

SUPPLEMENTARY MATERIAL

Novel redox-active enzymes of ligninolytic applications revealed from multiomics analyses of *Peniophora* sp. CBMAI 1063, a laccase hyper-producer strain

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Figure S1. The aminoacid sequence of the laccase with the highest spectrum counts (g1591.t1). Peptides identified by the LC-MS/MS analysis are shown in bold red. The coverage for this protein was 41%

MSSSWSLTL	FSLVATGAFA	AIGPTAQLTI	TNANIAPDGL	SR SSVL ANGV
FPAPLI TGNK	GDAFSLTVAD	SLTDTTMDLV	TSIHWHGLEFQ	KSTNYADGVS
GVTQCPIVPD	NSFEYAFSVP	GQAGTFWYHS	HYHAQYCDGL	R GALVI YDPA
DPAASLYD VD	DDSTVIT LAD	WYHYTSK NAP	AIPAPSAT LI	NGLGRYS GGP
ASDLAVIN VT	KGTRYR FRLV	SISCDTN FIF	SIDNHKF SVI	EVDGVNH KPQ
PIDNVQI FAG	QRYSLV MTAD	QDVGN YWVRA	QPNNIAA TFD	GGLNSAIL RY
KDATVAD PTT	TSSLSL ALNE	QDLHPLE SVD	YLSDKT PGGA	DVNLELD VTF
TGGLFAVNGK	SFEAPDVPVL	LQILSGTPPA	SLLPNGSVQL	LPPNAVVEIA
IPGGVAAGPH	PIHLHGHTFS	VVRSAGNATY	NYENPPIRD V	V SI GTAAT DR
TTIRFRTDNA	GPWFMHCHID	WHLTAGFAVV	MAEDSEDVPN	DVHPTDNWNA
LCPAWNTYSS	TTGITQGGLK	PIKAT		

Figure S2.

Comparison of the genomic and secretomic CAZyme content of the marine-derived *Peniophora* sp. CBMAI 1

