

SUPPLEMENTAL DATA FOR

A NEW GROUP OF AROMATIC PRENYLTRANSFERASES IN FUNGI, CATALYSING A 2,7-DIHYDROXYNAPHTHALENE DIMETHYLALLYL- TRANSFERASE REACTION

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Tables S1 to S5 show the genes surrounding the *ptf* genes in the genomes of the respective fungal genomes. Database searches for the closest orthologs were performed with the BLASTP programme (<http://www.ncbi.nlm.nih.gov/>).

Figures S1 and S2 show the $^1\text{H-NMR}$ and $^{13}\text{C-NMR}$ spectra of the enzymatic product formed by Ptf_{At} from 2,7-dihydroxynaphthalene and DMAPP.

Table S1: Genes surrounding the *ptf_{At}* gene in the genome of *Aspergillus terreus* NIH2624 (accession no. CH476594)

Gene	Size (aa)	Ortholog identified by BLAST search	Identity/ Similarity (%)	Origin	Protein accession No
ATEG_00811	401	hypothetical protein	66/81	<i>Aspergillus niger</i>	CAK96480
ATEG_00812	648	acetyl-coenzyme A synthetase	64/79	<i>Aspergillus fumigatus</i> Af293	EAL89682
ATEG_00813	1329	hypothetical protein	72/81	<i>Aspergillus oryzae</i>	BAE56163
ATEG_00814	522	putative choline transport protein	86/94	<i>Aspergillus flavus</i> NRRL3357	EED57752
ATEG_00815	377	conserved hypothetical protein	77/86	<i>Neosartorya fischeri</i> NRRL181	EAW22332
ATEG_00816	591	polysaccharide deacetylase family protein	79/87	<i>Neosartorya fischeri</i> NRRL181	EAW22333
ATEG_00817	528	hypothetical protein	72/83	<i>Aspergillus niger</i>	CAK44057
ATEG_00818	445	UDP-N-acetylglucosamine enolpyruvyl transferase	59/74	<i>Neosartorya fischeri</i> NRRL181	EAW18555
ATEG_00819	839	putative UDP-N-acetylmuramate--L-alanine ligase	94/97	<i>Aspergillus flavus</i> NRRL3357	EED46932
ATEG_00820	584	hypothetical protein	74/84	<i>Aspergillus nidulans</i> FGSC A4	EAA66650
ATEG_00821 = <i>ptf_{At}</i>	336	hypothetical protein SS1G_09465	48/64	<i>Sclerotinia sclerotiorum</i> 1980	EDN93598
ATEG_00822	188	Pc22g22620	31/54	<i>Penicillium chrysogenum</i> Wisconsin 54-1255	CAP99550
ATEG_00823	540	3-phytase A precursor	50/66	<i>Pyrenophora tritici-repentis</i> Pt-1C-BFP	EDU47362
ATEG_00824	1012	hypothetical protein	45/60	<i>Aspergillus niger</i>	CAK43185
ATEG_00825	929	hypothetical protein	91/96	<i>Aspergillus niger</i>	CAK96205
ATEG_00826	362	conserved hypothetical protein	73/84	<i>Aspergillus flavus</i> NRRL3357	EED57747
ATEG_00827	265	putative autophagy protein Atg27	61/78	<i>Aspergillus flavus</i> NRRL3357	EED57746
ATEG_00828	158	putative prefoldin subunit 4	70/78	<i>Aspergillus flavus</i> NRRL3357	EED57744
ATEG_00829	809	hypothetical protein	73/81	<i>Aspergillus oryzae</i>	BAE56155
ATEG_00830	110	hypothetical protein	27/43	<i>Aspergillus oryzae</i> RIB40	BAE64290
ATEG_00831	143	conserved hypothetical protein	78/86	<i>Aspergillus flavus</i> NRRL3357	EED57742

Table S2: Genes surrounding the *ptf_{BF}* gene in the genome of *Botryotinia fuckeliana* B05.10 (accession no. CH476844)

