

Table S1

Sequences of the matching peptides and functional classification of the identified proteins by MALDI-MS

Spot	Score	Accession	Description	Matching peptide(s)	Functional category
31	163	gi 2500828	RecName: Full=Superoxide dismutase [Mn], mitochondrial; AltName: Full=Mn-SOD; Flags: Precursor	FNGGGHINHSFLWK	Inorganic ion transport and metabolism
				ADYLAAIWIVINFK	
				SAIEQNWGSVDNFIK	
				HHQTYVNSLNAAEQAYAK	
				KHHQTYVNSLNAAEQAYAK	
32	268	gi 1519016	Manganese-superoxide dismutase, partial [Ganoderma tropicum]	FNGGGHINHSFLWK	Inorganic ion transport and metabolism
				AAIVQNWGSVDAFIK	
				HHQTYVNSLNAAEQAYAK	
				KHHQTYVNSLNAAEQAYAK	
33	92	gi 164564766	NAD-dependent formate dehydrogenase [Ceriporiopsis subvermispora]	VVG TIGAGR	Energy production and conversion; Coenzyme transport and metabolism
				KGAWLVNTAR	
				NFVPAHEMIER + Oxidation (M)	
				GLVNAELLKHFK	
41	93	gi 30172926	RecName: Full=Peroxisomal catalase	LFSYPTDTHR	Unclassified
				FPHFIHTQK	
				SNPPTYTTSQGCPVSDAFSTQR	
42	101	gi 28558774	Catalase [Lentinus sajor- caju]	LFSYPTDTHR	Unclassified
				FPHFIHTQK	
				QMHGYSGHTFK	
				LTADNPDYSTEMLFR + Oxidation (M)	
43	84	gi 169845435	Enolase [Coprinopsis cinerea okayama7#130]	ACNGLLLK	Unclassified
				EIDDFLIK	
				IALDVASSEFYK	
				YDLDFKNPNSDPTK	
				GKLGANAILGVSIAMVAEAGAGEK	
44	147	gi 172713	70kDa heat shock protein, partial [Saccharomyces cerevisiae]	STLDPVEKVLR	Unclassified
				SQVDEIVLVGGSTR	
				NFTPEQISSMVLGK + Oxidation (M)	
				IINEPTAAAIAYGLDK	
				ATAGDTHLGGEDFDNR	
				LDKSQVDEIVLVGGSTR	
45	461	gi 172713	70kDa heat shock protein, partial [Saccharomyces cerevisiae]	NEGIDFYTSITR	Unclassified
				SQVDEIVLVGGSTR	
				NFTPEQISSMVLGK + Oxidation (M)	
				IINEPTAAAIAYGLDK	
				ATAGDTHLGGEDFDNR	
				IINEPTAAAIAYGLDKK	
				LDKSQVDEIVLVGGSTR	
				TACESQENFVSSAQTVEIDSK	

NCBI nr (Fungi) database was employed for the identifications in MALDI-MS.

Table S2

Information for all the proteins identified by LC-MS in each analyzed spot

Spot	Distinct peptides (#)	Score	AA coverage (%)	Intensity	Relative volume (%)	Relative protein content (%)	Organism homology	Gene ID	Protein name
1	4	78.41	9	991000	3.90	100.00	<i>Grifola frondosa</i>	GME273_g	Lectin
2	9	155.75	11	2120000	8.98	100.00	<i>Grifola frondosa</i>	GME273_g	Lectin
3	8	126.28	11	1290000	7.23	99.97	<i>Grifola frondosa</i>	GME273_g	Lectin
3	2	25.05	5	28200	0.00	0.03	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
4	6	108.92	14	587000	1.22	85.33	<i>Grifola frondosa</i>	GME273_g	Lectin
4	5	73.56	40	115000	0.02	1.42	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
4	4	58.38	10	807000	0.17	11.93	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
4	3	43.59	28	19700	0.00	0.15	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
4	3	43.59	28	19700	0.00	0.15	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
4	2	35.61	30	76600	0.01	0.94	<i>Sclerotinia sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
4	2	24.72	10	17500	0.00	0.09	<i>Grifola frondosa</i>	GME272_g	Lectin
5	8	99.83	56	145000	0.34	9.11	<i>Moniliophthora perniciosa FA553</i>	GME7309_g	Hypothetical protein MPER_11381
5	6	94.14	52	118000	0.42	11.12	<i>Laccaria bicolor S238N-H82</i>	GME2234_g	Predicted protein
5	6	89.57	64	71300	0.13	3.36	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
5	4	72.37	12	164000	0.29	7.72	<i>Grifola frondosa</i>	GME273_g	Lectin
5	3	61.41	34	892000	2.38	63.02	<i>Sclerotinia sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
5	3	46.73	20	51000	0.06	1.60	<i>Grifola frondosa</i>	GME272_g	Lectin