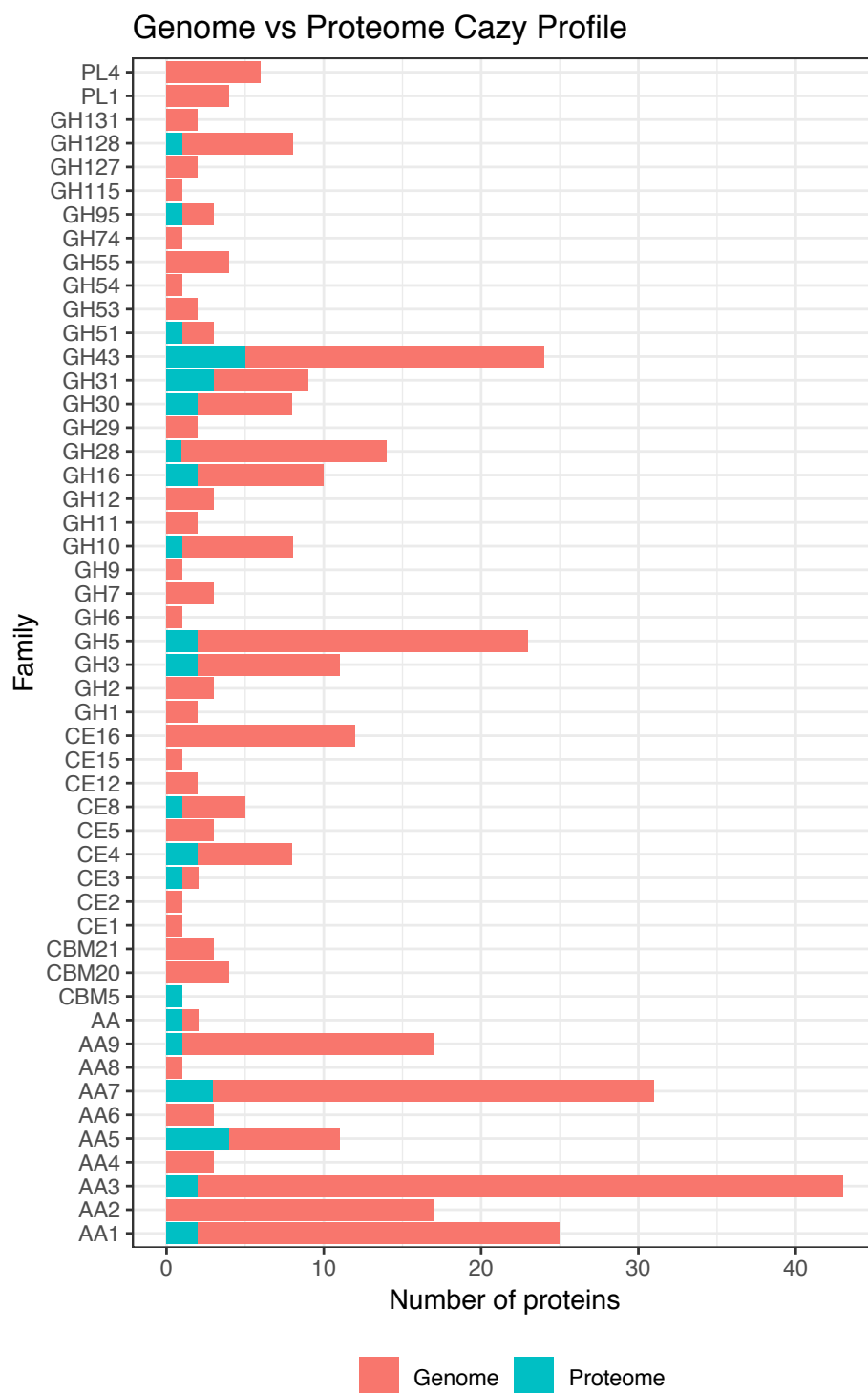


Figure S3. A Amino acid sequence alignment of Pnh_Lac1 with eight laccases from family AA1.1. Although the identity between Pnh_Lac1 with each is about 55 %, the fungal laccase signature segments, highlighted in blue (L1), green (L2), magenta (L3) and orange (4), showed high identity. Each laccase, except for Pnh_Lac1, is described by its genbank accession code.

