

Table 4.**Proteins (*Hericium erinaceum*) identified by 2-DGE and N-terminal amino acid sequencing**

The table lists indicated spot numbers, amino acid sequences, scores, accession numbers, protein names, identity/similarity, theoretical mass (kDa), theoretical pI, organism and function left to right.

Spot Number	Amino Acid Sequence	Score	Accession Number	Protein Name	Identity /Similarity	Analytical MW	Theoretical pI	Organism	Function
1	qlttkvrvlrdkrin	51	Q6FJ50	Guanine nucleotide-binding protein subunit gamma*	53 / 73	10251.63	6.05	Fungi	Signal transduction
2	gwfhdssdeaqaysq vndaphkael	118	Q4IID0	Hypothetical protein	67 / 83	11878.88	4.88	Fungi	Unclassified
3	anpggdyamn			No significant hit found					
4	qftvvlkaan	44	P58724	Blue-light photoreceptor*	70 / 80	28816.77	4.73	Bacteria	Signal transduction
5	qgatsikalgfnipl	59	Q9LA06	Serine protease do-like htrA*	62 / 92	41647.97	5.17	Bacteria	Amino acid transport and met:
6	hgeaeefilg	49	Q31G56	Ribonuclease HII*	70 / 90	22808.57	6.30	Bacteria	Nucleotide transport and meta
7	rakvyvmnls	40	P61174	50S ribosomal protein L36*	75 / 100	4694.62	12.14	Bacteria	Translation, ribosomal structu: biogenesis
8	txgdpsaavgflray			No significant hit found					
9	txgdpsaavgflraylef	57	Q9YAD8	Hypothetical protein APE2001	57 / 86	15980.57	5.40	Bacteria	Unclassified
10	txgdpsaavgflraylef	57	Q9YAD8	Hypothetical protein APE2001	57 / 86	15980.57	5.40	Bacteria	Unclassified
11	flekaqikvgekvsset vk	57	Q88QM6	30S ribosomal protein S17*	56 / 75	10057.76	9.81	Bacteria	Translation, ribosomal structu: biogenesis
12				N-terminal amino acid blocked					
13	axpasflekaqikvgek vsl	67	Q6H806	Putative ubiquitin fusion degradation protein*	50 / 94	35143.74	5.77	Plant	Posttranslational modification, turnover, chaperones
14	vektahaarsflekaqi kv	68	Q8U778	Transcriptional regulator, ROK family*	58 / 89	42235.10	5.97	Bacteria	Transcription
15	qpilfiaddgyafty	62	Q9AJ64	Antigenic heat-stable 120 kDa protein	64 / 79	108518.46	5.08	Bacteria	Unclassified
16				N-terminal amino acid blocked					
17				N-terminal amino acid blocked					
18				N-terminal amino acid blocked					
19	mllysdiiiddemfsda fpv	101	Q5K7S2	Translationally-controlled tumor protein homolog *	65 / 95	18763.25	4.55	Fungi	Signal transduction