5	3	40.75	8	86000	0.08	2.03	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
5	2	31.76	34	113000	0.07	1.77	<i>Laccaria bicolor S238N-H82</i>	GME3932_g	Predicted protein
5	2	31.53	8	17800	0.01	0.28	<i>Grifola frondosa</i>	GME271_g	Lectin
6	3	62.24	34	1290000	6.19	77.04	<i>Sclerotinia sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
6	2	51.09	6	194000	0.20	2.48	<i>Grifola frondosa</i>	GME273_g	Lectin
6	3	49.64	8	794000	1.63	20.32	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
6	2	30.36	11	18300	0.01	0.16	<i>Taiwanofungus camphoratus</i>	GME7546_g	Glutathione transferase
7	11	199.72	76	3600000	4.39	98.52	<i>Grifola frondosa</i>	GME270_g	Lectin
7	5	74.25	30	51700	0.02	0.42	<i>Grifola frondosa</i>	GME272_g	Lectin
7	3	58.1	10	128000	0.05	1.05	<i>Grifola frondosa</i>	GME273_g	Lectin
8	9	183.76	20	1660000	2.18	87.43	<i>Grifola frondosa</i>	GME273_g	Lectin
8	8	128.14	56	505000	0.30	12.19	<i>Grifola frondosa</i>	GME272_g	Lectin
8	4	52.31	30	21300	0.01	0.23	<i>Coprinopsis cinerea okayama7#130</i>	GME6204_g	Hypothetical protein CC1G_06180
8	2	32.11	8	21300	0.00	0.14	<i>Grifola frondosa</i>	GME271_g	Lectin
9	11	171.06	56	952000	1.21	89.09	<i>Grifola frondosa</i>	GME272_g	Lectin
9	5	74.05	17	116000	0.09	6.79	<i>Grifola frondosa</i>	GME273_g	Lectin
9	3	45.94	21	49400	0.02	1.73	<i>Grifola frondosa</i>	GME270_g	Lectin
9	3	42.6	10	102000	0.03	2.39	<i>Grifola frondosa</i>	GME271_g	Lectin
10	10	173.27	56	864000	1.08	88.14	<i>Grifola frondosa</i>	GME272_g	Lectin
10	5	87.71	17	267000	0.12	9.61	<i>Grifola frondosa</i>	GME273_g	Lectin
10	3	54.63	25	125000	0.03	2.25	<i>Grifola frondosa</i>	GME270_g	Lectin
11	8	131.88	72	2100000	1.56	97.66	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein

11	5	80.52	13	159000	0.04	2.34	<i>Grifola frondosa</i>	GME273_g	Lectin
12	5	78.66	39	295000	0.28	27.61	<i>Aspergillus nidulans</i> <i>FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
12	4	50.86	10	807000	0.65	64.74	<i>Hypsizygus</i> <i>marmoreus</i>	GME4347_g	Serine protease
12	2	36.82	6	66700	0.05	5.35	<i>Grifola frondosa</i>	GME273_g	Lectin
12	2	35.35	30	42900	0.02	2.29	<i>Sclerotinia</i> <i>sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
13	3	63.63	8	910000	1.62	65.97	<i>Grifola frondosa</i>	GME273_g	Lectin
13	3	48.19	42	248000	0.31	12.84	<i>Nectria</i> <i>haematococca mpVI</i> <i>77-13-4</i>	GME6455_g	Hypothetical protein NECHADRAFT_123372
13	2	44.94	42	485000	0.49	20.09	<i>Coprinopsis cinerea</i> <i>okayama7#130</i>	GME5894_g	Hypothetical protein CC1G_07172
13	3	37.79	21	21900	0.02	0.91	<i>Aspergillus nidulans</i> <i>FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
13	2	22.61	17	4580	0.00	0.09	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
13	2	22.61	17	4580	0.00	0.09	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
14	3	53.67	34	768000	3.49	90.74	<i>Sclerotinia</i> <i>sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
14	3	44.48	8	44700	0.10	2.64	<i>Hypsizygus</i> <i>marmoreus</i>	GME4347_g	Serine protease
14	2	37.34	6	112000	0.25	6.62	<i>Grifola frondosa</i>	GME273_g	Lectin
15	8	156.25	18	2020000	0.91	94.70	<i>Grifola frondosa</i>	GME273_g	Lectin
15	7	114.06	47	113000	0.02	2.30	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME777_g	Triose phosphate isomerase
15	6	81.4	34	133000	0.02	1.63	<i>Coprinopsis cinerea</i> <i>okayama7#130</i>	GME5178_g	ThiI/Pfpl
15	3	51.75	13	10500	0.00	0.09	<i>Schizophyllum</i> <i>commune H4-8</i>	GME7584_g	Hypothetical protein SCHCODRAFT_76790
15	4	49.09	15	15000	0.00	0.12	<i>Schizophyllum</i> <i>commune H4-8</i>	GME9837_g	Hypothetical protein SCHCODRAFT_103662