Pnh_Lac1	MSSWSLLTLFSL-VATGAFAAIGPTAQLTITNANIAPDGL-SRSSVLANGVFPAPLITG
CAE81289	MPSFASLKSLVLSLTSLSLAATVAL-DLHILNANLDPDGTGARS AVTAEGTTIAPLITG
CAA78144	MAKFQSLTLTFITLSLVASVYASIGPVADLTISNGAVSPDGF-SRQAILVNDVFPSPPLITG
ALE66817	MA-FKLTVSFLLGLSLSARAAIGPVADLKIVNANIQPDGF-TRPAVLAGGTFFPGPLIKG
AIT51846	MKALSFLTPIVTLALVAGAFASVGPVANLKIGNAAVSPDGY-TRDAVVNGATPGPLIVG
AGE13770	MAGFQTLLAYITLSLVASVYAGIGPVTDLTISDGPVSPDGF-TRQAILVNNQFSPSPPLITG
AFI41889	MASFKSIAALIAL-IFAVNAAQIGPVTDLHITNANISPDGF-SRPAVLAGGTFFPGPTIAG
AF118267	M--FKNLLSFALLAISVANAQIVNSVDTMTLTNANVSPDGF-TRAGILVNGVH-GPLIRG
ACC43989	MSRFQSLTLTFINISLVAVAHAAVGPVADLTITDAAVSPDGF-SRQAVVNGVTPGPLVAG
Pnh_Lac1	NKGDAFSLTVADSLTDTTMDLVTSIHHWGLFQKSTNYADGVSGVTQCP IVPDNSFEYAFS
CAE81289	NIDDRFQINVIDQLTDANMRRATSIHHWGFFQAGTTEMDGPAFVNQCPIIPNESFVYDFV
CAA78144	NKGDRFQLNVIDNMNHTMLKSTSIHHWGFFQHGTNWADGPAFVNQCPIISTGHAFLYDFQ
ALE66817	NKGDNFQLNVIDELENEDEMLKSTSIHHWGFFQHGTNWADGPAFVNQCPIITGHSFLYNFH
AIT51846	NKGDNFRLNVIDELTNHTMLKSTSIHHWGFFQHGTNWADGPAFVNQCPIISSGHSFSYNFQ
AGE13770	NKGDRFQLNVIDNMNHTMLKSTSIHHWGFFQHGTNWADGPAFVNQCPIISPGHSFLYDFQ
AFI41889	NTGDNFQITVFNDLTDPSMLTDTSIHHWGLFQKGTNWADGPAFVTQCP IITGQSFYDNFN
AF118267	GKNDNFELNVNDLDNPTMLRPTSIHHWGLFQKGTNWADGADGVNQCPIISPGHAFLYKFT
ACC43989	NIGDRFQLNVIDNLTNHTMLKSTSIHHWGFFQHGTNWADGPAFINQCPIISPGHSFLYDFQ
Pnh_Lac1	VPGQAGTFWYHSHYHAQYCDGLRGALVIYDPADPAASLYDVDDDSTVITLADWYHYTSK-
CAE81289	VPGQAGTYWYHSHLSTQYCDGLRGAFVVDPNPDLHSLYDVDDASTVITLADWYHSLSTV
CAA78144	VPDQAGTFWYHSHLSTQYCDGLRGFIVVDYPQDPHKSLYDVDDDSTVITLADWYHLAAKV
ALE66817	VPDQAGTFWYHSHLSTQYCDGLRGFPMVVDYPHDPKLYDVDDSTVMTLADWYHTLARQ
AIT51846	AKDQAGTFWYHSHLSTQYCDGLRGFVVDYPKDPHKKLYDVDDSTVITLEDWYHTAARL
AGE13770	VPDQAGTFWYHSHLSTQYCDGLRGFIVVDYPQDPHKDLYDVDDDSTVITLADWYHLAAKV
AFI41889	VPGQAGTFWYHSHLSTQYCDGLRGFVVDYPNDPNASLYDVDDDTTIITLADWYHTLAQQ
AF118267	PAGHAGTFWYHSHFGTQYCDGLRGFPMVIYDDNDPHAALYDEDDENTIIITLADWYHIPAP-
ACC43989	VPDQAGTFWYHSHLSTQYCDGLRGFVVDYPNDPHASRYDVDDDTVITLADWYHTAAKL
Pnh_Lac1	----NAPAIPAPSATLINGLGRYSGGPA-SDLAVINVTGKTRYRFRRLVLSISCDTNFIFSI
CAE81289	LFPNPNKAPPAPDTTLINGLGRNSANPSAGQLAVVSVQSGKRYRFRIVSTSCFPNYAFSI
CAA78144	----GPAVPTADATLINGLGRSI-NTLNADLAVITVTKGKRYRFRRLVLSLSCDPNHTFSI
ALE66817	----EPPGPVTPDSTLINGLGRAPQGTTPSELAVLTVKRGTRYRIRLINISCEPNYHYSI
AIT51846	----GPRFPLGSDSTLINGLGRSA-TTATGDLAVIKVTRGKRYRFRRLVLSLSCDPFFYTFSI
AGE13770	----GPAVPTADATLINGLGRSI-STLNADLAVISVTKGKRYRFRRLVLSLSCDPNHTFSI
AFI41889	---EPIGAAITADATLINGLGRSFTNTTASPLSVITVQSGKRYRMRLVLSISCDPNYLFSI
AF118267	----SIQGAAQPDATLINGKGRYVGGA-AELSIVNVEQGKKYRMRLISLSCDPNWQFSI
ACC43989	----GPRFPGGADATLINGKGRAP-SDSPAELSVIKVTKGKRYRFRRLVLSLSCPNHTFSI
Pnh_Lac1	DNHKFSVIEVDGVNHPQPIDNVQIFAGQRYSLVMTADQDVGNVWVRAQPNNIA----AT
CAE81289	DGHRMTVIEVDGVSHQPLTVDSLTI FAGQRYSVVVEANQAVGNYWIRANPSNGRN----G
CAA78144	DGHSLTVIEADSVNLKPQTVDLSIQIFAAQRYSFVLNADQDVVDNYWIRALPNSGT----RN
ALE66817	DNHDLTVIEADGVSTQSLTVSSLTIFAGQRYSFILNANQPVGNYWIRAQPNDAAD---VT
AIT51846	DGHNMTIIEADAVNTKPHTVDSLEIFAGQRYSFILNANQPVVDNYWVRANPNFGN----VG
AGE13770	DGHTMTVIEADSVNLKPQVVDLSIQIFAAQRYSFVLNADQDIGNYWIRAMPNSGT----RN
AFI41889	DGHDMTIEVDGVNSQQLTVDQIQIFAAQRYSFVLNANQPVGNYWIRAQPNSSG----QG
AF118267	DGHELTIEVDGQLTEPHTVDRLIQIFTGQRYSFVLDANQPVVDNYWIRAQPNKGRNGLAGT
ACC43989	DGHNLTIEVDVSNQPLEVDSIQIFAAQRYSFVLDANQAVDNYWIRANPNFGN----VG

