

**Table 2.****Proteins (*Sparassis crispa*) 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 /Similarlity	Analytical MW	Theoretical pI	Organism	Functional Category
1	gefsddsdqagaydq	74	A1CE10	Phosphoglycerate mutase*	73 / 87	12190.12	4.81	Fungi	Carbohydrate transport and metabolism
2	sntgvvaatv			No significant hits found					
3	sptvxvndvvpstgftfy vpy	74	Q2PCV2	Laccase*	69 / 81	5404.94	6.26	Fungi	Secondary metabolites biosynthesis, transport, and catabolism
4	sxraaxgsgavnags			No significant hits found					
5	raakgsgavnagstqsf vgnlseIn			No significant hits found					
6	rgkggsgvnnnggtqqf fv	65	Q6ZXX3	<b>Histone H4</b>	53 / 100	11382.34	11.36	Fungi	Chromatin structure and dynamics
7	aplgiavadapstaafg v	74	Q1IL41	Hypothetical protein	53 / 88	32116.70	5.64	Bacteria	Unclassified
8	aplsievadapstiafgv	61	Q9FAX2	DNA gyrase subunit B*	56 / 78	53556.69	6.33	Bacteria	DNA replication, recombination, and repair
9	sdsiearlhfieln	56	P46963	CTD kinase subunit gamma*	69 / 92	34809.18	5.88	Fungi	Transcription
10	sdsiearlhfieln	56	P46963	CTD kinase subunit gamma	69 / 92	34809.18	5.88	Fungi	Transcription
11	sdsiearlhfieln	56	P46963	CTD kinase subunit gamma	69 / 92	34809.18	5.88	Fungi	Transcription
12	sdsieaqlhfieln	54	Q753W3	Vacuolar sorting protein SNF7*	64 / 79	26685.19	4.84	Fungi	Intracellular trafficking and secretion
13	speqelaavngrllqss vgdldpvv	79	A0V740	Phosphatidylserine decarboxylase*	54 / 75	30888.40	9.09	Bacteria	Lipid metabolism
14	speqelaavngrllqss vgd			No significant hits found					
15	sldvearalyiesldifg	59	Q3IYU1	tRNA pseudouridine synthase B	56 / 88	32194.57	5.20	Bacteria	Translation, ribosomal structure and biogenesis
16	rvpktlidqlakay			No significant hits found					
17	gldklvnvnglqdm gvgdl	68	Q8ZVM9	Probable exosome complex exonuclease 1*	56 / 94	27148.26	6.86	Bacteria	Amino acid transport and metabolism
18	rlgkvgnvrgagg			No significant hits found					

19	spdkltnvnl			No significant hits found						
20	aapapkapkgvekrd			No significant hits found						
21	slnmvyrilmf			No significant hits found						
22	slimqlrltf			No significant hits found						
23	kldldllvrlrdah			No significant hits found						
24	kadmvtvril	47	Q9MUU6	Chloroplast 30S ribosomal protein S8*	75 / 100	14764.25	9.73	Plant	Translation, ribosomal structure and biogenesis	
25	kqsredlvylaklgr	64	Q562H7	14-3-3 protein	92 / 92	28815.19	4.76	Fungi	Signal transduction	
26	snprkpgqhdlll			No significant hits found						
27	kpgagengdg			No significant hits found						
28	kpgvhfmpfddfgl			No significant hits found						
29	kapegnilgggdr			No significant hits found						
30	lkdlqedhagvrlqv	80	O14460	Elongation factor 2	73 / 93	93230.90	6.02	Fungi	Translation, ribosomal structure and biogenesis	
31	kpqytpanigaprg	69	O57683	Splicing factor 3B subunit 1*	57 / 100	146214.52	6.48	Insect	RNA processing and modification	
32				N-terminal amino acid blocked						
33				N-terminal amino acid blocked						
34	asatehtlvrldgn	53	Q9B6D8	Cytochrome c oxidase subunit 3*	73 / 91	30467.04	6.32	Fungi	Energy production and conversion	
35	psakifydsdadlsl	73	Q46JF6	Ketol-acid reductoisomerase*	85 / 100	36309.51	5.21	Bacteria	Amino acid transport and metabolism	
36	slpegytvlsnrdsi			No significant hits found						
37	slgrygiggfl			No significant hits found						
38	pnvqrvtexvfqsps	50	Q9FNE0	Putative cytochrome c oxidase polypeptide Vc-4*	43 / 86	7421.61	8.03	Plant	Energy production and conversion	
39				N-terminal amino acid blocked						
40	qpgdelrdef	59	Q8DJ62	Urease accessory protein ureE*	89 / 100	16285.70	6.49	Bacteria	Amino acid transport and metabolism	
41	qpgydgvlaryrlgp	64	Q73V62	UPF0061 protein MAP 3154	67 / 87	53324.47	5.07	Bacteria	Unclassified	
42	spgnalevgy	54	P22553	S-locus-specific glycoprotein BS29-2 precursor*	70 / 100	49543.04	8.48	Plant	Sporulation	
43	qleydyngqh			No significant hits found						
44	lqtaadstqleda	52	P48465	Actin	82 / 100	41736.68	5.17	Bacteria	Cytoskeleton	
45	rigyngytnrfggrf			No significant hits found						
46				N-terminal amino acid blocked						