15	3	39.11	8	105000	0.01	0.86	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
15	2	29.16	7	11700	0.00	0.05	<i>Grifola frondosa</i>	GME3216_g	RNase Gf29
15	2	27.73	8	31600	0.00	0.13	<i>Grifola frondosa</i>	GME272_g	Lectin
15	3	27.63	12	10200	0.00	0.06	<i>Laccaria bicolor S238N-H82</i>	GME7807_g	Predicted protein
15	2	26.39	14	16900	0.00	0.07	<i>Grifola frondosa</i>	GME270_g	Lectin
16	7	103.52	19	1330000	1.45	91.95	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
16	5	81.25	17	214000	0.13	7.97	<i>Grifola frondosa</i>	GME273_g	Lectin
16	2	20.75	11	8190	0.00	0.09	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
17	9	143.14	40	105000	0.06	5.34	<i>Lentinula edodes</i>	GME1701_g	14-3-3-domain-containing protein
17	7	105.36	19	1360000	1.10	92.16	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
17	5	84.05	17	40300	0.02	1.82	<i>Grifola frondosa</i>	GME273_g	Lectin
17	4	44.62	26	30200	0.01	0.68	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
18	7	103.39	19	1160000	1.35	98.77	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
18	3	46.21	21	41600	0.01	1.06	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
18	2	16.16	12	6660	0.00	0.17	<i>Lentinula edodes</i>	GME1701_g	14-3-3-domain-containing protein
19	5	108.92	17	372000	0.19	10.39	<i>Grifola frondosa</i>	GME273_g	Lectin
19	7	105.59	19	1480000	1.67	89.61	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
20	7	98.46	19	1210000	1.05	98.16	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
20	4	59.25	15	47100	0.02	1.74	<i>Grifola frondosa</i>	GME273_g	Lectin
20	2	23.59	12	7060	0.00	0.10	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein

21	7	101.92	19	1200000	1.20	98.90	<i>Hypsizygos marmoreus</i>	GME4347_g	Serine protease
21	4	46.63	19	13500	0.01	0.56	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
21	2	31.52	5	26400	0.01	0.54	<i>Grifola frondosa</i>	GME273_g	Lectin
22	10	169.59	48	733000	0.48	71.45	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
22	6	100.17	62	498000	0.17	25.89	<i>Postia placenta Mad-698-R</i>	GME9375_g	Hypothetical protein POSPLDRAFT_134790
22	7	93.71	12	42400	0.02	2.48	<i>Laccaria bicolor S238N-H82</i>	GME8244_g	Phosphopyruvate hydratase
22	2	28.77	8	9040	0.00	0.18	<i>Grifola frondosa</i>	GME273_g	Lectin
23	8	155.01	48	1400000	0.63	65.79	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
23	6	108.56	66	633000	0.20	20.59	<i>Postia placenta Mad-698-R</i>	GME9375_g	Hypothetical protein POSPLDRAFT_134790
23	4	86.88	16	314000	0.13	13.62	<i>Grifola frondosa</i>	GME273_g	Lectin
24	8	134.94	48	723000	0.39	67.30	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
24	5	84.94	49	427000	0.15	25.29	<i>Postia placenta Mad-698-R</i>	GME9375_g	Hypothetical protein POSPLDRAFT_134790
24	3	50.75	10	125000	0.04	7.40	<i>Grifola frondosa</i>	GME273_g	Lectin
25	7	119.13	43	442000	0.31	44.15	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
25	5	87.86	17	210000	0.20	27.97	<i>Grifola frondosa</i>	GME273_g	Lectin
25	5	77.64	49	314000	0.20	27.88	<i>Postia placenta Mad-698-R</i>	GME9375_g	Hypothetical protein POSPLDRAFT_134790
26	5	81.56	13	535000	0.54	97.35	<i>Grifola frondosa</i>	GME273_g	Lectin
26	5	70.46	15	56300	0.01	2.36	<i>Coprinopsis cinerea okayama7#130</i>	GME9325_g	Endopeptidase

