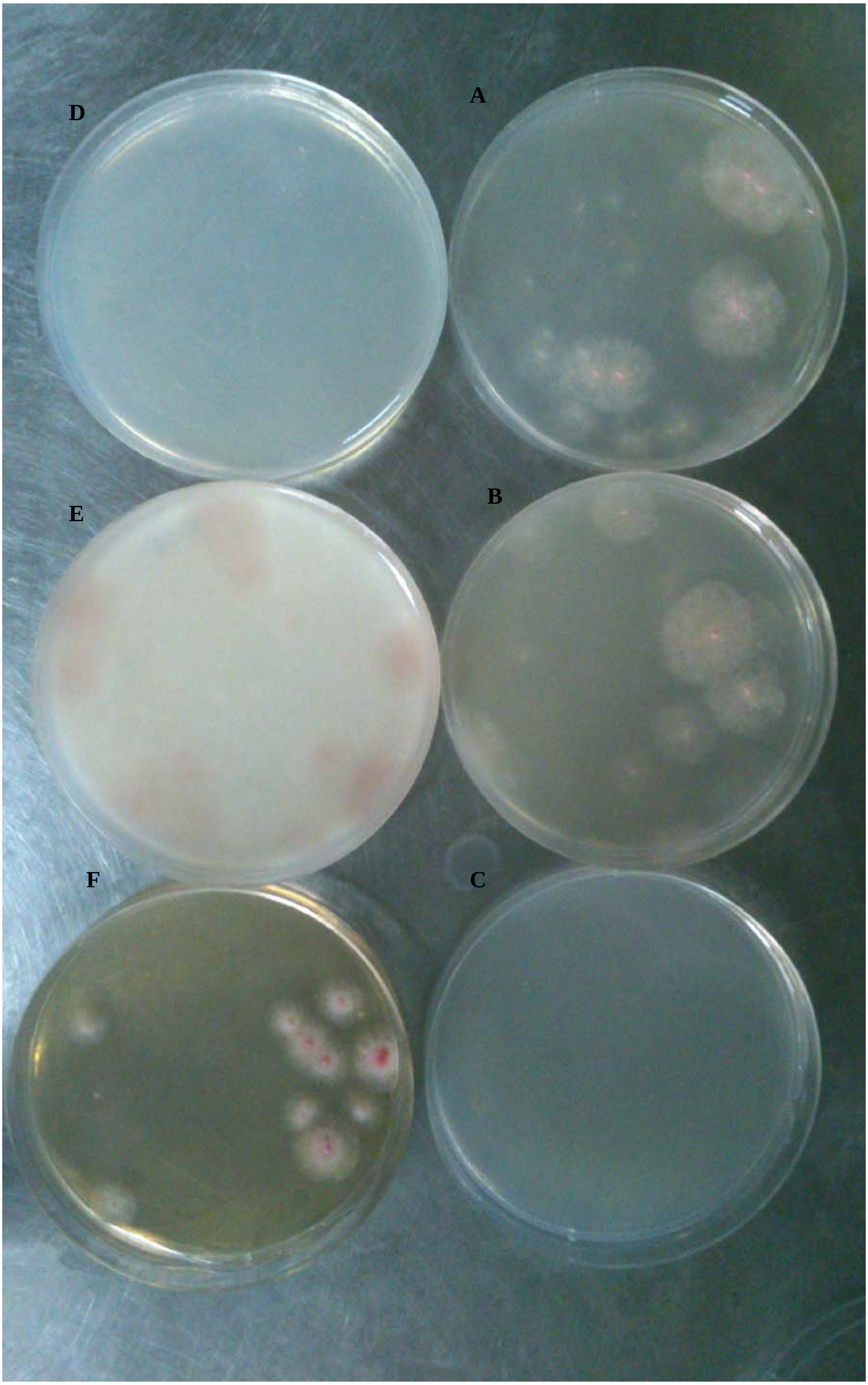

D
A
E
B
F
C

Figure S1. The growth phenotypes of *M. alpina* grown on medium containing glucose (A), phenylalanine (B), phenylacetate (C), phenylalanine and p-chlorophenylalanine (D), tyrosine (E), or glucose and phenylalanine (F) as the carbon source. The data shown are the results of three independent experiments.

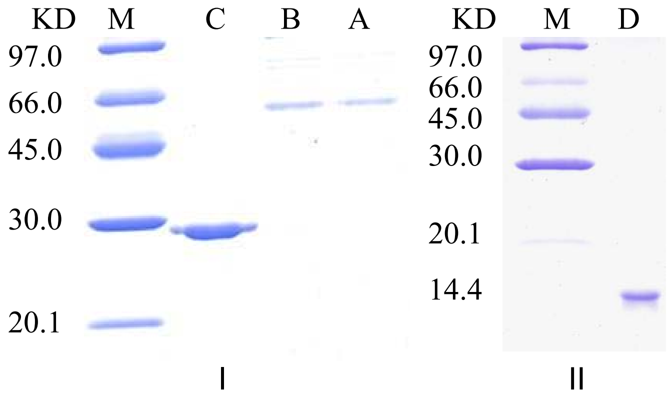


Fig. S2. SDS-polyacrylamide gel electrophoresis. The protein patterns are: (A) PAH-1; (B) PAH-2; (C) DHPR; (D) PCD; Proteins were denatured at 100°C for 5 min in 0.1% SDS and 1% 2-mercaptoehanol before being loaded in a 5% (wt/vol) stacking gel and separated in a 12% (I) or 15% (II) (wt/vol) separation gel. The gel was stained with coomassie bright blue R250. The molecular weight markers from GE Healthcare are indicated at each side of the panel.

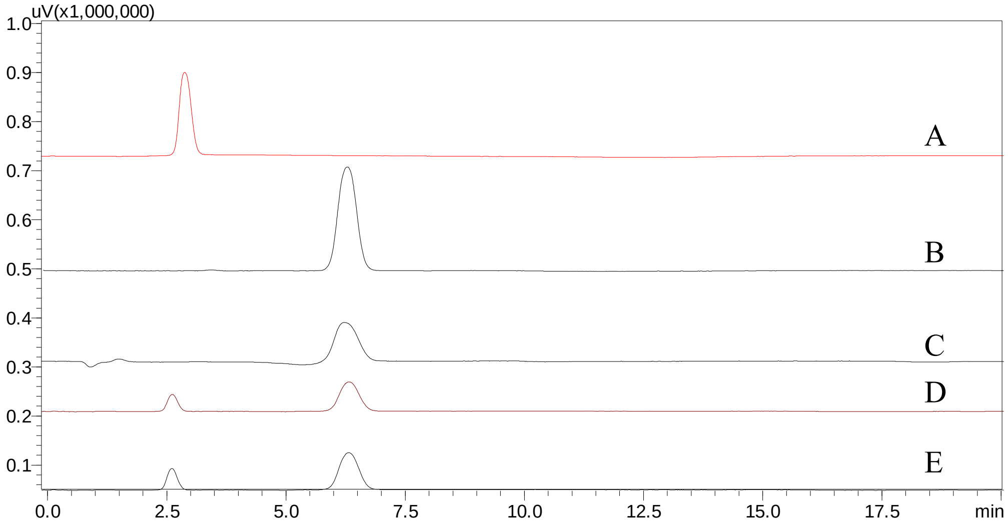


Figure S3. HPLC chromatographs of the reaction products: Tyrosine standard (A); Phenylalanine standard (B); Blank reaction (C); PAH-1 reaction (D); PAH-2 reaction (E).

