 435) 380 95.6 4.6e-17  
gi|497219|gb|AAB60302.1| chloroplast linoleate des ( 435) 380 95.6 4.6e-17  
gi|18700268|gb|AAL77744.1| AT5g05580/MOP10\_12 [Ara ( 435) 380 95.6 4.6e-17

gi|155090497|gb|ABS96096.1| Sequence 12 from paten ( 435) 380 95.6 4.6e-17  
gi|13605712|gb|AAK32849.1|AF361837\_1 AT5g05580/MOP ( 435) 380 95.6 4.6e-17  
gi|159888364|gb|ABX08578.1| Hypothetical protein P ( 180) 375 94.2 4.8e-17  
gi|143742469|gb|EDG55458.1| hypothetical protein G ( 226) 376 94.5 5e-17  
gi|137938899|gb|EBW86311.1| hypothetical protein G ( 243) 375 94.3 6.2e-17  
gi|141545071|gb|ECS26866.1| hypothetical protein G ( 306) 376 94.6 6.4e-17  
gi|143416270|gb|EDE83951.1| hypothetical protein G ( 240) 374 94.1 7.2e-17  
gi|143751027|gb|EDG60053.1| hypothetical protein G ( 386) 376 94.7 7.8e-17  
gi|111054802|gb|ABG88130.2| ER-type omega-3 fatty ( 395) 374 94.2 1.1e-16  
gi|17135417|dbj|BAB77963.1| omega-3 fatty acid des ( 359) 371 93.5 1.6e-16  
gi|4008402|emb|CAB05304.1| C. elegans protein W02A ( 376) 371 93.5 1.7e-16  
gi|62789973|gb|AAAY08322.1| Sequence 32 from patent ( 376) 371 93.5 1.7e-16  
gi|167279412|gb|ABZ32276.1| Sequence 6214 from pat ( 376) 371 93.5 1.7e-16  
gi|7546993|gb|AAF63745.1|AF240777\_1 delta 12 fatty ( 376) 371 93.5 1.7e-16  
gi|142200493|gb|ECW34394.1| hypothetical protein G ( 386) 371 93.5 1.7e-16  
gi|199601694|dbj|BAG70950.1| omega-3 fatty acid de ( 393) 371 93.5 1.7e-16  
gi|139519788|gb|ECF63159.1| hypothetical protein G ( 218) 367 92.5 2e-16  
gi|75704133|gb|ABA23809.1| Fatty acid desaturase [ ( 359) 369 93.0 2.2e-16  
gi|140863227|gb|ECO01526.1| hypothetical protein G ( 258) 366 92.3 2.7e-16  
gi|140667895|gb|ECM68585.1| hypothetical protein G ( 313) 366 92.3 3.2e-16  
gi|135781697|gb|EBJ80636.1| hypothetical protein G ( 309) 365 92.1 3.7e-16  
gi|139871797|gb|ECI04781.1| hypothetical protein G ( 154) 361 91.0 3.9e-16  
gi|140082397|gb|ECJ42398.1| hypothetical protein G ( 283) 364 91.8 4e-16  
gi|142362510|gb|ECS53443.1| hypothetical protein G ( 243) 362 91.3 4.9e-16  
gi|6503049|gb|AAF14564.1|AF181726\_1 delta-12 fatty ( 206) 361 91.1 5e-16  
gi|143131753|gb|EDD04630.1| hypothetical protein G ( 186) 360 90.8 5.3e-16  
gi|142755055|gb|EDA34189.1| hypothetical protein G ( 406) 363 91.7 6.4e-16  
gi|119214806|gb|ABL61262.1| chloroplast omega-3 de ( 445) 363 91.7 6.9e-16  
gi|155689133|gb|ABU29143.1| Sequence 13 from paten ( 375) 362 91.4 7e-16  
gi|45643651|gb|AAS72901.1| delta9 fatty acid conju ( 375) 362 91.4 7e-16  
gi|33766656|gb|AAQ52859.1| Sequence 13 from patent ( 375) 362 91.4 7e-16  
gi|140670558|gb|ECM70517.1| hypothetical protein G ( 320) 361 91.2 7.2e-16  
gi|3133289|gb|AAC16443.1| omega-3 desaturase [Pela ( 407) 362 91.5 7.5e-16  
gi|140541495|gb|ECM16089.1| hypothetical protein G ( 235) 359 90.7 7.6e-16  
gi|137615387|gb|EBV06629.1| hypothetical protein G ( 195) 358 90.4 7.6e-16  
gi|33640635|emb|CAE20424.1| fatty acid desaturase, ( 379) 361 91.2 8.2e-16  
gi|125661171|gb|ABN49521.1| fatty acid desaturase ( 389) 361 91.2 8.4e-16  
gi|50295115|gb|AAT72937.1| putative fatty acid des ( 389) 361 91.2 8.4e-16  
gi|112099617|gb|ABI10354.1| Sequence 15 from paten ( 351) 360 91.0 9.1e-16  
gi|45385976|gb|AAS59833.1| chloroplast omega-3 des ( 439) 361 91.3 9.3e-16  
gi|123964087|gb|ABM78843.1| fatty acid desaturase, ( 380) 360 91.0 9.7e-16  
gi|10050182|gb|AAE27089.1| Sequence 17 from patent ( 156) 355 89.6 1e-15  
gi|112099624|gb|ABI10360.1| Sequence 21 from paten ( 369) 359 90.8 1.1e-15  
gi|164521894|gb|ABY60736.1| microsomal omega-3 fat ( 371) 359 90.8 1.1e-15  
gi|118430556|gb|ABK91881.1| omega-3 fatty acid des ( 433) 359 90.8 1.3e-15  
gi|1694625|dbj|BAA11475.1| omega-3 fatty acid desa ( 441) 359 90.8 1.3e-15  
gi|21668486|dbj|BAC01274.1| plastid omega-3 fatty ( 441) 359 90.8 1.3e-15  
gi|62789972|gb|AAAY08321.1| Sequence 14 from patent ( 374) 358 90.5 1.3e-15  
gi|141233760|gb|ECQ54809.1| hypothetical protein G ( 176) 354 89.4 1.3e-15  
gi|138583392|gb|ECA60096.1| hypothetical protein G ( 162) 353 89.2 1.4e-15  
gi|137479245|gb|EBU32506.1| hypothetical protein G ( 237) 355 89.7 1.4e-15  
gi|167293297|gb|ABZ46161.1| Sequence 20099 from pa ( 347) 357 90.3 1.4e-15  
gi|186468713|gb|ACC84514.1| fatty acid desaturase ( 359) 357 90.3 1.5e-15  
gi|46849975|gb|AAT02410.1| chloroplast omega-3 fat ( 439) 358 90.6 1.5e-15  
gi|136982607|gb|EBR54408.1| hypothetical protein G ( 151) 352 88.9 1.6e-15  
gi|195612756|gb|ACG28208.1| omega-3 fatty acid des ( 408) 357 90.3 1.7e-15  
gi|141128901|gb|ECP82841.1| hypothetical protein G ( 234) 354 89.5 1.7e-15  
gi|135595996|gb|EBI65603.1| hypothetical protein G ( 166) 352 89.0 1.7e-15

gi|124423282|emb|CAK88077.1| unnamed protein produ ( 358) 356 90.1 1.7e-15  
gi|112099614|gb|ABI10351.1| Sequence 12 from paten ( 361) 356 90.1 1.7e-15  
gi|112099622|gb|ABI10358.1| Sequence 19 from paten ( 352) 355 89.8 2e-15  
gi|126633024|emb|CAM55477.1| unnamed protein produ ( 172) 351 88.8 2.1e-15  
gi|110084514|gb|ABG49414.1| chloroplast omega-3 fa ( 455) 356 90.1 2.1e-15  
gi|157351193|emb|CAO41380.1| unnamed protein produ ( 456) 356 90.1 2.1e-15  
gi|215700937|dbj|BAG92361.1| unnamed protein produ ( 385) 355 89.9 2.2e-15  
gi|76803810|gb|ABA55806.1| omega-3 fatty acid desa ( 385) 355 89.9 2.2e-15  
gi|77552800|gb|ABA95596.1| Omega-3 fatty acid desa ( 385) 355 89.9 2.2e-15  
gi|113648433|dbj|BAF28945.1| Os12g0104400 [Oryza s ( 385) 355 89.9 2.2e-15  
gi|5305302|gb|AAD41576.1|AF056565\_1 fatty acid des ( 163) 350 88.5 2.3e-15  
gi|870784|gb|AAA70334.1| omega-3 fatty acid desatu ( 447) 355 89.9 2.4e-15  
gi|112099620|gb|ABI10356.1| Sequence 17 from paten ( 377) 354 89.6 2.5e-15  
gi|125661167|gb|ABN49519.1| fatty acid desaturase ( 388) 354 89.6 2.5e-15  
gi|167292274|gb|ABZ45138.1| Sequence 19076 from pa ( 333) 353 89.4 2.6e-15  
gi|112099627|gb|ABI10362.1| Sequence 23 from paten ( 368) 353 89.4 2.9e-15  
gi|190613766|gb|ACE80931.1| omega-3 fatty acid des ( 445) 354 89.7 2.9e-15  
gi|91992438|gb|ABE72960.1| chloroplast omega-3 fat ( 455) 354 89.7 2.9e-15  
gi|414732|gb|AAA73511.1| linoleoyl desaturase ( 460) 354 89.7 2.9e-15  
gi|158307132|gb|ABW28749.1| omega-3 fatty acid des ( 353) 352 89.2 3.2e-15  
gi|126633508|emb|CAM55719.1| unnamed protein produ ( 437) 353 89.4 3.3e-15  
gi|4240385|gb|AAD13527.1| omega-3 fatty acid desat ( 437) 353 89.4 3.3e-15  
gi|76803815|gb|ABA55807.1| chloroplast omega-3 fat ( 438) 353 89.4 3.3e-15  
gi|116001285|emb|CAL49894.1| unnamed protein produ ( 363) 352 89.2 3.3e-15  
gi|162684238|gb|EDQ70642.1| predicted protein [Phy ( 445) 353 89.4 3.3e-15  
gi|137798840|gb|EBW06016.1| hypothetical protein G ( 213) 349 88.3 3.4e-15  
gi|1777376|dbj|BAA11397.1| w-3 fatty acid desatura ( 381) 352 89.2 3.4e-15  
gi|136237708|gb|EBM80780.1| hypothetical protein G ( 231) 349 88.4 3.6e-15  
gi|199601696|dbj|BAG70949.1| omega-3 fatty acid de ( 390) 351 88.9 4.1e-15  
gi|171700755|gb|ACB53736.1| fatty acid desaturase ( 349) 350 88.7 4.4e-15  
gi|126633530|emb|CAM55730.1| unnamed protein produ ( 429) 351 89.0 4.5e-15  
gi|125535471|gb|EAY81959.1| hypothetical protein O ( 355) 350 88.7 4.5e-15  
gi|125578209|gb|EAA21935.1| hypothetical protein O ( 355) 350 88.7 4.5e-15  
gi|112099641|gb|ABI10373.1| Sequence 34 from paten ( 356) 350 88.7 4.5e-15  
gi|3550663|emb|CAA07638.1| w-3 desaturase [Solanum ( 431) 351 89.0 4.5e-15  
gi|113735150|dbj|BAF30809.1| omega-3-desaturase [E ( 434) 351 89.0 4.5e-15  
gi|125575925|gb|EAA217147.1| hypothetical protein O ( 362) 350 88.7 4.5e-15  
gi|126632956|emb|CAM55443.1| unnamed protein produ ( 443) 351 89.0 4.6e-15  
gi|195627062|gb|ACG35361.1| omega-3 fatty acid des ( 443) 351 89.0 4.6e-15  
gi|2446998|dbj|BAA22441.1| fatty acid desaturase [ ( 443) 351 89.0 4.6e-15  
gi|140727720|gb|ECN10408.1| hypothetical protein G ( 294) 348 88.2 5.2e-15  
gi|110168938|gb|ABG53478.1| Delta(12)-fatty acid d ( 357) 349 88.5 5.2e-15  
gi|126633418|emb|CAM55674.1| unnamed protein produ ( 432) 350 88.7 5.2e-15  
gi|141315775|gb|ECQ99409.1| hypothetical protein G ( 203) 346 87.6 5.3e-15  
gi|134989727|gb|ABE77060.1| hypothetical protein G ( 204) 346 87.6 5.3e-15  
gi|110725975|gb|ABG88131.1| chloroplast omega-3 fa ( 436) 350 88.7 5.3e-15  
gi|141072386|gb|ECP43211.1| hypothetical protein G ( 252) 347 87.9 5.4e-15  
gi|139790774|gb|ECH48637.1| hypothetical protein G ( 255) 347 87.9 5.4e-15  
gi|138713287|gb|ECB49397.1| hypothetical protein G ( 211) 346 87.7 5.4e-15  
gi|112099616|gb|ABI10353.1| Sequence 14 from paten ( 375) 349 88.5 5.5e-15  
gi|167294087|gb|ABG24695.1| Sequence 20889 from pa ( 318) 348 88.2 5.6e-15  
gi|5101874|emb|CAB45155.1| omega-3 desaturase [Ver ( 387) 349 88.5 5.6e-15  
gi|164683927|gb|AAC98967.2| omega-3 fatty acid des ( 387) 349 88.5 5.6e-15  
gi|10050178|gb|AAE27085.1| Sequence 9 from patent ( 404) 349 88.5 5.8e-15  
gi|143646242|gb|EDG04607.1| hypothetical protein G ( 405) 349 88.5 5.8e-15  
gi|136026861|gb|EBL41763.1| hypothetical protein G ( 131) 343 86.9 5.9e-15  
gi|143564685|gb|EDF66080.1| hypothetical protein G ( 284) 347 88.0 5.9e-15  
gi|7378667|emb|CAB85467.1| chloroplast omega-3 fat ( 429) 349 88.5 6.1e-15

