## Table 1.

### A functional category list of proteins (*Sparassis crispa* ) identified by 1-DGE and nESI-LC-MS/MS

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

| Fraction Number | Matching Peptide | Score | Accession Number | Protein Name | Analytical MW | Theortical p*I* | Peptide |
|---|---|---|---|---|---|---|---|
| **Chromatin structure and dynamics** | | | | | | | |
| 6 | 1 | 92 | gi\|1742929 | Histone H2B * | 15165.40 | 10.16 | AMAILNSFVNDIFER |
| 6 | 1 | 67 | gi\|3142 | Histone H4* | 11366.34 | 11.36 | TVTALDVVYALK |
| **DNA replication, recombination, and repair** | | | | | | | |
| 2 | 1 | 57 | gi\|14245691 | Reverse transcriptase * | 40781.01 | 9.06 | QILADLK |
| 3 | 1 | 69 | gi\|908896 | DNA repair protein rad32* | 73688.98 | 5.48 | QINLLVK |
| 5 | 1 | 47 | gi\|47132515 | recQ family Helicase* | 169673.76 | 8.04 | LEAGTAHDSSDGVGGGSAPAAPGK |
| **Cell division and chromosome partitioning** | | | | | | | |
| 4 | 1 | 102 | gi\|10241488 | Cell division control protein 10 * | 38657.99 | 7.20 | STLINTIFASHLIDSK |
| 4 | 1 | 51 | gi\|6977953 | Septin* | 53737.59 | 5.41 | VNIIPIIAK |
| **Transcription** | | | | | | | |
| 4 | 1 | 49 | gi\|57228114 | Transcriptional activator* | 133338.53 | 8.14 | EEGEGLGEEGK |
| 4 | 1 | 47 | gi\|19068759 | Heat shock transcription factor * | 33685.36 | 6.62 | EDLLGFDDSLR |
| **Translation, ribosomal structure and biogenesis** | | | | | | | |
| 1 | 3 | 208 | gi\|58758727 | Translation elongation factor EF1-α * | 44184.90 | 8.55 | EHALLAFTLGVR,<br>TLLDAIDAIEPPVRPSDKPLRLPLQDVYK,<br>YAWVLDKLK, YAWVLDK,<br>AGMIVTFAPTNVTTEVK |
| 1 | 3 | 193 | gi\|11078214 | Translation elongation factor EF1-α | 46634.83 | 8.79 | IGGIGTVPVGR,<br>AGMIVTFAPTNVTTEVK |
| 3 | 5 | 263 | gi\|2897607 | Translation elongation factor EF1-α | 50133.84 | 9.21 | EHALLAFTLGVR,<br>TLLDAIDAIEPPVRPSDKPLRLPLQDVYK,<br>QTVAVGIIK, YAWVLDKLK, YAWVLDK |
| 3 | 5 | 259 | gi\|58758727 | Translation elongation factor EF1-α | 44184.90 | 8.55 | EHALLAFTLGVR,<br>TLLDAIDAIEPPVRPSDKPLRLPLQDVYK,<br>YAWVLDKLK, YAWVLDK,<br>AGMIVTFAPTNVTTEVK |
| 3 | 4 | 237 | gi\|2313 | Translation elongation factor EF1-α | 49828.51 | 9.12 | QLIVAINK, EHALLAFTLGVR,<br>YAWVLDKLK, YAWVLDK |

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|---|---|---|---|---|---|---|---|
| 3 | 2 | 149 | gi\|32567511 | Translation elongation factor EF1-α | 14692.27 | 6.95 | TLLDAIDANEPPVRPSDKPLR,<br>EHALLAFTLGVR |
| 3 | 1 | 71 | gi\|8927046 | Translation elongation factor EF2* | 89733.93 | 6.75 | GTVAFGSGLHGWAFTVR |
| 5 | 1 | 59 | gi\|46431916 | Ribosomal protein L3* | 43948.70 | 10.26 | HGSLGFLPR |
| 5 | 1 | 50 | gi\|3766376 | Ribosomal protein L10 * | 33565.30 | 4.71 | TSFFQALGIPTK |
| 6 | 2 | 109 | gi\|16943769 | Ribosomal protein S19* | 14522.61 | 9.48 | LEVPTWVDLVK, ELAPYDPDWYYVR |
| 6 | 1 | 81 | gi\|3806 | Translation initiation factor 5A-2* | 17114.28 | 4.81 | VHLVAIDIFTGK |
| 6 | 1 | 56 | gi\|3560198 | Ribosomal protein L18E * | 21189.79 | 11.66 | AGGEVLTLDQLALR |
| 6 | 1 | 56 | gi\|11595555 | Ribosomal protein S28* | 15909.58 | 10.60 | VSGVGLLALWK |