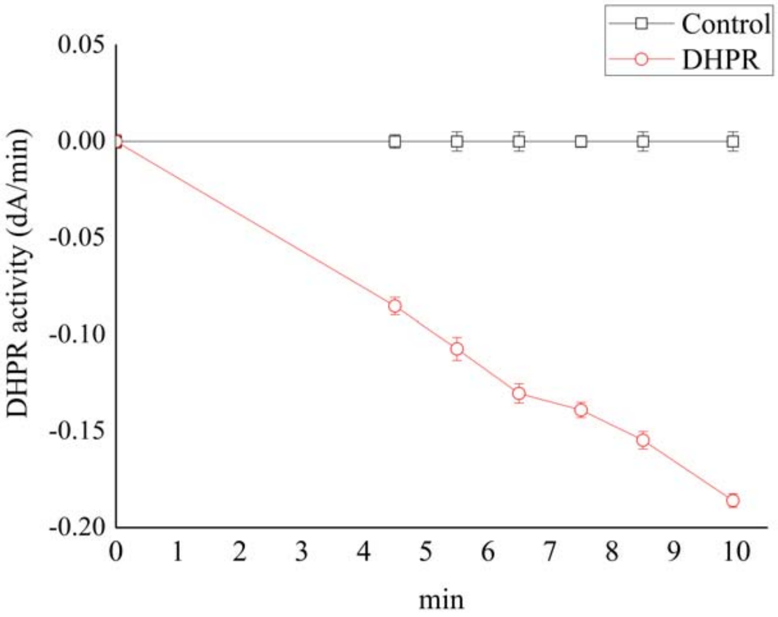
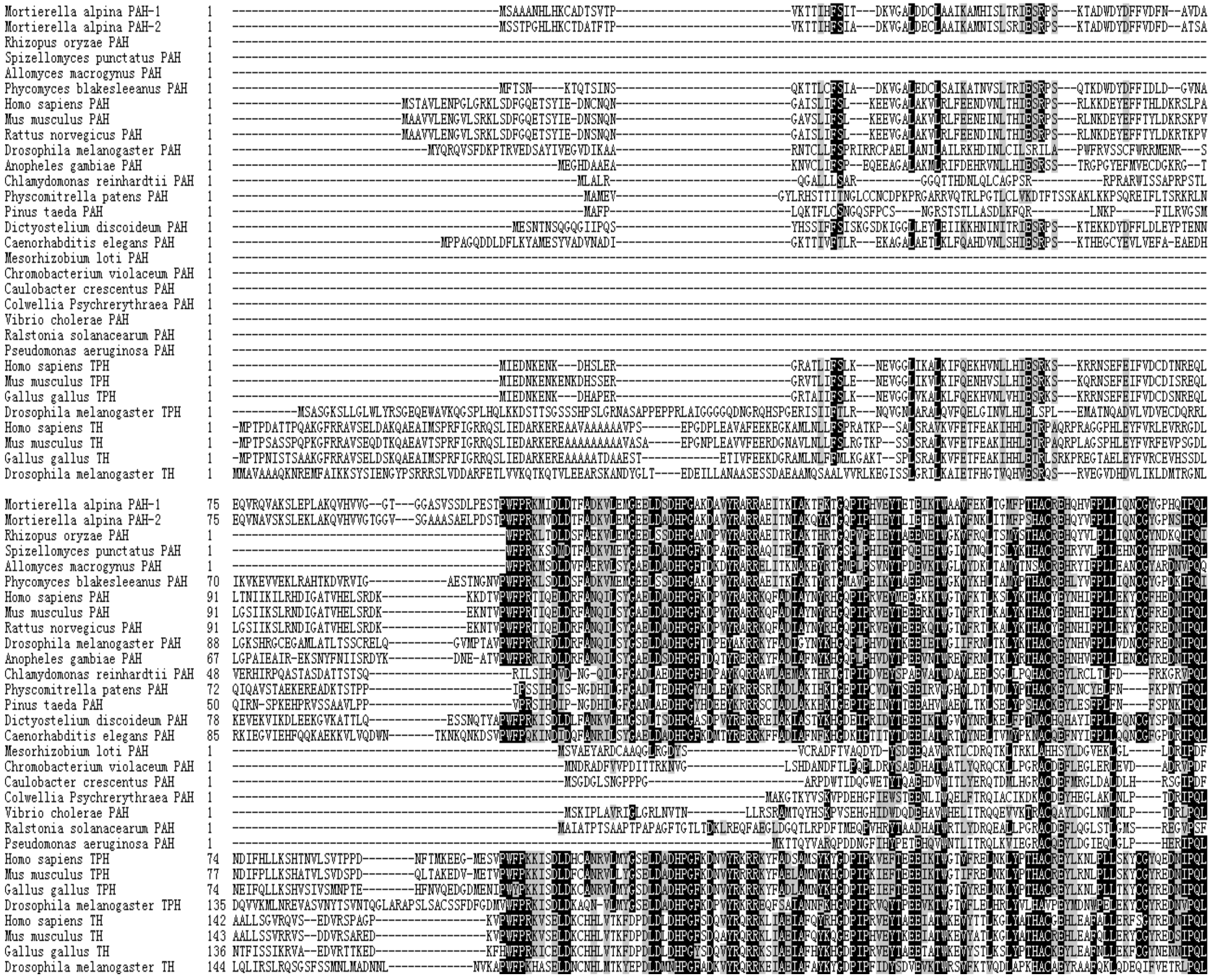


Figure S4. The purified DHPR protein shows DHPR enzyme activity. The open round circle (○) indicates the addition of a recombinant protein and the open square (□) indicates no addition of protein. The data shown are the averages of three independent experiments.


Mortierella alpina PAH-1
Mortierella alpina PAH-2
Rhizopus oryzae PAH
Spizellomyces punctatus PAH
Allomyces macrogynus PAH
Phycomyces blakesleeanus PAH
Homo sapiens PAH
Mus musculus PAH
Rattus norvegicus PAH
Drosophila melanogaster PAH
Anopheles gambiae PAH
Chlamydomonas reinhardtii PAH
Physcomitrella patens PAH
Pinus taeda PAH
Dictyostelium discoideum PAH
Caenorhabditis elegans PAH
Mesorhizobium loti PAH
Chromobacterium violaceum PAH
Caulobacter crescentus PAH
Colwellia Psychrerythraea PAH
Vibrio cholerae PAH
Ralstonia solanacearum PAH
Pseudomonas aeruginosa PAH
Homo sapiens TPH
Mus musculus TPH
Gallus gallus TPH
Drosophila melanogaster TPH
Homo sapiens TH
Mus musculus TH
Gallus gallus TH
Drosophila melanogaster TH
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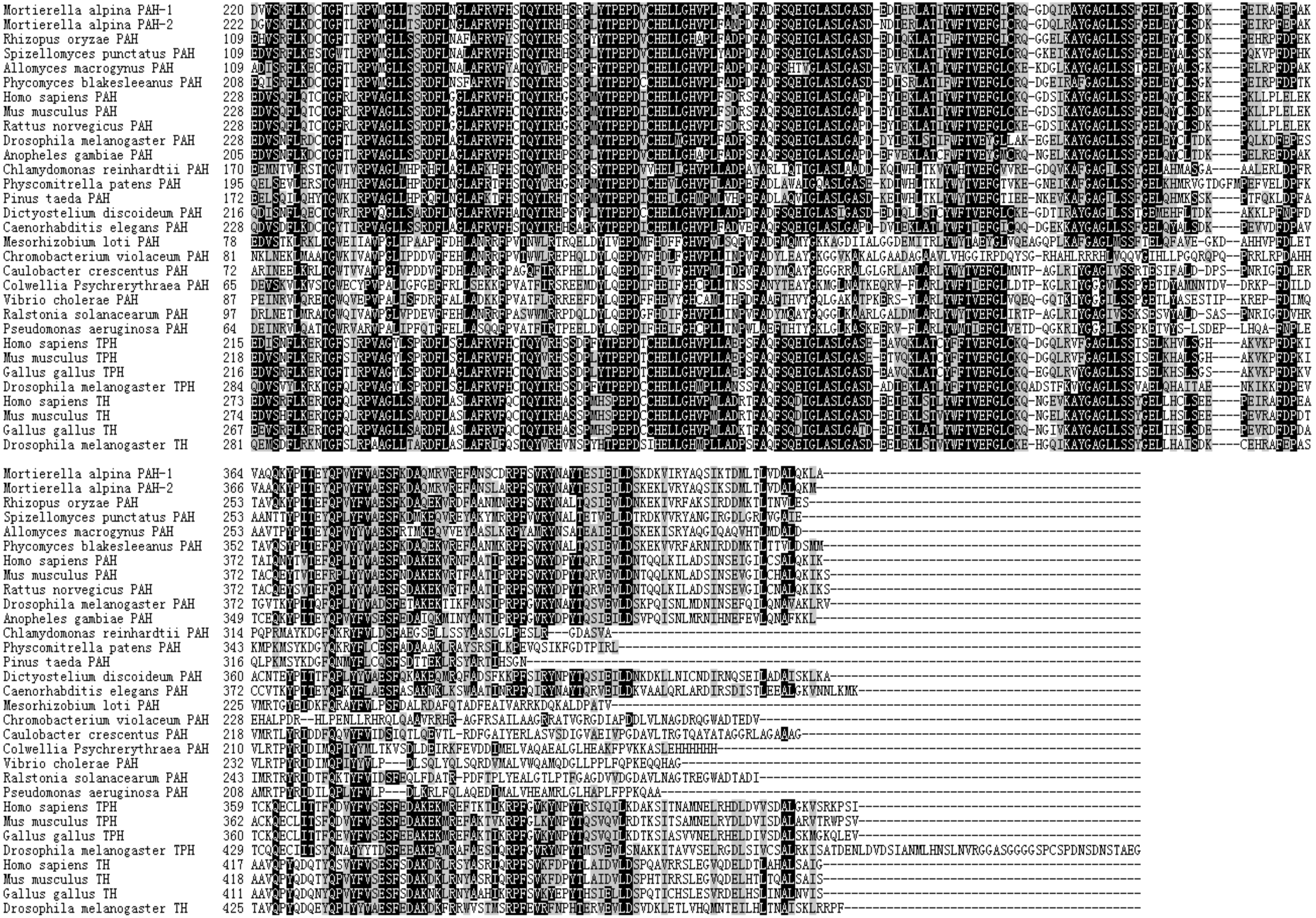