gi|112099618|gb|ABI10355.1| Sequence 16 from paten ( 358) 348 88.2 6.2e-15  
gi|32479366|gb|AAP82169.2| omega-3 fatty acid desa ( 435) 349 88.5 6.2e-15  
gi|32442202|gb|AAP82170.1| omega-3 fatty acid desa ( 435) 349 88.5 6.2e-15  
gi|112099635|gb|ABI10369.1| Sequence 30 from paten ( 362) 348 88.2 6.2e-15  
gi|33638914|emb|CAE07211.1| fatty acid desaturase, ( 382) 348 88.3 6.5e-15  
gi|43213399|gb|AAD15744.1| omega-3 fatty acid desat ( 391) 348 88.3 6.6e-15  
gi|136003587|gb|EBL26327.1| hypothetical protein G ( 242) 345 87.5 7.1e-15  
gi|23345023|gb|AAN17503.1| omega-3 fatty acid desa ( 444) 348 88.3 7.4e-15  
gi|11691870|emb|CAC18722.1| putative plastidial w- ( 449) 348 88.3 7.4e-15  
gi|140855361|gb|ECN95873.1| hypothetical protein G ( 211) 344 87.2 7.5e-15  
gi|162135888|gb|ABX82798.1| microsomal omega-3 fat ( 377) 347 88.0 7.5e-15  
gi|141430291|gb|ECR77185.1| hypothetical protein G ( 219) 344 87.2 7.7e-15  
gi|143454309|gb|EDF05453.1| hypothetical protein G ( 269) 345 87.5 7.8e-15  
gi|142738209|gb|EDA21987.1| hypothetical protein G ( 245) 344 87.2 8.4e-15  
gi|156219508|gb|EDD040389.1| predicted protein [Nem ( 361) 346 87.8 8.5e-15  
gi|112099637|gb|ABI10370.1| Sequence 31 from paten ( 369) 346 87.8 8.7e-15  
gi|139079064|gb|ECD26660.1| hypothetical protein G ( 235) 343 87.0 9.6e-15  
gi|699390|gb|AAA86690.1| delta-15 lineoyl desatura ( 436) 346 87.8 1e-14  
gi|112099623|gb|ABI10359.1| Sequence 20 from paten ( 363) 345 87.6 1e-14  
gi|156900674|gb|ABU96743.1| chloroplast omega-3 fa ( 446) 346 87.8 1e-14  
gi|139550120|gb|ECF83668.1| hypothetical protein G ( 149) 340 86.2 1.1e-14  
gi|74275357|gb|ABA02172.1| fatty acid desaturase 3 ( 392) 345 87.6 1.1e-14  
gi|145036529|gb|ABP30234.1| Sequence 8 from patent ( 392) 345 87.6 1.1e-14  
gi|135295560|gb|EBG69212.1| hypothetical protein G ( 153) 340 86.2 1.1e-14  
gi|196191998|gb|EDX86962.1| Fatty acid desaturase ( 351) 344 87.3 1.1e-14  
gi|541653|dbj|BAA03106.1| omega-3-desaturase [Arab ( 446) 345 87.6 1.2e-14  
gi|10050176|gb|AAE27083.1| Sequence 5 from patent ( 446) 345 87.6 1.2e-14  
gi|12321881|gb|AAG50977.1|AC073395\_19 omega-3 fatt ( 446) 345 87.6 1.2e-14  
gi|468434|dbj|BAA05040.1| plastid fatty acid desat ( 446) 345 87.6 1.2e-14  
gi|6016681|gb|AAF01508.1|AC009991\_4 omega-3 fatty ( 446) 345 87.6 1.2e-14  
gi|155090496|gb|ABS96095.1| Sequence 10 from paten ( 446) 345 87.6 1.2e-14  
gi|408481|gb|AAA61773.1| omega-3 fatty acid desatu ( 446) 345 87.6 1.2e-14  
gi|154813792|gb|ABS86961.1| chloroplast omega-3 fa ( 451) 345 87.6 1.2e-14  
gi|118489331|gb|ABK96470.1| unknown [Populus trich ( 452) 345 87.6 1.2e-14  
gi|160334210|gb|ABX24525.1| omega-3 fatty acid des ( 377) 344 87.3 1.2e-14  
gi|88697616|gb|ABD48788.1| endoplasmic reticulum 1 ( 383) 344 87.3 1.2e-14  
gi|195635609|gb|ACG37273.1| omega-3 fatty acid des ( 384) 344 87.3 1.2e-14  
gi|189308128|gb|ACD86948.1| fatty acyl desaturase ( 226) 341 86.5 1.3e-14  
gi|162684694|gb|EDQ71094.1| predicted protein [Phy ( 441) 344 87.4 1.4e-14  
gi|141069087|gb|ECP40955.1| hypothetical protein G ( 257) 341 86.6 1.4e-14  
gi|137359343|gb|EBT65630.1| hypothetical protein G ( 213) 340 86.3 1.4e-14  
gi|10050177|gb|AAE27084.1| Sequence 7 from patent ( 378) 343 87.1 1.4e-14  
gi|144576748|gb|ABO94816.1| predicted protein [Ost ( 387) 343 87.1 1.5e-14  
gi|155306965|gb|ABT62569.1| Sequence 150039 from p ( 164) 338 85.8 1.6e-14  
gi|162680781|gb|EDQ71204.1| predicted protein [Phy ( 431) 343 87.1 1.6e-14  
gi|158593298|gb|EDP31893.1| Fatty acid desaturase ( 376) 342 86.9 1.7e-14  
gi|140220184|gb|ECK34119.1| hypothetical protein G ( 151) 337 85.5 1.7e-14  
gi|50508696|gb|BAD31200.1| putative omega-3 fatty ( 327) 341 86.6 1.7e-14  
gi|33146890|dbj|BAC79888.1| putative omega-3 fatty ( 327) 341 86.6 1.7e-14  
gi|14787742|emb|CAC44309.1| C. elegans protein Y67 ( 402) 342 86.9 1.8e-14  
gi|125585886|gb|EAA226550.1| hypothetical protein O ( 402) 342 86.9 1.8e-14  
gi|140832739|gb|ECN82765.1| hypothetical protein G ( 285) 340 86.4 1.8e-14  
gi|124422313|emb|CAK87150.1| unnamed protein produ ( 358) 341 86.6 1.9e-14  
gi|108707600|gb|ABF95395.1| Omega-3 fatty acid des ( 458) 342 86.9 2e-14  
gi|140870390|gb|ECO06627.1| hypothetical protein G ( 150) 336 85.3 2e-14  
gi|50508695|dbj|BAD31199.1| putative omega-3 fatty ( 413) 341 86.7 2.1e-14  
gi|57014072|gb|AAW32557.1| FAD8 [Oryza sativa (jap ( 413) 341 86.7 2.1e-14  
gi|113612269|dbj|BAF22647.1| Os07g0693800 [Oryza s ( 413) 341 86.7 2.1e-14

gi|29837190|dbj|BAC75572.1| putative omega-3 fatty ( 413) 341 86.7 2.1e-14  
gi|215704382|dbj|BAG93816.1| unnamed protein produ ( 413) 341 86.7 2.1e-14  
gi|88606639|dbj|BAE79786.1| plastid omega-3 fatty ( 413) 341 86.7 2.1e-14  
gi|125601618|gb|EAZ41194.1| hypothetical protein O ( 413) 341 86.7 2.1e-14  
gi|88606635|dbj|BAE79784.1| plastid omega-3 fatty ( 413) 341 86.7 2.1e-14  
gi|215692568|dbj|BAG87988.1| unnamed protein produ ( 413) 341 86.7 2.1e-14  
gi|125992363|emb|CAM35355.1| unnamed protein produ ( 413) 341 86.7 2.1e-14  
gi|6752907|gb|AAF27933.1|AF222989\_1 omega-3 fatty ( 438) 341 86.7 2.2e-14  
gi|88606633|dbj|BAE79783.1| plastid omega-3 fatty ( 459) 341 86.7 2.3e-14  
gi|88606637|dbj|BAE79785.1| plastid omega-3 fatty ( 459) 341 86.7 2.3e-14  
gi|142738149|gb|EDA21944.1| hypothetical protein G ( 397) 340 86.4 2.4e-14  
gi|159025986|emb|CAO87893.1| unnamed protein produ ( 273) 338 85.9 2.4e-14  
gi|118430554|gb|ABK91880.1| omega-3 fatty acid des ( 449) 340 86.5 2.6e-14  
gi|141991317|gb|ECU67281.1| hypothetical protein G ( 280) 337 85.7 2.9e-14  
gi|159029904|emb|CAO90958.1| unnamed protein produ ( 345) 338 85.9 2.9e-14  
gi|166088576|dbj|BAG03284.1| omega 3 acyl-lipid de ( 350) 338 86.0 2.9e-14  
gi|112099634|gb|ABI10368.1| Sequence 29 from paten ( 354) 338 86.0 3e-14  
gi|196177223|gb|EDX72231.1| Fatty acid desaturase ( 358) 338 86.0 3e-14  
gi|116055853|emb|CAL57938.1| delta 12 fatty acid d ( 442) 339 86.2 3.1e-14  
gi|112099633|gb|ABI10367.1| Sequence 28 from paten ( 366) 338 86.0 3.1e-14  
gi|47028567|gb|AAT09135.1| omega-3 fatty acid desa ( 383) 338 86.0 3.2e-14  
gi|14124415|gb|AAE60611.1| Sequence 2 from patent ( 402) 338 86.0 3.3e-14  
gi|67581027|gb|AAY69963.1| Sequence 2 from patent ( 402) 338 86.0 3.3e-14  
gi|27278515|gb|AAN93253.1| Sequence 2 from patent ( 402) 338 86.0 3.3e-14  
gi|91145259|gb|ABE21477.1| Sequence 30 from patent ( 402) 338 86.0 3.3e-14  
gi|784870|gb|AAA67369.1| fatty acid desaturase ( 402) 338 86.0 3.3e-14  
gi|155102614|gb|ABT03237.1| Sequence 46 from paten ( 409) 338 86.0 3.4e-14  
gi|142522375|gb|ECY68815.1| hypothetical protein G ( 307) 336 85.5 3.6e-14  
gi|112099632|gb|ABI10366.1| Sequence 27 from paten ( 373) 337 85.7 3.6e-14  
gi|10050180|gb|AAE27087.1| Sequence 13 from patent ( 453) 338 86.0 3.7e-14  
gi|408792|gb|AAA61776.1| omega-3 fatty acid desatu ( 453) 338 86.0 3.7e-14  
gi|27902573|gb|AAO24263.1| microsomal omega-3-fatt ( 376) 337 85.7 3.7e-14  
gi|144583207|gb|ABP01320.1| microsomal omega three ( 376) 337 85.7 3.7e-14  
gi|34787276|dbj|BAC87757.1| microsomal omega-3 fat ( 376) 337 85.7 3.7e-14  
gi|157004277|gb|ABV00680.1| microsomal omega-3 fat ( 376) 337 85.7 3.7e-14  
gi|118430552|gb|ABK91879.1| omega-3 fatty acid des ( 386) 337 85.7 3.7e-14  
gi|74275359|gb|ABA02173.1| fatty acid desaturase 3 ( 391) 337 85.7 3.8e-14  
gi|2447000|dbj|BAA22442.1| fatty acid desaturase [ ( 398) 337 85.8 3.8e-14  
gi|2446996|dbj|BAA22440.1| fatty acid desaturase [ ( 398) 337 85.8 3.8e-14  
gi|147848500|emb|CAK24051.1| Fatty acid desaturase ( 331) 336 85.5 3.9e-14  
gi|169884460|gb|ACA98173.1| omega-3 acyl-lipid des ( 350) 336 85.5 4e-14  
gi|2197199|gb|AAB61352.1| omega-3 desaturase [Syn ( 350) 336 85.5 4e-14  
gi|41581197|emb|CAF18425.1| omega 3 acyl-lipid des ( 359) 336 85.5 4.1e-14  
gi|112099630|gb|ABI10365.1| Sequence 26 from paten ( 360) 336 85.5 4.1e-14  
gi|143598148|gb|EDF79303.1| hypothetical protein G ( 321) 335 85.2 4.4e-14  
gi|112099621|gb|ABI10357.1| Sequence 18 from paten ( 362) 335 85.3 4.9e-14  
gi|1786066|gb|AAB72241.1| omega-3 fatty acid desat ( 438) 336 85.5 4.9e-14  
gi|214028096|gb|ABS87969.2| omega-3 fatty acid des ( 372) 335 85.3 5e-14  
gi|122937801|gb|ABM68629.1| omega-3 fatty acid des ( 372) 335 85.3 5e-14  
gi|213053824|gb|ACJ39217.1| fatty acid desaturase ( 452) 336 85.6 5e-14  
gi|140220232|gb|ECK34154.1| hypothetical protein G ( 257) 333 84.7 5e-14  
gi|190898694|gb|ACE97860.1| fatty acid desaturase ( 197) 331 84.2 5.5e-14  
gi|46981930|gb|AAN62759.2| omega-3 fatty acid desa ( 435) 335 85.3 5.7e-14  
gi|1754795|gb|AAB39387.1| omega-3 fatty acid desat ( 438) 335 85.3 5.7e-14  
gi|164521896|gb|ABY60737.1| chloroplast omega-3 fa ( 451) 335 85.3 5.8e-14  
gi|154354069|gb|ABS76144.1| chloroplast omega-3 fa ( 453) 335 85.3 5.9e-14  
gi|112099643|gb|ABI10374.1| Sequence 35 from paten ( 329) 333 84.8 6.2e-14  
gi|190898688|gb|ACE97857.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14

gi|190898702|gb|ACE97864.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898664|gb|ACE97845.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
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gi|190898654|gb|ACE97840.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898652|gb|ACE97839.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898662|gb|ACE97844.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898666|gb|ACE97846.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898674|gb|ACE97850.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898692|gb|ACE97859.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898710|gb|ACE97868.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|190898708|gb|ACE97867.1| fatty acid desaturase ( 197) 330 84.0 6.5e-14  
gi|138639648|gb|ECA97978.1| hypothetical protein G ( 291) 332 84.5 6.5e-14  
gi|88606667|dbj|BAE79800.1| omega-3-desaturase [Cy ( 435) 334 85.1 6.6e-14  
gi|110565255|emb|CAL23344.1| unnamed protein produ ( 361) 333 84.8 6.7e-14  
gi|60220822|emb|CAI58910.1| unnamed protein produc ( 361) 333 84.8 6.7e-14  
gi|76059322|emb|CAJ30855.1| unnamed protein produc ( 361) 333 84.8 6.7e-14  
gi|126633856|emb|CAM55884.1| unnamed protein produ ( 361) 333 84.8 6.7e-14  
gi|140244294|gb|ECK50946.1| hypothetical protein G ( 300) 332 84.5 6.7e-14  
gi|143426844|gb|EDE89318.1| hypothetical protein G ( 338) 332 84.6 7.4e-14  
gi|190898670|gb|ACE97848.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898696|gb|ACE97861.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898678|gb|ACE97852.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898704|gb|ACE97865.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898684|gb|ACE97855.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898720|gb|ACE97873.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898700|gb|ACE97863.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898712|gb|ACE97869.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898726|gb|ACE97876.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898724|gb|ACE97875.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898716|gb|ACE97871.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898658|gb|ACE97842.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898676|gb|ACE97851.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898706|gb|ACE97866.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898690|gb|ACE97858.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898698|gb|ACE97862.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|144582279|gb|ABP00334.1| predicted protein [Ost ( 362) 331 84.4 9.2e-14  
gi|190898682|gb|ACE97854.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898718|gb|ACE97872.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898680|gb|ACE97853.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|190898714|gb|ACE97870.1| fatty acid desaturase ( 197) 329 83.8 7.6e-14  
gi|62789971|gb|AAY08320.1| Sequence 13 from patent ( 368) 332 84.6 7.9e-14  
gi|23345021|gb|AAN17502.1| omega-3 fatty acid desa ( 455) 333 84.9 8.1e-14  
gi|190898686|gb|ACE97856.1| fatty acid desaturase ( 197) 328 83.5 8.9e-14  
gi|112099628|gb|ABI10363.1| Sequence 24 from paten ( 353) 331 84.4 9e-14  
gi|144582279|gb|ABP00334.1| predicted protein [Ost ( 362) 331 84.4 9.2e-14  
gi|147845818|emb|CAN80104.1| hypothetical protein ( 452) 332 84.6 9.4e-14  
gi|157356207|emb|CAO50134.1| unnamed protein produ ( 452) 332 84.6 9.4e-14  
gi|167148|gb|AAA32994.1| linoleic acid desaturase ( 383) 331 84.4 9.6e-14  
gi|112099604|gb|ABI10344.1| Sequence 3 from patent ( 383) 331 84.4 9.6e-14  
gi|155090495|gb|ABS96094.1| Sequence 2 from patent ( 383) 331 84.4 9.6e-14  
gi|112099611|gb|ABI10349.1| Sequence 10 from paten ( 383) 331 84.4 9.6e-14  
gi|27278516|gb|AAN93254.1| Sequence 8 from patent ( 383) 331 84.4 9.6e-14  
gi|408483|gb|AAA61778.1| omega-3 fatty acid desatu ( 386) 331 84.4 9.7e-14  
gi|3420053|gb|AAC31854.1| omega-3 fatty acid desat ( 386) 331 84.4 9.7e-14  
gi|112099605|gb|ABI10345.1| Sequence 4 from patent ( 386) 331 84.4 9.7e-14  
gi|10050175|gb|AAE27082.1| Sequence 2 from patent ( 386) 331 84.4 9.7e-14  
gi|20465899|gb|AAM20102.1| putative omega-3 fatty ( 386) 331 84.4 9.7e-14  
gi|471091|dbj|BAA04505.1| fatty acid desaturase [A ( 386) 331 84.4 9.7e-14