Gene	Size (aa)	Ortholog identified by BLAST search	Identity/ Similarity (%)	Origin	Protein accession No
BC1G_01285	497	Ca ²⁺ /H ⁺ antiporter	89/94	Sclerotinia sclerotiorum 1980	EDN93607
BC1G_01286	245	hypothetical protein SS1G_09475 (carboxypeptidase 4)	89/94	Sclerotinia sclerotiorum 1980	EDN93608
BC1G_01287	122	hypothetical protein SS1G_09475 (carboxypeptidase 4)	88/93	Sclerotinia sclerotiorum 1980	EDN93608
BC1G_01288	553	hypothetical protein SS1G_09476 (hypothetical protein)	76/82	Sclerotinia sclerotiorum 1980	EDN93609
BC1G_01289	678	hypothetical protein SS1G_09477 (peptidoglycan binding domain containing protein)	64/77	Sclerotinia sclerotiorum 1980	EDN93610
BC1G_01290	168	hypothetical protein SS1G_09470 (RPEL repeat protein)	92/95	Sclerotinia sclerotiorum 1980	EDN93603
BC1G_01291	624	hypothetical protein SS1G_09467 (DNA-Polymerase K)	86/91	Sclerotinia sclerotiorum 1980	EDN93600
BC1G_01292	804	hypothetical protein SS1G_09468 (elongation factor G)	97/98	Sclerotinia sclerotiorum 1980	EDN93601
BC1G_01293	306	hypothetical protein	52/69	Aspergillus oryzae RIB40	BAE65671
BC1G_01294	804	conserved hypothetical protein	40/58	Penicillium marneffeii ATCC 18224	EEA19618
BC1G_01295 = <i>ptf_{BF}</i>	309	hypothetical protein SS1G_09465	81/89	Sclerotinia sclerotiorum 1980	EDN93598
BC1G_01296	56	--			
BC1G_01297	474	hypothetical protein SS1G_09461 (proteasome regulatory subunit)	92/94	Sclerotinia sclerotiorum 1980	EDN93594
BC1G_01298	190	hypothetical protein SS1G_09462 (dihydrofolate reductase)	87/92	Sclerotinia sclerotiorum 1980	EDN93595
BC1G_01299	174	conserved hypothetical protein	49/63	Aspergillus flavus NRRL3357	EED55112
BC1G_01300	135	pyridoxamine 5'-phosphate oxidase-related FMN-binding	33/46	Methylobacterium nodulans ORS 2060	ACL59804
BC1G_01301	63	molybdopterin-guanine dinucleotide biosynthesis protein B	35/49	Desulfatibacillum alkenivorans AK-01	ACL05682
BC1G_01302	55	--			
BC1G_01303	677	hypothetical protein SS1G_09456 (hypothetical protein)	79/87	Sclerotinia sclerotiorum 1980	EDN93589
BC1G_01304	70	--			
BC1G_01305	80	hypothetical protein BACCAC_03661	46/66	Bacteroides caccae ATCC43185	EDM19155

Table S3: Genes surrounding the *ptf_{ss}* gene in the genome of *Sclerotinia sclerotiorum* 1980 (accession no. CH476633)

