

Table 3.**A functional category list of proteins (*Hericium erinaceum*) identified by 1-DGE and nESI-LC-MS/MS**

The table lists indicated fraction numbers, matching peptides, scores, accession numbers, protein names, theoretical mass (kDa), theoretical pI left to right.

Fraction Number	Matching Peptide	Score	Accession Number	Protein Name	Analytical MW	Theoretical pI	Peptide
Chromatin structure and dynamics							
2	1	44	gi 44982537	Chromatin remodeling complex subunit RSC8*	64437.55	5.46	DLAQLNISKK
6	1	91	gi 1742929	Histone H2B *	15165.40	10.16	AMAILNSFVNDIFER
6	1	77	gi 3142	Histone H4.2 *	11366.34	11.36	TVTALDVVYALKR
DNA replication, recombination, and repair							
1	1	42	gi 57898980	DNA topoisomerase II *	176899.32	7.14	SIGMGRRGK
2	1	47	gi 550429	Helicases*	124537.62	6.82	EINSNTKTLENIR
4	1	49	gi 2213553	DNA repair protein RAD4 *	79023.81	8.76	EEALLPNAKPVK
6	1	42	gi 2340169	Telomerase reverse transcriptase 1 *	116457.25	9.75	KFLNLSLR
Cell division and chromosome partitioning							
3	1	73	gi 5725417	Septin *	40119.94	5.01	VNVIPVIGK
3	1	56	gi 38704270	Beta-tubulin	25238.83	5.07	AVLNDLEPGTMDAVR
4	1	100	gi 10241488	Cell division control protein 10 *	38657.99	7.20	STLINTIFASHLIDSK
5	1	44	gi 984572	Beta-tubulin*	48984.54	4.92	AVLIDLEPGTMDAVR
Transcription							
3	1	45	gi 21745321	Transcription factor *	56479.77	9.38	LPPITNHSEK
4	1	45	gi 5055	RNA polymerase II large subunit *	194162.51	5.62	QILSLIPK
Translation, ribosomal structure and biogenesis							
1	2	151	gi 11078222	Translation elongation factor EF1- α	40282.27	8.71	TLLEAIDAIEPPSRPSDKPLR LPLQDVYK, TLLEAIDAIEPPSRPSDKPLRPLQD VYK
1	2	119	gi 27960789	Translation elongation factor EF1- α	36015.52	8.81	SVEMHHEQLQEGLPGDNGVFNVK , QLIVAINK
1	1	45	gi 42547595	60S ribosomal protein L15 *	24017.93	11.27	YYEVILVDPQHK
2	2	113	gi 10637881	Translation elongation factor EF1-α *	50051.61	9.15	GDVASDSKNDPAK ,YMVTVIDAPC
2	1	70	gi 1364060	Translation elongation factor EF1- α	49663.33	9.22	DDLFNNTNASIVR, IQFGGDEVVK