gi|17381020|gb|AAL36322.1| putative omega-3 fatty ( 386) 331 84.4 9.7e-14  
gi|112099613|gb|ABI10350.1| Sequence 11 from paten ( 386) 331 84.4 9.7e-14  
gi|1197795|dbj|BAA05514.1| microsomal omega-3 fatt ( 386) 331 84.4 9.7e-14  
gi|62789969|gb|AAY08318.1| Sequence 11 from patent ( 389) 331 84.4 9.7e-14  
gi|164521898|gb|ABY60738.1| omega-3 fatty acid des ( 454) 331 84.4 1.1e-13  
gi|113735152|dbj|BAF30810.1| omega-3-desaturase [E ( 340) 329 83.9 1.2e-13  
gi|137646878|gb|EBV23208.1| hypothetical protein G ( 240) 327 83.3 1.2e-13  
gi|154813794|gb|ABS86962.1| omega-3 fatty acid des ( 386) 329 83.9 1.3e-13  
gi|62789968|gb|AAY08317.1| Sequence 10 from patent ( 387) 329 83.9 1.3e-13  
gi|125559707|gb|EAO25243.1| hypothetical protein O ( 250) 326 83.1 1.5e-13  
gi|32306982|gb|AAP78965.1| omega-3 fatty acid desa ( 443) 329 84.0 1.5e-13  
gi|45385321|gb|AAM77643.2|AF517831\_1 chloroplast o ( 449) 329 84.0 1.5e-13  
gi|10050179|gb|AAE27086.1| Sequence 11 from patent ( 380) 328 83.7 1.5e-13  
gi|34787274|dbj|BAC82756.1| microsomal omega-3 fatt ( 380) 328 83.7 1.5e-13  
gi|157004275|gb|ABV00679.1| microsomal omega-3 fat ( 380) 328 83.7 1.5e-13  
gi|408794|gb|AAA61777.1| omega-3 fatty acid desatu ( 380) 328 83.7 1.5e-13  
gi|27902575|gb|AAO24264.1| microsomal omega-3-fatt ( 380) 328 83.7 1.5e-13  
gi|3157460|dbj|BAA28358.1| omega-3 fatty acid desa ( 383) 328 83.7 1.5e-13  
gi|139522922|gb|ECF65248.1| hypothetical protein G ( 318) 327 83.4 1.6e-13  
gi|190898668|gb|ACE97847.1| fatty acid desaturase ( 197) 324 82.6 1.7e-13  
gi|112099640|gb|ABI10372.1| Sequence 33 from paten ( 349) 327 83.4 1.7e-13  
gi|116061930|emb|CAL52648.1| delta 12 fatty acid d ( 442) 328 83.7 1.7e-13  
gi|162696041|gb|EDQ827382.1| predicted protein [Phy ( 380) 327 83.5 1.8e-13  
gi|94959240|gb|ABF47510.1| truncated delta-12 fatt ( 107) 320 81.6 1.9e-13  
gi|190898672|gb|ACE97849.1| fatty acid desaturase ( 197) 323 82.4 2e-13  
gi|190898660|gb|ACE97843.1| fatty acid desaturase ( 197) 323 82.4 2e-13  
gi|162677068|gb|EDQ63543.1| predicted protein [Phy ( 364) 326 83.2 2e-13  
gi|14488094|gb|AAK63867.1|AF389295\_1 AT3g11170/F9F ( 446) 327 83.5 2.1e-13  
gi|20908084|gb|AAM26725.1| AT3g11170/F9F8\_4 [Arabi ( 446) 327 83.5 2.1e-13  
gi|23345025|gb|AAN17504.1| microsomal omega-3 fatt ( 386) 326 83.2 2.1e-13  
gi|60220802|emb|CAI58900.1| unnamed protein produc ( 361) 325 83.0 2.4e-13  
gi|160830400|emb|CAP40270.1| unnamed protein produc ( 361) 325 83.0 2.4e-13  
gi|76059302|emb|CAJ30845.1| unnamed protein produc ( 361) 325 83.0 2.4e-13  
gi|76059411|emb|CAJ30870.1| unnamed protein produc ( 361) 325 83.0 2.4e-13  
gi|126633852|emb|CAM55882.1| unnamed protein produc ( 361) 325 83.0 2.4e-13  
gi|141620606|gb|ECS58022.1| hypothetical protein G ( 212) 322 82.2 2.4e-13  
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gi|21668465|dbj|BAA07785.3| plastid omega-3 fatty ( 381) 325 83.0 2.5e-13  
gi|112099638|gb|ABI10371.1| Sequence 32 from paten ( 348) 324 82.8 2.7e-13  
gi|112099629|gb|ABI10364.1| Sequence 25 from paten ( 356) 323 82.5 3.2e-13  
gi|138600399|gb|ECA72044.1| hypothetical protein G ( 306) 322 82.3 3.3e-13  
gi|62789966|gb|AAY08315.1| Sequence 8 from patent ( 397) 323 82.6 3.5e-13  
gi|138259907|gb|EBY63590.1| hypothetical protein G ( 235) 320 81.7 3.6e-13  
gi|136011793|gb|EBL31511.1| hypothetical protein G ( 197) 319 81.5 3.7e-13  
gi|53952283|gb|AAV02280.1| Sequence 14237 from pat ( 110) 315 80.4 4.3e-13  
gi|27902577|gb|AAO24265.1| microsomal omega-3-fatt ( 380) 321 82.1 4.7e-13  
gi|188509991|gb|ACD56667.1| omega-3 fatty acid des ( 380) 321 82.1 4.7e-13  
gi|15430570|dbj|BAB18135.2| microsomal omega-3 fat ( 380) 321 82.1 4.7e-13  
gi|189014684|gb|ACD69578.1| omega-3 fatty acid des ( 380) 321 82.1 4.7e-13  
gi|287562|dbj|BAA03306.1| hypothetical protein [Vi ( 380) 321 82.1 4.7e-13  
gi|157004279|gb|ABV00681.1| microsomal omega-3 fat ( 380) 321 82.1 4.7e-13  
gi|113548266|dbj|BAF11709.1| Os03g0290300 [Oryza s ( 276) 319 81.6 4.9e-13  
gi|62789967|gb|AAY08316.1| Sequence 9 from patent ( 413) 321 82.1 5e-13  
gi|158283651|gb|EDP09401.1| chloroplast glycerolip ( 418) 321 82.1 5e-13  
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gi|5305298|gb|AAD41574.1|AF056562\_1 unknown [Brass ( 169) 316 80.8 5.2e-13  
gi|187424523|gb|ACD03846.1| omega-3 fatty acid des ( 436) 321 82.1 5.2e-13  
gi|3452132|gb|AAC32756.1| putative oleate 12-desat ( 181) 316 80.8 5.5e-13

gi|5305300|gb|AAD41575.1|AF056563\_1 unknown [Brass ( 165) 315 80.5 6e-13  
gi|5305760|gb|AAD41802.1|AF140057\_1 unknown [Brass ( 165) 315 80.5 6e-13  
gi|112099615|gb|ABI10352.1| Sequence 13 from paten ( 359) 319 81.6 6.1e-13  
gi|155362912|gb|ABU18517.1| Sequence 205986 from p ( 162) 314 80.3 6.9e-13  
gi|5305756|gb|AAD41801.1|AF140055\_1 unknown [Brass ( 166) 314 80.3 7.1e-13  
gi|408492|gb|AAA61775.1| omega-3 fatty acid desatu ( 377) 318 81.4 7.4e-13  
gi|91125673|gb|ABE12621.1| Sequence 34 from patent ( 377) 318 81.4 7.4e-13  
gi|112099602|gb|ABI10343.1| Sequence 2 from patent ( 377) 318 81.4 7.4e-13  
gi|112099610|gb|ABI10348.1| Sequence 9 from patent ( 377) 318 81.4 7.4e-13  
gi|49355342|gb|AAT65204.1| omega-3 fatty acid desa ( 378) 318 81.4 7.4e-13  
gi|112099601|gb|ABI10342.1| Sequence 1 from patent ( 380) 318 81.4 7.5e-13  
gi|62319074|dbj|BAD94215.1| omega-3 fatty acid des ( 206) 314 80.3 8.4e-13  
gi|197111726|gb|ACH43027.1| microsomal omega-3 fat ( 380) 317 81.2 8.8e-13  
gi|189014682|gb|ACD69577.1| omega-3 fatty acid des ( 380) 317 81.2 8.8e-13  
gi|137943424|gb|EBW88866.1| hypothetical protein G ( 332) 316 80.9 9.2e-13  
gi|600598|dbj|BAA02924.1| delta 15 desaturase [Syn ( 359) 316 80.9 9.8e-13  
gi|167275943|gb|ABZ28807.1| Sequence 2745 from pat ( 359) 316 80.9 9.8e-13  
gi|1653388|dbj|BAA18302.1| delta 15 desaturase [Sy ( 359) 316 80.9 9.8e-13  
gi|139034378|gb|ECC95336.1| hypothetical protein G ( 151) 311 79.6 1e-12  
gi|193299732|gb|ABU54076.2| omega 3 desaturase O3D ( 434) 315 80.7 1.3e-12  
gi|112099644|gb|ABI10375.1| Sequence 36 from paten ( 329) 313 80.2 1.5e-12  
gi|136211167|gb|EBM62811.1| hypothetical protein G ( 189) 310 79.4 1.5e-12  
gi|155707466|gb|ABU33115.1| Sequence 6 from patent ( 358) 313 80.2 1.6e-12  
gi|182916824|gb|ACC10859.1| Sequence 4 from patent ( 358) 313 80.2 1.6e-12  
gi|145025096|gb|ABP24253.1| Sequence 44 from paten ( 358) 313 80.2 1.6e-12  
gi|155070722|gb|ABS91067.1| Sequence 54 from paten ( 358) 313 80.2 1.6e-12  
gi|118822322|gb|ABL20744.1| Sequence 4 from patent ( 358) 313 80.2 1.6e-12  
gi|144998359|gb|ABP16932.1| Sequence 28 from paten ( 358) 313 80.2 1.6e-12  
gi|160830402|emb|CAP40271.1| unnamed protein produ ( 358) 313 80.2 1.6e-12  
gi|38426733|gb|AAR20444.1| omega-3 fatty acid desa ( 358) 313 80.2 1.6e-12  
gi|155102608|gb|ABT03231.1| Sequence 26 from paten ( 358) 313 80.2 1.6e-12  
gi|155102613|gb|ABT03236.1| Sequence 45 from paten ( 358) 313 80.2 1.6e-12  
gi|112099647|gb|ABI10377.1| Sequence 38 from paten ( 251) 311 79.7 1.6e-12  
gi|157347450|emb|CAO18087.1| unnamed protein produ ( 368) 313 80.3 1.6e-12  
gi|6466197|gb|AAF12821.1|AF200717\_1 omega-3 fatty ( 451) 314 80.5 1.6e-12  
gi|2446994|dbj|BAA22439.1| fatty acid desaturase [ ( 262) 311 79.7 1.7e-12  
gi|162686680|gb|EDQ73067.1| predicted protein [Phy ( 383) 313 80.3 1.7e-12  
gi|138707809|gb|ECB45598.1| hypothetical protein G ( 261) 310 79.5 1.9e-12  
gi|15811218|dbj|BAD08867.1| omega-3 fatty acid desa ( 302) 310 79.5 2.2e-12  
gi|139690344|gb|ECG79948.1| hypothetical protein G ( 252) 309 79.2 2.2e-12  
gi|159888363|gb|ABX08577.1| Hypothetical protein P ( 141) 305 78.2 2.6e-12  
gi|112099664|gb|ABI10390.1| Sequence 69 from paten ( 382) 310 79.6 2.7e-12  
gi|141437295|gb|ECR82204.1| hypothetical protein G ( 177) 305 78.3 3.1e-12  
gi|140939661|gb|ECO53532.1| hypothetical protein G ( 194) 305 78.3 3.3e-12  
gi|5305296|gb|AAD41573.1|AF056561\_1 unknown [Brass ( 163) 304 78.0 3.4e-12  
gi|141373649|gb|ECR37601.1| hypothetical protein G ( 177) 304 78.0 3.6e-12  
gi|134996864|gb|EBE81927.1| hypothetical protein G ( 171) 303 77.8 4.1e-12  
gi|61162223|dbj|BAD36812.2| microsomal omega-3 fat ( 381) 307 78.9 4.3e-12  
gi|143457875|gb|EDF08039.1| hypothetical protein G ( 165) 302 77.5 4.7e-12  
gi|138993987|gb|ECC71640.1| hypothetical protein G ( 172) 302 77.6 4.9e-12  
gi|141025864|gb|ECP12238.1| hypothetical protein G ( 174) 302 77.6 4.9e-12  
gi|135975138|gb|EBL08479.1| hypothetical protein G ( 176) 302 77.6 5e-12  
gi|38564809|gb|AAR23833.1| delta-12 oleate desatur ( 419) 306 78.7 5.4e-12  
gi|76007352|gb|ABA38266.1| Sequence 9 from patent ( 302) 304 78.1 5.7e-12  
gi|17918538|gb|AAE85972.1| Sequence 9 from patent ( 302) 304 78.1 5.7e-12  
gi|17909755|gb|AAE82562.1| Sequence 9 from patent ( 302) 304 78.1 5.7e-12  
gi|141619566|gb|ECS57491.1| hypothetical protein G ( 186) 301 77.3 6.1e-12  
gi|110739886|dbj|BAF01848.1| omega-3 fatty acid de ( 225) 302 77.6 6.1e-12

gi|141103895|gb|ECP65231.1| hypothetical protein G ( 123) 296 76.1 9.5e-12  
gi|137018838|gb|EBR74904.1| hypothetical protein G ( 153) 296 76.2 1.1e-11  
gi|139880277|gb|ECI09568.1| hypothetical protein G ( 178) 296 76.2 1.3e-11  
gi|136984566|gb|EBR55532.1| hypothetical protein G ( 195) 295 76.0 1.6e-11  
gi|112099625|gb|ABI10361.1| Sequence 22 from paten ( 351) 298 76.8 1.7e-11  
gi|599592|dbj|BAA0515.1| microsomal omega-3 acid ( 379) 298 76.8 1.8e-11  
gi|21668484|dbj|BAC01273.1| microsomal omega-3 fat ( 379) 298 76.8 1.8e-11  
gi|137790912|gb|EBW01485.1| hypothetical protein G ( 170) 292 75.3 2.3e-11  
gi|136351800|gb|EBN58293.1| hypothetical protein G ( 255) 294 75.8 2.4e-11  
gi|155311457|gb|ABT67061.1| Sequence 154531 from p ( 145) 290 74.8 2.8e-11  
gi|155327923|gb|ABT83527.1| Sequence 170997 from p ( 138) 289 74.5 3.2e-11  
gi|154354067|gb|ABS76143.1| chloroplast omega-3 fa ( 248) 292 75.4 3.2e-11  
gi|17918537|gb|AAE85971.1| Sequence 8 from patent ( 309) 292 75.4 3.9e-11  
gi|17909754|gb|AAE82561.1| Sequence 8 from patent ( 309) 292 75.4 3.9e-11  
gi|76007351|gb|ABA38265.1| Sequence 8 from patent ( 309) 292 75.4 3.9e-11  
gi|157337097|emb|CAO21443.1| unnamed protein produ ( 329) 292 75.4 4.1e-11  
gi|155367161|gb|ABU22766.1| Sequence 210235 from p ( 138) 287 74.1 4.3e-11  
gi|144600655|gb|ABP01593.1| microsomal omega-3 fat ( 105) 285 73.6 4.7e-11  
gi|134987868|gb|EBE75801.1| hypothetical protein G ( 171) 286 73.9 6.1e-11  
gi|139880513|gb|ECI09723.1| hypothetical protein G ( 157) 285 73.7 6.6e-11  
gi|5305764|gb|AAD41803.1|AF140059\_1 fatty acid des ( 177) 284 73.5 8.6e-11  
gi|141600306|gb|ECS52576.1| hypothetical protein G ( 173) 283 73.2 9.9e-11  
gi|157337096|emb|CAO21442.1| unnamed protein produ ( 329) 286 74.1 1.1e-10  
gi|172402595|dbj|BAB78717.1| omega-3 fatty acid des ( 418) 287 74.3 1.1e-10  
gi|210028781|emb|CAR94991.1| unnamed protein produ ( 115) 280 72.4 1.1e-10  
gi|138224268|gb|EBY53079.1| hypothetical protein G ( 139) 281 72.7 1.1e-10  
gi|17224294|gb|AAL36934.1|AF213482\_1 delta-15 desa ( 390) 285 73.9 1.4e-10  
gi|6900316|emb|CAB71341.1| omega-3 fatty acid desa ( 164) 280 72.5 1.5e-10  
gi|137799086|gb|EBW06156.1| hypothetical protein G ( 136) 278 72.0 1.8e-10  
gi|155363868|gb|ABU19473.1| Sequence 206942 from p ( 169) 279 72.3 1.8e-10  
gi|141600305|gb|ECS52575.1| hypothetical protein G ( 123) 277 71.8 1.9e-10  
gi|155334563|gb|ABT90167.1| Sequence 177637 from p ( 137) 277 71.8 2.1e-10  
gi|139974114|gb|ECI74768.1| hypothetical protein G ( 122) 276 71.5 2.2e-10  
gi|139351796|gb|ECE59526.1| hypothetical protein G ( 135) 276 71.6 2.4e-10  
gi|144600653|gb|ABP01592.1| microsomal omega-3 fat ( 105) 274 71.0 2.7e-10  
gi|125543438|gb|EAY89577.1| hypothetical protein O ( 387) 279 72.5 3.6e-10  
gi|140139588|gb|ECJ80227.1| hypothetical protein G ( 140) 273 70.9 4e-10  
gi|5305752|gb|AAD41800.1|AF140053\_1 unknown [Brass ( 157) 273 70.9 4.4e-10  
gi|112099645|gb|ABI10376.1| Sequence 37 from paten ( 321) 272 70.9 9.5e-10  
gi|179185401|gb|AAE85974.1| Sequence 11 from patent ( 224) 270 70.3 9.6e-10  
gi|62789096|gb|AAY07979.1| Sequence 10 from patent ( 224) 270 70.3 9.6e-10  
gi|115833236|gb|ABJ40714.1| Sequence 10 from paten ( 224) 270 70.3 9.6e-10  
gi|215072601|gb|AAM57795.1| Sequence 10 from patent ( 224) 270 70.3 9.6e-10  
gi|17909757|gb|AAE82564.1| Sequence 11 from patent ( 224) 270 70.3 9.6e-10  
gi|5305884|gb|ABA17988.1| Sequence 10 from patent ( 224) 270 70.3 9.6e-10  
gi|76007354|gb|ABA38268.1| Sequence 11 from patent ( 224) 270 70.3 9.6e-10  
gi|408490|gb|AAA61774.1| omega-3 fatty acid desatu ( 329) 272 70.9 9.7e-10  
gi|140855362|gb|ECN95874.1| hypothetical protein G ( 136) 265 69.1 1.4e-09  
gi|5305308|gb|AAD41579.1|AF056568\_1 unknown [Brass ( 106) 262 68.3 1.8e-09  
gi|5305306|gb|AAD41578.1|AF056567\_1 unknown [Brass ( 104) 261 68.1 2.1e-09  
gi|5305304|gb|AAD41577.1|AF056566\_1 unknown [Brass ( 108) 261 68.1 2.2e-09  
gi|112099663|gb|ABI10389.1| Sequence 68 from paten ( 379) 264 69.1 3.9e-09  
gi|112099666|gb|ABI10391.1| Sequence 70 from paten ( 384) 262 68.6 5.4e-09  
gi|140873904|gb|ECO09092.1| hypothetical protein G ( 227) 259 67.8 5.5e-09  
gi|144600657|gb|ABP01594.1| microsomal omega-3 fat ( 105) 254 66.5 6.4e-09  
gi|134135879|gb|ABO56993.1| fatty acid desaturase ( 365) 260 68.1 7e-09  
gi|142490019|gb|ECY45889.1| hypothetical protein G ( 103) 253 66.2 7.4e-09  
gi|137372058|gb|EBT72798.1| hypothetical protein G ( 137) 254 66.5 8e-09