| 6 | 1 | 53 | gi\|1164943 | Ribosomal protein S7e* | 21987.65 | 9.73 | ILEDLVFPTEIVGK |
| 6 | 1 | 42 | gi\|1850540 | Ribosomal P2 phosphoprotein* | 11145.20 | 4.17 | DINELIASGPEK |
| **Posttranslational modification, protein turnover, chaperones** |  |  |  |  |  |  |  |
| 2 | 4 | 271 | gi\|7521943 | Heat shock protein 70 * | 71055.79 | 5.02 | IINEPTAAAIAYGLDKK<br>TQDLLLLDVAPLSLGIETAGGVMTALIK,<br>SINPDEAVAYGAAVQAAILSGDTSEK,<br>IINEPTAAAIAYGLDK |
| 2 | 1 | 66 | gi\|19069227 | 26S Proteasome regulatory subunit 4* | 47377.75 | 6.39 | TMLELLNQLDGFDTR |
| 2 | 1 | 65 | gi\|56199674 | 60 kDa Chaperonin* | 19860.09 | 5.99 | GFISPYFITDVK |
| 3 | 2 | 160 | gi\|7521943 | Heat shock protein 70 | 71055.79 | 5.02 | IINEPTAAAIAYGLDKK<br>TQDLLLLDVAPLSLGIETAGGVMTALIK,<br>SINPDEAVAYGAAVQAAILSGDTSEK,<br>IINEPTAAAIAYGLDK |
| 4 | 1 | 56 | gi\|7521943 | Heat shock protein 70 | 71055.79 | 5.02 | IINEPTAAAIAYGLDKK<br>TQDLLLLDVAPLSLGIETAGGVMTALIK,<br>SINPDEAVAYGAAVQAAILSGDTSEK,<br>IINEPTAAAIAYGLDK |
| 5 | 1 | 60 | gi\|172714 | Heat shock protein 70 | 16141.27 | 5.42 | FELSGIPPAPR |
| **Energy production and conversion** |  |  |  |  |  |  |  |
| 2 | 1 | 50 | gi\|4376093 | Pyruvate kinase * | 58248.74 | 5.88 | GDLGIEIPASQVFLAQK |
| 3 | 1 | 45 | gi\|4376093 | Pyruvate kinase | 58248.74 | 5.88 | GDLGIEIPASQVFLAQK |
| 3 | 2 | 140 | gi\|584806 | ATP synthase alpha chain* | 59522.39 | 9.07 | STVAQLVKTLEENDAMK,<br>TGEIVDVPVGPELLGR |
| 3 | 1 | 79 | gi\|44985523 | F0F1-type ATP synthase* | 58941.62 | 9.29 | TAVALDTILNQK |
| 3 | 1 | 76 | gi\|5190 | Phosphoglycerate kinase * | 44406.05 | 6.15 | DGAITNNNR |
| 3 | 1 | 53 | gi\|2654 | Vacuolar ATPase subunit b * | 57199.76 | 4.96 | TIFESLDLAWSLLR |
| 3 | 1 | 52 | gi\|469103 | Fumarase * | 53156.73 | 6.84 | SLQNFDIGGPTER |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 4 | 2 | 130 | gi\|46444820 | Malate dehydrogenase * | 34728.38 | 5.72 | DDLFNTNASIVR,<br>VAVLGAGGGIGQPLSLLLK |
| 4 | 1 | 77 | gi\|4029338 | Malate dehydrogenase * | 33029.29 | 6.13 | VAVLGAAGGIGQPLSLLLK |
| 4 | 1 | 81 | gi\|46433360 | NAD-formate dehydrogenase * | 41801.55 | 5.51 | LLGTVENELGIR |
| 4 | 1 | 74 | gi\|13785197 | Inorganic pyrophosphatase * | 32390.49 | 5.24 | VLGIMALLDEGETDWK |
| 4 | 1 | 45 | gi\|218041 | Phosphoglycerate kinase * | 44656.34 | 8.14 | ALESPQRPFLAILGGAK |
| **Carbohydrate transport and metabolism** | | | | | | | |
| 1 | 1 | 44 | gi\|929983 | Glycerol-3-aldehyde dehydrogenase * | 30768.23 | 6.13 | VPTNDVSVVDLVVR |
| 1 | 1 | 42 | gi\|5441844 | Polygalacturonase 1* | 38063.31 | 6.53 | FFYAHSLDDSTITGLNVK |
| 2 | 1 | 56 | gi\|15808971 | Glycogen synthase * | 80847.52 | 6.03 | GVDMFIESLAR |
| 2 | 1 | 88 | gi\|6651233 | Trehalose phosphorylase * | 83653.35 | 6.38 | IINEPTAAAIAYGLDK |
| 2 | 1 | 51 | gi\|171569 | 1,4-glucan-6-(1,4-glucano)-transferase* | 81129.57 | 5.76 | LPAWITR |
| 3 | 1 | 95 | gi\|169852 | Glyceraldehyde-3-phosphate dehydrogenase* | 36055.25 | 7.01 | VPTLDVSVVDLVVR |
| 3 | 1 | 74 | gi\|3367647 | Enolase * | 46877.80 | 5.15 | LGANAILGVSLAVAKAGAAEK |