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Mortierella alpina PAH-2          222 DGVSKFLKDCTGFTLRPVMGLLTSRDFLNGLAFRVFHSTQYIRHHSKPLYTPEPDVCHELLGHVPLFANPDFADFSQEIGLASLGASD-NDIERLATIYWFTVEFGICRQ-GDQLRAYGAGLLSSFGELEYCLSDK----PEIRPFEPAK
Rhizopus oryzae PAH               109 EHVSRFLKDCTGFTIRPVMGLLSSRDFLNAFAFRVFYSTQYIRHSSKPYYTPEPDVCHELLGHAPLFADPDFADFSQEIGLASLGASD-EDIQKLATIFWFTVEFGICRQ-GGELKAYGAGLLSSFGELEYCLSDK----PEHRPFDPEK
Spizellomyces punctatus PAH       109 EDVSRFLKESTGWTLRPVMGLLSSRDFLNALAFRVFHSTQYIRHHSKPLYTPEPDVCHELLGHVPLYADPDFADFSQEIGLASLGASD-EDIEKLATIYWFTVEFGLCRQ-GKEIKAYGAGLLSSFGELEYALSSK----PQKVPFDPHK
Allomyces macrogynus PAH          109 ADISRFLKECTGFTLRPVMGLLSSRDFLNALAFRVFYATQYVRHPSMPFYTPEPDICHELLGHVPLFADPDFADFSHTVGLASLGASD-EEVKKLATLYWFTVEFGLCKE-KDGLKAYGAGLLSSTGELEYALSGK----PELRPFDPAK
Phycomyces blakesleeanus PAH      208 EQISRFLKDCTGFTIRPVMGLLSSRDFLNSFAFRVFYSTQYIRHSSKPLYTPEPDCCHELLGHVPLFADPDFADFSQEIGLASLGASD-EDISRLATIFWFTVEFGLCRQ-DGEIRAFGAGLLSSFGELEYCLSGK----PEIRPFDPTK
Homo sapiens PAH                  228 EDVSQFLQTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPD-EYIEKLATIYWFTVEFGLCKQ-GDSIKAYGAGLLSSFGELQYCLSEK----PKLLPLELEK
Mus musculus PAH                  228 EDVSQFLQTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPD-EYIEKLATIYWFTVEFGLCKE-GDSIKAYGAGLLSSFGELQYCLSDK----PKLLPLELEK
Rattus norvegicus PAH             228 EDVSQFLQTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPD-EYIEKLATIYWFTVEFGLCKE-GDSIKAYGAGLLSSFGELQYCLSDK----PKLLPLELEK
Drosophila melanogaster PAH       228 EDVSNFLRDCTGFTLRPVAGLLSSRDFLAGLAFRVFHCTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPSFAQFSQEIGLASLGAPD-DYIEKLSTIFWFTVEYGLLAK-EGELKAYGAGLLSSYGELEYCLTDK----PQLKDFEPES
Anopheles gambiae PAH             205 EDVSNFLKDCTGFTLRPVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPLYTPEPDVCHELLGHAPLFADPSFAQFSQEIGLASLGAPD-EFVEKLATCFWFTVEYGMCRQ-NGELKAYGAGLLSSFGELQYCLTDK----PELREFDPAK
Chlamydomonas reinhardtii PAH     170 EEMNTVLRSTTGWTVRPVAGLMHPRHFLAGLAFKHFHSTQYMRHPSKPSYTPEPDVVHELIGHVPLLADPAYARLIQTIGLASLAADD-KQIWHLTKVYWHTVEFGVVRE-GDQVKAFGAGILSSYGELAHMASGA----AALERLDPFR
Physcomitrella patens PAH         195 QELSEVLERSTGWHIRPVAGLLHPRDFLNGLAFRTFHSTQYVRHGSNPMYTPEPDICHEVLGHVPILADPEFADLAWAIGQASLGASE-KDIWHLTKLYWYTVEFGTVKE-GNEIKAFGAGLLSSFGELKHMRVGTDGFMPEFVELDPFK
Pinus taeda PAH                   172 EELSQILQHYTGWKIRPVAGLLHPRQFLNGLAFKTFHSTQYIRHTSNPMYTPEPDICHEILGHMPMLVHPEFADLAQVIGLASLGASD-KEIWHLTKLYWYTVEFGTIEE-NKEVKAFGAGILSSFGELQHMKSSK----PTFQKLDPFA
Dictyostelium discoideum PAH      216 QDISNFLQECTGWRIRPVQGLLSARDFLNGLAFRVFHATQYIRHPSVPLYTPEPDCCHELLGHVPLLADPDFADFSQEIGLASIGASD-EDIQLLSTCYWFTVEFGLCKE-GDTIRAYGAGILSSTGEMEHFLTDK----AKKLPFNPFD
Caenorhabditis elegans PAH        228 QDVSDFLKDCTGYTIRPVAGLLSSRDFLAGLAFRVFHSTQYIRHHSAPKYTPEPDICHELLGHVPLFADVEFAQFSQEIGLASLGAPD-DVIEKLATLYWFTIEFGICQQ-DGEKKAYGAGLLSSFGELQYALSDK----PEVVDFDPAV
Mesorhizobium loti PAH            78  EDVSTKLRKLTGWEIIAVPGLIPAAPFFDHLANRRFPVTNWLRTRQELDYIVEPDMFHDFFGHVPVLSQPVFADFMQMYGKKAGDIIALGGDEMITRLYWYTAEYGLVQEAGQPLKAFGAGLMSSFTELQFAVE-GKD--AHHVPFDLET
Chromobacterium violaceum PAH     81  NKLNEKLMAATGWKIVAVPGLIPDDVFFEHLANRRFPVTWWLREPHQLDYLQEPDVFHDLFGHVPLLINPVFADYLEAYGKGGVKAKALGAADAGAAVLVHGGIRPDQYSG-RHAHLRRRHLVQQVGIHLLPGQRQPQ--PRRLRPDAHH
Caulobacter crescentus PAH        72  ARINEELKRLTGWTVVAVPGLVPDDVFFDHLANRRFPAGQFIRKPHELDYLQEPDIFHDVFGHVPMLTDPVFADYMQAYGEGGRRALGLGRLANLARLYWYTVEFGLMNTP-AGLRIYGAGIVSSRTESIFALD-DPS--PNRIGFDLER
Colwellia Psychrerythraea PAH     65  DEVSKVLKVSTGWECYPVPALIGFGEFFRLLSEKKFPVATFIRSREEMDYLQEPDIFHEIFGHCPLLTNSSFANYTEAYGKMGLNATKEQRV-FLARLYWFTIEFGLLDTP-KGLRIYGGGVLSSPGETDYAMNNTDV--DRKP-FDILD
Vibrio cholerae PAH               87  PEINRVLQRETGWQVEPVPALISFDRFFALLADKKFPVATFLRRREEFDYLQEPDFFHEVYGHCAMLTHPDFAAFTHVYGQLGAKATPKERS-YLARLYWFTVEFGLVQEQ-GQTKIYGGGILSSPGETLYASESTIP--KREP-FDIMQ
Ralstonia solanacearum PAH        97  DRLNETLMRATGWQIVAVPGLVPDEVFFEHLANRRFPASWWMRRPDQLDYLQEPDGFHDIFGHVPLLINPVFADYMQAYGQGGLKAARLGALDMLARLYWYTVEFGLIRTP-AGLRIYGAGIVSSKSESVYALD-SAS--PNRIGFDVHR
Pseudomonas aeruginosa PAH        64  DEINRVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHCPLLTNPWLAEFTHTYGKLGLKASKEERV-FLARLYWMTIEFGLVETD-QGKRIYGGGILSSPKETVYS-LSDEP--LHQA-FNPLE
Homo sapiens TPH                  215 EDISNFLKERTGFSIRPVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELLGHVPLLAEPSFAQFSQEIGLASLGASE-EAVQKLATCYFFTVEFGLCKQ-DGQLRVFGAGLLSSISELKHVLSGH----AKVKPFDPKI
Mus musculus TPH                  218 EDVSNFLKERTGFSIRPVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFSQEIGLASLGASE-ETVQKLATCYFFTVEFGLCKQ-DGQLRVFGAGLLSSISELKHALSGH----AKVKPFDPKI
Gallus gallus TPH                 216 EDVSRFLKERTGFTIRPVAGYLSPRDFLAGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFSQEIGLASLGASD-EAVQKLATCYFFTVEFGLCKQ-EGQLRVYGAGLLSSISELKHSLSGS----AKVKPFDPKV
Drosophila melanogaster TPH       284 QDVSVYLKRKTGFQLRPVAGYLSPRDFLSGLAFRVFHCTQYIRHSSDPFYTPEPDCCHELLGHMPLLANSSFAQFSQEIGLASLGASD-ADIEKLATLYFFTVEFGLCKQADSTFKVYGAGLLSSVAELQHAITAE----NKIKKFDPEV
Homo sapiens TH                   273 EDVSRFLKERTGFQLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFSQDIGLASLGASD-EEIEKLSTLYWFTVEFGLCKQ-NGEVKAYGAGLLSSYGELLHCLSEE----PEIRAFDPEA
Mus musculus TH                   274 EDVSHFLKERTGFQLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFSQDIGLASLGASD-EEIEKLSTVYWFTVEFGLCKQ-NGELKAYGAGLLSSYGELLHSLSEE----PEVRAFDPDT
Gallus gallus TH                  267 EEVSRFLKERTGFQLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADKTFAQFSQDIGLASLGATD-EEIEKLATLYWFTVEFGLCRQ-NGIVKAYGAGLLSSYGELIHSLSDE----PEVRDFDPDA
Drosophila melanogaster TH        281 QEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQSTQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIGLASLGASD-EEIEKLSTVYWFTVEFGLCKE-HGQIKAYGAGLLSSYGELLHAISDK----CEHRAFEPAS