gi|167018792|gb|ABZ05366.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018790|gb|ABZ05365.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018864|gb|ABZ05402.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018728|gb|ABZ05334.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018722|gb|ABZ05331.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018778|gb|ABZ05359.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018696|gb|ABZ05318.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018826|gb|ABZ05383.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018724|gb|ABZ05332.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018846|gb|ABZ05393.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018762|gb|ABZ05351.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018760|gb|ABZ05350.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018690|gb|ABZ05315.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018756|gb|ABZ05348.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018768|gb|ABZ05354.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018738|gb|ABZ05339.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018698|gb|ABZ05319.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018794|gb|ABZ05367.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018832|gb|ABZ05386.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
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gi|167018830|gb|ABZ05350.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018862|gb|ABZ05401.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018776|gb|ABZ05358.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018700|gb|ABZ05320.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
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gi|167018802|gb|ABZ05371.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018740|gb|ABZ05340.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018718|gb|ABZ05329.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018858|gb|ABZ05399.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
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gi|167018744|gb|ABZ05342.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018758|gb|ABZ05349.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018716|gb|ABZ05328.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018732|gb|ABZ05336.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018766|gb|ABZ05353.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018774|gb|ABZ05357.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018808|gb|ABZ05374.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018828|gb|ABZ05384.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018810|gb|ABZ05375.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018806|gb|ABZ05373.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018848|gb|ABZ05394.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018838|gb|ABZ05389.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018806|gb|ABZ05311.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018704|gb|ABZ05322.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018804|gb|ABZ05372.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018788|gb|ABZ05364.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018784|gb|ABZ05362.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018764|gb|ABZ05352.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018856|gb|ABZ05398.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018798|gb|ABZ05369.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018824|gb|ABZ05382.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018730|gb|ABZ05335.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018840|gb|ABZ05390.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018816|gb|ABZ05378.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018860|gb|ABZ05400.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09  
gi|167018726|gb|ABZ05333.1| fatty acid desaturase ( 118) 253 66.3 8.3e-09

|                             |                           |        |     |      |         |                             |                           |        |     |      |         |
|-----------------------------|---------------------------|--------|-----|------|---------|-----------------------------|---------------------------|--------|-----|------|---------|
| gi 167018772 gb ABZ05356.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 167018818 gb ABZ05379.1  | fatty acid desaturase     | ( 111) | 217 | 58.0 | 2.4e-06 |
| gi 167018710 gb ABZ05325.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 50261903 gb AAT72504.1   | AT4G30950 [Arabidopsis    | ( 203) | 220 | 58.9 | 2.4e-06 |
| gi 167018742 gb ABZ05341.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 167018822 gb ABZ05381.1  | fatty acid desaturase     | ( 110) | 216 | 57.8 | 2.7e-06 |
| gi 167018786 gb ABZ05363.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 33634986 emb CAE20972.1  | Fatty acid desaturase,    | ( 361) | 221 | 59.2 | 3.4e-06 |
| gi 167018708 gb ABZ05324.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 488509 dbj BAA02921.1    | delta 12 desaturase [Syn  | ( 349) | 220 | 59.0 | 3.8e-06 |
| gi 167018836 gb ABZ05388.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 2696717 dbj BAA23881.1   | chloroplast w6 desatura   | ( 424) | 221 | 59.3 | 3.8e-06 |
| gi 167018782 gb ABZ05361.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 158277870 gb EDP03637.1  | omega-6-FAD, chloropla    | ( 424) | 221 | 59.3 | 3.8e-06 |
| gi 167018680 gb ABZ05310.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 194342553 gb EDX23519.1  | fatty acid desaturase     | ( 367) | 219 | 58.8 | 4.7e-06 |
| gi 167018702 gb ABZ05321.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 111055893 gb EAT77013.1  | hypothetical protein S    | ( 374) | 219 | 58.8 | 4.7e-06 |
| gi 167018754 gb ABZ05347.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 141139091 gb ECP89709.1  | hypothetical protein G    | ( 108) | 212 | 56.9 | 5.1e-06 |
| gi 167018688 gb ABZ05314.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 76059320 emb CAJ30854.1  | unnamed protein produc    | ( 418) | 219 | 58.8 | 5.2e-06 |
| gi 167018686 gb ABZ05313.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 126633854 emb CAM55883.1 | unnamed protein produ     | ( 418) | 219 | 58.8 | 5.2e-06 |
| gi 167018748 gb ABZ05344.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 60220820 emb CAI58909.1  | unnamed protein produc    | ( 418) | 219 | 58.8 | 5.2e-06 |
| gi 167018780 gb ABZ05360.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 17135418 dbj BAB77964.1  | phosphatidylcholine de    | ( 350) | 218 | 58.5 | 5.3e-06 |
| gi 167018736 gb ABZ05338.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 493225 dbj BAA03435.1    | fatty-acid desaturase [A  | ( 350) | 218 | 58.5 | 5.3e-06 |
| gi 167018868 gb ABZ05404.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 167292275 gb ABZ45139.1  | Sequence 19077 from pa    | ( 350) | 218 | 58.5 | 5.3e-06 |
| gi 167018720 gb ABZ05330.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 75704134 gb ABA23810.1   | Fatty acid desaturase [   | ( 350) | 218 | 58.5 | 5.3e-06 |
| gi 167018684 gb ABZ05312.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 1653254 dbj BAA18169.1   | fatty acid desaturase [   | ( 351) | 217 | 58.3 | 6.2e-06 |
| gi 167018866 gb ABZ05403.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 40652 emb CAA37584.1     | unnamed protein product [ | ( 351) | 217 | 58.3 | 6.2e-06 |
| gi 167018694 gb ABZ05317.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 167275936 gb ABZ28800.1  | Sequence 2738 from pat    | ( 351) | 217 | 58.3 | 6.2e-06 |
| gi 167018750 gb ABZ05345.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 108863908 gb ABA91057.2  | Omega-3 fatty acid des    | ( 415) | 217 | 58.4 | 7.1e-06 |
| gi 167018854 gb ABZ05397.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 138773117 gb ECB81856.1  | hypothetical protein G    | ( 111) | 210 | 56.4 | 7.1e-06 |
| gi 167018752 gb ABZ05346.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 137634104 gb EBV16995.1  | hypothetical protein G    | ( 153) | 211 | 56.7 | 8e-06   |
| gi 167018706 gb ABZ05323.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 137012142 gb EBR71172.1  | hypothetical protein G    | ( 125) | 209 | 56.2 | 9.2e-06 |
| gi 167018852 gb ABZ05396.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 159028367 emb CAO87265.1 | unnamed protein produ     | ( 346) | 214 | 57.6 | 9.8e-06 |
| gi 167018870 gb ABZ05405.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 141103894 gb ECP65230.1  | hypothetical protein G    | ( 133) | 208 | 56.0 | 1.1e-05 |
| gi 167018844 gb ABZ05392.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 166090471 dbj BAG05179.1 | delta 12 acyl-lipid d     | ( 346) | 213 | 57.4 | 1.1e-05 |
| gi 167018812 gb ABZ05376.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 41581195 emb CAF18424.1  | delta 12 acyl-lipid de    | ( 350) | 213 | 57.4 | 1.2e-05 |
| gi 167018746 gb ABZ05343.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 143683191 gb EDG25391.1  | hypothetical protein G    | ( 274) | 211 | 56.9 | 1.3e-05 |
| gi 167018734 gb ABZ05337.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 118487416 gb ABK95536.1  | unknown [Populus trich    | ( 444) | 213 | 57.5 | 1.4e-05 |
| gi 167018820 gb ABZ05380.1  | fatty acid desaturase     | ( 118) | 253 | 66.3 | 8.3e-09 | gi 149390715 gb ABR25375.1  | omega 6 fatty acid des    | ( 79)  | 203 | 54.8 | 1.6e-05 |
| gi 155289548 gb ABT45152.1  | Sequence 132622 from p    | ( 224) | 250 | 65.7 | 2.3e-08 | gi 54873456 gb AAV41001.1   | chloroplast fatty acid    | ( 443) | 211 | 57.0 | 1.9e-05 |
| gi 62789970 gb AAY08319.1   | Sequence 12 from patent   | ( 289) | 251 | 66.0 | 2.4e-08 | gi 55772330 dbj BAD70771.1  | fatty acid desaturase     | ( 345) | 209 | 56.5 | 2.2e-05 |
| gi 138003596 gb EBX22343.1  | hypothetical protein G    | ( 103) | 244 | 64.2 | 3.1e-08 | gi 46196514 gb AAS80930.1   | omega-(3) fatty acid de   | ( 345) | 209 | 56.5 | 2.2e-05 |
| gi 162669532 gb EDQ56117.1  | predicted protein [Phy    | ( 173) | 244 | 64.3 | 4.8e-08 | gi 35214308 dbj BAC91676.1  | delta 12 acyl-lipid de    | ( 355) | 209 | 56.5 | 2.2e-05 |
| gi 167018692 gb ABZ05316.1  | fatty acid desaturase     | ( 118) | 241 | 63.5 | 5.5e-08 | gi 42408692 dbj BAD09911.1  | putative Omega-6 fatty    | ( 414) | 209 | 56.5 | 2.5e-05 |
| gi 155102612 gb ABT03235.1  | Sequence 44 from paten    | ( 359) | 246 | 64.9 | 6.4e-08 | gi 42408677 dbj BAD09897.1  | putative Omega-6 fatty    | ( 414) | 209 | 56.5 | 2.5e-05 |
| gi 167018714 gb ABZ05327.1  | fatty acid desaturase     | ( 117) | 240 | 63.3 | 6.5e-08 | gi 167293298 gb ABZ46162.1  | Sequence 20100 from pa    | ( 347) | 208 | 56.3 | 2.5e-05 |
| gi 169887016 gb ACB00730.1  | phosphatidylcholine de    | ( 347) | 245 | 64.7 | 7.3e-08 | gi 186468714 gb ACC84515.1  | fatty acid desaturase     | ( 353) | 208 | 56.3 | 2.6e-05 |
| gi 6649528 gb AAF21445.1    | U36388_2 delta-12 desatur | ( 347) | 245 | 64.7 | 7.3e-08 | gi 196176135 gb EDX71152.1  | Fatty acid desaturase     | ( 354) | 208 | 56.3 | 2.6e-05 |
| gi 488511 dbj BAA02922.1    | delta_12 desaturase [Syn  | ( 347) | 245 | 64.7 | 7.3e-08 | gi 58013371 gb AAW63039.1   | plastidial delta-12 ole   | ( 443) | 209 | 56.5 | 2.7e-05 |
| gi 147847464 gb CAK23015.1  | Fatty acid desaturase     | ( 354) | 245 | 64.7 | 7.4e-08 | gi 155090528 gb ABS96125.1  | Sequence 72 from paten    | ( 418) | 206 | 55.8 | 4.1e-05 |
| gi 140312354 gb ECK90461.1  | hypothetical protein G    | ( 118) | 238 | 62.8 | 8.9e-08 | gi 493068 gb AAA92800.1     | chloroplast omega-6 fatty | ( 418) | 206 | 55.8 | 4.1e-05 |
| gi 134412622 gb EBB20102.1  | hypothetical protein G    | ( 120) | 237 | 62.6 | 1.1e-07 | gi 623344 emb CAA55121.1    | n-6 fatty acid desaturas  | ( 447) | 206 | 55.9 | 4.3e-05 |
| gi 34600646 gb AAQ78503.1   | Sequence 8 from patent    | ( 59)  | 233 | 61.5 | 1.1e-07 | gi 14813796 gb AAK73979.1   | chloroplast delta-12 f    | ( 447) | 206 | 55.9 | 4.3e-05 |
| gi 10278520 emb CAC09647.1  | unnamed protein produc    | ( 59)  | 233 | 61.5 | 1.1e-07 | gi 114384177 gb ABI73993.1  | omega-6 fatty acid des    | ( 447) | 206 | 55.9 | 4.3e-05 |
| gi 137892068 gb EBW59749.1  | hypothetical protein G    | ( 117) | 233 | 61.7 | 2e-07   | gi 7269997 emb CAB79813.1   | chloroplast omega-6 fat   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 186469984 gb ACW85610.1  | delta 12 desaturase [A    | ( 350) | 238 | 63.1 | 2.2e-07 | gi 15010640 gb AAK73979.1   | AT4g30950/F6I18_140 [Ar   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 805064 emb CAA60415.1    | delta 12 desaturase [Art  | ( 351) | 238 | 63.1 | 2.2e-07 | gi 2980771 emb CAA18198.1   | chloroplast omega-6 fat   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 147851166 emb CAK28660.1 | Fatty acid desaturase     | ( 351) | 237 | 62.9 | 2.6e-07 | gi 16604360 gb AAL24186.1   | AT4g30950/F6I18_140 [Ar   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 141492535 gb ECS05464.1  | hypothetical protein G    | ( 161) | 229 | 60.9 | 4.8e-07 | gi 18958032 gb AAL79589.1   | AT4g30950/F6I18_140 [Ar   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 155289549 gb ABT45153.1  | Sequence 132623 from p    | ( 328) | 232 | 61.7 | 5.4e-07 | gi 16604468 gb AAL24240.1   | AT4g30950/F6I18_140 [Ar   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 35213192 dbj BAC90564.1  | delta 12 acyl-lipid de    | ( 352) | 231 | 61.5 | 6.7e-07 | gi 21593581 gb AAM65548.1   | chloroplast omega-6 fat   | ( 448) | 206 | 55.9 | 4.3e-05 |
| gi 7381157 gb AAF61413.1    | AF134896_1 delta 12 desat | ( 352) | 231 | 61.5 | 6.7e-07 | gi 142830407 gb EDA90356.1  | hypothetical protein G    | ( 380) | 205 | 55.6 | 4.4e-05 |
| gi 3452135 gb AAC32757.1    | putative oleate 12-desat  | ( 161) | 225 | 60.0 | 9.1e-07 | gi 140563764 gb ECM22629.1  | hypothetical protein G    | ( 95)  | 197 | 53.4 | 4.9e-05 |
| gi 143452461 gb EDF04111.1  | hypothetical protein G    | ( 127) | 223 | 59.4 | 1e-06   | gi 196191947 gb EDX86911.1  | Fatty acid desaturase     | ( 346) | 203 | 55.1 | 5.6e-05 |
| gi 123963403 gb ABM78159.1  | Fatty acid desaturase,    | ( 361) | 228 | 60.8 | 1.1e-06 | gi 136641202 gb EBP45594.1  | hypothetical protein G    | ( 287) | 201 | 54.6 | 6.6e-05 |
| gi 138327289 gb EBY99311.1  | hypothetical protein G    | ( 118) | 219 | 58.5 | 1.8e-06 | gi 5821436 dbj BAA83822.1   | chloroplast w6 desatura   | ( 421) | 203 | 55.2 | 6.6e-05 |