Gene	Size (aa)	Ortholog identified by BLAST search	Identity/ Similarity (%)	Origin	Protein accession No
SS1G_09455	178	predicted protein	43/55	Botryotinia fuckeliana B05.10	EDN25746
SS1G_09456	849	hypothetical protein BC1G_01303 (hypothetical protein)	79/87	Botryotinia fuckeliana B05.10	EDN25743
SS1G_09457	119	3-oxoacyl-(acyl-carrier-protein) synthase	44/63	Bdellovibrio bacteriovorus HD100	CAE79862
SS1G_09458	70	hypothetical protein TRIADDRAFT_55459	38/56	Trichoplax adhaerens	EDV25400
SS1G_09459	60	predicted protein	42/62	Aspergillus terreus NIH2624	EAU33099
SS1G_09460	55	conserved hypothetical protein	42/57	Corynebacterium genitalium ATCC 33030	EEV90421
SS1G_09461	493	hypothetical protein	92/94	Botryotinia fuckeliana B05.10	EDN25737
SS1G_09462	284	hypothetical protein BC1G_01298 (dihydrofolate reductase)	87/92	Botryotinia fuckeliana B05.10	EDN25738
SS1G_09463	38	--			
SS1G_09464	131	putative 1,4- α -glucan branching enzyme	32/51	Toxoplasma gondii GT1	EEE26148
SS1G_09465	309	hypothetical protein BC1G_01295 = <i>ptf_{ss}</i>	81/89	Botryotinia fuckeliana B05.10	EDN25735
SS1G_09466	66	--			
SS1G_09467	562	hypothetical protein BC1G_01291 (DNA polymerase K)	86/91	Botryotinia fuckeliana B05.10	EDN25731
SS1G_09468	804	hypothetical protein BC1G_01292 (elongation factor G)	97/98	Botryotinia fuckeliana B05.10	EDN25732
SS1G_09469	55	--			
SS1G_09470	168	hypothetical protein BC1G_01290 (RPEL repeat protein)	92/95	Botryotinia fuckeliana B05.10	EDN25730
SS1G_09471	518	hypothetical protein NECHADRAFT_88411	44/58	Nectria haematococca mp VI 77-13-4	EEU34828
SS1G_09472	144	predicted protein	58/71	Botryotinia fuckeliana B05.10	EDN25723
SS1G_09473	65	predicted protein	96/98	Botryotinia fuckeliana B05.10	EDN25724
SS1G_09474	493	hypothetical protein BC1G_01285 (Ca ²⁺ /H ⁺ antiporter)	90/94	Botryotinia fuckeliana B05.10	EDN25725
SS1G_09475	554	carboxypeptidase	60/71	Aspergillus fumigatus	AAR96056

Table S4: Genes surrounding the *ptf_{Pm}* gene in the genome of *Penicillium marneffe* ATCC18224 (accession no. DS995899)

Gene	Size (aa)	Ortholog identified by BLAST search	Identity/ Similarity (%)	Origin	Protein accession No
PMAA_022220	660	putative sulfur metabolite repression control protein SconB	91/93	Talaromyces stipitatus ATCC10500	EED19784
PMAA_022230	129	Pc12g02210	41/58	Penicillium chrysogenum Wisconsin 54-1255	CAP79848
PMAA_022240					
A	349	putative alcohol dehydrogenase	88/95	Talaromyces stipitatus ATCC10500	EED19785
B	339	putative alcohol dehydrogenase	87/94	Talaromyces stipitatus ATCC10500	EED19785
PMAA_022250	131	DNA mismatch repair protein MutL	31/48	Microscilla marina ATCC23134	EAY29540
PMAA_022260	507	conserved hypothetical protein	83/89	Talaromyces stipitatus ATCC10500	EED19787
PMAA_022270	871	putative MHYT domain signaling protein	78/86	Talaromyces stipitatus ATCC10500	EED19788
PMAA_022280	608	putative dihydroxy acid dehydratase Ilv3	95/98	Talaromyces stipitatus ATCC10500	EED19792
PMAA_022290	687	putative protein kinase	86/90	Talaromyces stipitatus ATCC10500	EED19793
PMAA_022300	206	putative mitochondrial import inner membrane translocase subunit, TIM-family	94/96	Talaromyces stipitatus ATCC10500	EED19800
PMAA_022310	1666	HEAT repeat protein	79/88	Talaromyces stipitatus ATCC10500	EED19802
PMAA_022320 364		hypothetical protein BC1G_01295	36/55	Botryotinia fuckeliana B05.10	EDN25735
= <i>ptf_{Pm}</i>					
PMAA_022330	636	putative autophagy protein Atg20	95/97	Talaromyces stipitatus ATCC10500	EED19803
PMAA_022340	1448	putative ubiquitin C-terminal hydrolase	90/94	Talaromyces stipitatus ATCC10500	EED19804
PMAA_022350					
A	438	hypothetical protein	47/56	Talaromyces stipitatus ATCC10500	EED19805
B	422	hypothetical protein	48/57	Talaromyces stipitatus ATCC10500	EED19805
C	312	hypothetical protein	47/58	Talaromyces stipitatus ATCC10500	EED19805
D	308	hypothetical protein	47/58	Talaromyces stipitatus ATCC10500	EED19805
E	308	hypothetical protein	47/58	Talaromyces stipitatus ATCC10500	EED19805
PMAA_022360	102	putative conidiation protein Con-6	78/89	Talaromyces stipitatus ATCC10500	EED19807
PMAA_022370	125	conserved hypothetical protein	84/90	Talaromyces stipitatus ATCC10500	EED19809
PMAA_022380	650	putative GPI anchored endo-1,3(4)- β -glucanase	58/67	Talaromyces stipitatus ATCC10500	EED19810
PMAA_022390	305	conserved hypothetical protein	79/87	Talaromyces stipitatus ATCC10500	EED19811
PMAA_022400	166	hypothetical protein TSTA_030760	36/45	Talaromyces stipitatus ATCC10500	EED19813
PMAA_022410	266	hypothetical protein TSTA_030770	63/79	Talaromyces stipitatus ATCC10500	EED19814
PMAA_022420	151	conserved hypothetical protein	89/96	Talaromyces stipitatus ATCC10500	EED17425