Pnh_Lac1	FDGGLNSAILRYKDATVADPTTT--SSLALNEQDLHPLESVDYLSDKTPGGADVNL
CAE81289	FTGGINSALFRYEGAAVAEPTTS--QNSGTALNEANLIPLINPGAPGNPVPGGADINLN
CAA78144	FDGGVNSAILRYDGAAAPVEPTTT-QTPSTQPLVESALTTLEGTAAPGNPTPGGVDLALNM
ALE66817	FNGGINSAILRYEGAPVAEPNTT-AGPDNTPLLEVNIIRPFVFTVPVGPQPHAGGADFVKNL
AIT51846	FTNGINSAILRYDGAAVAEPATAIPPASVTPLLETDLHPLVSTPVPGPSVAGGVDKALNF
AGE13770	FDGGVNSAILRYDGADPVEPTTT-QTPSSQPLVESALTTLEGTAAPGSPTAGGVDLAINM
AFI41889	FDGGINSAILRYEGATVEDPTTTAPTTFSNPLVETDLHPLADLGVPGQPFRRGGADDPVLV
AF118267	FANGVNSAILRYAGAAANADPTTS-ANPNPAQLNEADLHALIDPAAPGIPTPGAADVNLRF
ACC43989	FDGGINSAILRYDGAPAVEPTTN-QTTSVKPLNEVDLHPLVSTPVPGPSVSSGGVDKAINM

Pnh_Lac1	DVTFTGG-L-FAVNGKSFEAPDVPVLLQILSGTPPAS-LLPNGSVQLLPNAVVEIAIPG
CAE81289	RIGRNATTADFTINGAPFIPPTVPVLLQILSGVTNPNDLLPGGAVISLPANQVIEISIPG
CAA78144	AFGFAGG--RFTINGASFTPPTVPVLLQILSGAQSAQDLLPSGSVYSLPANADIEISLPA
ALE66817	LFSFNGT--NFQVDNVSEVPPTVPILLQILSGAHTAQDLMPAGSIIPLPKNAVIEFSMPG
AIT51846	VFNFDGT--NFFINDATFTPPSVVLLQILSGAQAAQDLLPSGSVIPLPALSTIELSFPA
AGE13770	AFGFAGG--RFTINGASFTPPTVPVLLQILSGAQNAQDLLPTGSVYSLPANADIEISLPA
AFI41889	NLAFANG--RFSIDGVSEVPPTVPVLLQILSGAQNAQDLLPAGSVISLPSNSVIEVALPA
AF118267	QLGFSGG--RFTINGTAYESPSVPTLLQIMSGAQSAQDLLPAGSVYELPRNQVVELVVA
ACC43989	AFNFNGS--NFFINGASFPPTVPVLLQILSGAQTAQDLLPSGSVYVLPNASIEISFPA