26	2	34.98	8	20500	0.00	0.29	<i>Chlorobium phaeobacteroides BS1</i>	GME4019_g	Phosphatidylserine decarboxylase-related
27	7	106.09	18	756000	0.55	81.29	<i>Hypsizygos marmoreus</i>	GME8711_g	Serine protease
27	4	58.44	10	117000	0.05	6.86	<i>Hypsizygos marmoreus</i>	GME4347_g	Serine protease
27	2	49.65	6	303000	0.08	11.85	<i>Grifola frondosa</i>	GME273_g	Lectin
28	2	45.67	6	127000	1.01	81.91	<i>Grifola frondosa</i>	GME273_g	Lectin
28	2	27.84	21	18700	0.11	9.05	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
28	2	27.84	21	18700	0.11	9.05	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
29	13	234.96	30	860000	0.32	92.39	<i>Laccaria bicolor S238N-H82</i>	GME590_g	Predicted protein
29	9	120.76	40	57000	0.01	3.34	<i>Laccaria bicolor S238N-H82</i>	GME7966_g	Predicted protein
29	6	90.39	22	14900	0.00	0.51	<i>Laccaria bicolor S238N-H82</i>	GME1791_g	Mannitol-1-phosphate dehydrogenase MPDH1
29	4	52.29	19	20400	0.00	0.40	<i>Coprinopsis cinerea okayama7#130</i>	GME3375_g	D-isomer specific 2-hydroxyacid dehydrogenase
29	4	48.28	9	15500	0.00	0.30	<i>Laccaria bicolor S238N-H82</i>	GME133_g	Predicted protein
29	2	46.51	6	118000	0.01	2.30	<i>Grifola frondosa</i>	GME273_g	Lectin
29	2	25.26	6	9320	0.00	0.09	<i>Coprinopsis cinerea okayama7#130</i>	GME6542_g	Ketol-acid reductoisomerase
29	2	23.61	3	7980	0.00	0.08	<i>Pleurotus eryngii</i>	GME1553_g	Aryl-alcohol oxidase
29	2	21.6	12	23500	0.00	0.34	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
29	2	19.27	13	16400	0.00	0.24	<i>Postia placenta Mad-698-R</i>	GME2238_g	Predicted protein
30	12	206.17	26	531000	0.17	91.19	<i>Laccaria bicolor S238N-H82</i>	GME590_g	Predicted protein
30	4	52.42	16	102000	0.01	6.81	<i>Grifola frondosa</i>	GME273_g	Lectin

30	4	49.4	22	22800	0.00	1.09	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
30	3	35.75	11	14700	0.00	0.70	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME1791_g	Mannitol-1-phosphate dehydrogenase MPDH1
30	2	20.04	2	11200	0.00	0.21	<i>Schizophyllum</i> <i>commune H4-8</i>	GME5848_g	Hypothetical protein SCHCODRAFT_73898
31	9	150.49	37	1770000	0.38	87.65	<i>Heterobasidion</i> <i>annosum</i>	GME441_g	Manganese superoxide dismutase
31	7	111.8	53	131000	0.02	3.78	<i>Moniliophthora</i> <i>perniciosa FA553</i>	GME7309_g	Hypothetical protein MPER_11381
31	5	81.76	20	77100	0.01	1.59	<i>Schizophyllum</i> <i>commune H4-8</i>	GME5825_g	Hypothetical protein SCHCODRAFT_233273
31	4	54.98	27	133000	0.01	2.74	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
31	3	44.2	3	39400	0.00	0.49	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME2527_g	Linoleate diol synthase
31	3	44.09	31	41500	0.00	0.51	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
31	3	44.09	31	41500	0.00	0.51	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
31	3	37.62	21	63500	0.00	0.79	<i>Grifola frondosa</i>	GME270_g	Lectin
31	3	36.66	8	41600	0.00	0.51	<i>Schizophyllum</i> <i>commune H4-8</i>	GME9537_g	Hypothetical protein SCHCODRAFT_83719
31	3	34.95	15	47700	0.00	0.59	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME3972_g	20S proteasome subunit
31	2	26.91	8	13700	0.00	0.11	<i>Grifola frondosa</i>	GME272_g	Lectin
31	2	25.72	4	42500	0.00	0.35	<i>Hypsizygus</i> <i>marmoreus</i>	GME4347_g	Serine protease
31	2	22.3	12	15500	0.00	0.13	<i>Coprinopsis cinerea</i> <i>okayama7#130</i>	GME7414_g	Peptide methionine sulfoxide reductase
31	2	19.03	13	28600	0.00	0.24	<i>Laccaria bicolor</i> <i>S238N-H82</i>	GME7754_g	Predicted protein
32	10	159.68	34	1100000	0.41	98.99	<i>Heterobasidion</i> <i>annosum</i>	GME441_g	Manganese superoxide dismutase
32	3	45.65	11	22500	0.00	0.38	<i>Schizophyllum</i> <i>commune H4-8</i>	GME5825_g	Hypothetical protein SCHCODRAFT_233273