Table S5: Genes surrounding the *ptf_{Mc}* gene in the genome of *Microsporium canis* CBS113480 (accession no. DS995704, DS995705)

Gene	Size (aa)	Ortholog identified by BLAST search	Identity/ Similarity (%)	Origin	Protein accession No
MCYG_05050	237	conserved hypothetical protein	32/44	Neosartorya fischeri NRRL181	EAW19675
MCYG_05051	387	FG-GAP repeat domain-containing protein	39/51	Microsporium canis CBS113480	EEQ28605
MCYG_05052	314	hypothetical protein SS1G_05679	45/63	Sclerotinia sclerotiorum 1980	EDO03199
MCYG_05053	137	conserved hypothetical protein (cercosporin toxin biosynthesis protein)	55/74	Microsporium canis CBS113480	EEQ33879
MCYG_05054	2143	conidial pigment polyketide synthase PksP/Alb1	48/65	Penicillium marneffeii ATCC18224	EEA24206
MCYG_05055	534	DHA14-like major facilitator	38/58	Botryotinia fuckeliana	AF238225
MCYG_05056	202	hypothetical protein (nitro reductase)	51/71	Aspergillus oryzae RIB40	BAE64439
MCYG_05057	370	hypothetical protein SNOG_07051 (Zn-II 2Cys6 regulatory protein)	27/44	Phaeosphaeria nodorum SN15	EAT85702
MCYG_05058	270	hypothetical protein SS1G_13322 (polyketide synthase I)	35/50	Sclerotinia sclerotiorum 1980	EDN98463
MCYG_05059	389	beta-lactamase	36/50	Ajellomyces dermatitidis SLH14081	EEQ72609
MCYG_05060 = <i>ptf_{Mc}</i>	314	hypothetical protein SS1G_09465	39/59	Sclerotinia sclerotiorum 1980	EDN93598
MCYG_05061	117	hypothetical protein MGG_08523	47/64	Magnaporthe grisea 70-15	EDJ97021
MCYG_05062	652	hypothetical protein UREG_05020 (kinesin family protein)	65/75	Uncinocarpus reesii 1704	EEP80178
MCYG_05063	555	translation initiation factor eif-2b delta subunit	63/76	Aspergillus clavatus NRRL 1	EAW13156
MCYG_05064	157	hypothetical protein CIMG_09271	64/70	Coccidioides immitis RS	XP_001239650
MCYG_05065	664	DNA polymerase alpha subunit B family protein	64/79	Coccidioides posadasii C735 delta SOWgp	EER25067
MCYG_05066	390	conserved hypothetical protein	74/83	Uncinocarpus reesii 1704	EEP80183
MCYG_05067	379	nuclear protein SNF4	72/76	Paracoccidioides brasiliensis Pb01	EEH40501
MCYG_05068	658	predicted protein	41/57	Uncinocarpus reesii 1704	EEP80185
MCYG_05069	178	--			
MCYG_05070	479	putative 3-hydroxyisobutyryl-CoA hydrolase	70/82	Coccidioides posadasii C735 delta SOWgp	EER25075