47	rvtgklgavairv	57	Q8NSS8	Hypothetical transport protein Cgl0590/cg0683	67 / 87	55665.64	5.78	Bacteria	Unclassified
48	kgnggllgqnadlgr	64	P43852	Bifunctional purine biosynthesis protein purH*	83 / 92	58349.59	5.75	Bacteria	Nucleotide transport and metabolism
49	qiggasgggr			No significant hits found					
50	mvlveelnvlva	45	Q83PY1	Protein slyX	64 / 82	8184.30	4.89	Bacteria	Unclassified
51	kgyatpiftmd			No significant hits found					
52	ateatgtigqvktvigav vd	86	Q98EV8	ATP synthase subunit beta*	65 / 95	50775.77	4.97	Bacteria	Energy production and conversion
53	slgahgakry	59	Q00094	Gene 73 protein kinase*	80 / 100	106567.73	8.80	Viruses	Signal transduction
54	pltfsqqfntsv	52	Q8CWA2	Cation efflux system protein cusB precursor*	67 / 92	44409.95	5.70	Bacteria	Cell envelope biogenesis, outer membrane
55	rtagepydtv			No significant hits found					
56	paiaiekvpathkti	53	Q4WGM4	Ubiquinol-cytochrome c reductase complex*	47 / 80	14662.88	5.55	Fungi	Energy production and conversion
57	apqtkllqatgdaay	51	P94186	Mercuric transport protein periplasmic component precursor*	73 / 91	9505.12	9.26	Bacteria	Inorganic ion transport and metabolism
58	ahkdikfsnegrasi	70	Q0H0L2	Heat shock protein 60	71 / 83	63039.38	5.91	Fungi	Posttranslational modification, protein turnover, chaperones
59	slqvaliayqkndyh	55	Q7VI68	L-seryl-tRNA(Sec) selenium transferase*	53 / 93	50580.15	8.50	Bacteria	Translation, ribosomal structure and biogenesis
60	klgdklgrkg	67	Q0K852	NADH dehydrogenase type2 *	100 / 100	47467.77	8.64	Bacteria	Energy production and conversion
61	glearvptdsqp	67	Q2H0Z4	Hypothetical protein	75 / 100	51089.66	4.91	Fungi	Unclassified
62	qteeyfvitlqflhv	52	P37485	Hypothetical protein yybS	64 / 91	34534.02	9.65	Bacteria	Unclassified
63	spgtlprgkhrmgms	77	Q2LEM4	Hypothetical protein	71 / 86	25414.61	5.89	Bacteria	Unclassified
64	sqgeglgtmier			No significant hits found					
65	atvsegnigaty			No significant hits found					
66	alvgeggrgt			No significant hits found					
67				N-terminal amino acid blocked					
68	slgrvdlirt			No significant hits found					
69	slrvgygth			No significant hits found					
70	klraelnen			No significant hits found					

71	klrayrnvlk	49	Q6EW16	Chloroplast 30S ribosomal protein S8*	88 / 100	15447.03	11.30	Plant	Translation, ribosomal structure and biogenesis
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Asterisks indicate unique proteins identified from *S. crispa* fruiting body using Tandem MS analysis and Edman sequencing. Commonly identified proteins in *S. crispa* and *H. erinaceum* are shown in red letters.