32	2	27.28	5	27600	0.00	0.31	<i>Coprinopsis cinerea okayama7#130</i>	GME4000_g	Aspartyl aminopeptidase
32	2	21.16	8	19000	0.00	0.32	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
33	23	440.33	63	1760000	0.29	86.05	<i>Ceriporiopsis subvermispora</i>	GME5414_g	NAD-dependent formate dehydrogenase
33	5	80.59	9	447000	0.01	3.05	<i>Ceriporiopsis subvermispora</i>	GME8390_g	NAD-dependent formate dehydrogenase
33	15	222.65	58	124000	0.01	2.26	<i>Laccaria bicolor S238N-H82</i>	GME3894_g	NAD-malate dehydrogenase
33	9	150.73	8	74400	0.00	0.85	<i>Laccaria bicolor S238N-H82</i>	GME7808_g	Glycosyltransferase family 31 protein
33	7	112.32	8	132000	0.00	1.05	<i>Schizophyllum commune H4-8</i>	GME5315_g	Glycoside hydrolase family 92 protein
33	7	106.48	17	92200	0.00	0.84	<i>Taiwanofungus camphoratus</i>	GME6571_g	Catalase
33	7	104.47	21	60900	0.00	0.48	<i>Ganoderma lucidum</i>	GME9039_g	Glyceraldehyde-3-phosphate dehydrogenase
33	4	60.1	6	658000	0.01	2.99	<i>Schizophyllum commune H4-8</i>	GME7281_g	Hypothetical protein SCHCODRAFT_52674
33	4	58.96	16	44200	0.00	0.20	<i>Laccaria bicolor S238N-H82</i>	GME7966_g	Predicted protein
33	4	58.15	16	97700	0.00	0.44	<i>Laccaria bicolor S238N-H82</i>	GME1791_g	Mannitol-1-phosphate dehydrogenase MPDH1
33	3	45.43	5	42400	0.00	0.14	<i>Laccaria bicolor S238N-H82</i>	GME6007_g	Predicted protein
33	3	45.43	9	42400	0.00	0.14	<i>Laccaria bicolor S238N-H82</i>	GME10741_g	Predicted protein
33	3	41.76	5	82900	0.00	0.28	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
33	3	40.26	8	58300	0.00	0.20	<i>Schizophyllum commune H4-8</i>	GME4142_g	Hypothetical protein SCHCODRAFT_230667
33	3	39.41	12	41700	0.00	0.14	<i>Postia placenta Mad-698-R</i>	GME2238_g	Predicted protein
33	2	37.81	4	97100	0.00	0.22	<i>Grifola frondosa</i>	GME273_g	Lectin
33	3	35.5	5	44600	0.00	0.15	<i>Coprinopsis cinerea okayama7#130</i>	GME10100_g	Microtubule binding protein

33	2	29.66	4	35400	0.00	0.08	<i>Postia placenta Mad-698-R</i>	GME4760_g	Candidate aryl-alcohol dehydrogenase
33	2	25.46	9	46500	0.00	0.11	<i>Laccaria bicolor S238N-H82</i>	GME7514_g	GTP binding protein
33	2	24.27	3	26300	0.00	0.06	<i>Laccaria bicolor S238N-H82</i>	GME5452_g	Predicted protein
33	2	21.68	4	21900	0.00	0.05	<i>Postia placenta Mad-698-R</i>	GME1408_g	Candidate G-protein beta subunit
33	2	21.25	10	90600	0.00	0.21	***	GME5765_g	NA
34	6	93.37	37	64200	0.52	29.71	<i>Taiwanofungus camphoratus</i>	GME7546_g	Glutathione transferase
34	4	56.37	15	56100	0.30	17.31	<i>Pleurotus ostreatus</i>	GME1549_g	Hypothetical protein
34	3	41.94	13	47000	0.19	10.88	<i>Laccaria bicolor S238N-H82</i>	GME36_g	Thaumatococcus-like protein
34	3	41.25	31	28400	0.15	8.76	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
34	3	41.25	31	28400	0.15	8.76	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
34	3	38.75	10	20100	0.08	4.65	<i>Coprinopsis cinerea okayama7#130</i>	GME1812_g	Proteasome component pts1
34	2	33.59	3	39500	0.11	6.09	<i>Postia placenta Mad-698-R</i>	GME6245_g	Predicted protein
34	2	29.08	11	24000	0.07	3.70	<i>Laccaria bicolor S238N-H82</i>	GME9376_g	Glycoside hydrolase family 27 protein
34	2	28.88	5	20000	0.05	3.09	<i>Laccaria bicolor S238N-H82</i>	GME590_g	Predicted protein
34	2	27.34	8	45700	0.12	7.05	<i>Heterobasidion annosum</i>	GME441_g	Manganese superoxide dismutase
35	9	155.44	58	406000	0.73	87.11	<i>Grifola frondosa</i>	GME270_g	Lectin
35	9	143.6	56	507000	0.05	6.53	<i>Grifola frondosa</i>	GME272_g	Lectin
35	8	113.86	57	139000	0.01	1.19	<i>Moniliophthora perniciosa FA553</i>	GME7309_g	Hypothetical protein MPER_11381
35	4	88.1	13	415000	0.02	2.23	<i>Grifola frondosa</i>	GME273_g	Lectin
35	4	74.94	38	78800	0.00	0.34	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
35	4	74.94	38	78800	0.00	0.34	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
35	5	66.95	24	141000	0.01	0.91	<i>Grifola frondosa</i>	GME271_g	Lectin