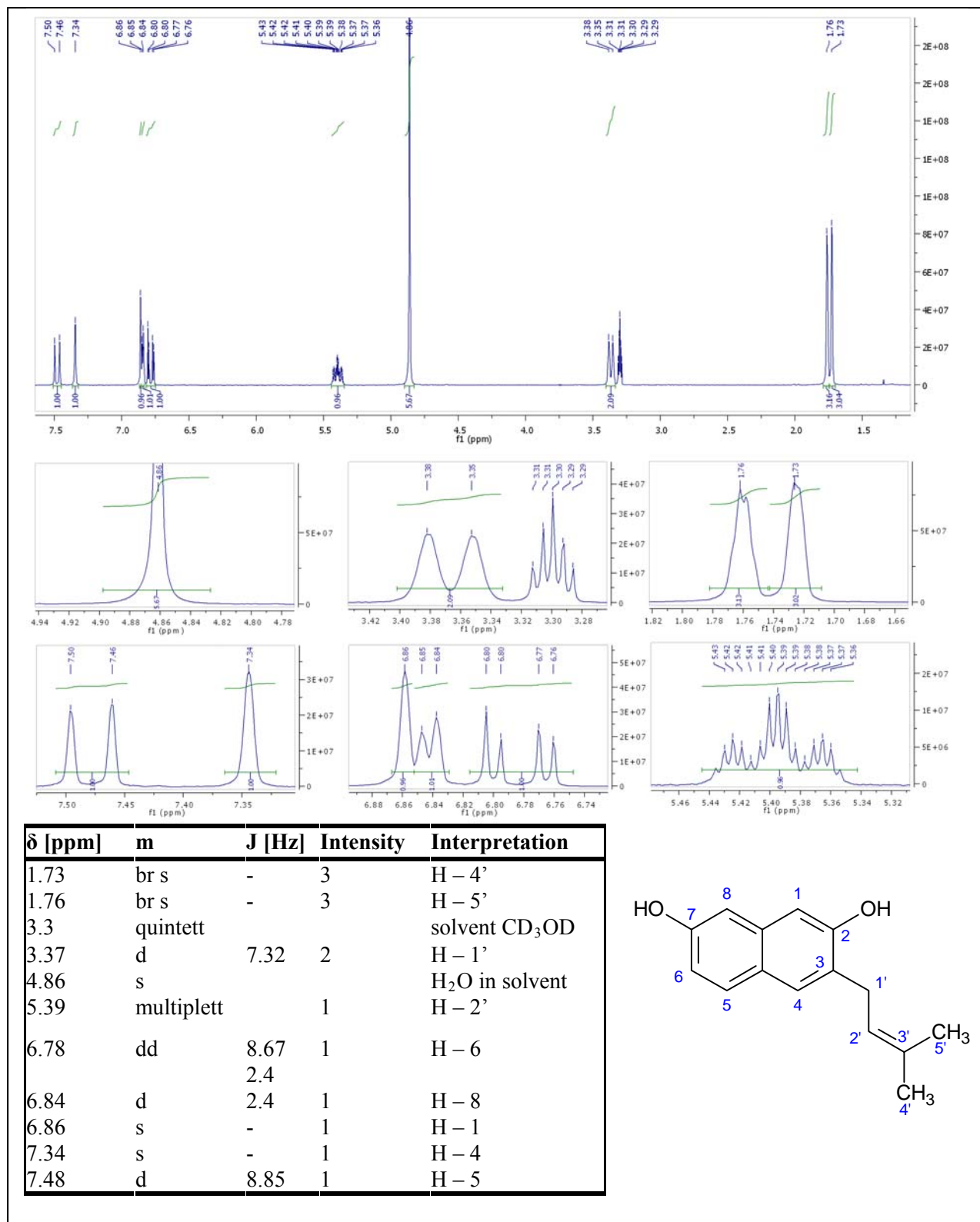


Fig. S1. ¹H-NMR spectrum of the enzymatic product 3-dimethylallyl-2,7-dihydroxynaphthalene formed by Ptf_{A1} with 2,7-dihydroxynaphthalene and DMAPP. The ¹H-NMR spectrum was recorded at 250 MHz in a Bruker AC-250, with CD₃OD as solvent.