Pnh_Lac1	GVA--AGPHPIHLHGHTFSVRSAGNATYNYENPPIRDVVSIGTA-ATDRTTIRFRTDNA
CAE81289	-----GGNHPPFHLHGHNFDVVRTPGSSVYNYVNPVRRDVVSIGGG--GDNVTFRFVTDNP
CAA78144	TSAAPGFPHPPFHLHGHTFAVRSAGSSTYNYANPVYRDVVSIGSP--GDNVTIRFRTDNP
ALE66817	GVV--GGGHPPIHLHGHNFWVIRSANSVYNYNDPVIRDVVNIGTT--GDNVTIRFETNNP
AIT51846	TANAPGVPHPPFHLHGHTFAVRSAGSTAYNYEDPVWRDVVSTGTPAAGDNVTIRFVTDNP
AGE13770	TAAAPGFPHPPFHLHGHTFAVRSAGSSTYNYANPVYRDVVSIGSP--GDNVTIRFRTDNP
AFI41889	GAA--GGPHPPFHLHGHNFAVVQSANNATPNYVNPVWRDVSIGGT--GDNVTIRFTTNNP
AF118267	GVL--GGPHPPFHLHGHAFSVRSAGSSTYNFVNPVKRDVVSIGVT--GDEVTVIRFVTDNP
ACC43989	TAAAPGAPHPFHLHGHTFAVRSAGSTVYNYDNPIFRDVVSTGTPAAGDNVTIRFDTNNP

Pnh_Lac1	GPWFMHCHIDWHLTAGFAVVMAEDSEDVPNDVHPTDNWNALCPAWN-----TYSS-----
CAE81289	GPWFLHCHIDWHLEAGLAVVFAEDIPNIPIANAISPADDLCPKYN-----ANN-----
CAA78144	GPWFLHCHIDFHLEAGFAVVMAEDIPDVAATNPVPQAWSDLCPITYD-----ALS-----
ALE66817	GPWFLHCHIDWHLDLGFAVVMAEDIPDAAAANPVPAAWNELCPLYD-----ALT-----
AIT51846	GPWFLHCHIDFHLEAGFAVVFAEDLPGTAAANPVQPQAWSDLCPITYD-----ALA-----
AGE13770	GPWFLHCHIDFHLEAGFAVVMAEDIPDVAANPVQPQAWSDLCPITYN-----ALD-----
AFI41889	GPWFLHCHIDWHLEAGFAIVFAEDIPDTASANPVQPQAWSDLCPAYDQAHNISTATRQDFQ
AF118267	GPWFFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPEATSIQT---
ACC43989	GPWFLHCHIDFHLEGGFAVVMAEDTPDVKAVNPVPQAWSDLCPITYD-----ALD-----

Pnh_Lac1	---TTGITQGGLKP---IKAT
CAE81289	-----PDSGLA-----
CAA78144	-----PDDQ-----
ALE66817	-----PGNQ-----
AIT51846	-----EDDQ-----
AGE13770	-----PNDQ-----
AFI41889	ILCICGILHVNFRQEERCIS
AF118267	--VVRRAEPTGFSAKFRREGL
ACC43989	-----PNDQ-----

Figure S4. Structural alignment of Pnh_Lac1 model with the structures of the eight laccases from family AA1.1, used in the sequence alignment described in figure S2. The Pnh_Lac1 structure, generated by homology modelling, resulted in a high structural identity (RMSD about 0.5 Å) with the other members, evidencing the conserved folding of the family and the reliability of the model.