Mortierella alpina PAH-1          364 VAQQKYPITEYQPVYFVAESFKDAQMRVREFANSCDRPFSVRYNAYTESIEILDSKDKVIRYAQSIKTDMLTLVDALQKLA---------------------------------------------
Mortierella alpina PAH-2          366 VAAQKYPITEYQPVYFVAESFKDAQMRVREFANSLARPFSVRYNAYTESIEILDSKEKLVRYAQSIKSDMLTLVDALQKM----------------------------------------------
Rhizopus oryzae PAH               253 TAVQKYPITEFQPVYFVAESFKDAQEKVRDFAANMNRPFSVRYNALTQSIEVLDNKEKIVRFAKSIRDDMKTLTNVLES-----------------------------------------------
Spizellomyces punctatus PAH       253 AANTTYPITEYQPLYFVAESFKDMKEQVREYAKYMRRPFVVRYNALTETVELLDTRDKVVRYANGIRGDLGRLVGAIE------------------------------------------------
Allomyces macrogynus PAH          253 AAVTPYPITEYQPVYYVAESFRTMKEQVVEYAASLKRPYAMRYNSATEAIEILDSKEKISRYAQGIQAQVHTLMDALD------------------------------------------------
Phycomyces blakesleeanus PAH      352 TAVQSYPITEFQPVYYVAESFKDAQEKVREFAANMKRPFSVRYNALTQSIEVLDSKEKVVRFARNIRDDMKTLTTVLDSMM---------------------------------------------
Homo sapiens PAH                  372 TAIQNYTVTEFQPLYYVAESFNDAKEKVRNFAATIPRPFSVRYDPYTQRIEVLDNTQQLKILADSINSEIGILCSALQKIK---------------------------------------------
Mus musculus PAH                  372 TACQEYTVTEFRPLYYVAESFNDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLDNTQQLKNLADSINSEVGILCHALQKIKS--------------------------------------------
Rattus norvegicus PAH             372 TACQEYSVTEFQPLYYVAESFSDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLDNTQQLKILADSINSEVGILCNALQKIKS--------------------------------------------
Drosophila melanogaster PAH       372 TGVTKYPITQFQPLYYVADSFETAKEKTIKFANSIPRPFGVRYNAYTQSVEVLDSKPQISNLMDNINSEFQILQNAVAKLRV--------------------------------------------
Anopheles gambiae PAH             349 TCEQKYPITEYQPVYFVSESFEDAIQKMINYANTIPRPFGVRYDPYTQSIEILDSVPQISNLMRNIHNEFEVLQNAFKKL----------------------------------------------
Chlamydomonas reinhardtii PAH     314 PQPRMAYKDGFQKRYFVLDSFAEGSELLSSYAASLGLPESLR---GDASVA---------------------------------------------------------------------------
Physcomitrella patens PAH         343 KMPKMSYKDGYQKRYFLCESFADAAAKLRAYSRSILKPEVQSIKFGDTPIRL--------------------------------------------------------------------------
Pinus taeda PAH                   316 QLPKMSYKDGFQNMYFLCQSFSDTTEKLRSYARTIHSGN---------------------------------------------------------------------------------------
Dictyostelium discoideum PAH      360 ACNTEYPITTFQPLYYVAESFQKAKEQMRQFADSFKKPFSIRYNPYTQSIEILDNKDKLLNICNDIRNQSEILADAISKLKA--------------------------------------------
Caenorhabditis elegans PAH        372 CCVTKYPITEYQPKYFLAESFASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKVAALQRLARDIRSDISTLEEALGKVNNLKMK----------------------------------------
Mesorhizobium loti PAH            225 VMRTGYEIDKFQRAYFVLPSFDALRDAFQTADFEAIVARRKDQKALDPATV---------------------------------------------------------------------------
Chromobacterium violaceum PAH     228 EHALPDR--HLPENLLRHRQLQAAVRRHR-AGFRSAILAAGRRATVGRGDIAPDDLVLNAGDRQGWADTEDV------------------------------------------------------
Caulobacter crescentus PAH        218 VMRTLYRIDDFQQVYFVIDSIQTLQEVTL-RDFGAIYERLASVSDIGVAEIVPGDAVLTRGTQAYATAGGRLAGAAAG------------------------------------------------
Colwellia Psychrerythraea PAH     210 VLRTPYRIDIMQPIYYMLTKVSDLDEIRKFEVDDIMELVAQAEALGLHEAKFPVKKASLEHHHHHH------------------------------------------------------------
Vibrio cholerae PAH               232 VLRTPYRIDIMQPIYYVLP---DLSQLYQLSQRDVMALVWQAMQDGLLPPLFQPKEQQHAG-----------------------------------------------------------------
Ralstonia solanacearum PAH        243 IMRTRYRIDTFQKTYFVIDSFEQLFDATR-PDFTPLYEALGTLPTFGAGDVVDGDAVLNAGTREGWADTADI------------------------------------------------------
Pseudomonas aeruginosa PAH        208 AMRTPYRIDILQPLYFVLP---DLKRLFQLAQEDIMALVHEAMRLGLHAPLFPPKQAA--------------------------------------------------------------------
Homo sapiens TPH                  359 TCKQECLITTFQDVYFVSESFEDAKEKMREFTKTIKRPFGVKYNPYTRSIQILKDAKSITNAMNELRHDLDVVSDALGKVSRKPSI----------------------------------------
Mus musculus TPH                  362 ACKQECLITSFQDVYFVSESFEDAKEKMREFAKTVKRPFGLKYNPYTQSVQVLRDTKSITSAMNELRYDLDVISDALARVTRWPSV----------------------------------------
Gallus gallus TPH                 360 TCKQECLITTFQEVYFVSESFEEAKEKMREFAKTIKRPFGVKYNPYTQSVQILKDTKSIASVVNELRHELDIVSDALSKMGKQLEV----------------------------------------
Drosophila melanogaster TPH       429 TCQQECIITSYQNAYYYTDSFEEAKEQMRAFAESIQRPFGVRYNPYTMSVEVLSNAKKITAVVSELRGDLSIVCSALRKISATDENLDVDSIANMLHNSLNVRGGASGGGGSPCSPDNSDNSTAEG
Homo sapiens TH                   417 AAVQPYQDQTYQSVYFVSESFSDAKDKLRSYASRIQRPFSVKFDPYTLAIDVLDSPQAVRRSLEGVQDELDTLAHALSAIG---------------------------------------------
Mus musculus TH                   418 AAVQPYQDQTYQPVYFVSESFSDAKDKLRNYASRIQRPFSVKFDPYTLAIDVLDSPHTIRRSLEGVQDELHTLTQALSAIS---------------------------------------------
Gallus gallus TH                  411 AAVQPYQDQNYQPVYFVSESFSDAKNKLRNYAAHIKRPFSVKYEPYTHSIELLDSPQTICHSLESVRDELHSLINALNVIS---------------------------------------------
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Fig. S5. Multiple amino acid sequence alignment of amino acid hydroxylases from fungi, animal, protist, plant and bacteria. Multiple alignments were performed with the ClustalW program using the BioEdit sequence alignment software. The corresponding nucleotide sequences encoding *M. alpina* PAH has been deposited in the GenBank/EMBL database with Accession No. (JN982953 and JN982954). Accession numbers for the other PAH protein sequences above are: *Rhizopus_oryzae* (RO3G_07757.1), *Spizellomyces punctatus* (SPPG_07026T0), *Allomyces macrogynus* (AMAG_15797T0), *Phycomyces blakesleeanus* (Jgi|Phybl2|161646), *Homo sapiens* (AAH26251.1), *Mus musculus* (CAA36205.1), *Rattus norvegicus* (AAA41843.1),*Drosophila melanogaster* (AAA69513.1), *Anopheles gambiae* (EAA10731.4|), *Chlamydomonas reinhardtii* (HQ003816.1), *Physcomitrella patens* (HQ003815.1), *Pinus taeda* (HQ003814.1),*Dictyostelium discoideum* (EAL67992.1), *Caenorhabditis elegans* (CAA91286.1), *Mesorhizobium loti* (BAB51399.1), *Chromobacterium violaceum* (AAA23115.1), *Caulobacter crescentus* (AAK23591.1), *Colwellia Psychrerythraea* (150261591), *Vibrio cholerae* (AAF96726.1), *Ralstonia solanacearum* (CAD17143.1), and *Pseudomonas aeruginosa* (AAA25936.1). Accession numbers for the TPH protein sequences above are: *Homo sapiens* (AAA67050.1), *Mus musculus* (AAA63401.1), *Gallus gallus* (AAC60036.1), and *Drosophila melanogaster* (AAF47444.1). Accession numbers for the TH protein sequences above are: *Homo sapiens* (AAI04968.1), *Mus musculus* (AAA40434.1), *Gallus gallus* (CAB62388.1), and *Drosophila melanogaster* (CAA53802.1).

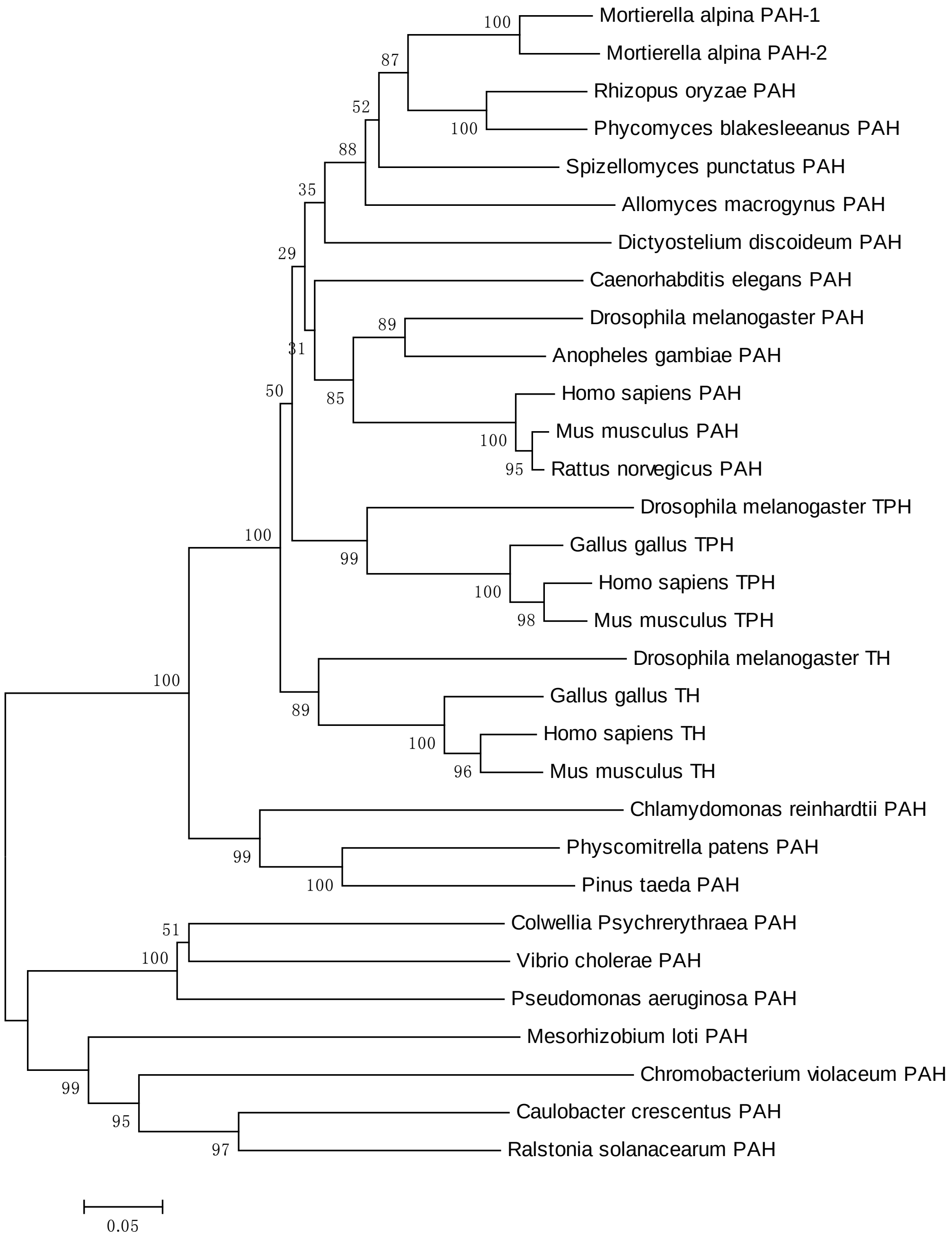

Fig. S6. Phylogenetic tree of amino acid hydroxylases from different organisms (PAH: Phenylalanine hydroxylase; TPH: Tryptophan hydroxylase; TH: Tyrosine hydroxylase). The tree was constructed using the neighbor-joining method with CLUSTAL W NJPLOT. The horizontal branch length is proportional to the amino acid substitution rate per site.