|                             |                          |        |     |      |         |                             |                           |        |     |      |         |
|-----------------------------|--------------------------|--------|-----|------|---------|-----------------------------|---------------------------|--------|-----|------|---------|
| gi 156900672 gb ABU96742.1  | chloroplast omega-6 fa   | ( 440) | 203 | 55.2 | 6.8e-05 | gi 154358245 gb ABS79146.1  | At4g30950-like protein    | ( 111) | 184 | 50.5 | 0.00044 |
| gi 142370756 gb ECX58803.1  | hypothetical protein G   | ( 116) | 195 | 53.0 | 8e-05   | gi 171699545 gb ACBS2526.1  | fatty acid desaturase     | ( 349) | 190 | 52.1 | 0.00044 |
| gi 167018834 gb ABZ05387.1  | fatty acid desaturase    | ( 102) | 193 | 52.5 | 9.8e-05 | gi 154358193 gb ABS79120.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 167018842 gb ABZ05391.1  | fatty acid desaturase    | ( 102) | 193 | 52.5 | 9.8e-05 | gi 154358187 gb ABS79117.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 112099608 gb ABI10347.1  | Sequence 6 from patent   | ( 217) | 196 | 53.4 | 0.00011 | gi 154358195 gb ABS79121.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 112099662 gb ABI10388.1  | Sequence 64 from paten   | ( 218) | 196 | 53.4 | 0.00012 | gi 154358203 gb ABS79125.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 139465389 gb ECF29015.1  | hypothetical protein G   | ( 152) | 193 | 52.6 | 0.00014 | gi 154358183 gb ABS79115.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 162682735 gb EDQ69151.1  | predicted protein [Phy   | ( 342) | 197 | 53.7 | 0.00014 | gi 154358191 gb ABS79119.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 112099607 gb ABI10346.1  | Sequence 5 from patent   | ( 283) | 196 | 53.5 | 0.00014 | gi 154358239 gb ABS79143.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 139342629 gb ECE56642.1  | hypothetical protein G   | ( 119) | 191 | 52.1 | 0.00015 | gi 154358189 gb ABS79118.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 167018850 gb ABZ05395.1  | fatty acid desaturase    | ( 100) | 190 | 51.8 | 0.00016 | gi 154358205 gb ABS79126.1  | At4g30950-like protein    | ( 112) | 184 | 50.5 | 0.00044 |
| gi 112099669 gb ABI10393.1  | Sequence 72 from paten   | ( 218) | 194 | 52.9 | 0.00016 | gi 154358239 gb ABS79143.1  | At4g30950-like protein    | ( 113) | 184 | 50.5 | 0.00044 |
| gi 49355354 gb AAT65208.1   | omega-6 desaturase [Bra  | ( 443) | 197 | 53.8 | 0.00018 | gi 12655937 gb AAK00664.1   | AF229392_1 omega 6 reduc  | ( 201) | 187 | 51.3 | 0.00045 |
| gi 155316475 gb ABT72079.1  | Sequence 159549 from p   | ( 81)  | 188 | 51.3 | 0.00018 | gi 125603557 gb EAAZ42882.1 | hypothetical protein O    | ( 370) | 190 | 52.2 | 0.00046 |
| gi 112099667 gb ABI10392.1  | Sequence 71 from paten   | ( 283) | 194 | 53.0 | 0.0002  | gi 125561683 gb EAAZ07131.1 | hypothetical protein O    | ( 372) | 190 | 52.2 | 0.00047 |
| gi 110165097 gb ABG49637.1  | fatty acid desaturase    | ( 351) | 195 | 53.3 | 0.0002  | gi 68348070 gb AAAY95676.1  | delta 12 desaturase [Ps   | ( 659) | 193 | 53.0 | 0.00047 |
| gi 33639203 emb CAB08211.1  | possible fatty acid de   | ( 378) | 195 | 53.3 | 0.00021 | gi 146218708 emb CAM96526.1 | putative chloroplast      | ( 167) | 185 | 50.8 | 0.00053 |
| gi 116787557 gb ABK24556.1  | unknown [Picea sitchen   | ( 460) | 196 | 53.6 | 0.00021 | gi 88911216 gb ABD58898.1   | chloroplast omega-6 fat   | ( 439) | 190 | 52.2 | 0.00053 |
| gi 134996528 gb EBE81702.1  | hypothetical protein G   | ( 394) | 195 | 53.3 | 0.00022 | gi 5305312 gb AAD41581.1    | AF056571_1 unknown [Brass | ( 141) | 184 | 50.6 | 0.00053 |
| gi 84787828 gb ABC64010.1   | putative fatty acid des  | ( 344) | 194 | 53.1 | 0.00023 | gi 112099651 gb ABI10380.1  | Sequence 41 from paten    | ( 141) | 184 | 50.6 | 0.00053 |
| gi 12655933 gb AAK00662.1   | AF229390_1 omega 6 reduc | ( 202) | 191 | 52.2 | 0.00024 | gi 61620777 gb AAAX47480.1  | microsomal omega-6-des    | ( 151) | 184 | 50.6 | 0.00057 |
| gi 457631 gb AAA50157.1     | omega-6 desaturase       | ( 443) | 195 | 53.3 | 0.00024 | gi 12655931 gb AAK00661.1   | AF229389_1 omega 6 reduc  | ( 222) | 186 | 51.1 | 0.00057 |
| gi 154358219 gb ABS79133.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 140516970 gb ECMO8249.1  | hypothetical protein G    | ( 246) | 185 | 50.9 | 0.00073 |
| gi 154358243 gb ABS79145.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 5305310 gb AAD41580.1    | AF056570_1 unknown [Brass | ( 141) | 182 | 50.1 | 0.00073 |
| gi 154358221 gb ABS79134.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 112099652 gb ABI10381.1  | Sequence 42 from paten    | ( 141) | 182 | 50.1 | 0.00073 |
| gi 154358235 gb ABS79141.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 140873905 gb ECO09093.1  | hypothetical protein G    | ( 68)  | 178 | 49.0 | 0.00075 |
| gi 154358201 gb ABS79124.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 134906514 gb EBE21366.1  | hypothetical protein G    | ( 261) | 185 | 50.9 | 0.00076 |
| gi 154358217 gb ABS79132.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 142875988 gb EDB20702.1  | hypothetical protein G    | ( 191) | 183 | 50.4 | 0.00081 |
| gi 154358207 gb ABS79127.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 112099648 gb ABI10378.1  | Sequence 39 from paten    | ( 257) | 183 | 50.5 | 0.001   |
| gi 154358213 gb ABS79130.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 1785856 dbj BAA11396.1   | w-3 fatty acid desatura   | ( 269) | 183 | 50.5 | 0.0011  |
| gi 154358181 gb ABS79114.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 138969562 gb ECC63594.1  | hypothetical protein G    | ( 278) | 183 | 50.5 | 0.0011  |
| gi 154358231 gb ABS79139.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 113623875 dbj BAF23820.1 | Os08g0440900 [Oryza s     | ( 184) | 179 | 49.5 | 0.0015  |
| gi 154358185 gb ABS79116.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 34600645 gb AAQ78502.1   | Sequence 6 from patent    | ( 183) | 177 | 49.0 | 0.002   |
| gi 154358251 gb ABS79149.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 10278518 emb CAC09646.1  | unnamed protein produc    | ( 183) | 177 | 49.0 | 0.002   |
| gi 154358211 gb ABS79129.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 138090575 gb EBX69101.1  | hypothetical protein G    | ( 283) | 179 | 49.6 | 0.0021  |
| gi 154358233 gb ABS79140.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 143207578 gb EDD59354.1  | hypothetical protein G    | ( 368) | 180 | 49.9 | 0.0022  |
| gi 154358249 gb ABS79148.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 136415656 gb EB001902.1  | hypothetical protein G    | ( 315) | 179 | 49.6 | 0.0023  |
| gi 154358199 gb ABS79123.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 144066402 gb EDI62561.1  | hypothetical protein G    | ( 196) | 176 | 48.8 | 0.0025  |
| gi 154358237 gb ABS79142.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 157388522 gb ABV51227.1  | Fatty acid desaturase,    | ( 368) | 179 | 49.6 | 0.0026  |
| gi 154358225 gb ABS79136.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 134825520 gb EBD68131.1  | hypothetical protein G    | ( 220) | 176 | 48.8 | 0.0028  |
| gi 154358197 gb ABS79122.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 52346891 gb AAU39525.1   | hypothetical protein BL   | ( 342) | 178 | 49.4 | 0.0029  |
| gi 154358227 gb ABS79137.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 46408141 emb CAG26642.1  | unnamed protein produc    | ( 342) | 178 | 49.4 | 0.0029  |
| gi 154358209 gb ABS79128.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 52002229 gb AAU22171.1   | fatty acid desaturase [   | ( 342) | 178 | 49.4 | 0.0029  |
| gi 154358241 gb ABS79144.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 136733729 gb EBQ04834.1  | hypothetical protein G    | ( 303) | 177 | 49.1 | 0.0031  |
| gi 154358229 gb ABS79138.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 108863907 gb ECS90863.1  | Omega-3 fatty acid des    | ( 271) | 176 | 48.9 | 0.0033  |
| gi 154358215 gb ABS79131.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 459962 gb AAA50158.1     | plastid omega-6 desatur   | ( 424) | 178 | 49.4 | 0.0035  |
| gi 154358223 gb ABS79135.1  | At4g30950-like protein   | ( 128) | 188 | 51.4 | 0.00026 | gi 91125674 gb ABE12622.1   | Sequence 35 from patent   | ( 424) | 178 | 49.4 | 0.0035  |
| gi 162684523 gb EDQ70964.1  | predicted protein [Phy   | ( 340) | 193 | 52.8 | 0.00027 | gi 33238186 gb AAQ00253.1   | Fatty acid desaturase [   | ( 370) | 177 | 49.2 | 0.0036  |
| gi 157330281 emb CAO45069.1 | unnamed protein produ    | ( 301) | 192 | 52.6 | 0.00028 | gi 113644232 dbj BAF27373.1 | Os11g0104400 [Oryza s     | ( 269) | 175 | 48.7 | 0.0038  |
| gi 195628958 gb ACG36241.1  | hypothetical protein [   | ( 443) | 194 | 53.1 | 0.00029 | gi 171991123 gb ACB62045.1  | fatty acid desaturase     | ( 339) | 175 | 48.7 | 0.0046  |
| gi 162669755 gb EDQ56336.1  | predicted protein [Phy   | ( 454) | 194 | 53.1 | 0.00029 | gi 141716287 gb ECS90863.1  | hypothetical protein G    | ( 306) | 174 | 48.5 | 0.005   |
| gi 113881936 gb ABT46894.1  | possible fatty acid de   | ( 399) | 193 | 52.9 | 0.00031 | gi 189184986 gb ACD82171.1  | Fatty acid desaturase     | ( 295) | 173 | 48.2 | 0.0057  |
| gi 126559291 gb AAK00660.1  | AF229388_1 omega 6 reduc | ( 213) | 189 | 51.8 | 0.00034 | gi 108467859 gb ABF93044.1  | fatty acid desaturase     | ( 361) | 174 | 48.5 | 0.0057  |
| gi 12655935 gb AAK00663.1   | AF229391_1 omega 6 reduc | ( 216) | 189 | 51.8 | 0.00035 | gi 24193921 gb AAN47701.1   | AE011236_10 Fatty acid d  | ( 365) | 174 | 48.5 | 0.0058  |
| gi 49355339 gb AAT65203.1   | omega-6 desaturase [Bra  | ( 443) | 192 | 52.7 | 0.00039 | gi 198248261 gb ACH83854.1  | fatty acid desaturase     | ( 374) | 174 | 48.5 | 0.0059  |
| gi 155273457 gb ABT29061.1  | Sequence 116531 from p   | ( 443) | 192 | 52.7 | 0.00039 | gi 142453372 gb ECY18908.1  | hypothetical protein G    | ( 259) | 172 | 48.0 | 0.0059  |
| gi 136874329 gb EBQ98333.1  | hypothetical protein G   | ( 259) | 189 | 51.8 | 0.0004  | gi 120324979 gb ABM19294.1  | fatty acid desaturase     | ( 362) | 173 | 48.3 | 0.0067  |
| gi 90655389 gb ABD96230.1   | possible fatty acid des  | ( 379) | 191 | 52.4 | 0.0004  | gi 45602124 gb AAS71602.1   | fatty acid desaturase [   | ( 365) | 173 | 48.3 | 0.0068  |