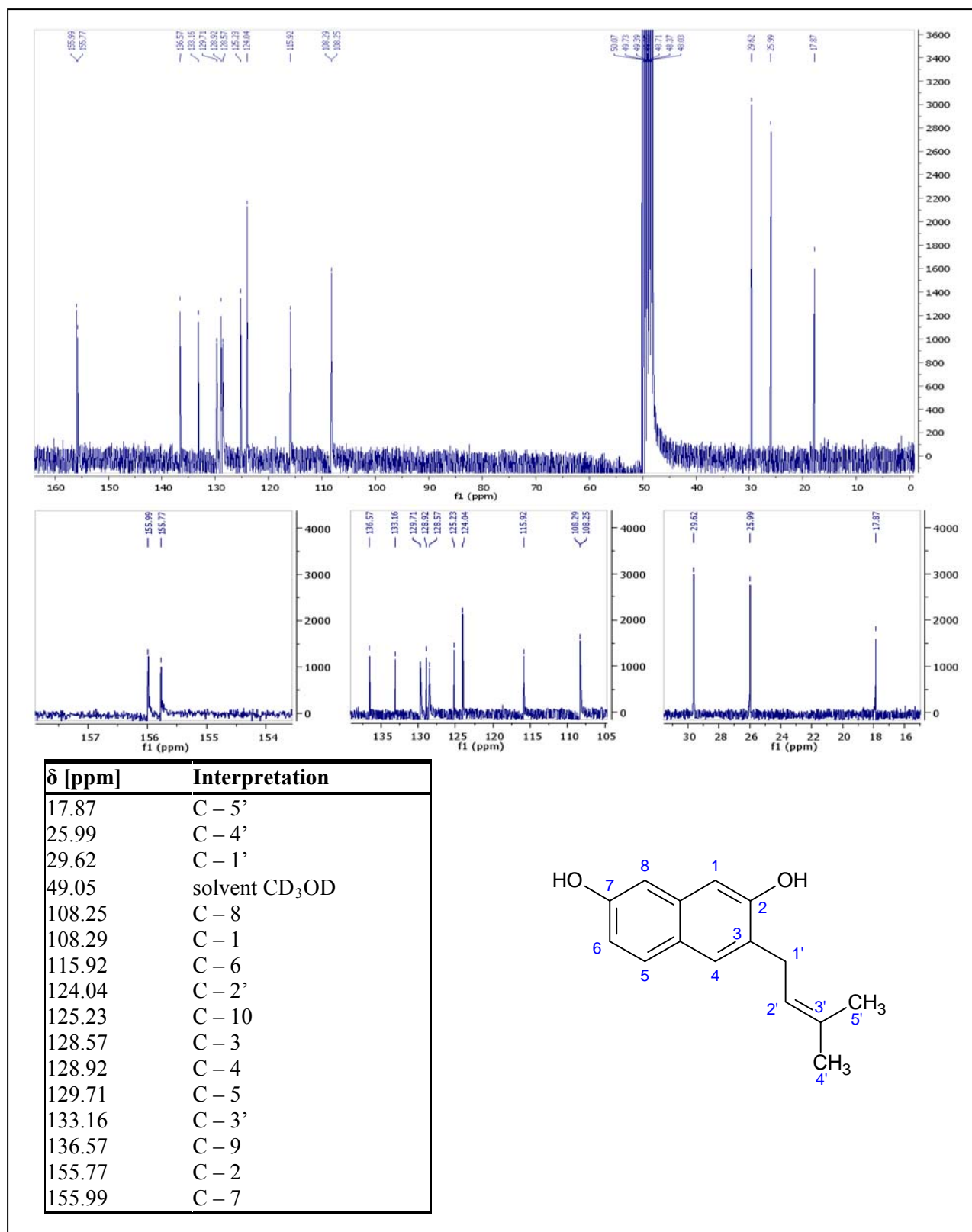


Fig. S2. ¹³C-NMR spectrum of the enzymatic product 3-dimethylallyl-2,7-dihydroxynaphthalene formed by Ptf_{At} with 2,7-dihydroxynaphthalene and DMAPP. The ¹³C-NMR spectrum was broadband decoupled and recorded at 250 MHz in a Bruker AC-250, with CD₃OD as solvent.