2	1	63	gi 4056551	Translation initiation factor 3 subunit*	62636.95	6.59	EQRGRQGAFAGR EHALLAFTLGVR.
3	5	333	gi 58618695	Translation elongation factor EF1- α	46048.02	8.79	YMVTVIDAPGHR, LPLQDVYK, LVPSKPMCYESYNEYPPPLGR, YMVTVIDAPGHRDFIK EHALLAFTLGVR.
3	4	278	gi 58758729	Translation elongation factor EF1- α	34283.63	8.28	SVEMHHEQLEQGLPGDNVGFNVK , LPLQDVYK, LVPSKPMCYESYNEYPPPLGR TLLEAIDAIEPPSRPSDKPLR
3	3	213	gi 11078222	Translation elongation factor EF1- α	40282.27	8.71	LPLQDVYK, TLLEAIDAIEPPSRPSDKPLRLPLQD VYK
3	1	70	gi 542225	Ribosomal protein L4.e *	39005.13	10.64	NIPGVEIVNVR TLLEAIDAIEPPSRPSDKPLR
4	1	80	gi 11078222	Translation elongation factor EF1- α	40282.27	8.71	LPLQDVYK, TLLEAIDAIEPPSRPSDKPLRLPLQD VYK
4	1	79	gi 32810507	Translation elongation factor EF1- α	20360.35	8.66	AGMIVTFAPNTVTTEVK
4	1	78	gi 3766376	Ribosomal protein L10*	33565.30	4.71	TSFFQALGIPTK
4	1	77	gi 1039443	Ribosome-associated protein*	31684.85	4.91	FTPGSFTNYITR
4	1	63	gi 57225965	60s Ribosomal protein l5-b*	34650.37	8.79	ELDAEVLQK
4	1	42	gi 2104451	Threonyl-tRNA synthetase *	80138.01	6.84	WELNAGDGAFYGP
5	2	135	gi 1364060	Translation elongation factor EF1- α	49663.33	9.22	DDLFNNTNASIVR, IQFGGDEVVK ILEDLVFPTEIVGK, ILEDLVFPTEIVGKR
5	2	118	gi 1164943	Ribosomal protein S7e*	21987.65	9.73	ILEDLVFPTEIVGK, ILEDLVFPTEIVGKR
5	2	106	gi 46098158	40S Ribosomal protein S9 *	22237.86	10.68	QIVNVPSFVVR, LFEGNAIRR
5	2	94	gi 32563304	Translation elongation factor EF1- α	30650.33	6.61	YAWVLDKLLK, IGGNGTVPVGR
5	1	72	gi 1039443	Ribosome-associated protein	31684.85	4.91	FTPGSFTNYITR
5	1	62	gi 12329975	Ribosomal protein S2 *	28310.92	10.16	SMEEIYLFSLPVK
5	1	53	gi 3859691	Ribosomal protein L13e *	23053.64	10.61	GFTLAELK
5	1	49	gi 44885669	S-phase specific ribosomal protein	29423.16	9.87	LFAIGFTK
5	1	48	gi 16944409	related to GTPase MSS1 *	56936.39	4.98	SQDPILISCR
5	1	48	gi 2414648	60S ribosomal protein L7*	28449.26	10.06	QAANFLWPFK
5	1	46	gi 3766376	Ribosomal protein L10	33565.30	4.71	TSFFQALGIPTK
5	1	44	gi 14994314	40S Ribosomal protein S8*	23557.83	10.93	LIGVVYNASNELVR
6	2	150	gi 19571756	Ribosomal protein L18E *	11145.20	4.17	APTGSNTVLLR
6	3	148	gi 1742935	40S Ribosomal protein S13 *	17080.03	10.78	GISSALPYR, KGLTPSQIGVTLR, LILIESR
6	2	137	gi 46098158	40S Ribosomal protein S9	22237.86	10.68	QIVNVPSFVVR, LFEGNAIRR

6	1	86	gi 11595555	Ribosomal protein S28 *	15909.58	10.60	VSGVGLLALWK
6	1	74	gi 1039443	Ribosome-associated protein	31684.85	4.91	FTPGSFTNYITR
6	1	56	gi 38524278	40S Ribosomal protein S5*	23680.17	9.30	DISLTDYIQIR
6	1	55	gi 3620	Ribosomal protein L29 *	16721.55	10.62	INMDKYHPGYFGK
6	1	54	gi 3859690	40S Ribosomal protein rps16 *	15739.42	10.29	INMDKYHPGYFGK
6	1	53	gi 3806	Hypusine containing protein HP2 *	17114.28	4.81	VHLVAIDIFTGK
6	1	49	gi 6323236	Ribosomal protein L6*	95480.78	6.15	AFKQGNIDAGVVAGDIYFQMQNY;
Posttranslational modification, protein turnover, chaperones							
1	1	45	gi 2551	Ubiquitin *	8540.78	6.56	IQDKEGIPPDQQR
1	1	44	gi 21388600	Heat shock protein 70	25092.47	5.52	DAGVIAGLNVLR
2	5	385	gi 7521943	Heat shock protein 70	71055.79	5.02	IINEPTAAAIAYGLDKK, IINEPTAAAIAYGLDK, TQDLLLLDVAPLSLGIETAGGVMT ALIK, NGLESYAYNLR, FELSGIPPAPR
2	3	222	gi 44983832	Heat shock protein 70 *	70303.76	5.12	IINEPTAAAIAYGLDKK, IINEPTAAAIAYGLDK,FELTGIPPA PR
2	2	135	gi 25990446	Heat-shock protein 90 *	79295.85	4.92	HSEFISYPIQLVVTK, DSPFLEVVK
2	2	100	gi 44981480	Heat shock protein 70 *	73898.47	4.91	FELSGIPPAPR, EDIDDIVLVGGSTR
3	1	81	gi 19069227	26S Proteasome regulatory subunit 4 *	47377.75	6.39	TMLELLNQLDGFDR
3	1	60	gi 3687465	26S Proteasome regulatory subunit*	43552.98	5.28	ENAPAIIFIDEIDAIATK
5	1	65	gi 984687	Proteasome alpha type 1*	25604.02	6.90	LFQVEYALEAIK
6	2	109	gi 16943775	Cyclophilin *	17614.90	9.36	FADENFQLK, VIPQFMLQGGDFTK
6	1	77	gi 849081	Cyclophilin B *	21969.06	8.59	VIKDFMIQGGDFTR
6	1	49	gi 6323236	Ubiquitin *	95480.78	6.15	AFKQGNIDAGVVAGDIYFQMQNY;
Energy production and conversion							
1	5	347	gi 57227717	Pyruvate carboxylase*	121206.58	6.27	NIIVEQGPEAFK, TWTFIDDTPELFK, SAFGDGTVFIER, LVPNIPLQALVR, HYFIEINPR
1	2	108	gi 4255	Pyruvate carboxylase *	130907.76	6.25	QFNGTLLMDTTWR, HYFIEINPR
1	1	51	gi 46433360	NAD-formate dehydrogenase *	41801.55	5.51	LLGTVENELGIR
1	1	49	gi 7320601	Pyruvate carboxylase	43215.42	5.57	ASDSSVFDHEMPGGQYTNLMFQA SQLGLGTQWTEIK
2	1	81	gi 1749734	Succinate dehydrogenase*	53767.12	7.71	LGANSLLDIVVFR
3	2	160	gi 584806	ATP synthase alpha chain*	59522.39	9.07	STVAQLVKTLLEENDAMK,TGEIVD VPVGPPELLGR