|                             |                                 |     |      |        |                             |                                |     |      |       |
|-----------------------------|---------------------------------|-----|------|--------|-----------------------------|--------------------------------|-----|------|-------|
| gi 126543953 gb ABO18195.1  | Fatty acid desaturase, ( 368)   | 173 | 48.3 | 0.0068 | gi 142848386 gb EDB03752.1  | hypothetical protein G ( 326)  | 163 | 46.0 | 0.03  |
| gi 135949122 gb EBK90918.1  | hypothetical protein G ( 368)   | 173 | 48.3 | 0.0068 | gi 139409156 gb ECE91420.1  | hypothetical protein G ( 153)  | 159 | 44.9 | 0.03  |
| gi 144056605 gb ED155295.1  | hypothetical protein G ( 369)   | 173 | 48.3 | 0.0068 | gi 109454449 gb ABG30654.1  | fatty acid desaturase, ( 350)  | 163 | 46.0 | 0.032 |
| gi 136114208 gb EBM00849.1  | hypothetical protein G ( 374)   | 173 | 48.3 | 0.0069 | gi 189335465 dbj BAG44535.1 | putative fatty acid d ( 361)   | 163 | 46.0 | 0.033 |
| gi 210028779 emb CAR94990.1 | unnamed protein produ ( 89)     | 165 | 46.1 | 0.0074 | gi 142399062 gb ECX78387.1  | hypothetical protein G ( 368)  | 163 | 46.0 | 0.033 |
| gi 143730985 gb EDA9314.1   | hypothetical protein G ( 86)    | 172 | 48.0 | 0.008  | gi 142248916 gb ECW70653.1  | hypothetical protein G ( 309)  | 162 | 45.7 | 0.034 |
| gi 136362146 gb EBN65337.1  | hypothetical protein G ( 390)   | 172 | 48.1 | 0.0084 | gi 160341224 gb ABX14310.1  | fatty acid desaturase ( 378)   | 163 | 46.0 | 0.034 |
| gi 215765755 dbj BAG87452.1 | unnamed protein produ ( 162)    | 167 | 46.7 | 0.0089 | gi 138257509 gb EBY61921.1  | hypothetical protein G ( 181)  | 159 | 44.9 | 0.035 |
| gi 142760554 gb EDA38161.1  | hypothetical protein G ( 196)   | 168 | 47.0 | 0.0089 | gi 135823807 gb EBK07194.1  | hypothetical protein G ( 322)  | 162 | 45.7 | 0.035 |
| gi 136276686 gb EBN07445.1  | hypothetical protein G ( 377)   | 171 | 47.8 | 0.0095 | gi 60172920 gb AAX14502.1   | delta-8 fatty acid desa ( 476) | 164 | 46.3 | 0.035 |
| gi 155315801 gb ABT71405.1  | Sequence 158875 from p ( 177)   | 167 | 46.7 | 0.0095 | gi 60220814 emb CAI58906.1  | unnamed protein produc ( 476)  | 164 | 46.3 | 0.035 |
| gi 134324014 gb EBA64569.1  | hypothetical protein G ( 160)   | 166 | 46.5 | 0.01   | gi 76059314 emb CAJ30851.1  | unnamed protein produc ( 476)  | 164 | 46.3 | 0.035 |
| gi 137661488 gb EBV31099.1  | hypothetical protein G ( 175)   | 166 | 46.5 | 0.011  | gi 126633752 emb CAM55832.1 | unnamed protein produ ( 476)   | 164 | 46.3 | 0.035 |
| gi 49330597 gb AAT61243.1   | delta5 acyl-lipid desat ( 319)  | 169 | 47.3 | 0.011  | gi 40193163 gb AAR78135.1   | Sequence 33 from patent ( 29)  | 149 | 42.2 | 0.036 |
| gi 49179721 gb AAT55097.1   | fatty acid desaturase [ ( 319)  | 169 | 47.3 | 0.011  | gi 158473916 gb ABW47816.1  | Sequence 22 from paten ( 29)   | 149 | 42.2 | 0.036 |
| gi 30257588 gb AAP26818.1   | fatty acid desaturase [ ( 319)  | 169 | 47.3 | 0.011  | gi 118901317 gb ABL51032.1  | Sequence 22 from paten ( 29)   | 149 | 42.2 | 0.036 |
| gi 47503442 gb AAT32118.1   | fatty acid desaturase [ ( 319)  | 169 | 47.3 | 0.011  | gi 83349275 gb ABC14928.1   | Sequence 33 from patent ( 29)  | 149 | 42.2 | 0.036 |
| gi 143665885 gb EDG16525.1  | hypothetical protein G ( 334)   | 169 | 47.3 | 0.012  | gi 20230167 gb AAE91310.1   | Sequence 33 from patent ( 29)  | 149 | 42.2 | 0.036 |
| gi 118417547 gb ABK85966.1  | delta5 acyl-lipid desa ( 343)   | 169 | 47.3 | 0.012  | gi 110293129 gb ABG66302.1  | omega-3 fatty acid des ( 91)   | 155 | 43.8 | 0.037 |
| gi 217068320 gb ACJ82570.1  | fatty acid desaturase ( 343)    | 169 | 47.3 | 0.012  | gi 142821377 gb EDA83492.1  | hypothetical protein G ( 197)  | 159 | 44.9 | 0.037 |
| gi 15975993 gb AAU17543.1   | delta5 acyl-lipid desat ( 343)  | 169 | 47.3 | 0.012  | gi 91800948 gb ABE63323.1   | fatty acid desaturase [ ( 349) | 162 | 45.7 | 0.037 |
| gi 29896651 gb AAP09930.1   | delta5 acyl-lipid desat ( 343)  | 169 | 47.3 | 0.012  | gi 20230171 gb AAE91314.1   | Sequence 37 from patent ( 36)  | 150 | 42.5 | 0.037 |
| gi 143633755 gb EDF97335.1  | hypothetical protein G ( 306)   | 168 | 47.1 | 0.013  | gi 83349279 gb ABC14932.1   | Sequence 37 from patent ( 36)  | 150 | 42.5 | 0.037 |
| gi 123201151 gb ABM72759.1  | Fatty acid desaturase, ( 368)   | 168 | 47.1 | 0.015  | gi 40193167 gb AAR78139.1   | Sequence 37 from patent ( 36)  | 150 | 42.5 | 0.037 |
| gi 33640302 emb CAE19837.1  | Fatty acid desaturase, ( 368)   | 168 | 47.1 | 0.015  | gi 118901322 gb ABL51037.1  | Sequence 27 from paten ( 36)   | 150 | 42.5 | 0.037 |
| gi 154350851 gb ABS72930.1  | putitative fatty acid ( 342)    | 167 | 46.9 | 0.017  | gi 158473921 gb ABW47821.1  | Sequence 27 from paten ( 36)   | 150 | 42.5 | 0.037 |
| gi 206685961 gb ED246443.1  | fatty acid desaturase ( 344)    | 167 | 46.9 | 0.017  | gi 136840519 gb EBQ75828.1  | hypothetical protein G ( 200)  | 159 | 44.9 | 0.038 |
| gi 136409502 gb EBN97900.1  | hypothetical protein G ( 236)   | 165 | 46.3 | 0.017  | gi 139594873 gb ECG14809.1  | hypothetical protein G ( 244)  | 160 | 45.2 | 0.038 |
| gi 138556163 gb ECA41253.1  | hypothetical protein G ( 287)   | 166 | 46.6 | 0.017  | gi 78713356 gb ABB50533.1   | fatty acid desaturase, ( 368)  | 162 | 45.8 | 0.039 |
| gi 111608891 gb ABH11003.1  | omega-6 fatty acid des ( 216)   | 164 | 46.1 | 0.018  | gi 136740857 gb EBQ09515.1  | hypothetical protein G ( 149)  | 157 | 44.4 | 0.04  |
| gi 167324306 gb AB260899.1  | Sequence 11698 from pa ( 344)   | 166 | 46.7 | 0.019  | gi 88865995 gb ABD56872.1   | fatty acid desaturase [ ( 330) | 161 | 45.5 | 0.042 |
| gi 136121332 gb EBM05702.1  | hypothetical protein G ( 322)   | 165 | 46.4 | 0.022  | gi 20230169 gb AAE91312.1   | Sequence 35 from patent ( 36)  | 149 | 42.2 | 0.044 |
| gi 136961755 gb EBR42583.1  | hypothetical protein G ( 326)   | 165 | 46.4 | 0.022  | gi 40193165 gb AAR78137.1   | Sequence 35 from patent ( 36)  | 149 | 42.2 | 0.044 |
| gi 143157154 gb EDD23046.1  | hypothetical protein G ( 395)   | 166 | 46.7 | 0.022  | gi 118901320 gb ABL51035.1  | Sequence 25 from paten ( 36)   | 149 | 42.2 | 0.044 |
| gi 136491773 gb EBO51081.1  | hypothetical protein G ( 343)   | 165 | 46.4 | 0.023  | gi 158473919 gb ABW47819.1  | Sequence 25 from paten ( 36)   | 149 | 42.2 | 0.044 |
| gi 42738016 gb AAS41947.1   | fatty acid desaturase [ ( 343)  | 165 | 46.4 | 0.023  | gi 83349277 gb ABC14930.1   | Sequence 35 from patent ( 36)  | 149 | 42.2 | 0.044 |
| gi 20230199 gb AAE91342.1   | Sequence 66 from patent ( 36)   | 153 | 43.2 | 0.023  | gi 140824677 gb ECN77005.1  | hypothetical protein G ( 292)  | 160 | 45.2 | 0.044 |
| gi 118901340 gb ABL51055.1  | Sequence 49 from paten ( 36)    | 153 | 43.2 | 0.023  | gi 142215690 gb ECW45999.1  | hypothetical protein G ( 204)  | 158 | 44.7 | 0.045 |
| gi 40193196 gb AAR78168.1   | Sequence 66 from patent ( 36)   | 153 | 43.2 | 0.023  | gi 142341924 gb ECX39321.1  | hypothetical protein G ( 300)  | 160 | 45.3 | 0.045 |
| gi 83349307 gb ABC14960.1   | Sequence 66 from patent ( 36)   | 153 | 43.2 | 0.023  | gi 123199229 gb ABM70870.1  | Fatty acid desaturase, ( 368)  | 161 | 45.5 | 0.046 |
| gi 158473939 gb ABW47839.1  | Sequence 49 from paten ( 36)    | 153 | 43.2 | 0.023  | gi 163862930 gb ABY43989.1  | fatty acid desaturase ( 343)   | 160 | 45.3 | 0.05  |
| gi 5955839 gb AAE07495.1    | Sequence 21 from patent ( 37)   | 153 | 43.2 | 0.024  | gi 138546994 gb ECA34812.1  | hypothetical protein G ( 239)  | 158 | 44.7 | 0.051 |
| gi 5955833 gb AAE07489.1    | Sequence 15 from patent ( 37)   | 153 | 43.2 | 0.024  | gi 190696256 gb ACE90341.1  | probable fatty acid de ( 350)  | 160 | 45.3 | 0.051 |
| gi 2492210 gb AAB80346.1    | I66157 Sequence 15 from p ( 37) | 153 | 43.2 | 0.024  | gi 139660029 gb ECG58793.1  | hypothetical protein G ( 294)  | 159 | 45.0 | 0.052 |
| gi 2492216 gb AAB80352.1    | I66163 Sequence 21 from p ( 37) | 153 | 43.2 | 0.024  | gi 141725778 gb ECX96738.1  | hypothetical protein G ( 145)  | 155 | 43.9 | 0.054 |
| gi 143544394 gb EDF55390.1  | hypothetical protein G ( 368)   | 165 | 46.4 | 0.024  | gi 136684917 gb EBP72872.1  | hypothetical protein G ( 177)  | 156 | 44.2 | 0.054 |
| gi 136003365 gb EBL26198.1  | hypothetical protein G ( 368)   | 165 | 46.4 | 0.024  | gi 143447253 gb EDF01011.1  | hypothetical protein G ( 384)  | 160 | 45.3 | 0.055 |
| gi 143444755 gb EDE99441.1  | hypothetical protein G ( 370)   | 165 | 46.4 | 0.024  | gi 83349276 gb ABC14929.1   | Sequence 34 from patent ( 29)  | 146 | 41.5 | 0.059 |
| gi 20230165 gb AAE91308.1   | Sequence 31 from patent ( 29)   | 151 | 42.6 | 0.027  | gi 40193164 gb AAR78136.1   | Sequence 34 from patent ( 29)  | 146 | 41.5 | 0.059 |
| gi 158473938 gb ABW47838.1  | Sequence 48 from paten ( 29)    | 151 | 42.6 | 0.027  | gi 158473917 gb ABW47817.1  | Sequence 23 from paten ( 29)   | 146 | 41.5 | 0.059 |
| gi 158473914 gb ABW47814.1  | Sequence 20 from paten ( 29)    | 151 | 42.6 | 0.027  | gi 118901318 gb ABL51033.1  | Sequence 23 from paten ( 29)   | 146 | 41.5 | 0.059 |
| gi 83349273 gb ABC14926.1   | Sequence 31 from patent ( 29)   | 151 | 42.6 | 0.027  | gi 20230168 gb AAE91311.1   | Sequence 34 from patent ( 29)  | 146 | 41.5 | 0.059 |
| gi 40193161 gb AAR78133.1   | Sequence 31 from patent ( 29)   | 151 | 42.6 | 0.027  | gi 40193166 gb AAR78138.1   | Sequence 36 from patent ( 36)  | 147 | 41.8 | 0.06  |
| gi 118901339 gb ABL51054.1  | Sequence 48 from paten ( 29)    | 151 | 42.6 | 0.027  | gi 83349278 gb ABC14931.1   | Sequence 36 from patent ( 36)  | 147 | 41.8 | 0.06  |
| gi 118901315 gb ABL51030.1  | Sequence 20 from paten ( 29)    | 151 | 42.6 | 0.027  | gi 118901321 gb ABL51036.1  | Sequence 26 from paten ( 36)   | 147 | 41.8 | 0.06  |
| gi 186464974 gb ACC80775.1  | fatty acid desaturase ( 351)    | 164 | 46.2 | 0.027  | gi 20230170 gb AAE91313.1   | Sequence 36 from patent ( 36)  | 147 | 41.8 | 0.06  |
| gi 88863496 gb ABD54373.1   | fatty acid desaturase [ ( 362)  | 164 | 46.2 | 0.028  | gi 158473920 gb ABW47820.1  | Sequence 26 from paten ( 36)   | 147 | 41.8 | 0.06  |
| gi 143600341 gb EDF80364.1  | hypothetical protein G ( 312)   | 163 | 45.9 | 0.029  | gi 143629263 gb EDF94858.1  | hypothetical protein G ( 370)  | 159 | 45.1 | 0.063 |

|                             |                                 |     |      |       |                             |                                  |     |      |      |
|-----------------------------|---------------------------------|-----|------|-------|-----------------------------|----------------------------------|-----|------|------|
| gi 143884086 gb EDH32508.1  | hypothetical protein G ( 307)   | 158 | 44.8 | 0.063 | gi 167285169 gb ABZ38033.1  | Sequence 11971 from pa ( 340)    | 153 | 43.7 | 0.15 |
| gi 139693866 gb ECG82229.1  | hypothetical protein G ( 87)    | 151 | 42.9 | 0.066 | gi 136963384 gb EBR43477.1  | hypothetical protein G ( 136)    | 148 | 42.3 | 0.16 |
| gi 27350502 dbj BAC47512.1  | blr2247 [Bradyrhizobiu ( 493)   | 160 | 45.4 | 0.068 | gi 140930891 gb ECO47251.1  | hypothetical protein G ( 199)    | 150 | 42.9 | 0.16 |
| gi 115282774 gb ABI88291.1  | fatty acid desaturase ( 340)    | 158 | 44.8 | 0.068 | gi 144002551 gb EDI16748.1  | hypothetical protein G ( 356)    | 153 | 43.7 | 0.16 |
| gi 115517589 gb ABJ05573.1  | fatty acid desaturase ( 349)    | 158 | 44.8 | 0.07  | gi 77968224 gb ABB09604.1   | Fatty acid desaturase [ ( 360)   | 153 | 43.7 | 0.16 |
| gi 140248747 gb ECK54112.1  | hypothetical protein G ( 304)   | 157 | 44.6 | 0.073 | gi 198035352 emb CAR51227.1 | fatty acid desaturase ( 360)     | 153 | 43.7 | 0.16 |
| gi 47028617 gb AAT09160.1   | delta-5 fatty acid desa ( 475)  | 159 | 45.1 | 0.077 | gi 143529043 gb EDF47704.1  | hypothetical protein G ( 252)    | 151 | 43.2 | 0.16 |
| gi 61661518 gb AA51386.1    | delta-5 fatty acid desa ( 476)  | 159 | 45.1 | 0.077 | gi 134613509 gb EBC39000.1  | hypothetical protein G ( 254)    | 151 | 43.2 | 0.16 |
| gi 142654294 gb EC261904.1  | hypothetical protein G ( 225)   | 155 | 44.0 | 0.078 | gi 5955841 gb AAE07497.1    | Sequence 23 from patent ( 40)    | 141 | 40.4 | 0.17 |
| gi 171192396 gb ACB43357.1  | fatty acid desaturase ( 344)    | 157 | 44.6 | 0.081 | gi 2492212 gb AAB80348.1    | I66159 Sequence 17 from p ( 40)  | 141 | 40.4 | 0.17 |
| gi 40193157 gb AAR78129.1   | Sequence 27 from patent ( 30)   | 144 | 41.1 | 0.083 | gi 2492218 gb AAB80354.1    | I66165 Sequence 23 from p ( 40)  | 141 | 40.4 | 0.17 |
| gi 118901310 gb ABL51025.1  | Sequence 15 from paten ( 30)    | 144 | 41.1 | 0.083 | gi 5955835 gb AAE07491.1    | Sequence 17 from patent ( 40)    | 141 | 40.4 | 0.17 |
| gi 83349269 gb ABC14922.1   | Sequence 27 from patent ( 30)   | 144 | 41.1 | 0.083 | gi 135702350 gb EBJ31380.1  | hypothetical protein G ( 222)    | 150 | 42.9 | 0.17 |
| gi 158473909 gb ABW47809.1  | Sequence 15 from paten ( 30)    | 144 | 41.1 | 0.083 | gi 196193075 gb EDX88034.1  | Fatty acid desaturase ( 328)     | 152 | 43.4 | 0.17 |
| gi 20230161 gb AAE91304.1   | Sequence 27 from patent ( 30)   | 144 | 41.1 | 0.083 | gi 142640255 gb ECZ52013.1  | hypothetical protein G ( 329)    | 152 | 43.4 | 0.17 |
| gi 134810286 gb EBD58450.1  | hypothetical protein G ( 295)   | 156 | 44.3 | 0.083 | gi 137677701 gb EBV40288.1  | hypothetical protein G ( 236)    | 150 | 42.9 | 0.18 |
| gi 182635565 gb ACB96339.1  | fatty acid desaturase ( 363)    | 157 | 44.6 | 0.085 | gi 121588613 gb ABM61193.1  | fatty acid desaturase ( 349)     | 152 | 43.5 | 0.18 |
| gi 142059971 gb ECK61602.1  | hypothetical protein G ( 250)   | 155 | 44.1 | 0.085 | gi 134772240 gb EBD32686.1  | hypothetical protein G ( 351)    | 152 | 43.5 | 0.18 |
| gi 136533675 gb EBO78016.1  | hypothetical protein G ( 254)   | 155 | 44.1 | 0.086 | gi 136921855 gb EBR20091.1  | hypothetical protein G ( 242)    | 150 | 42.9 | 0.18 |
| gi 136997190 gb EBR62659.1  | hypothetical protein G ( 313)   | 156 | 44.3 | 0.088 | gi 91802797 gb ABE65169.1   | fatty acid desaturase [ ( 354)   | 152 | 43.5 | 0.18 |
| gi 158473918 gb ABW47818.1  | Sequence 24 from paten ( 29)    | 143 | 40.8 | 0.094 | gi 142019328 gb ECU89817.1  | hypothetical protein G ( 246)    | 150 | 42.9 | 0.19 |
| gi 118901316 gb ABL51031.1  | Sequence 21 from paten ( 29)    | 143 | 40.8 | 0.094 | gi 5823006 gb AAD53003.1    | AF076471_1 MocD [Sinorhiz ( 361) | 152 | 43.5 | 0.19 |
| gi 40193162 gb AAR78134.1   | Sequence 32 from patent ( 29)   | 143 | 40.8 | 0.094 | gi 144135916 gb EDJ12565.1  | hypothetical protein G ( 363)    | 152 | 43.5 | 0.19 |
| gi 118901319 gb ABL51034.1  | Sequence 24 from paten ( 29)    | 143 | 40.8 | 0.094 | gi 139074519 gb ECD23377.1  | hypothetical protein G ( 254)    | 150 | 42.9 | 0.19 |
| gi 83349274 gb ABC14927.1   | Sequence 32 from patent ( 29)   | 143 | 40.8 | 0.094 | gi 136348703 gb EBN56170.1  | hypothetical protein G ( 318)    | 151 | 43.2 | 0.2  |
| gi 20230166 gb AAE91309.1   | Sequence 32 from patent ( 29)   | 143 | 40.8 | 0.094 | gi 138159875 gb EBY09754.1  | hypothetical protein G ( 224)    | 149 | 42.7 | 0.2  |
| gi 158473915 gb ABW47815.1  | Sequence 21 from paten ( 29)    | 143 | 40.8 | 0.094 | gi 22778539 dbj BAC14808.1  | fatty-acid desaturase ( 349)     | 151 | 43.2 | 0.21 |
| gi 145046627 gb ABP33254.1  | fatty acid desaturase ( 346)    | 156 | 44.4 | 0.095 | gi 115260472 emb CAK03576.1 | putative transmembran ( 362)     | 151 | 43.2 | 0.22 |
| gi 155082204 gb ABS94944.1  | Sequence 37 from paten ( 509)   | 158 | 44.9 | 0.096 | gi 154156969 gb ABS64186.1  | fatty acid desaturase ( 371)     | 151 | 43.2 | 0.22 |
| gi 155095505 gb ABS99960.1  | Sequence 37 from paten ( 509)   | 158 | 44.9 | 0.096 | gi 143086273 gb EDC71371.1  | hypothetical protein G ( 174)    | 147 | 42.2 | 0.22 |
| gi 111979073 gb ABH83316.1  | Sequence 37 from paten ( 509)   | 158 | 44.9 | 0.096 | gi 141273638 gb ECQ82648.1  | hypothetical protein G ( 217)    | 148 | 42.4 | 0.23 |
| gi 155116369 gb ABT11295.1  | Sequence 37 from paten ( 509)   | 158 | 44.9 | 0.096 | gi 126633754 emb CAM55833.1 | unnamed protein produ ( 482)     | 152 | 43.5 | 0.24 |
| gi 158473923 gb ABW47823.1  | Sequence 29 from paten ( 36)    | 144 | 41.1 | 0.096 | gi 60220816 emb CAI58907.1  | unnamed protein produc ( 482)    | 152 | 43.5 | 0.24 |
| gi 118901324 gb ABL51039.1  | Sequence 29 from paten ( 36)    | 144 | 41.1 | 0.096 | gi 76059316 emb CAJ30852.1  | unnamed protein produc ( 482)    | 152 | 43.5 | 0.24 |
| gi 146218710 emb CAM96527.1 | putative microsomal o ( 116)    | 150 | 42.7 | 0.099 | gi 136665182 gb EBP60030.1  | hypothetical protein G ( 275)    | 149 | 42.7 | 0.24 |
| gi 206680127 gb EDZ44614.1  | fatty acid desaturase ( 309)    | 155 | 44.1 | 0.1   | gi 142643368 gb ECZ54224.1  | hypothetical protein G ( 337)    | 150 | 43.0 | 0.24 |
| gi 143304298 gb EDE21795.1  | hypothetical protein G ( 341)   | 155 | 44.1 | 0.11  | gi 138742267 gb ECB69817.1  | hypothetical protein G ( 231)    | 148 | 42.5 | 0.24 |
| gi 168990272 gb ACA37812.1  | Fatty acid desaturase ( 343)    | 155 | 44.1 | 0.11  | gi 144056168 gb EDI54978.1  | hypothetical protein G ( 165)    | 146 | 41.9 | 0.25 |
| gi 140942966 gb ECO55750.1  | hypothetical protein G ( 238)   | 153 | 43.6 | 0.11  | gi 83349270 gb ABC14923.1   | Sequence 28 from patent ( 30)    | 137 | 39.5 | 0.25 |
| gi 136001020 gb EBL24809.1  | hypothetical protein G ( 242)   | 153 | 43.6 | 0.11  | gi 118901311 gb ABL51026.1  | Sequence 16 from paten ( 30)     | 137 | 39.5 | 0.25 |
| gi 137209426 gb EBS81473.1  | hypothetical protein G ( 166)   | 151 | 43.1 | 0.11  | gi 20230162 gb AAE91305.1   | Sequence 28 from patent ( 30)    | 137 | 39.5 | 0.25 |
| gi 143423631 gb EDE87807.1  | hypothetical protein G ( 382)   | 155 | 44.2 | 0.12  | gi 158473910 gb ABW47810.1  | Sequence 16 from paten ( 30)     | 137 | 39.5 | 0.25 |
| gi 137327946 gb EBT47954.1  | hypothetical protein G ( 291)   | 153 | 43.6 | 0.13  | gi 40193158 gb AAR78130.1   | Sequence 28 from patent ( 30)    | 137 | 39.5 | 0.25 |
| gi 137844667 gb EBW32573.1  | hypothetical protein G ( 78)    | 146 | 41.7 | 0.13  | gi 124872059 gb EAY63775.1  | Fatty acid desaturase ( 360)     | 150 | 43.0 | 0.25 |
| gi 169817288 gb ACA91871.1  | fatty acid desaturase ( 360)    | 154 | 43.9 | 0.14  | gi 146406616 gb ABQ35122.1  | putative fatty acid de ( 374)    | 150 | 43.0 | 0.26 |
| gi 134461097 gb EBB48299.1  | hypothetical protein G ( 140)   | 149 | 42.6 | 0.14  | gi 143029156 gb EDC29503.1  | hypothetical protein G ( 385)    | 150 | 43.0 | 0.27 |
| gi 3411183 gb AAC31186.1    | putative hydrocarbon oxy ( 361) | 154 | 43.9 | 0.14  | gi 143139481 gb EDD10306.1  | hypothetical protein G ( 385)    | 150 | 43.0 | 0.27 |
| gi 167285093 gb ABZ37957.1  | Sequence 11895 from pa ( 363)   | 154 | 43.9 | 0.14  | gi 139308454 gb ECE49396.1  | hypothetical protein G ( 267)    | 148 | 42.5 | 0.27 |
| gi 150031672 gb ABR63788.1  | fatty acid desaturase ( 363)    | 154 | 43.9 | 0.14  | gi 138908835 gb ECC37941.1  | hypothetical protein G ( 193)    | 146 | 42.0 | 0.29 |
| gi 14022428 dbj BAB49037.1  | probable hydrocarbon o ( 363)   | 154 | 43.9 | 0.14  | gi 142744786 gb EDA26768.1  | hypothetical protein G ( 351)    | 149 | 42.8 | 0.29 |
| gi 58532810 gb AAW78909.1   | fatty acid desaturase [ ( 66)   | 145 | 41.5 | 0.14  | gi 52349044 gb AAU41678.1   | Des [Bacillus lichenifo ( 352)   | 149 | 42.8 | 0.29 |
| gi 142884493 gb EBD26892.1  | hypothetical protein G ( 301)   | 153 | 43.7 | 0.14  | gi 52004370 gb AAU24312.1   | fatty acid desaturase [ ( 352)   | 149 | 42.8 | 0.29 |
| gi 137811454 gb EBW13315.1  | hypothetical protein G ( 250)   | 152 | 43.4 | 0.14  | gi 135839244 gb EBK16908.1  | hypothetical protein G ( 94)     | 142 | 40.9 | 0.29 |
| gi 143312578 gb EBD26503.1  | hypothetical protein G ( 383)   | 154 | 43.9 | 0.14  | gi 143268760 gb EDE02855.1  | hypothetical protein G ( 295)    | 148 | 42.5 | 0.3  |
| gi 135404309 gb EBH41061.1  | hypothetical protein G ( 318)   | 153 | 43.7 | 0.14  | gi 105893807 gb ABF76972.1  | fatty acid desaturase ( 360)     | 149 | 42.8 | 0.3  |
| gi 139033775 gb ECC94899.1  | hypothetical protein G ( 277)   | 152 | 43.4 | 0.15  | gi 116648791 gb ABK09432.1  | fatty acid desaturase ( 360)     | 149 | 42.8 | 0.3  |
| gi 138189358 gb EBY30327.1  | hypothetical protein G ( 278)   | 152 | 43.4 | 0.15  | gi 142388028 gb ECX70339.1  | hypothetical protein G ( 301)    | 148 | 42.5 | 0.3  |
| gi 14023557 dbj BAB50163.1  | fatty acid desaturase ( 340)    | 153 | 43.7 | 0.15  | gi 140964139 gb ECO70818.1  | hypothetical protein G ( 250)    | 147 | 42.2 | 0.3  |