The numbers represent the frequencies with which the tree topology presented here was replicated after 1000 bootstrap iterations.

Table. S1[a]

1	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>jgi|Phybl2|112460|e_gw1.10.203.1	Length =	245	Score =	312 bits	800	Expect =	1.00E-84	Method: Compositional matrix adjust.	Identities = 149/222	(67%	149/222	67%
2	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>CIMT_06798 | CIMG_06516 | Coccidioides immitis RS GTP cyclohydrolase I (translat	Length =	338	Score =	308 bits	789	Expect =	2.00E-83	Method: Compositional matrix adjust.	Identities = 150/223	(67%	150/223	67%
3	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>gnl|GLV|YALI0A10310g similar to uniprot|P51601 Saccharomyces cerevisiae YGR267c	Length =	301	Score =	303 bits	775	Expect =	1.00E-81	Method: Compositional matrix adjust.	Identities = 145/221	(65%	145/221	65%
4	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>HCAG_00487T0 | HCAG_00487 | Histoplasma capsulatum NAm1 GTP cyclohydrolase (tran	Length =	390	Score =	295 bits	754	Expect =	3.00E-79	Method: Compositional matrix adjust.	Identities = 147/220	(66%	147/220	66%
5	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>PTRT_10930 | PTRG_10930 | Pyrenophora tritici-repentis GTP cyclohydrolase I (tra	Length =	329	Score =	294 bits	752	Expect =	4.00E-79	Method: Compositional matrix adjust.	Identities = 142/224	(63%	142/224	63%
6	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>BDET_01270 | BDEG_01266 | Batrachochytrium dendrobatidis GTP cyclohydrolase I (t	Length =	264	Score =	291 bits	745	Expect =	3.00E-78	Method: Compositional matrix adjust.	Identities = 145/250	(58%	145/250	58%
7	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>SPPG_01175T0 | SPPG_01175 | Spizellomyces punctatus DAOM BR117 GTP cyclohydrolas	Length =	274	Score =	287 bits	735	Expect =	4.00E-77	Method: Compositional matrix adjust.	Identities = 137/227	(60%	137/227	60%
8	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>NFIA_038970 | Neosartorya fischeri null (translation) (335 aa)	Length =	334	Score =	286 bits	731	Expect =	1.00E-76	Method: Compositional matrix adjust.	Identities = 145/234	(61%	145/234	61%
9	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>ANID_08188T0 | ANID_08188 | Aspergillus nidulans FGSC A4 GTP cyclohydrolase I (t	Length =	329	Score =	285 bits	728	Expect =	3.00E-76	Method: Compositional matrix adjust.	Identities = 142/220	(64%	142/220	64%
10	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AO090102000517 | Aspergillus oryzae Unknown (translation) (279 aa)	Length =	278	Score =	280 bits	717	Expect =	5.00E-75	Method: Compositional matrix adjust.	Identities = 142/220	(64%	142/220	64%
11	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>Afu5g03140 | Aspergillus fumigatus GTP cyclohydrolase i (translation) (335 aa)	Length =	334	Score =	280 bits	715	Expect =	8.00E-75	Method: Compositional matrix adjust.	Identities = 139/212	(65%	139/212	65%
12	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AMAG_12870T0 | AMAG_12870 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	238	Score =	279 bits	713	Expect =	2.00E-74	Method: Compositional matrix adjust.	Identities = 139/229	(60%	139/229	60%
13	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>Pa_0_1000|chrm2_SCA|Putative GTP cyclohydrolase I	Length =	446	Score =	279 bits	713	Expect =	2.00E-74	Method: Compositional matrix adjust.	Identities = 133/215	(61%	133/215	61%
14	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>orf19.3957 | Candida Albicans sc5314 assembly 21 orf19.3957 (translation) (277	Length =	276	Score =	278 bits	710	Expect =	3.00E-74	Method: Compositional matrix adjust.	Identities = 132/219	(60%	132/219	60%
15	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AMAG_14237T0 | AMAG_14237 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	235	Score =	277 bits	709	Expect =	5.00E-74	Method: Compositional matrix adjust.	Identities = 130/171	(76%	130/171	76%
16	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AMAG_15175T0 | AMAG_15175 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	267	Score =	277 bits	709	Expect =	5.00E-74	Method: Compositional matrix adjust.	Identities = 135/211	(63%	135/211	63%
17	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>VDAG_05019T0 | VDAG_05019 | Verticillium dahliae VdLs.17 GTP cyclohydrolase I (t	Length =	352	Score =	276 bits	706	Expect =	9.00E-74	Method: Compositional matrix adjust.	Identities = 129/220	(58%	129/220	58%
18	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AMAG_11330T0 | AMAG_11330 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	269	Score =	276 bits	705	Expect =	1.00E-73	Method: Compositional matrix adjust.	Identities = 135/209	(64%	135/209	64%
19	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>BC1T_07979 | BC1G_07979 | Botrytis cinerea GTP cyclohydrolase I (translation) (3	Length =	303	Score =	275 bits	702	Expect =	3.00E-73	Method: Compositional matrix adjust.	Identities = 135/243	(55%	135/243	55%
20	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>SPAC17A5_13.1 | SPAC17A5_13 | Schizosaccharomyces pombe 972h- GTP cyclohydrolase	Length =	235	Score =	274 bits	701	Expect =	4.00E-73	Method: Compositional matrix adjust.	Identities = 133/209	(63%	133/209	63%
21	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>SS1T_09610 | SS1G_09610 | Sclerotinia sclerotiorum GTP cyclohydrolase (translati	Length =	303	Score =	274 bits	701	Expect =	4.00E-73	Method: Compositional matrix adjust.	Identities = 130/216	(60%	130/216	60%
22	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>MGG_09458T0 | MGG_09458 | Magnaporthe grisea 70-15 GTP cyclohydrolase I (transla	Length =	310	Score =	274 bits	700	Expect =	5.00E-73	Method: Compositional matrix adjust.	Identities = 131/220	(59%	131/220	59%
23	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>CNAG_04010T0 | CNAG_04010 | Cryptococcus neoformans grubii H99 GTP cyclohydrolas	Length =	435	Score =	271 bits	694	Expect =	2.00E-72	Method: Compositional matrix adjust.	Identities = 129/209	(61%	129/209	61%
24	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>jgi|Phchr1|32514|gwh2.3.518.1	Length =	215	Score =	270 bits	691	Expect =	5.00E-72	Method: Compositional matrix adjust.	Identities = 130/212	(61%	130/212	61%
25	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>YGR267C FOL2 SGDID:S000003499, Chr VII from 1025741-1025010, reverse complement,	Length =	243	Score =	266 bits	681	Expect =	7.00E-71	Method: Compositional matrix adjust.	Identities = 131/228	(57%	131/228	57%
26	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>FGST_06700 | FGSG_05854 | Fusarium graminearum conserved hypothetical protein (t	Length =	322	Score =	265 bits	678	Expect =	2.00E-70	Method: Compositional matrix adjust.	Identities = 136/216	(62%	136/216	62%
27	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>jgi|Lacbi1|171534|estExt_Genewise1_human.C_20975	Length =	181	Score =	260 bits	665	Expect =	6.00E-69	Method: Compositional matrix adjust.	Identities = 117/169	(69%	117/169	69%
28	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>SNOT_11256 | SNOG_11256 | Stagonospora nodorum GCH1_PHYBL GTP cyclohydrolase I (	Length =	177	Score =	259 bits	662	Expect =	1.00E-68	Method: Compositional matrix adjust.	Identities = 123/173	(71%	123/173	71%
29	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>NCUT_07956 | NCU07774 | Neurospora crassa GTP cyclohydrolase I (translation) (18	Length =	182	Score =	255 bits	652	Expect =	2.00E-67	Method: Compositional matrix adjust.	Identities = 117/168	(69%	117/168	69%
30	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>AO090001000235 | Aspergillus oryzae Unknown (translation) (238 aa)	Length =	237	Score =	237 bits	604	Expect =	7.00E-62	Method: Compositional matrix adjust.	Identities = 106/172	(61%	106/172	61%
31	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>CC1G_14672T0 | CC1G_14672 | Coprinus cinereus okayama7#130 GTP cyclohydrolase I	Length =	284	Score =	221 bits	562	Expect =	5.00E-57	Method: Compositional matrix adjust.	Identities = 107/177	(60%	107/177	60%
32	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>CHGT_06822 | CHGG_06822 | Chaetomium globosum hypothetical protein (translation)	Length =	233	Score =	207 bits	527	Expect =	5.00E-53	Method: Compositional matrix adjust.	Identities = 98/175	(56%)	98/175	56%
33	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>MGG_05045T0 | MGG_05045 | Magnaporthe grisea 70-15 GTP cyclohydrolase I (transla	Length =	258	Score =	207 bits	526	Expect =	7.00E-53	Method: Compositional matrix adjust.	Identities = 93/171	(54%)	93/171	54%
34	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>UM06446 | Ustilago maydis hypothetical protein (translation) (124 aa)	Length =	123	Score =	195 bits	496	Expect =	2.00E-49	Method: Compositional matrix adjust.	Identities = 93/123	(75%)	93/123	75%
35	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>CHGT_10779 | CHGG_10779 | Chaetomium globosum hypothetical protein similar to GT	Length =	124	Score =	188 bits	478	Expect =	2.00E-47	Method: Compositional matrix adjust.	Identities = 89/121	(73%)	89/121	73%
36	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>PAAG_04343T0 | PAAG_04343 | Paracoccidioides brasiliensis Pb01 GTP cyclohydrolas	Length =	347	Score =	176 bits	447	Expect =	9.00E-44	Method: Compositional matrix adjust.	Identities = 92/172	(53%)	92/172	53%
37	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>RO3T_02061 | RO3G_02062 | Rhizopus oryzae GTP cyclohydrolase I (translation) (10	Length =	102	Score =	143 bits	360	Expect =	1.00E-33	Method: Compositional matrix adjust.	Identities = 64/89	(71%)	64/89	71%
38	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>BC1T_02106 | BC1G_02106 | Botrytis cinerea GTP cyclohydrolase I (translation) (1	Length =	1504	Score =	113 bits	283	Expect =	1.00E-24	Method: Compositional matrix adjust.	Identities = 52/82	(63%)	52/82	63%
39	3.5.4.16_evm.TU.scaffold00173.121_3.5.4.16_a	(268 letters)	268	>Afu3g13710 | Aspergillus fumigatus GTP cyclohydrolase I precursor (translation)	Length =	98	Score =	112 bits	280	Expect =	3.00E-24	Method: Compositional matrix adjust.	Identities = 55/99	(55%)	55/99	55%
40	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>jgi|Phybl2|112460|e_gw1.10.203.1	Length =	245	Score =	345 bits	886	Expect =	1.00E-94	Method: Compositional matrix adjust.	Identities = 163/222	(73%	163/222	73%
41	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>CIMT_06798 | CIMG_06516 | Coccidioides immitis RS GTP cyclohydrolase I (translat	Length =	338	Score =	336 bits	861	Expect =	1.00E-91	Method: Compositional matrix adjust.	Identities = 157/213	(73%	157/213	73%