35	4	54.17	10	151000	0.01	0.65	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
35	3	44.32	5	54900	0.00	0.18	<i>Chlorobium phaeobacteroides BS1</i>	GME4019_g	Phosphatidylserine decarboxylase-related
35	3	44.03	15	42400	0.00	0.14	<i>Cryptococcus neoformans var. neoformans B-3501A</i>	GME3300_g	Hypothetical protein CNBD4370
35	3	43.47	26	28100	0.00	0.09	<i>Nectria haematococca mpVI 77-13-4</i>	GME10521_g	Hypothetical protein NECHADRAFT_88285
35	2	39.42	30	31800	0.00	0.10	<i>Sclerotinia sclerotiorum 1980</i>	GME3505_g	Hypothetical protein SS1G_10096
35	2	30.61	16	66300	0.00	0.14	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
35	2	28.88	5	10400	0.00	0.02	<i>Coprinopsis cinerea okayama7#130</i>	GME9565_g	TAL1
35	2	20.87	10	20500	0.00	0.04	<i>Taiwanofungus camphoratus</i>	GME6641_g	1-Cys peroxiredoxin isozyme
36	9	148.16	56	1020000	0.42	39.24	<i>Grifola frondosa</i>	GME272_g	Lectin
36	8	147.35	20	1060000	0.57	53.32	<i>Grifola frondosa</i>	GME273_g	Lectin
36	6	82.86	32	136000	0.03	2.82	<i>Grifola frondosa</i>	GME271_g	Lectin
36	4	54.23	27	46300	0.01	0.68	<i>Coprinopsis cinerea okayama7#130</i>	GME399_g	Eukaryotic translation initiation factor 1A
36	4	53.02	10	66500	0.01	0.79	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
36	4	49.87	26	18800	0.00	0.22	<i>Schizophyllum commune H4-8</i>	GME2106_g	Hypothetical protein SCHCODRAFT_14451
36	2	41.39	19	172000	0.02	1.53	<i>Grifola frondosa</i>	GME270_g	Lectin
36	3	38.63	31	41700	0.00	0.37	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
36	3	38.63	31	41700	0.00	0.37	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
36	2	29.14	16	56000	0.00	0.33	<i>Aspergillus nidulans FGSC A4</i>	GME4537_g	TPA: conserved hypothetical protein
36	2	28.38	12	37600	0.00	0.33	<i>Postia placenta Mad-698-R</i>	GME636_g	Eukaryotic translation initiation factor 5A

37	13	236.97	67	2880000	0.96	47.18	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
37	13	236.97	67	2880000	0.96	47.18	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
37	6	99.18	59	1060000	0.09	4.48	<i>Nectria haematococca mpVI 77-13-4</i>	GME10521_g	Hypothetical protein NECHADRAFT_88285
37	4	74.35	16	279000	0.02	0.74	<i>Grifola frondosa</i>	GME273_g	Lectin
37	4	58.73	31	103000	0.01	0.33	<i>Grifola frondosa</i>	GME272_g	Lectin
37	2	33.79	15	22300	0.00	0.02	***	GME2109_g	NA
37	2	25.28	16	33200	0.00	0.04	<i>Laccaria bicolor S238N-H82</i>	GME8574_g	Predicted protein
37	2	24.73	4	35700	0.00	0.04	<i>Hypsizygus marmoreus</i>	GME4347_g	Serine protease
38	5	100.98	11	865000	0.50	92.99	<i>Grifola frondosa</i>	GME273_g	Lectin
38	3	40.42	31	42900	0.01	1.73	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
38	3	40.42	31	42900	0.01	1.73	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
38	2	29.99	8	29500	0.01	1.19	<i>Grifola frondosa</i>	GME271_g	Lectin
38	2	27.91	14	77800	0.01	2.09	***	GME2110_g	NA
38	2	23.07	10	10200	0.00	0.27	<i>Grifola frondosa</i>	GME272_g	Lectin
39	4	80.58	40	940000	1.10	94.68	<i>Schizophyllum commune H4-8</i>	GME1771_g	Hypothetical protein SCHCODRAFT_109126
39	2	40.8	9	92500	0.06	5.32	<i>Grifola frondosa</i>	GME273_g	Lectin
40	7	133.85	41	2520000	1.14	97.17	<i>Schizophyllum commune H4-8</i>	GME1771_g	Hypothetical protein SCHCODRAFT_109126
40	5	76.16	42	69000	0.00	0.31	***	GME2109_g	NA
40	5	72.84	39	97200	0.01	0.61	<i>Ganoderma lucidum</i>	GME10641_g	Immunomodulatory protein 8
40	5	72.84	39	97200	0.01	0.61	<i>Ganoderma lucidum</i>	GME7566_g	Immunomodulatory protein 8
40	2	36	6	30800	0.00	0.08	<i>Grifola frondosa</i>	GME273_g	Lectin
40	2	28.3	10	25200	0.00	0.05	<i>Schizophyllum commune H4-8</i>	GME9537_g	Hypothetical protein SCHCODRAFT_83719
40	2	25.44	10	654000	0.01	1.17	***	GME5765_g	NA

L. rhinocerotis TM02 genome database was employed for the identifications in LC-MS. Abbreviations: AA, amino acid; MW, molecular weight; NA, not annotated.