|                            |                                 |     |      |      |
|----------------------------|---------------------------------|-----|------|------|
| gi 140218683 gb ECK33115.1 | hypothetical protein G ( 172)   | 145 | 41.7 | 0.3  |
| gi 114340763 gb ABI66043.1 | fatty acid desaturase ( 311)    | 148 | 42.5 | 0.31 |
| gi 137385866 gb EBT80458.1 | hypothetical protein G ( 85)    | 141 | 40.6 | 0.32 |
| gi 135644423 gb EBI95603.1 | hypothetical protein G ( 268)   | 147 | 42.3 | 0.32 |
| gi 136177948 gb EBM40697.1 | hypothetical protein G ( 222)   | 146 | 42.0 | 0.32 |
| gi 142269902 gb ECW86122.1 | hypothetical protein G ( 155)   | 144 | 41.4 | 0.33 |
| gi 143763977 gb EDG66623.1 | hypothetical protein G ( 334)   | 148 | 42.5 | 0.33 |
| gi 40193195 gb AAR78167.1  | Sequence 65 from patent ( 29)   | 135 | 39.0 | 0.33 |
| gi 158473913 gb ABW47813.1 | Sequence 19 from patent ( 29)   | 135 | 39.0 | 0.33 |
| gi 20230198 gb AAE91341.1  | Sequence 65 from patent ( 29)   | 135 | 39.0 | 0.33 |
| gi 118901314 gb ABL51029.1 | Sequence 19 from patent ( 29)   | 135 | 39.0 | 0.33 |
| gi 83349306 gb ABC14959.1  | Sequence 65 from patent ( 29)   | 135 | 39.0 | 0.33 |
| gi 138383837 gb EBZ29515.1 | hypothetical protein G ( 295)   | 147 | 42.3 | 0.35 |
| gi 163664008 gb ABY31375.1 | fatty acid desaturase ( 358)    | 148 | 42.6 | 0.35 |
| gi 124894086 gb EAY67966.1 | Fatty acid desaturase ( 361)    | 148 | 42.6 | 0.35 |
| gi 138456706 gb EBZ80160.1 | hypothetical protein G ( 254)   | 146 | 42.0 | 0.36 |
| gi 142447364 gb ECY14572.1 | hypothetical protein G ( 317)   | 147 | 42.3 | 0.37 |
| gi 139773585 gb ECH36273.1 | hypothetical protein G ( 226)   | 145 | 41.8 | 0.38 |
| gi 140553831 gb ECM19576.1 | hypothetical protein G ( 236)   | 145 | 41.8 | 0.4  |
| gi 157682103 gb ABV63247.1 | fatty acid desaturase ( 351)    | 147 | 42.3 | 0.4  |
| gi 36958688 gb AAQ87156.1  | putative hydrocarbon ox ( 361)  | 147 | 42.3 | 0.41 |
| gi 86284822 gb ABC93881.1  | hydrocarbon oxygenase p ( 362)  | 147 | 42.3 | 0.41 |
| gi 190699629 gb ACE93713.1 | hydrocarbon oxygenase ( 362)    | 147 | 42.3 | 0.41 |
| gi 142373528 gb ECX60602.1 | hypothetical protein G ( 301)   | 146 | 42.1 | 0.41 |
| gi 140968244 gb EC073358.1 | hypothetical protein G ( 80)    | 139 | 40.1 | 0.41 |
| gi 140827068 gb ECN78717.1 | hypothetical protein G ( 319)   | 146 | 42.1 | 0.43 |
| gi 138361544 gb EBZ15949.1 | hypothetical protein G ( 277)   | 145 | 41.8 | 0.45 |
| gi 114227321 gb ABI57120.1 | fatty acid desaturase ( 349)    | 146 | 42.1 | 0.47 |
| gi 141112148 gb ECP71052.1 | hypothetical protein G ( 242)   | 144 | 41.5 | 0.47 |
| gi 196170643 gb ACG71616.1 | Linoleoyl-CoA desatura ( 364)   | 146 | 42.1 | 0.48 |
| gi 142120546 gb ECV74038.1 | hypothetical protein G ( 302)   | 145 | 41.8 | 0.49 |
| gi 3378264 gb AAD03847.1   | unknown [Novosphingobium ( 309) | 145 | 41.8 | 0.5  |
| gi 145322189 gb ABP64133.1 | fatty acid desaturase ( 309)    | 145 | 41.8 | 0.5  |
| gi 135247052 gb EBG40726.1 | hypothetical protein G ( 258)   | 144 | 41.6 | 0.5  |
| gi 142407392 gb ECX84610.1 | hypothetical protein G ( 181)   | 142 | 41.0 | 0.51 |
| gi 134772826 gb EBD33094.1 | hypothetical protein G ( 276)   | 144 | 41.6 | 0.53 |
| gi 135954332 gb EBK94439.1 | hypothetical protein G ( 283)   | 144 | 41.6 | 0.54 |
| gi 143117833 gb EDC94407.1 | hypothetical protein G ( 134)   | 140 | 40.5 | 0.54 |
| gi 141828284 gb ECT53004.1 | hypothetical protein G ( 295)   | 144 | 41.6 | 0.56 |
| gi 192283939 gb ACF00320.1 | fatty acid desaturase ( 357)    | 145 | 41.9 | 0.56 |
| gi 2492201 gb AAB80337.1   | I66148 Sequence 6 from pa ( 37) | 133 | 38.6 | 0.56 |
| gi 5955840 gb AAE07496.1   | Sequence 22 from patent ( 37)   | 133 | 38.6 | 0.56 |
| gi 2492217 gb AAB80353.1   | I66164 Sequence 22 from p ( 37) | 133 | 38.6 | 0.56 |
| gi 5955824 gb AAE07480.1   | Sequence 6 from patent U ( 37)  | 133 | 38.6 | 0.56 |
| gi 217063951 gb ACJ78201.1 | fatty acid desaturase ( 361)    | 145 | 41.9 | 0.56 |
| gi 49177306 gb AAT52682.1  | fatty acid desaturase [ ( 361)  | 145 | 41.9 | 0.56 |
| gi 29894149 gb AAP07440.1  | Fatty acid desaturase [ ( 361)  | 145 | 41.9 | 0.56 |
| gi 42735462 gb AAS39401.1  | fatty acid desaturase [ ( 361)  | 145 | 41.9 | 0.56 |
| gi 49331599 gb AAT62245.1  | possible fatty acid des ( 361)  | 145 | 41.9 | 0.56 |
| gi 47500784 gb AAT29460.1  | fatty acid desaturase [ ( 361)  | 145 | 41.9 | 0.56 |
| gi 51978352 gb AAU19902.1  | possible fatty acid des ( 361)  | 145 | 41.9 | 0.56 |
| gi 118415337 gb ABK83756.1 | fatty acid desaturase ( 361)    | 145 | 41.9 | 0.56 |
| gi 30253902 gb AAP24397.1  | fatty acid desaturase [ ( 361)  | 145 | 41.9 | 0.56 |
| gi 14024924 dbj BAB51526.1 | putative hydrocarbon o ( 363)   | 145 | 41.9 | 0.57 |
| gi 135993001 gb EBL20112.1 | hypothetical protein G ( 250)   | 143 | 41.3 | 0.57 |
| gi 137615900 gb EBV06925.1 | hypothetical protein G ( 257)   | 143 | 41.3 | 0.58 |
| gi 143213186 gb EDD63444.1 | hypothetical protein G ( 332)   | 144 | 41.6 | 0.62 |
| gi 137862788 gb EBW42988.1 | hypothetical protein G ( 231)   | 142 | 41.1 | 0.62 |

|                             |                                 |     |      |      |
|-----------------------------|---------------------------------|-----|------|------|
| gi 135475063 gb EBH88481.1  | hypothetical protein G ( 135)   | 139 | 40.3 | 0.64 |
| gi 138053809 gb EBX48750.1  | hypothetical protein G ( 241)   | 142 | 41.1 | 0.65 |
| gi 139857852 gb ECH95363.1  | hypothetical protein G ( 245)   | 142 | 41.1 | 0.66 |
| gi 138433799 gb EBZ64427.1  | hypothetical protein G ( 297)   | 143 | 41.4 | 0.66 |
| gi 136763277 gb EBQ24339.1  | hypothetical protein G ( 246)   | 142 | 41.1 | 0.66 |
| gi 142439034 gb ECY08406.1  | hypothetical protein G ( 299)   | 143 | 41.4 | 0.66 |
| gi 209539265 gb ACI59198.1  | fatty acid desaturase ( 362)    | 144 | 41.6 | 0.66 |
| gi 141714707 gb ECS89892.1  | hypothetical protein G ( 252)   | 142 | 41.1 | 0.67 |
| gi 143369933 gb EDE60968.1  | hypothetical protein G ( 209)   | 141 | 40.8 | 0.67 |
| gi 196193799 gb EDX88758.1  | Fatty acid desaturase ( 373)    | 144 | 41.7 | 0.68 |
| gi 140460181 gb ECL89651.1  | hypothetical protein G ( 83)    | 136 | 39.5 | 0.69 |
| gi 56680208 gb AAV96874.1   | fatty acid desaturase f ( 314)  | 143 | 41.4 | 0.69 |
| gi 2492204 gb AAB80340.1    | I66151 Sequence 9 from pa ( 40) | 132 | 38.4 | 0.7  |
| gi 5955827 gb AAE07483.1    | Sequence 9 from patent U ( 40)  | 132 | 38.4 | 0.7  |
| gi 2492198 gb AAB80334.1    | I66145 Sequence 3 from pa ( 40) | 132 | 38.4 | 0.7  |
| gi 5955821 gb AAE07477.1    | Sequence 3 from patent U ( 40)  | 132 | 38.4 | 0.7  |
| gi 135351893 gb EBH05844.1  | hypothetical protein G ( 269)   | 142 | 41.1 | 0.71 |
| gi 144124815 gb EDJ04372.1  | hypothetical protein G ( 326)   | 143 | 41.4 | 0.71 |
| gi 136058406 gb EBL62852.1  | hypothetical protein G ( 339)   | 143 | 41.4 | 0.73 |
| gi 84366874 dbj BAE68032.1  | putative RtxC homolog ( 346)    | 143 | 41.4 | 0.75 |
| gi 3064243 gb AAC38355.1    | membrane bound delta 5 a ( 352) | 143 | 41.4 | 0.76 |
| gi 2619012 gb AAB84436.1    | fatty acid desaturase [B ( 352) | 143 | 41.4 | 0.76 |
| gi 2634311 emb CAB13810.1   | fatty acid desaturase [ ( 352)  | 143 | 41.4 | 0.76 |
| gi 167296359 gb ABZ49223.1  | Sequence 23161 from pa ( 352)   | 143 | 41.4 | 0.76 |
| gi 46408065 emb CAG26605.1  | unnamed protein produc ( 352)   | 143 | 41.4 | 0.76 |
| gi 58425606 gb AAW74643.1   | RtxC [Xanthomonas oryza ( 355)  | 143 | 41.4 | 0.76 |
| gi 144115985 gb EDI97942.1  | hypothetical protein G ( 360)   | 143 | 41.4 | 0.77 |
| gi 163860553 gb ABY41612.1  | fatty acid desaturase ( 361)    | 143 | 41.4 | 0.77 |
| gi 144212727 gb EDJ68662.1  | hypothetical protein G ( 299)   | 142 | 41.1 | 0.77 |
| gi 186929487 emb CAC48958.2 | MocD [Sinorhizobium m ( 363)    | 143 | 41.4 | 0.78 |
| gi 141672141 gb ECST3663.1  | hypothetical protein G ( 253)   | 141 | 40.9 | 0.79 |
| gi 135299436 gb EBG71506.1  | hypothetical protein G ( 371)   | 143 | 41.4 | 0.79 |
| gi 136241577 gb EBM83404.1  | hypothetical protein G ( 177)   | 139 | 40.3 | 0.8  |
| gi 142467276 gb ECY29127.1  | hypothetical protein G ( 326)   | 142 | 41.2 | 0.83 |
| gi 140347395 gb ECL15019.1  | hypothetical protein G ( 284)   | 141 | 40.9 | 0.87 |
| gi 143772505 gb EDG70880.1  | hypothetical protein G ( 285)   | 141 | 40.9 | 0.87 |
| gi 138585842 gb ECA61869.1  | hypothetical protein G ( 236)   | 140 | 40.6 | 0.87 |
| gi 39648523 emb CAE27044.1  | putative fatty acid de ( 355)   | 142 | 41.2 | 0.89 |
| gi 134519477 gb EBB82703.1  | hypothetical protein G ( 202)   | 139 | 40.4 | 0.9  |
| gi 84787975 gb ABC64157.1   | hypothetical protein EL ( 304)  | 141 | 40.9 | 0.92 |
| gi 193786708 dbj BAG52031.1 | unnamed protein produ ( 210)    | 139 | 40.4 | 0.93 |
| gi 45503662 emb CAF86845.1  | unnamed protein produc ( 210)   | 139 | 40.4 | 0.93 |
| gi 136020166 gb EBL37299.1  | hypothetical protein G ( 270)   | 140 | 40.7 | 0.98 |
| gi 139522233 gb ECF64931.1  | hypothetical protein G ( 272)   | 140 | 40.7 | 0.98 |