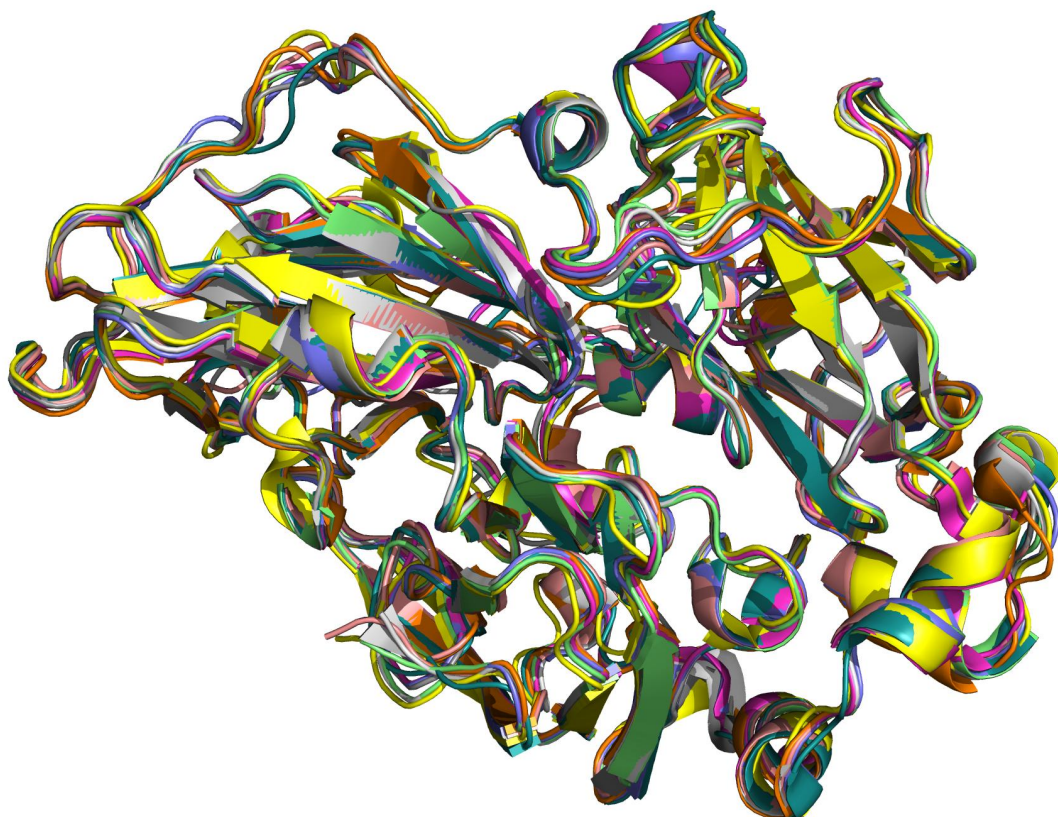


Table S1. Statistics of the marine *Peniophora* sp. CBMAI 1063 draft genome assembly.

Assembly statistics	<i>Peniophora</i> sp. CBMAI 1063
# Number of QC reads	39442518
Estimated coverage	165X
# contigs (≥ 0 bp)	939
# scaffolds	833
# contigs (≥ 5000 bp)	618
# contigs (≥ 10000 bp)	509
# contigs (≥ 25000 bp)	376
# contigs (≥ 50000 bp)	249
Total length (bp)	46982497
Largest contig (bp)	1115204
GC (%)	55,21
N50	155805
N75	73455
L50	84
L75	191
Number of predicted genes	17219
Number of predicted transcripts	17714
Average gene length (bp)	1416
rRNA	1
tRNA	74
Genome completeness (%)	93

Table S2. Non-CAZymes identified in the secretome of *Peniophora* sp. CBMAI 1063 cultivated in a bioreactor under saline conditions.