Table S3Coding sequences of some selected LC-MS-identified *L. rhinocerotis* sclerotial proteins (by Gene ID)

Gene ID	Protein name	Coding sequences (CDS)	CDS length (AA)
GME1701_g	14-3-3-domain-containing protein	MAQSREDSVYLAKLAEQAERYEEMVENMKRVASSDQELTVEERNLLSVAYKNVIGARRASWRIVSSIEQKEESKGNVQVKMIKGY REKIEGELAKICEDILDVLDKHLIPSAASGESKVFYHKMMGDYHRYLAEFATGDKRKESADKSLEAYKAASDVAVTELPPTHPIRLGLAL NFSVFYYEILNSPDRACHLAKQAFDDAIAELDTLSEESYKDESTLIMQLLRDNLTLWTSDMQESEKPADKDDVADAPAEEGA	257
GME7309_g	Aegerolysin-domain-containing protein	MSTDDPVLRAYAQWVTIRINNIGTIPIKLNLSLSWGKLYVNGNKDNEVGTDREYEGSVISPNNEWLEFSSCGRSDASSGTEGRFDLVD PGAGDKIIRNFYWDPCPWGSKSNQWSVSGSNSKFMIEHYGANYSSEGALGTITVDVLNKPQVPA	149
GME3505_g	Cerato-platanin	MQFTTSLALAAIVSAAFAIRVTYDPVYDNESQSLNTVACSDGKNGLITKGYSTFGDLPTFPNIGGAHVVEGWNSTQCGSCWQLTY NGNKVIVTAIDHTHTGFNIGPRAMQDLTGSPIGMVENAQAQQLDRSACGL	136
GME7546_g	Glutathione transferase	MVLKLYGNPQSTCTSRVRVVAEELKIPELVLVVDVDFSKGEHKAPEFLAIQPFQVQPYLDDGFKLYESRAIARYLALKYGGIGKLIPDPTD LQTTALFEQAASIENSNFDPASSTLAFENIFKPMFGNKDTGTVVQQLTEVLEKKLAVYDVILGKSKYLAGDNLTADLHFLPYGALLEKQ GINFLVSDKFPNVKRWVTEISSRPSWTKVTS	212
GME9376_g	Glycoside hydrolase family 27 protein	MTEPTWSSIASAINELSFVSWASDFYGHNDLDFLQIGQGGLTFEEKTHFTAWALFKSPLIINTDLSKISNQDLSILKNEEIIAINQDPV VGKAVTPFRWGANPDHTNDPARPAQYWSGETQNGVVMLINTLSTQADMFFNLTESPWIRAGRQYSVRDLWAHTDNGIAVRN YTARGVAPHGVVALLLKDAGDEPEGAGPPCAHASSSQCLPAPK	215
GME10641_g	Immunomodulatory protein 8	MRYTLLTAPNPASKNLSKPLHNIHSTSPMSDLTITYFQVITHDVKFSVDYTPNWKRGNPNNYIDNVVFPKVLTNKKYSYGVVVDGA SLGVQAGYEVSSDGSQKVNFLYNSGYGISDKKKIQVYAVDPDTGNQFKVAQWN	141
GME273_g	Lectin	MLMAKTPLPIAIAEIVVLADVILGEPHRNPLYATKPIASIDVFSSGEAVDGIGVTYNLSDGDTVTLIHGSGPGSDHLDHTWRWAW LPPKIVAVHGRAGSMSGYGRSLVTTFDIIIIDTANDKVRLEGVTRFYFVYLCCELGGCAGNCCWTLQMFQDMHHGNEGTPPYSCN SLAFGGFAEDNADALETGTEQPHRLRLSRNPLPSTAISSALNFELYEGMTTPRYMVVTLVGGHDGTPFDDVIFMQNSNGNFIID DSNKNQIDPKKPIINTIEVYSGWVVDGISVTYNTIGGGTTTTLKHGSGPASGRTTSKVTLSGDELLVGVGLAGPQSYKRDVLNKLFSVI CNVSKQSVRVEGPFNGNNSNEGTPFYCSDVLAFFGGCAQDVSQLGLSGLCFSQACPKIFLPLSRIRIYYNMQEFTTSLVGGNVG TIFRDILFKDGDGSFVLDTSSQGILDVNHPIITNITVYHGWWVDGFDVTHQLDSGDTVTLRHGSGPATGRTTSSVTFGADEVLTGVFG LAGPQSTFRDMLNRIGFTIQNTATGVVRNAGPFGDGRNTNEGTSFYASDVIAFGGFAQDTPSVGLSGLFFYSKGG	598
GME270_g	Lectin	MSQMKNKAMVQKFDNSSLVGGQDNKWFNDVLMQTKDGNVILNTDNKEQLDLNHPHQITVYHGWIVDGTVDYQTKDGGKVT KQHGSNKQRSTRDLGDNEIVTGIFGRAGKQSYEREMVNSIGFIIYDTKKNTARTEGPVGNNGKSDGEDTFYASNVVAFGGFSKD DAYDLGLSGLFFLMKTT	184
GME272_g	Lectin	MQQFIQTSLLAGDDGVNFNDIYLRKNDGSFVNDTNKDTLDIKHPIKTIVVHGIGPVRGLSVTYRLASGDTTINHGSTGHPRQPTY PVPFEDNEVLVGFHGHYKPDGFYSMGMFVINDQEKGTVRTFGPFGNPEGATPFYCSDVIAFGGFAKDDPEWESRICGLYFFKNVGA	173
GME441_g	Manganese superoxide dismutase	MAHSLPDLPGYDALEPFISKQIMELHHRKHHQTYVNSLNAEQAAYAKATTPKERIALQAALKFNGGGHINHSLFWKNLAPSASEG KGGHGLTRDGPLKTAIENGWGSVDNFKKEFNTITAAIQSGSGWGWLGYSMTKVLEITTTANQDPLLHVPLIGVDIWEHAFYLQYY NVKMDYLNAIWDVIDFDEAEKRLVEAQAACL	204
GME5414_g	NAD-dependent formate dehydrogenase	MTMLGVSYSYLRGLLSTTARPPRLSSTRLLAPSLSRQSIAGMKILAVLYSGGEAAKQEPRLGTIENQLALRPWLES LGHEYIVTDDK EGPESVFQKNIVDAEVLITPPHFGYLTRDLIEKAKNLKLCITAGVGS DHIDLNAAA EKGLQVLEVSGSNVVSVAEHVVM SILLV RNF VPAHEMIERGDWQVSEIARDAYDLEGKVVGTIGAGRIGYRVLQRLVFPNTKELVYDYDYNPLPEEA AKAVGARRVLDLKDFVSQC DVI	400