>>gi|88181398|gb|EAQ88866.1| hypothetical protein CHGG\_0 (400 aa)  
 initn: 1699 initl: 964 opt: 1886 Z-score: 2327.3 bits: 439.6 E(): 1.2e-120  
 Smith-Waterman score: 1886; 67.519% identity (84.399% similar) in 391 aa  
 overlap (32-422:15-397)

|        |  |    |    |     |     |     |
|--------|--|----|----|-----|-----|-----|
|        | 10   | 20 | 30 | 40  | 50  | 60  |
| del_15 | AVTTRSHKAAAATEPEVVSTGVDAVSAAAPSSSSSSSQSAEPIEYPDIKTIRDAIPDH |    |    |     |     |     |
|        | :  | :  | :  | :   | :   | :   |
| gi 881 | MATTTTTTTRSRRAAEVKSAPIKLVEGPQYPIQTIRDAIPAH                 |    |    |     |     |     |
|        |  | 10 | 20 | 30  | 40  |     |
|        | 70   | 80 | 90 | 100 | 110 | 120 |



[illegible]



Smith-Waterman score: 1369; 52.868% identity (75.062% similar) in 401 aa overlap (30-427:2-393)

```

      10      20      30      40      50      60
del_15 MAVTTRSHKAAAAATEPEVVSTGVDVSAAPSSSSSSSQKSAEPIEYDICTIRDAIPD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114      MATSTMTLRKSPVEQDESVPSLTKLTKDAIPK
      10      20      30
```

```

      70      80      90      100      110      120
del_15 HCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 DCFESSVVTSLLYLARDILYCAALTYAAFQ-IHLLPWLSLRVAAWTAYGFLQGCVCVTGLW
      40      50      60      70      80      90
```

```

      130      140      150      160      170      180
del_15 ILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHRRFTGHMEKDMAFVPAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 ILAHECGHGAFSRYQGFDVFGWATHSFLMVPYFSWKFTHARHHRFTGHMEKDTVFPVWT
      100      110      120      130      140      150
```

```

      190      200      210      220      230      240
del_15 EADRNQRKLANLYMDKETAEEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSQWET
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 DDQLAQKKNVRLEQLKHLAE---ETPIVSFVQLVAHQFLGWQLYLLNVNTAG--AKSCPD
      160      170      180      190      200
```

```

      250      260      270      280      290
del_15 GKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYLQAAQVVG-WQMVGLLYF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 GSAEV-W-PASHFNPFSLFTSSQWIYIALSDLGLAIMGAVLYYAATQIGAWNVT-LLYV
      210      220      230      240      250      260
```

```

      300      310      320      330      340      350
del_15 QQYFWVHHWLVAITYLHHTHEEVHHFDADSWTFVKALATVDRDFGFIGKHLFHNIIIDHH
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 VPFYFWVHHWLIATYQLQHTHPAVPHYTAETWTYTKGALATIDRTTGFGRHFFHEIIDYH
      270      280      290      300      310      320
```

```

      360      370      380      390      400      410
del_15 VVHHLFPRIPFYAAEATNSIRPMLGPLYHRD-DRSFMGQLWYNFTHCKWVVPDPQ-VPG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 VVHHLFSRIPFYKAERATKAIQPLLGENYHEQKDESFLYSLMMTFRKCIYVSDKGRGMFG
      330      340      350      360      370      380
```

```

      420
del_15 ALIWAHTVQS
      : : : : : :
gi|114 VLHFFVRAEESQ
      390
```

>>gi|134082006|emb|CAK46691.1| unnamed protein product [ (398 aa)  
initn: 1189 initl: 626 opt: 1349 Z-score: 1664.4 bits: 316.9 E(): 9.9e-84  
Smith-Waterman score: 1349; 51.918% identity (76.471% similar) in 391 aa  
overlap (35-419:9-389)

```

      10      20      30      40      50      60
del_15 TRSHKAAAAATEPEVVSTGVDVSAAPSSSSSSSQKSAEPIE----YPDICTIRDAIPD
```

```

      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134      MAELRKVPASQAAQQQQQPIHNDDNVPSLTKLTKDAIPE
      10      20      30
```

```

      70      80      90      100      110      120
del_15 HCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 ECFDSSVVTSLLYLARDILYCAILTYGAF-HIHLPSLPLRALAWAVYGFQGCVCVTGIW
      40      50      60      70      80      90
```

```

      130      140      150      160      170      180
del_15 ILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHRRFTGHMEKDMAFVPAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 ILAHECGHGAFSKHQTFNDIVGWAHSFLMVPYFSWKITHARHHRFTGHMEKDTVFPVWT
      100      110      120      130      140      150
```

```

      190      200      210      220      230      240
del_15 EADRNQRKLANLYMDKETAEEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSQWET
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 DNELAKKK--NVRIEQ-LKHLTEETPIVSFLQLIGHQLFGWQLYFLNVTAGPKSLPENR
      160      170      180      190      200      210
```

```

      250      260      270      280      290
del_15 GKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYLQAAQVVG-WQMVGLLYF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 PIRGAA---SHFNPFGLFTKSYFSIALTDLGLLIMGSILYASTQIGAWNVT-LLYF
      220      230      240      250      260
```

```

      300      310      320      330      340      350
del_15 QQYFWVHHWLVAITYLHHTHEEVHHFDADSWTFVKALATVDRDFGFIGKHLFHNIIIDHH
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 VPYLWVHHWLIATYQLQHTHPAVPHYTAESWTYTKALATIDRSIGFIGRHFHEIIDYH
      270      280      290      300      310      320
```

```

      360      370      380      390      400      410
del_15 VVHHLFPRIPFYAAEATNSIRPMLGPLYHRD-DRSFMGQLWYNFTHCKWVVPDPQVPGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 VVHHLFSRIPFYKAAEATRAIQPLLGVNYHEEKESFLYSLMTTFRKCIYV-SDGKKNV
      330      340      350      360      370      380
```

```

      420
del_15 LIWAHTVQS
      :
gi|134 LHFVLPPEAK
      390
```

>>gi|83776412|dbj|BAE66531.1| unnamed protein product [A (392 aa)  
initn: 1158 initl: 625 opt: 1337 Z-score: 1649.7 bits: 314.2 E(): 6.5e-83  
Smith-Waterman score: 1337; 52.604% identity (75.781% similar) in 384 aa  
overlap (39-419:9-383)

```

      10      20      30      40      50      60
del_15 KAAATEPEVVSTGVDVSAAPSSSSSSSQKSAEPIEYDICTIRDAIPDHCFRPRVW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|837      MAELHNRKAKEAIEKDTTPTLTKELKDAIPKCEFFESSAV
      10      20      30

      70      80      90      100      110      120
```





```

280          290          300          310          320          330
      370      380      390      400      410      420
del_15 PFYYAAEEATNSIRPMLGPLYHRD-DRSFMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS
      .....: ...: ..: ..: ..:
gi|211 PFYHAEKATPAIQPMLGENYHEQKDEGFLYSIMMTFRCKIYVESKGRANGEPEGVLHFLVL
      340      350      360      370      380      390

gi|211 SDESK

>>gi|119398366|gb|EAW08796.1| oleate delta-12 desaturase (391 aa)
initn: 1131 initl: 600 opt: 1305 Z-score: 1610.2 bits: 306.9 E(): 1e-80
Smith-Waterman score: 1305; 52.419% identity (76.075% similar) in 372 aa
overlap (49-419:23-384)

      20      30      40      50      60      70
del_15 VSTGVDVAASAAAPSSSSSSSSQKSAEPIEYPDIKTIRDAIPDHCFRPRVWISMAYFIRDF
      .....: ..: ..:
gi|119 MAEAEVRKRTPEAEAVVPQDNTPSLKSILKDAIPQECFESSLVTSLLYLARDI
      10      20      30      40      50

      80      90      100      110      120      130
del_15 AMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFN
      .: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..:
gi|119 LYCAVLAYGAF-HIHLPLSLPLRIVAWAAYTFFQGCVGVTGLWILAHECGHGAFSRYPRI
      60      70      80      90      100      110

      140      150      160      170      180      190
del_15 NVMGWIGHSFLLVPYFSWKFSHRRHRRFTGHMEKDMAFVPATEADNRNQRKLANLYMDKET
      .: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..:
gi|119 DFIGWAAHSFLLVPYFSWKITHARHRRYTGHMDRDTVFVPWT-ADQLAAK-KNVRLDQ-L
      120      130      140      150      160

      200      210      220      230      240      250
del_15 AEMFEDVPVQLVKLIAHQLAGWQMYLLFNVSAGKSGKWETGKGGMGLRVSHFEPSSA
      ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..:
gi|119 RHLAETPIVTFVQLLGHQLGWQLYLLTNATAGALS--WPESTPKTGV--ASHFNPVGA
      170      180      190      200      210      220

      260      270      280      290      300      310
del_15 VFRNSEAIYIALSDLGLMIMGYILYQAAQVVGWQMVGLLYFQQYFVWHVLVAITYLHHT
      ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..:
gi|119 LWTPAQRLSIALSDLGLIMGAVLWFASTRIGVANVILYFIPYLVVHHLIAITYLQHT
      230      240      250      260      270      280

      320      330      340      350      360      370
del_15 HEEVHHFDADSWTFVKGALATVDRDFGFIGKHLFHNIDHHVVVHHLFPRIPFYAAEEATN
      : ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..: ..:
gi|119 HPALPHYTAETWTYTKGALATVDRTMGFIGRHFFHEIIDYHVVVHHLFSRIPFYEAERATR
      290      300      310      320      330      340

      380      390      400      410      420
del_15 SIRPMLGPLYHRDDR-SFMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS
      .....: ..: ..: ..: ..: ..:
gi|119 AIQPLLGAQYNEDKQESFLGSLVSTFRSCVYVAPSE--PGVLHVFTRRE
      350      360      370      380      390

```





```

gi|826 HKATGNMERDMVFVPR---REQQATRLGKMTHELAHTEETPAFTLMLVLVQLVGVW
      200      210      220      230      240      250
del_15 230      240      250      260      270
YLLFNVSAGKSGKQWETGK-----GMGWLRVSHFEPSSAVFRNSEAYIALSDLGLMIM
::: ::::: . . . .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|826 YLITNVTGHNYHERQREGRGKGKHNGLGG-GVNHFDPRSPLYENSADAKLIVLSDIGILM
      260      270      280      290      300
del_15 280      290      300      310      320      330
GYILYQAAQVVGWQMVGLLYFQQYFWVHHWLVAITYLHHTHEEVHHFDADSWTFVKGALA
. : : . : . . . .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|826 ATALYFLVQKGFYNMAIWFVPYLVVNHVLVAITFLOHTDPTLPHYTNDEWNFVRGAAA
      310      320      330      340      350      360
del_15 340      350      360      370      380      390
TVDRDFGFIGKHLFHNIIDHHVVHHLFPRIPFYAAEATNSIRPMLGPLYHRD----DRS
: . . . .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|826 TIDREMGFIGRHLHGLIETHVLHHYVSSIPFNADEATEAIKPIMGKHRYADVQDGPGRG
      370      380      390      400      410      420
del_15 400      410      420
FMGQLWYNFTHCKWVVPDPQVPGALIIWAHTVQS
. . . .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|826 FIRAMYSARMCQWVEPSAGAEGAGKGVLFFRNRNNVGTTPPAVIKPPA
      430      440      450      460      470
>>gi|144998356|gb|ABP16929.1| Sequence 20 from patent US (477 aa)
initn: 1110 initl: 513 opt: 1141 Z-score: 1406.4 bits: 269.5 E()
Smith-Waterman score: 1141; 42.271% identity (69.082% similar) in
overlap (21-418:47-453)
      10      20      30      40      50
del_15 MAVTTRSHKAAAAATEPEVVSTGVDVAASAPSSSSSSSSQKSAEPIEYPD
      . . . .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|144 TVTSTTVTDSESAAVSPSDSPRHSASSTSLSSMSEVDIAKPKSEYGVMLDTYGNQFEVPD
      20      30      40      50      60      70
del_15 60      70      80      90      100
--IKTIRDAIPDHCFRPRVWISMAYFIRDFAM--AFGLGY--LAWQYIPLIASTPLRYG
: : : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|144 FTIKDIYNAIPKHCFKRSALKGYGILRDIVLLTTFSIWNFVTEYIP---STPARAG
      80      90      100      110      120      130
del_15 110      120      130      140      150      160
AWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFNVMVGWIGHSFLLVPYFSWKFSHHRH
: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|144 LWAVYTVLQGLFGTLGWVIAHECGHGAFSDSRIINDITGWVLHSSLVLVPYFSWQISHRKH
      140      150      160      170      180      190
del_15 170      180      190      200      210      220
HRFTGHMEKDMAFVPATEADRNRKLANLYMDKETAEFMFEDVPIVQLVKLIAHQLAGWQM
. : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|144 HKATGNMERDMVFVPR---REQQATRLGKMTHELAHTEETPAFTLMLVLVQLVGVW
      200      210      220      230      240      250
del_15 230      240      250      260      270

```

```

      230      240      250      260      270
del_15 YLLFNVSAGKSGKQWETGKG-----GMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIM
      ::  ::::  . . . . ::  ::  ::::  . . . . ::  ::::  . .
gi|158 YLITNVTGHNHYHERQREGRGKGKGNHGLGG-GVNHFDPRSPLYENSADAKLIVLSDIGIGLM
      260      270      280      290      300

```

```

      280      290      300      310      320      330
del_15  GYILYQAAQVVGWQMVGLLYFQQYFWVHHHLVAITYLHHTHEEVHHFDASWTFVKGALA
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi|155  ATALYFLVQKFGFYNNMAIWFVPYLWNHHLVAITFLQHTDPTLPHYTNDEWNEFVGGAAA
      310      320      330      340      350      360

```



gi|119 HTGWTGFFKALWTSARTCQWVEPTGAKGESQHVLFYRNINGIGVPPAKIPAK  
420 430 440 450 460

427 residues in 1 query sequences  
3787527556 residues in 14717352 library sequences  
Scomplib [34t26]  
start: Tue Oct 20 14:41:34 2009 done: Tue Oct 20 15:07:36 2009  
Total Scan time: 1517.490 Total Display time: 15.080

Function used was FASTA [version 3.4t26 July 7, 2006]

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Database checksum values:

|   |                                  |
|---|----------------------------------|
| Tue Oct 20 15:07:38 CDT 2009<br>/home/andre/db/AD_2009  | 5c91759664b0377022cf35e7d5a0d23c |
| Tue Oct 20 15:07:38 CDT 2009<br>/home/andre/db/TOX_2009 | fa2987b358e662a0d03802f0cfba9676 |
| Tue Oct 20 15:09:46 CDT 2009<br>/home/andre/db/PRT_2009 | a155ebc7632842e917ba5dd4cce1dc09 |