3	1	69	gi 46433360	NAD-formate dehydrogenase *	41801.55	5.51	LLGTVENELGIR
3	1	59	gi 4376093	Pyruvate kinase *	58248.74	5.88	GDLGIEIPASQVFLAQK
3	1	51	gi 1420756	PYK2 *	55195.22	6.43	IENQQGLDNFDEILEVTDGVMIAI
4	2	137	gi 59803007	Malate dehydrogenase*	35191.31	8.26	DDLFTNASIVR, LFGVTTLDVVR
4	2	110	gi 4029338	Malate dehydrogenase *	33029.29	6.13	IQFGGDEVVK, VAVLGAAGGIGQPLSLLLF
4	2	96	gi 462075	Formate dehydrogenase *	39910.56	6.84	GLVNAELLK, GAWLVNTAR
4	1	81	gi 46433360	NAD-formate dehydrogenase	41801.55	5.51	LLGTVENELGIR
4	1	66	gi 13785197	Inorganic pyrophosphatase *	32390.49	5.24	VLGIMALLDEGETDVK
4	1	42	gi 18149179	Aryl alcohol dehydrogenase *	44382.60	6.88	NITAVAIAIYVMQK
5	1	72	gi 34765759	NADH-ubiquinone oxidoreductase*	30373.33	8.83	VVYEPLQLTQAFR
Carbohydrate transport and metabolism							
1	1	89	gi 929983	Glycerol-3-aldehyde dehydrogenase *	30768.23	6.13	VPTNDVSVDLVVR
2	1	53	gi 29409959	Transketolase *	74759.56	5.98	ANSGHPGAPMGMAPVSHVLFNK
2	1	43	gi 21264637	Endo beta 1,4 glucanase *	36395.44	4.40	VASATAWLK
3	2	123	gi 870831	Glucose-6-phosphate 1-dehydrogenase	58950.31	6.17	GGYFDEFGIIR,TFPALFGLYR
3	1	87	gi 929983	Glycerol-3-aldehyde dehydrogenase	30768.23	6.13	VPTNDVSVDLVVR
3	1	70	gi 40713647	Glucose-6-phosphate isomerase *	61445.79	6.38	ILLSNFFAQPEALAFGK
4	3	237	gi 57232460	Glyceraldehyde 3-phosphate dehydrogenase *	25354.62	8.81	VVNDKFGIVEGLMSTIHATTATQK , FGIVEGLMSTIHATTATQK
4	1	80	gi 30525994	Glyceraldehyde 3-phosphate dehydrogenase	11364.02	9.10	GVNGNIIPSTGAAK
4	1	63	gi 3289019	Xylose reductase *	36021.33	5.77	TPAEVLLR
5	1	81	gi 929983	Glycerol-3-aldehyde dehydrogenase	30768.23	6.13	VPTNDVSVDLVVR
5	1	74	gi 40739109	Triosephosphate isomerase *	27156.97	5.88	VVIAIYEPVWAIGTGK
6	1	58	gi 929983	Glycerol-3-aldehyde dehydrogenase	30768.23	6.13	VPTNDVSVDLVVR
Amino acid transport and metabolism							
4	2	151	gi 6746633	Glutamine synthetase*	38306.81	5.88	IWDFDGSSTNQAPGNDSDVYLRF AAIFKDPFR, IWDFDGSSTNQAPGNDSDVYLRF AAIFK
4	1	55	gi 57223024	Endopeptidase*	47547.37	4.77	EPGLAFAFGK
Nucleotide transport and metabolism							
6	1	47	gi 44981739	Carbamoyl-phosphate synthase *	248131.78	5.48	AASTVDEALEAVK
Lipid metabolism							