Accession Number	Molecular Weight ^a	Amino acid length ^b	PFAM Domain ^c	PFAM description	Signal Peptide ^d	Location ^e	Unique peptides	Spectrum counts
g1019.t1	34 kDa	305	PF00240 PF11976 F14560 PF13881	Ubiquitin family	NO	C	2	43
g10257.t1	42 kDa	394	PF01161	Phosphatidylethanolamine-binding protein	NO	SP	2	1
g6425.t1	35 kDa	348	PF03067	Lytic polysaccharide monooxygenase	YES	SP	2	1
g10717.t1	45 kDa	424	PF00026 PF14543	Eukaryotic aspartyl protease Xylanase inhibitor N-terminal	YES	SP	3	3
g11007.t1	36 kDa	321	PF00248	Aldo/keto reductase family	NO	C	3	9
g11209.t1	44 kDa	393	PF04389 PF01546	Peptidase family M28/ M20/M25/M40	YES	SP	5	11
g11268.t1	120 kDa	1084	PF00282	Pyridoxal-dependent decarboxylase conserved domain	NO	C	15	20
g1175.t1	29 kDa	258	PF01182	Glucosamine-6-phosphate isomerases 6-phosphogluconolactonase	NO	C	2	9
g12242.t1	53 kDa	505	PF07992 PF02852 PF00070 PF12831 PF01134 PF00890	Pyridine nucleotide-disulphide oxidoreductase; FAD dependent oxidoreductase:	NO	M	8	10
g1234.t1	31 kDa	279	PF01738	Dienelactone hydrolase Family	NO	M	4	13
g12438.t1	14 kDa	135	PF07249	Cerato-platanin	YES	SP	3	29
g12440.t1	14 kDa	135	PF07249	Cerato-platanin	YES	SP	2	26

g1251.t1	39 kDa	397	not identified		YES	SP	3	8
g12536.t1	166 kDa	1524	PF00168	C2 domain	NO	X	4	9
g13042.t1	43 kDa	395	PF06516	Purine nucleoside permease (NUP)	NO	SP	4	13
g1333.t1	61 kDa	561	PF02878 PF02880 PF02879	Phosphoglucomutase/ phosphomannomutase, alpha/beta/alpha domain I	NO	C	3	4
g13681.t1	87 kDa	793	not identified		NO	C	4	2
g13797.t1	39 kDa	379	not identified		YES	SP	3	58
g13878.t1	52 kDa	479	PF04389	Peptidase family M28	YES	SP	4	7
g14070.t1	26 kDa	231	PF13417 PF13409 PF02798	Glutathione S-transferase	NO	M	2	6
g14182.t1	21 kDa	200	not identified		YES	SP	2	7
g14619.t1	61 kDa	548	PF00262	Calreticulin Family	YES	SP	2	3
g14686.t1	38 kDa	358	PF10282	Lactonase, 7-bladed beta-propeller	NO	SP	4	3
g14843.t1	22 kDa	198	not identified		NO	M	3	43
g14865.t1	34 kDa	317	PF01014 PF01014	Uricase;Uricase	NO	M	3	5
g15561.t1	38 kDa	374	not identified		YES	SP	3	5
g16265.t1	47 kDa	438	PF01546 PF07687	Peptidase family M20/M25/M40	NO	C	2	1
g16319.t1	26 kDa	253	PF00314	Thaumatococcus Family	YES	SP	3	9

g16410.t1	17 kDa	152	PF00334	Nucleoside diphosphate kinase	NO	M	2	7
g16808.t1	26 kDa	236	PF13419 PF00702 PF13242	Haloacid dehalogenase-like hydrolase	NO	C	2	6
g16849.t1	67 kDa	617	PF09423 PF16655	PhoD-like phosphatase	YES	SP	7	10
g1891.t1	27 kDa	256	PF00314	Thaumatococcus Family	YES	SP	3	18
g312.t1	62 kDa	581	PF12222	Peptide N-acetyl-beta-D-glucosaminyl asparaginase amidase A	YES	SP	2	4
g329.t1	76 kDa	696	PF03571	Peptidase family M49	NO	C	16	13
g3731.t1	54 kDa	497	PF01266	FAD dependent oxidoreductase	YES	SP	2	1
g4046.t1	33 kDa	305	not identified		YES	SP	3	2
g414.t1	35 kDa	348	PF03330	Lytic transglycolase	YES	SP	2	1
g4288.t1	35 kDa	322	PF03372	Endonuclease/Exonuclease/phosphatase family	NO	C	11	68
g514.t1	41 kDa	396	not identified		YES	SP	6	25
g5214.t1	61 kDa	568	PF00026	Eukaryotic aspartyl protease	YES	SP	2	1
g5591.t1	55 kDa	515	PF00883 PF02789	Cytosol aminopeptidase family, catalytic domain	NO	M	2	1
g5969.t1	11 kDa	99	PF11976 PF00240	Ubiquitin-2 like Rad60 SUMO-like	NO	N	2	7
g6000.t1	19 kDa	168	PF14566	Inositol hexakisphosphate	NO	C	3	14
g620.t1	44 kDa	405	PF08450 PF03088	SMP-30/Gluconolactonase/LRE-like region;Strictosidine synthase	YES	M	4	4