20	mllysiitddemfsda	79	Q5K7S2	Translationally-controlled tumor protein homolog	65 / 94	18763.25	4.55	Fungi	Signal transduction
21	vhtlpdlpyaydalepy fsr	123	Q9P4T6	Superoxide dismutase [Mn]*	90 / 100	22194.25	6.03	Fungi	Inorganic ion transport and me
22	vhtlpdlpyayd	77	Q9P4T6	Superoxide dismutase [Mn]	80 / 90	22194.25	6.03	Fungi	Inorganic ion transport and me
23	vlklhgspstgttrvvv vl	84	Q1EBD9	Glutathione S-transferase*	75 / 85	23889.39	6.60	Fungi	Secondary metabolites biosyn transport, and catabolism
24	snavkeglffta			No significant hit found					
25				N-terminal amino acid blocked					
26	tltggrgafgir	56	Q1CX38	ATP synthase epsilon chain*	78 / 89	14595.68	5.54	Bacteria	Energy production and conver
27	aprkkffvggnfkmnps tqae	97	P04828	Triosephosphate isomerase	71 / 94	27156.97	5.88	Fungi	Carbohydrate transport and m
28				N-terminal amino acid blocked					
29	rplaglyrga			No signifcant hit found					
30	kplfgv			No significant hit found					
31	tqgpivtgtsilalk	71	A1CE34	Proteasome component Pre4*	67 / 100	29023.61	5.67	Fungi	Posttranslational modification. turnover, chaperones
32	mlgng			No significant hit found					
33	qglpganyit			No significant hit found					
34	kvgges			No significant hit found					
35				N-terminal amino acid blocked					
36				N-terminal amino acid blocked					
37	pesredsvylaklaeqa ery	125	Q4G2I8	14-3-3 protein	100 / 100	28721.07	4.71	Fungi	Signal transduction
38				N-terminal amino acid blocked					
39	sihpevllgq			No significant hit found					
40	mrlirddktavgdy	73	Q4PDU5	hypothetical protein	73 / 86	32424.87	6.35	Fungi	Unclassified
41				N-terminal amino acid blocked					
42				N-terminal amino acid blocked					
43	nkynagkygl	58	A1FRZ0	Lytic transglycosylase*	80 / 90	35129.87	8.28	Bacteria	Cell envelope biogenesis, outc
44				N-terminal amino acid blocked					
45	tkvavlgaggigqpls	113	P17505	Malate dehydrogenase*	95 / 100	35649.96	8.46	Fungi	Energy production and conver
46	spryilatdq			No significant hit found					
47	pkavvlgaaggigqp	75	P17505	Malate dehydrogenase	79 / 100	35649.96	8.46	Fungi	Energy production and conver
48	skavvlgaaggigqp	75	P17505	Malate dehydrogenase	79 / 100	35649.96	8.46	Fungi	Energy production and conver

49				N-terminal amino acid blocked								
50				N-terminal amino acid blocked								
51	dyqtakpaievgklk	62	P36498	Transport protein comB*	83 / 92	49601.49	5.64	Bacteria	Cell envelope biogenesis, oute			
52	paltvtklnt	45	P92133	Caurepsin B-like CF3 protease*	83 / 100	32673.83	5.19	Insect	Amino acid transport and met			
53				N-terminal amino acid blocked								
54	dillfkvlr	49	Q5VV43	Uncharacterized protein KIAA0319 precursor	89 / 100	117762.74	5.34	Human	Unclassified			
55				N-terminal amino acid blocked								
56				N-terminal amino acid blocked								
57	vvkvgingfgrigri	97	Q8J1H3	Glyceraldehyde-3-phosphate dehydrogenase	100 / 100	36400.27	6.46	Fungi	Carbohydrate transport and m			
58				N-terminal amino acid blocked								
59				N-terminal amino acid blocked								
60				N-terminal amino acid blocked								
61				N-terminal amino acid blocked								
62	ivgrpghqlvmv	61	P10982	Actin-1	75 / 83	15693.88	5.30	Fungi	Cytoskeleton			
63	mltelekalnsidsv	68	P05109	Protein S100-A8*	87 / 93	10834.51	6.51	Human	Signal transduction			
64	mltelekalnsidsv	68	P05109	Protein S100-A8	87 / 93	10834.51	6.51	Human	Signal transduction			
65				N-terminal amino acid blocked								
66	lpiheyqsvkllnsy	82	Q5KN95	Succinate-CoA ligase*	87 / 93	44998.54	5.62	Fungi	Energy production and conver			
67				N-terminal amino acid blocked								
68	vykvadislaafgrkei ega	104	P39954	Adenosylhomocysteinase*	90 / 95	49125.51	5.83	Fungi	Amino acid transport and met			
69	vaywepgtqynygsiv eyeg	81	Q8U1H4	Putative chitinase*	65 / 88	39701.99	5.18	Bacteria	Carbohydrate transport and m			
70	vaydepgtqynhgsi	54	P47009	Hypothetical 11.7 kDa protein in IDS2-MPI2 intergenic region	64 / 91	11659.54	6.40	Fungi	Unclassified			
71				N-terminal amino acid blocked								
72				N-terminal amino acid blocked								
73	ginkgklg	53	Q5NF19	Probable inorganic polyphosphate /ATP-NAD kinase*	100 / 100	32505.52	8.63	Bacteria	Coenzyme metabolism			
74				N-terminal amino acid blocked								
75				N-terminal amino acid blocked								