5	1	55	gi 1907190	Acyl-CoA sterol acyltransferase *	71613.08	8.53	ESLSPETREILQK
Inorganic ion transport and metabolism							
2	1	46	gi 30580366	Catalase 3*	79227.71	5.75	FEASHVTNEQVKK
4	1	66	gi 57226036	Voltage-dependent ion-selective channel*	30636.63	9.13	INNAGVLSLGYTQALRPGVK
6	1	51	gi 38566870	Glutathione peroxidase *	18888.76	6.43	FLIGKDGKVK
Secondary metabolites biosynthesis, transport, and catabolism							
1	1	44	gi 44982853	Cytochrome P450 *	60505.74	6.77	VMTVYLGTK
Cytoskeleton							
3	3	164	gi 5053107	Actin 1 *	41617.51	5.30	TTGIVLDSGDGVTHTVPIYEGFALP HAILR, LDLAGRDLTDFLIK, DLTDFLIK
4	1	62	gi 31581446	Actin 1	33445.88	5.46	SYENPDGQVITIGNER
5	1	91	gi 31581482	Actin 1	33559.39	5.46	SYENPDGQVITIGNER
Cell envelope biogenesis, outer membrane							
3	1	87	gi 15321714	UDP-glucose dehydrogenase *	51311.93	5.53	ILTVGLWSSSELSK
Intracellular trafficking and secretion							
5	1	84	gi 46099486	GTP-binding protein ypt1*	22931.88	5.89	SATNVEQAFLTMAK
5	1	64	gi 46444053	Clathrin-associated protein AP-1 complex *	50205.14	7.08	LKTFPGGK
5	1	61	gi 30024664	Ras-related protein Rab7 *	22969.85	4.75	EAINVEQAFQTVAK
5	1	48	gi 311752	Ran*	24810.36	6.12	SNYNFEKPFLWLR
6	2	108	gi 461532	ADP-ribosylation factor*	20912.06	5.79	ILMVGLDAAGK, DALLVFANK
6	1	82	gi 46099486	GTP-binding protein ypt1	22931.88	5.89	SATNVEQAFLTMAK
Signal transduction							
1	1	54	gi 3560251	Serine/Threonine protein kinases*	55222.27	8.00	EVSILER
2	1	44	gi 3560	Calmodulin-binding protein 2*	68499.64	5.92	SSDAIRNTEQINAAIKIENK
2	1	42	gi 44985926	Serine/Threonine protein kinases*	51673.68	5.61	NLKPDAVDLLEK
4	1	50	gi 474400	Serine/Threonine protein kinases*	42450.42	9.35	TVLLADQLISR

5	6	414	gi 11262436	14-3-3 protein homolog *	28913.33	4.67	LAEQAERYEEMVENMKR, QAFDDAIAELDTLSEESYKDSTLI MQLLR, AASDVAVTELPPTHPIR, DSTLIMQLLR, YLAEFATGDKR, NLLSVAYK
Unclassified							
2	1	53	gi 28950128	Related to sporulation protein SPO72 *	219672.55	4.84	HILLDNLR
2	1	48	gi 44981703	ACR227Wp	87703.32	5.52	MISECLGDDSESILVPRLK
3	1	43	gi 57222792	protein-nucleus import-related protein	78291.35	5.11	LIDLGRISGNLK
4	1	45	gi 44983595	AER010Cp	84506.58	8.70	SDEVALLKHRR
6	1	71	gi 1052793	SPAC2F7.10	72521.60	8.74	QALISNGLK
6	1	53	gi 531492	RRP3p	122491.61	4.52	ENNGNEEDK
6	1	45	gi 27948809	SNT1	93751.27	7.77	ISNFMGGLR

Asterisks indicate unique proteins identified from *H. erinaceum* fruiting body using Tandem MS analysis and Edman sequencing.
Commonly identified proteins in *S. crispa* and *H. erinaceum* are shown in red letters.

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