g6204.t1	36 kDa	343	not identified		YES	SP	2	2
g621.t1	44 kDa	409	PF08450 PF03088	SMP-30/Gluconolactonase/LRE-like region;Strictosidine synthase	YES	SP	3	2
g690.t1	97 kDa	905	PF13449 F01266	Esterase-like activity of phytase;FAD dependent oxidoreductase	YES	SP	18	42
g7075.t1	24 kDa	227	not identified		YES	SP	4	13
g7191.t1	58 kDa	529	PF05577	Serine carboxypeptidase S28	YES	SP	5	7
g7314.t1	74 kDa	691	PF17168 PF16335 PF08760	Domains of unknown function	YES	SP	6	13
g7338.t1	74 kDa	687	PF03372	Endonuclease/Exonuclease/phosphatase family	NO	C	2	2
g7407.t1	106 kDa	960	PF04253 PF04389 PF02225	Transferrin receptor-like dimerisation domain; Peptidase family M28;PA domain	NO	N	5	8
g7610.t1	68 kDa	615	PF00149	Calcineurin-like phosphoesterase	YES	SP	3	2
g7664.t1	39 kDa	403	not identified		YES	SP	4	5
g780.t1	37 kDa	338	PF07991 PF01450 PF03807 PF03446	Acetohydroxy acid isomeroreductase, NADPH-binding domain	NO	C	4	6
g7893.t1	63 kDa	590	PF09286 PF00082		YES	SP	8	13

g8153.t1	51 kDa	470	PF07992 PF02852 PF00070 PF13738 PF03486 PF13434	Pyridine nucleotide-disulphide oxidoreductase	NO	C	10	16
g8392.t1	102 kDa	934	not identified		NO	SP	7	6
g8584.t1	87 kDa	774	PF01432	Peptidase family M3	NO	SP	4	3
g8812.t1	100 kDa	903	PF01433 PF11838	Peptidase family M1;ERAP1-like C-terminal domain	NO	C	6	3
g8977.t1	64 kDa	580	PF05577	Serine carboxypeptidase S28	NO	C	3	2
g9286.t1	33 kDa	308	not identified		YES	SP	2	2
g9390.t1	44 kDa	427	PF00445	Ribonuclease T2 family	YES	SP	6	28
g9486.t1	42 kDa	389	PF01263	Aldose 1-epimerase	YES	SP	3	3
g9536.t1	50 kDa	466	PF00557	Metallopeptidase family M24	NO	N	5	9
g9683.t1	14 kDa	125	PF00173	Cytochrome b5-like Heme/Steroid binding domain	NO	M	2	7
g1396.t1	58 kDa	541	PF00135 PF07859	Carboxylesterase family 10	YES	SP	2	3
g1415.t1	58 kDa	541	PF00135 PF07859	Carboxylesterase family 10	YES	SP	4	5
g1747.t1	59 kDa	549	PF00135 PF07859	Carboxylesterase family 10	YES	SP	3	4
g5988.t1	63 kDa	584	PF00135	Carboxylesterase family 10	NO	SP	8	8

Legend. ^aMolecular Weight and ^bAmino acid length determined by LC-MS/MS analysis . The results were processed by Mascot v. 2.3.01 engine (Matrix Science Ltd.) software against the genome sequencing database of *Peniophora* sp. CBMAI 1063 and Scaffold – Proteome Software (version Scaffold_4.3.2 20140225). ^cPfam protein family Domain analysis. ^dThe presence of a signal peptide of secreted proteins predicted by SignalP v.4.0. ^eThe subcellular localization of proteins predicted by YLoc (Interpretable Subcellular Localization Prediction): SP – secreted pathway; C – cytoplasm; M – mitochondrial location; N – Nucleus