42	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>PTRT_10930 | PTRG_10930 | Pyrenophora tritici-repentis GTP cyclohydrolase I (tra	Length =	329	Score =	322 bits	825	Expect =	1.00E-87	Method: Compositional matrix adjust.	Identities = 152/223	(68%	152/223	68%
43	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>HCAG_00487T0 | HCAG_00487 | Histoplasma capsulatum NAm1 GTP cyclohydrolase (tran	Length =	390	Score =	320 bits	821	Expect =	4.00E-87	Method: Compositional matrix adjust.	Identities = 152/213	(71%	152/213	71%
44	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>gnl|GLV|YALI0A10310g similar to uniprot|P51601 Saccharomyces cerevisiae YGR267c	Length =	301	Score =	318 bits	816	Expect =	2.00E-86	Method: Compositional matrix adjust.	Identities = 151/213	(70%	151/213	70%
45	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>SPPG_01175T0 | SPPG_01175 | Spizellomyces punctatus DAOM BR117 GTP cyclohydrolas	Length =	274	Score =	318 bits	815	Expect =	2.00E-86	Method: Compositional matrix adjust.	Identities = 151/241	(62%	151/241	62%
46	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AO090102000517 | Aspergillus oryzae Unknown (translation) (279 aa)	Length =	278	Score =	316 bits	810	Expect =	8.00E-86	Method: Compositional matrix adjust.	Identities = 152/213	(71%	152/213	71%
47	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>BDET_01270 | BDEG_01266 | Batrachochytrium dendrobatidis GTP cyclohydrolase I (t	Length =	264	Score =	316 bits	810	Expect =	1.00E-85	Method: Compositional matrix adjust.	Identities = 147/212	(69%	147/212	69%
48	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>NFIA_038970 | Neosartorya fischeri null (translation) (335 aa)	Length =	334	Score =	315 bits	808	Expect =	1.00E-85	Method: Compositional matrix adjust.	Identities = 153/216	(70%	153/216	70%
49	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>ANID_08188T0 | ANID_08188 | Aspergillus nidulans FGSC A4 GTP cyclohydrolase I (t	Length =	329	Score =	315 bits	808	Expect =	2.00E-85	Method: Compositional matrix adjust.	Identities = 151/212	(71%	151/212	71%
50	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>Afu5g03140 | Aspergillus fumigatus GTP cyclohydrolase i (translation) (335 aa)	Length =	334	Score =	313 bits	802	Expect =	7.00E-85	Method: Compositional matrix adjust.	Identities = 152/213	(71%	152/213	71%
51	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>jgi|Phchr1|32514|gwh2.3.518.1	Length =	215	Score =	310 bits	795	Expect =	5.00E-84	Method: Compositional matrix adjust.	Identities = 147/215	(68%	147/215	68%
52	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>Pa_0_1000|chrm2_SCA|Putative GTP cyclohydrolase I	Length =	446	Score =	309 bits	791	Expect =	1.00E-83	Method: Compositional matrix adjust.	Identities = 143/215	(66%	143/215	66%
53	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>BC1T_07979 | BC1G_07979 | Botrytis cinerea GTP cyclohydrolase I (translation) (3	Length =	303	Score =	303 bits	777	Expect =	5.00E-82	Method: Compositional matrix adjust.	Identities = 146/243	(60%	146/243	60%
54	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>MGG_09458T0 | MGG_09458 | Magnaporthe grisea 70-15 GTP cyclohydrolase I (transla	Length =	310	Score =	303 bits	775	Expect =	9.00E-82	Method: Compositional matrix adjust.	Identities = 142/220	(64%	142/220	64%
55	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>SS1T_09610 | SS1G_09610 | Sclerotinia sclerotiorum GTP cyclohydrolase (translati	Length =	303	Score =	302 bits	774	Expect =	1.00E-81	Method: Compositional matrix adjust.	Identities = 141/215	(65%	141/215	65%
56	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>VDAG_05019T0 | VDAG_05019 | Verticillium dahliae VdLs.17 GTP cyclohydrolase I (t	Length =	352	Score =	302 bits	773	Expect =	2.00E-81	Method: Compositional matrix adjust.	Identities = 138/220	(62%	138/220	62%
57	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>CNAG_04010T0 | CNAG_04010 | Cryptococcus neoformans grubii H99 GTP cyclohydrolas	Length =	435	Score =	301 bits	770	Expect =	4.00E-81	Method: Compositional matrix adjust.	Identities = 139/209	(66%	139/209	66%
58	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>SPAC17A5_13.1 | SPAC17A5_13 | Schizosaccharomyces pombe 972h- GTP cyclohydrolase	Length =	235	Score =	300 bits	767	Expect =	7.00E-81	Method: Compositional matrix adjust.	Identities = 143/222	(64%	143/222	64%
59	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AMAG_11330T0 | AMAG_11330 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	269	Score =	300 bits	767	Expect =	9.00E-81	Method: Compositional matrix adjust.	Identities = 156/269	(57%	156/269	57%
60	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AMAG_14237T0 | AMAG_14237 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	235	Score =	299 bits	766	Expect =	1.00E-80	Method: Compositional matrix adjust.	Identities = 152/239	(63%	152/239	63%
61	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AMAG_12870T0 | AMAG_12870 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	238	Score =	299 bits	765	Expect =	2.00E-80	Method: Compositional matrix adjust.	Identities = 152/237	(64%	152/237	64%
62	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AMAG_15175T0 | AMAG_15175 | Allomyces macrogynus ATCC 38327 GTP cyclohydrolase I	Length =	267	Score =	298 bits	763	Expect =	2.00E-80	Method: Compositional matrix adjust.	Identities = 151/266	(56%	151/266	56%
63	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>orf19.3957 | Candida Albicans sc5314 assembly 21 orf19.3957 (translation) (277	Length =	276	Score =	298 bits	762	Expect =	3.00E-80	Method: Compositional matrix adjust.	Identities = 139/208	(66%	139/208	66%
64	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>FGST_06700 | FGSG_05854 | Fusarium graminearum conserved hypothetical protein (t	Length =	322	Score =	291 bits	746	Expect =	3.00E-78	Method: Compositional matrix adjust.	Identities = 145/215	(67%	145/215	67%
65	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>YGR267C FOL2 SGDID:S000003499, Chr VII from 1025741-1025010, reverse complement,	Length =	243	Score =	286 bits	732	Expect =	9.00E-77	Method: Compositional matrix adjust.	Identities = 137/216	(63%	137/216	63%
66	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>jgi|Lacbi1|171534|estExt_Genewise1_human.C_20975	Length =	181	Score =	279 bits	713	Expect =	2.00E-74	Method: Compositional matrix adjust.	Identities = 128/182	(70%	128/182	70%
67	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>NCUT_07956 | NCU07774 | Neurospora crassa GTP cyclohydrolase I (translation) (18	Length =	182	Score =	273 bits	697	Expect =	1.00E-72	Method: Compositional matrix adjust.	Identities = 125/177	(70%	125/177	70%
68	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>SNOT_11256 | SNOG_11256 | Stagonospora nodorum GCH1_PHYBL GTP cyclohydrolase I (	Length =	177	Score =	266 bits	680	Expect =	1.00E-70	Method: Compositional matrix adjust.	Identities = 127/178	(71%	127/178	71%
69	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>AO090001000235 | Aspergillus oryzae Unknown (translation) (238 aa)	Length =	237	Score =	245 bits	626	Expect =	2.00E-64	Method: Compositional matrix adjust.	Identities = 112/199	(56%	112/199	56%
70	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>CC1G_14672T0 | CC1G_14672 | Coprinus cinereus okayama7#130 GTP cyclohydrolase I	Length =	284	Score =	238 bits	608	Expect =	2.00E-62	Method: Compositional matrix adjust.	Identities = 132/271	(48%	132/271	48%
71	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>CHGT_06822 | CHGG_06822 | Chaetomium globosum hypothetical protein (translation)	Length =	233	Score =	237 bits	604	Expect =	6.00E-62	Method: Compositional matrix adjust.	Identities = 108/175	(61%	108/175	61%
72	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>MGG_05045T0 | MGG_05045 | Magnaporthe grisea 70-15 GTP cyclohydrolase I (transla	Length =	258	Score =	215 bits	547	Expect =	3.00E-55	Method: Compositional matrix adjust.	Identities = 103/203	(50%	103/203	50%
73	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>PAAG_04343T0 | PAAG_04343 | Paracoccidioides brasiliensis Pb01 GTP cyclohydrolas	Length =	347	Score =	204 bits	520	Expect =	4.00E-52	Method: Compositional matrix adjust.	Identities = 103/172	(59%	103/172	59%
74	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>UM06446 | Ustilago maydis hypothetical protein (translation) (124 aa)	Length =	123	Score =	196 bits	497	Expect =	2.00E-49	Method: Compositional matrix adjust.	Identities = 94/124	(75%)	94/124	75%
75	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>CHGT_10779 | CHGG_10779 | Chaetomium globosum hypothetical protein similar to GT	Length =	124	Score =	188 bits	478	Expect =	3.00E-47	Method: Compositional matrix adjust.	Identities = 89/121	(73%)	89/121	73%
76	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>RO3T_02061 | RO3G_02062 | Rhizopus oryzae GTP cyclohydrolase I (translation) (10	Length =	102	Score =	156 bits	395	Expect =	1.00E-37	Method: Compositional matrix adjust.	Identities = 70/97	(72%)	70/97	72%
77	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>BC1T_02106 | BC1G_02106 | Botrytis cinerea GTP cyclohydrolase I (translation) (1	Length =	1504	Score =	119 bits	298	Expect =	2.00E-26	Method: Compositional matrix adjust.	Identities = 55/92	(59%)	55/92	59%
78	3.5.4.16_evm.TU.scaffold00326.155_3.5.4.16_b	(268 letters)	268	>Afu3g13710 | Aspergillus fumigatus GTP cyclohydrolase I precursor (translation)	Length =	98	Score =	109 bits	272	Expect =	2.00E-23	Method: Compositional matrix adjust.	Identities = 55/99	(55%)	55/99	55%
79	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>SPPG_04785T0 | SPPG_04785 | Spizellomyces punctatus DAOM BR117 6-pyruvoyl-tetrah	Length =	137	Score =	184 bits	467	Expect =	1.00E-46	Method: Compositional matrix adjust.	Identities = 84/137	(61%)	84/137	61%
80	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>RO3T_04822 | RO3G_04823 | Rhizopus oryzae hypothetical protein (translation) (17	Length =	177	Score =	177 bits	448	Expect =	2.00E-44	Method: Compositional matrix adjust.	Identities = 81/142	(57%)	81/142	57%
81	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>jgi|Phybl2|132802|estExt_Genewise1Plus.C_80027	Length =	166	Score =	167 bits	423	Expect =	2.00E-41	Method: Compositional matrix adjust.	Identities = 76/142	(53%)	76/142	53%
82	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>AMAG_03379T0 | AMAG_03379 | Allomyces macrogynus ATCC 38327 6-pyruvoyl tetrahydr	Length =	209	Score =	144 bits	363	Expect =	1.00E-34	Method: Compositional matrix adjust.	Identities = 75/143	(52%)	75/143	52%