		TVNCP LHDGTRGLVNADLLKHFKKGAWLVNTARGAICDKDAVAAALKSGQJSGYSGDVWNVQPAPRDHIWRTMKNPLGAGNG MVPHYSGTTLDAQARYAAGTKSILENYLSGKPQEAQNIIVGKTGYETKAYGQR	
GME590_g	Phosphoglycerate mutase-like protein	MSAHHDLGAVVLARNGDRTECYQHPVSQKASSTRSTPLGEVQAYQLGQHLRNLYLNPDSASFIRGIHSDLVDLSEVAVRVKVGGE GAAVFD SATALLQGLFPPNPNHRITLANETT VVAPLNGYQYVPVETVEPSNDRSLEPWTD CPAFEKHAQKMHN SAEFKEVAKQAQ PFFHALKDFAFGRELSLENAYNVWDLVSSQLIHNKTYAHLRPPFTFIEQARGFANFRENAIYSDSAMGGIGNIASRTALSSILKALQRIA FNGDPLQLMVIETTYQPFISFFHQADVHRHADRLRPLPCAHTDAFPDPSCVISLTSMHDPYPPYPADFGSAIAIELRRAPPPDQRD FLRFKFRNGTNEEFRTIHVFKHREDIPLTEFIYRENSVVNSNREWAQACSSSGATASAASLLGLPERATTGSTVADASIGVFLALVML TLTFFAAKVVRCCRRAVHLGAPEDNLSAVPSEIIVQRRDDKAPVRY	482
GME4347_g	Serine protease	MRLFAIVSVA FALLAPAFAGPSTPLKAVLKSGGETKPN SYIVKLKDGVAKDAHIHWLSSKHGSSTNVTHPDWSSKVLHGYAGSYILSA RMLMSFPLTG VFGTDALNALRMSPDV DYIEEDAIVNIEDTNTQENAPWGLQRISQDPPLPAGSNPNLLAYNYTYEVTAGEYVDIYII DTGIRITHTEFN GRAKWGKTFGGYPDADGNHGHTHCAGTAAGR TYGVAKNANLIAVKVLS DGGQVWFPSHLRCECLLV LFGSSGS LSDVISGVDYVVVEAGQTGAPSIASMSLSSPPSIAVDNAVQAATIAGVHVVAAGNQQIPASGRSPARAPAAVTVAASDIRDFAPF SNYGPSVDIAPGVS VISAWFTSDTAINIISGTSMATPHVAGLVACLISDGGNLLPEAMSDRLQQLATKNAISGVPPGTVNYLARNQV	435
GME8711_g	Serine protease	MKFFTAVSAALLLLVPVIAAPPAALKTVRASGGESLPDSYIVKLKDGVS KDAHLRWLSSNHGSDAVITHPQWSSRVLHGYAGTLHTD ALNALRASDDVEYIEE DAIAHHS AVVTQIDAPWGLQRISQDERLPDGS DPSLLVYNYTYEESAGSGVDIYILD TGIRTTTHNEFGGRAR WGPTFTGTPDEDIYGHGTHCAGTAGGSRVGVAKKASLIAVKVLGDDGSGPWSSIISGLDYVVTEFIRTVGPSIASMSLSGLASDAMD SAVEAATNAGIHVVCSAGNTGQPSDTRSPARAPSAITVAASDIQDQFASFSSYGS AVDIIAPGVVVFSA SNTNDAEYRPASGTS MST PHVAGLLATLVSDVGNFLPVEAKV KLTQLATKDAITGVPPD TVNYLARNQV	400

Abbreviation: AA, amino acids.