76				N-terminal amino acid blocked					
77				N-terminal amino acid blocked					
78				N-terminal amino acid blocked					
79				N-terminal amino acid blocked					
80	atavtqgpftvttl	61	Q9Y8B5	Mitochondrial-processing peptidase subunit beta*	60 / 93	51162.66	5.69	Fungi	Amino acid transport and met:
81	ateakgaigavktviga vxd	81	Q6FYM3	ATP synthase subunit beta*	60 / 83	57135.98	5.61	Bacteria	Energy production and conver
82	apegvgdigliglah			No significant hit found					
83				N-terminal amino acid blocked					
84				N-terminal amino acid blocked					
85				N-terminal amino acid blocked					
86				N-terminal amino acid blocked					
87				N-terminal amino acid blocked					
88				N-terminal amino acid blocked					
89				N-terminal amino acid blocked					
90	papadflkgvdsneeaf iqr	66	Q98N59	Elongation factor G*	50 / 77	77208.28	5.28	Bacteria	Translation, ribosomal structu: biogenesis
91	hlqqvf			No signifcant hit found					
92	pnqtvfdirdgavyt	62	Q93LL2	Acetyl-coenzyme A synthetase*	62 / 85	37143.22	6.14	Bacteria	Energy production and conver
93	ahkeikfsnegraai	73	P50142	Heat shock protein 60*	73 / 93	61888.74	5.69	Fungi	Posttranslational modification, turnover, chaperones
94	qlgseadftqisfdh			No signifcant hit found					
95	lggggvlslg			No signifcant hit found					
96				N-terminal amino acid blocked					
97				N-terminal amino acid blocked					
98	qglpnprqgaed	60	P36627	Cellular nucleic acid-binding protein homolog*	100 / 100	19342.51	8.34	Fungi	Signal transduction
99	rlkvggpogg			No signifcant hit found					
100				N-terminal amino acid blocked					
101	qtdpaeitdgvfgi	55	P01007	Plasminostreptin*	54 / 85	11398.86	6.07	Bacteria	Defense
102				N-terminal amino acid blocked					
103				N-terminal amino acid blocked					
104	qglnlpg	50	Q927D8	UPF0133 protein	100 / 100	11438.28	4.59	Bacteria	Unclassified
105				N-terminal amino acid blocked					

106	dasnkseygtvigig	60	Q24895	78 kDa glucose-regulated protein precursor*	83 / 92	71675.38	5.09	Insect	Posttranslational modification, turnover, chaperones
107	pgqlaqanphgdsg			No significant hit found					
108	qgqlaqanphg			No significant hit found					
109				N-terminal amino acid blocked					
110				N-terminal amino acid blocked					
111	spgnllgdgarg	61	P04922	Circumsporozoite protein precursor	67 / 83	34782.33	5.38	Insect	Unclassified
112	fpapgateqvkgvis			No significant hit found					
113	aapvstndrfvpsaa	57	P78972	WD repeat containing protein	64 / 91	53417.86	9.30	Fungi	Unclassified
114	aapvsln dqfgpsaa	60	Q5A387	Hypothetical Protein MSS1	73 / 91	42895.97	5.98	Fungi	Unclassified
115	gghsvpltnfm	65	P07267	Saccharopepsin precursor*	73 / 100	44499.00	4.70	Fungi	Amino acid transport and metabolism

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