83	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>BDET_08489 | BDEG_08464 | Batrachochytrium dendrobatidis 6-pyruvoyl tetrahydrobi	Length =	127	Score =	139 bits	351	Expect =	4.00E-33	Method: Compositional matrix adjust.	Identities = 66/138	(47%)	66/138	47%
84	4.2.3.12 evm.TU.scaffold00184.409_4.2.3.12	(146 letters)	146	>AMAG_04684T0 | AMAG_04684 | Allomyces macrogynus ATCC 38327 6-pyruvoyl tetrahydr	Length =	237	Score =	128 bits	321	Expect =	1.00E-29	Method: Compositional matrix adjust.	Identities = 73/171	(42%)	73/171	42%
85	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>jgi|Phybl2|159803|fgenesh1_kg.21_#_45_#_1737_1_CBNA_CBNB_CBNC_CBNF	Length =	273	Score =	214 bits	544	Expect =	6.00E-55	Method: Compositional matrix adjust.	Identities = 121/285	(42%	121/285	42%
86	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>SPPG_07804T0 | SPPG_07804 | Spizellomyces punctatus DAOM BR117 sepiapterin reduc	Length =	261	Score =	141 bits	356	Expect =	4.00E-33	Method: Compositional matrix adjust.	Identities = 94/276	(34%)	94/276	34%
87	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>BDET_01123 | BDEG_01119 | Batrachochytrium dendrobatidis conserved hypothetical	Length =	223	Score =	131 bits	329	Expect =	6.00E-30	Method: Compositional matrix adjust.	Identities = 77/212	(36%)	77/212	36%
88	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>RO3T_12510 | RO3G_12511 | Rhizopus oryzae hypothetical protein (translation) (19	Length =	198	Score =	123 bits	308	Expect =	2.00E-27	Method: Compositional matrix adjust.	Identities = 82/219	(37%)	82/219	37%
89	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>SNOT_02538 | SNOG_02538 | Stagonospora nodorum hypothetical protein (translation	Length =	259	Score = 7	71.6 bits	174	Expect =	5.00E-12	Method: Compositional matrix adjust.	Identities = 84/290	(28%)	84/290	28%
90	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>PTRT_08144 | PTRG_08144 | Pyrenophora tritici-repentis short chain dehydrogenase	Length =	262	Score = 6	65.9 bits	159	Expect =	3.00E-10	Method: Compositional matrix adjust.	Identities = 71/272	(26%)	71/272	26%
91	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>orf19.6837 | Candida Albicans sc5314 assembly 21 orf19.6837 (translation) (254	Length =	253	Score = 6	65.5 bits	158	Expect =	4.00E-10	Method: Compositional matrix adjust.	Identities = 75/287	(26%)	75/287	26%
92	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>HCAG_03338T0 | HCAG_03338 | Histoplasma capsulatum NAm1 short-chain dehydrogenas	Length =	262	Score = 6	62 bits	149	Expect =	5.00E-09	Method: Compositional matrix adjust.	Identities = 74/275	(26%)	74/275	26%
93	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>AO090120000042 | Aspergillus oryzae Unknown (translation) (254 aa)	Length =	253	Score = 6	61.6 bits	148	Expect =	6.00E-09	Method: Compositional matrix adjust.	Identities = 75/270	(27%)	75/270	27%
94	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>YIR036C IRC24 SGDID:S000001475, Chr IX from 422862-422071, reverse complement, U	Length =	263	Score = 6	61.2 bits	147	Expect =	7.00E-09	Method: Compositional matrix adjust.	Identities = 38/119	(31%)	38/119	31%
95	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>CHGT_06529 | CHGG_06529 | Chaetomium globosum hypothetical protein (translation)	Length =	269	Score = 5	58.2 bits	139	Expect =	5.00E-08	Method: Compositional matrix adjust.	Identities = 71/278	(25%)	71/278	25%
96	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>PAAG_01557T0 | PAAG_01557 | Paracoccidioides brasiliensis Pb01 short-chain dehyd	Length =	257	Score = 5	57 bits	136	Expect =	1.00E-07	Method: Compositional matrix adjust.	Identities = 67/270	(24%)	67/270	24%
97	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>BC1T_09610 | BC1G_09610 | Botrytis cinerea hypothetical protein similar to short	Length =	255	Score = 5	56.6 bits	135	Expect =	2.00E-07	Method: Compositional matrix adjust.	Identities = 65/262	(24%)	65/262	24%
98	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>orf19.5194.1 | Candida Albicans sc5314 assembly 21 orf19.5194.1 (translation) (	Length =	253	Score = 5	55.8 bits	133	Expect =	3.00E-07	Method: Compositional matrix adjust.	Identities = 62/262	(23%)	62/262	23%
99	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>CIMT_00697 | CIMG_00647 | Coccidioides immitis RS NADP-dependent L-serine/L-allo	Length =	270	Score = 5	55.1 bits	131	Expect =	6.00E-07	Method: Compositional matrix adjust.	Identities = 53/235	(22%)	53/235	22%
100	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>NFIA_003520 | Neosartorya fischeri null (translation) (254 aa)	Length =	253	Score = 5	54.3 bits	129	Expect =	9.00E-07	Method: Compositional matrix adjust.	Identities = 70/278	(25%)	70/278	25%
101	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>AO090026000725 | Aspergillus oryzae Unknown (translation) (270 aa)	Length =	269	Score = 5	53.5 bits	127	Expect =	1.00E-06	Method: Compositional matrix adjust.	Identities = 58/236	(24%)	58/236	24%
102	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>ANID_09357T0 | ANID_09357 | Aspergillus nidulans FGSC A4 short-chain dehydrogena	Length =	262	Score = 5	52.8 bits	125	Expect =	2.00E-06	Method: Compositional matrix adjust.	Identities = 51/180	(28%)	51/180	28%
103	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>YIR035C YIR035C SGDID:S000001474, Chr IX from 421787-421023, reverse complement,	Length =	254	Score = 5	52.4 bits	124	Expect =	3.00E-06	Method: Compositional matrix adjust.	Identities = 46/150	(30%)	46/150	30%
104	1.1.1.153evm.TU.scaffold00213.635_1.1.1.153	(282 letters)	282	>jgi|Phybl2|61319|Phybl1.fgeneshPB_pg.3__944	Length =	256	Score = 5	52 bits	123	Expect =	4.00E-06	Method: Compositional matrix adjust.	Identities = 39/148	(26%)	39/148	26%
105	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>RO3T_07756 | RO3G_07757 | Rhizopus oryzae hypothetical protein (translation) (43	Length =	433	Score =	648 bits	1672	Expect =	0	Method: Compositional matrix adjust.	Identities = 304/433	(70%	304/433	70%
106	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>jgi|Phybl2|161646|fgenesh1_pg.1_#_731	Length =	432	Score =	640 bits	1650	Expect =	0	Method: Compositional matrix adjust.	Identities = 297/430	(69%	297/430	69%
107	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>SPPG_07026T0 | SPPG_07026 | Spizellomyces punctatus DAOM BR117 phenylalanine hyd	Length =	495	Score =	583 bits	1502	Expect =	1.00E-165	Method: Compositional matrix adjust.	Identities = 277/445	(62%	277/445	62%
108	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>RO3T_12091 | RO3G_12092 | Rhizopus oryzae hypothetical protein (translation) (36	Length =	360	Score =	555 bits	1429	Expect =	1.00E-157	Method: Compositional matrix adjust.	Identities = 260/359	(72%	260/359	72%
109	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>AMAG_15797T0 | AMAG_15797 | Allomyces macrogynus ATCC 38327 phenylalanine-4-hydr	Length =	545	Score =	523 bits	1346	Expect =	1.00E-147	Method: Compositional matrix adjust.	Identities = 259/456	(56%	259/456	56%
110	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>AMAG_14369T0 | AMAG_14369 | Allomyces macrogynus ATCC 38327 phenylalanine-4-hydr	Length =	544	Score =	518 bits	1334	Expect =	1.00E-146	Method: Compositional matrix adjust.	Identities = 256/451	(56%	256/451	56%
111	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>BDET_00193 | BDEG_00192 | Batrachochytrium dendrobatidis phenylalanine-4-hydroxy	Length =	227	Score =	330 bits	846	Expect =	1.00E-89	Method: Compositional matrix adjust.	Identities = 150/222	(67%	150/222	67%
112	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>BDET_00194 | BDEG_00193 | Batrachochytrium dendrobatidis conserved hypothetical	Length =	228	Score =	131 bits	329	Expect =	1.00E-29	Method: Compositional matrix adjust.	Identities = 71/148	(47%)	71/148	47%
113	1.14.16.1evm.TU.scaffold00112.263_1.14.16.1_a	(444 letters)	444	>AMAG_15877T0 | AMAG_15877 | Allomyces macrogynus ATCC 38327 mitochondrial interm	Length =	475	Score = 7	77 bits	188	Expect =	2.00E-13	Method: Compositional matrix adjust.	Identities = 45/100	(45%)	45/100	45%
114	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>RO3T_07756 | RO3G_07757 | Rhizopus oryzae hypothetical protein (translation) (43	Length =	433	Score =	656 bits	1693	Expect =	0	Method: Compositional matrix adjust.	Identities = 307/427	(71%	307/427	71%
115	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>jgi|Phybl2|161646|fgenesh1_pg.1_#_731	Length =	432	Score =	639 bits	1647	Expect =	0	Method: Compositional matrix adjust.	Identities = 297/434	(68%	297/434	68%
116	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>SPPG_07026T0 | SPPG_07026 | Spizellomyces punctatus DAOM BR117 phenylalanine hyd	Length =	495	Score =	588 bits	1516	Expect =	1.00E-167	Method: Compositional matrix adjust.	Identities = 279/446	(62%	279/446	62%
117	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>RO3T_12091 | RO3G_12092 | Rhizopus oryzae hypothetical protein (translation) (36	Length =	360	Score =	561 bits	1446	Expect =	1.00E-159	Method: Compositional matrix adjust.	Identities = 263/361	(72%	263/361	72%
118	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>AMAG_15797T0 | AMAG_15797 | Allomyces macrogynus ATCC 38327 phenylalanine-4-hydr	Length =	545	Score =	530 bits	1364	Expect =	1.00E-149	Method: Compositional matrix adjust.	Identities = 258/455	(56%	258/455	56%
119	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>AMAG_14369T0 | AMAG_14369 | Allomyces macrogynus ATCC 38327 phenylalanine-4-hydr	Length =	544	Score =	527 bits	1358	Expect =	1.00E-149	Method: Compositional matrix adjust.	Identities = 256/450	(56%	256/450	56%
120	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>BDET_00193 | BDEG_00192 | Batrachochytrium dendrobatidis phenylalanine-4-hydroxy	Length =	227	Score =	332 bits	852	Expect =	2.00E-90	Method: Compositional matrix adjust.	Identities = 151/222	(68%	151/222	68%
121	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>BDET_00194 | BDEG_00193 | Batrachochytrium dendrobatidis conserved hypothetical	Length =	228	Score =	132 bits	331	Expect =	6.00E-30	Method: Compositional matrix adjust.	Identities = 73/156	(46%)	73/156	46%
122	1.14.16.1evm.TU.scaffold00320.72_1.14.16.1_b	(445 letters)	445	>AMAG_15877T0 | AMAG_15877 | Allomyces macrogynus ATCC 38327 mitochondrial interm	Length =	475	Score = 8	80.5 bits	197	Expect =	2.00E-14	Method: Compositional matrix adjust.	Identities = 47/100	(47%)	47/100	47%

[a] Genome sequences of Candida albicans(1), Rhizopus oryzae(16), Aspergillus fumigatus Af293(19), Ashbya gossypii (Eremothecium gossypii) ATCC 10895(4), Aspergillus nidulans FGSC A4(8), Aspergillus niger CBS 513.88(20), Aspergillus oryzae RIB40(17), Botryotinia fuckeliana B05.10, Candida glabrata CBS138(5), Cryptococcus neoformans JEC21 (Filobasidiella neoformans JEC21)(15), Debaryomyces hansenii CBS767(5), Encephalitozoon cuniculi GB-M1(12), Fusarium graminearum (Gibberella zeae PH-1)v(2), Kluyveromyces lactis NRRL Y-1140(5), Kluyveromyces waltii NCYC 2644(13), Laccaria bicolor S238N-H82(18), Malassezia globosa CBS 7966(24), Magnaporthe

grisea 70-15(3), Neurospora crassa OR74A(7), Neosartorya fischeri NRRL 181, Podospora anserina DSM 980(6), Phanerochaete chrysosporium, Pichia stipitis CBS 6054(10), Saccharomyces bayanus(14), Saccharomyces cerevisiae S288C(9), Saccharomyces mikatae(14), Saccharomyces paradoxus(14), Schizosaccharomyces pombe 972h(23), Sclerotinia sclerotiorum 1980 UF-70, Ustilago maydis 521(11), Yarrowia lipolytica CLIB122(5), Schizosaccharomyces cryophilus OY26, Schizosaccharomyces japonicus yFS275 and Schizosaccharomyces octosporus ATCC4206 (21), and Vanderwaltozyma polyspora DSM 70294(22) were published. Genome sequences of Nectria haematococca MPVI (Fusarium solani) (Joint Genome Institute), Trichoderma atroviride P1 (Joint Genome Institute), Trichoderma virens Gv29-8 (Joint Genome Institute), Batrachochytrium dendrobatidis JAM81 (Joint Genome Institute), Mucor circinelloides (Joint Genome Institute), Trichoderma reese QM6a (Joint Genome Institute), Neosartorya fischeri NRRL 181 (Broad Institute), and Phytophthora infestans T30-4 (Broad Institute) were downloaded from the corresponding websites.

Table. S2. The status of fatty acids in *M. alpina* and *A. oryza* grown on PAH inhibitor medium[a]

Medium	Cell dry weight (CDW) (g/L)	Cell lipid (mg/g CDW)	SAFA						MUFA							
			14:0	16:0	18:0	20:0	22:0	24:0	14:1	16:1	total 18:1	oleate	vaccenate	20:1	22:1	24:1
Inhibitor (*M. alpina*)	5.3±0.2	24.1±1.3	2.4±0.1	18.5±1.1	8.7±0.6	0.5±0.1	1.4±0.2	2.9±0.1		0.1±0.0	24.2±1.4	23.8±1.2	0.4±0.1	0.8±0.1		0.2±0.0
Inhibitor+Tyrosine (*M. alpina*)	5.1±0.2	24.2±1.2	2.2±01	19.7±09	7.9±0.3	0.5±0.1	1.6±0.2	4.2±0.2		0.1±0.0	24.9±1.3	24.5±1.2	0.4±0.1	0.7±0.1		0.1±0.0
Control (*M. alpina*)	6.6±0.2	35.5±1.5	1.3±0.1	16.2±1.5	11.0±0.8	0.6±0.1	1.3±0.1	1.9±0.1		0.1±0.0	11.7±1.8	11.4±1.6	0.3±0.0	0.3±0.0		0.2±0.0
Inhibitor (*A. oryzae*)	7.0±0.2	11.6±0.2	0.4±0.0	11.8±03	15.4±0.5	0.4±0.0	0.4±0.0	2.2±0.1		0.3±0.0	20.7±1.0	20.6±1.0	0.1±0.0	0.1±0.0		
Control (*A. oryzae*)	7.3±0.3	11.2±0.2	0.4±0.0	11.7±0.2	14.8±0.8	0.4±0.0	0.4±0.0	2.1±0.1		0.3±0.0	21.2±1.2	21.1±1.2	0.1±0.0	0.1±0.0		

Medium	ω6 PUFA					ω3 PUFA					
	18:2	20:2	18:3 n-6	20:3	20:4	18:3 n-3	20:5	22:5	22:6	24:5	24:6
Inhibitor (*M. alpina*)	18.8±1.2	0.7±0.1			20.8±0.8		0.1±0.0				
Inhibitor+Tyrosine (*M. alpina*)	19.1±0.9	0.6±0.1			18.1±0.7		0.1±0.0				
Control (*M. alpina*)	20.8±1.7	0.8±0.1			33.9±2.1		0.1±0.0				
Inhibitor (*A. oryzae*)	46.7±2.3	0.1±0.0				1.5±0.1					
Control (*A. oryzae*)	47.0±2.0	0.1±0.0				1.5±0.1					

[a] Molar percent of each fatty acid in day 6 mycelia. 14:0 myristic acid (tetradecanoic acid), 14:1 myristoleic acid (tetradecenoic acid), 16:0 palmitic acid (hexadecanoic acid), 16:1 palmitoleic acid (hexadecenoic acid), 18:0 stearic acid (octadecanoic acid), 18:1 oleic acid (9Z-octadecenoic acid) and vaccenic acid (11Z-octadecenoic acid), 18:2 linoleic acid (octadecadienoic acid), 18:3 α-linolenic acid (9Z,12Z,15Zoctadecatrienoic acid) and γ-linolenic acid (6Z,9Z,12Z-octadecatrienoic acid), 20:0 arachidic acid (eicosanoic acid), 20:1 gondoic acid (eicosenoic acid), 20:2 (Eicosadienoic acid), 20:3 dihomo-γ-linolenic acid (eicosatrienoic acid), 20:4 arachidonic acid (eicosatetraenoic acid), 20:5 EPA (eicosapentaenoic acid), 22:0 behenic acid (docosanoic acid), 22:1 erucic acid

(docosenoic acid), 22:5 DPA (docosapentaenoic acid), 22:6 DHA (docosahexaenoic acid), 24:0 lignoceric acid (tetracosanoic acid), 24:1 nervonic acid (tetracosenoic acid), 24:5 (tetracosapentaenoic acid), and 24:6 (tetracosahexaenoic acid). The data shown are the averages of three independent experiments.

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