| 3 | 1 | 47 | gi\|40713647 | Glucose-6-phosphate isomerase* | 61445.79 | 6.38 | ILLSNFFAQPEALAFGK |
| 4 | 2 | 175 | gi\|30038515 | Glyceraldehyde-3-phosphate dehydrogenase | 36607.76 | 7.67 | VPTIDVSVVDLVVR,<br>AVGNNIIPSSTGAAK |
| 4 | 2 | 152 | gi\|929979 | Glycerol-3-phosphate dehydrogenase * | 30895.28 | 5.71 | VPTLDVSVVDLVVR,<br>KVIISAPSSDAPMFVCGVNLDAYDPK |
| 4 | 1 | 59 | gi\|3289019 | Xylose reductase * | 36021.33 | 5.77 | WAAQRGIAVIPK |
| 4 | 1 | 44 | gi\|19068698 | Alpha alpha trehalase * | 76692.14 | 5.92 | LFEVVEGKRSK |
| 5 | 1 | 65 | gi\|68429 | Triose-phosphate isomerase * | 27234.99 | 6.13 | IVIAYEPVWAIGTGK |
| 5 | 1 | 42 | gi\|19068698 | Alpha alpha trehalase | 76692.14 | 5.92 | LFEVVEGKRSK |
| 6 | 1 | 74 | gi\|169852 | Glyceraldehyde-3-phosphate dehydrogenase | 36055.25 | 7.01 | VPTLDVSVVDLVVR |
| **Amino acid transport and metabolism** | | | | | | | |
| 3 | 1 | 97 | gi\|16415894 | Aspartyl-proteinase* | 18517.90 | 5.77 | VILDTGSSNLWVPSTK |
| 3 | 1 | 51 | gi\|44980853 | Aminopeptidase I * | 53590.96 | 6.08 | FFAGFLTDWR |
| **Nucleotide transport and metabolism** | | | | | | | |
| 1 | 1 | 49 | gi\|44981739 | Carbamoylphosphate synthase * | 248131.78 | 5.48 | AASTVDEALEAVK |
| 1 | 1 | 45 | gi\|22095310 | C1-tetrahydrofolate synthase * | 67745.49 | 6.28 | AGCVNLKKHIQNAK |
| **Lipid metabolism** | | | | | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2 | 1 | 43 | gi\|4959943 | Esterase * | 170506.56 | 4.67 | DLHLADWDGDGACDIIWTDPDNLNR |
| 3 | 1 | 43 | gi\|12718322 | C-8, 7 sterol isomerase* | 30464.65 | 6.51 | AGDVGGGLLEKVVR |
| 4 | 1 | 47 | gi\|44986286 | Diacylglycerol kinase * | 63153.68 | 5.37 | SSIISVDGENFPFEPIQVEVLPR |
| 5 | 1 | 42 | gi\|5725410 | Phosphocholine cytidylyltransferase * | 41556.61 | 5.39 | FFYAHSLDDSTITGLNVK |
| **Inorganic ion transport and metabolism** | | | | | | | |
| 3 | 1 | 44 | gi\|2776 | Catalase * | 57848.89 | 6.42 | LFSYPDTHR |
| **Cytoskeleton** | | | | | | | |
| 3 | 2 | 137 | gi\|508701 | Actin * | 41736.68 | 5.17 | SYELPDGQVITIGNER,<br>TTGIVLDSGDGVTHTVPIYEGFSLPHAIL |
| **Cell envelope biogenesis, outer membrane** | | | | | | | |
| 6 | 1 | 60 | gi\|46442658 | GPI-protein transamidase * | 55466.46 | 5.40 | EQTNVKDLIVK |
| 6 | 1 | 44 | gi\|51215619 | Chitin biosynthesis protein * | 27327.64 | 5.31 | K.NGLRLGKIPK.A |
| **Intracellular trafficking and secretion** | | | | | | | |
| 6 | 1 | 48 | gi\|2072023 | GABA-receptor-associated protein* | 22479.01 | 6.66 | YLVPSDLTVGQFVYVIR |
| **Signal transduction** | | | | | | | |
| 4 | 5 | 314 | gi\|11262436 | 14-3-3 protein homolog * | 28913.33 | 4.67 | QAFDDAIAELDTLSEESYKDSTLIMQLL<br>, AASDVAVTELPPTHPIR,<br>QAFDDAIAELDTLSEESYK,<br>DSTLIMQLLR, YLAEFATGDK |
| 5 | 1 | 53 | gi\|3218407 | Adenylate cyclase* | 190334.33 | 5.86 | ELNIANNK |
| **Unclassified** | | | | | | | |
| 1 | 1 | 53 | gi\|6321879 | Protein involved in RNA metabolism | 12009.47 | 5.05 | IEEVIDLILR |
| 2 | 1 | 52 | gi\|6321879 | Protein involved in RNA metabolism | 12009.47 | 5.05 | IEEVIDLILR |
| 4 | 3 | 179 | gi\|30024660 | guanine nucleotide binding protein | 34556.86 | 5.98 | DGITMLWDLNEGK,<br>GWVTAIATSSENPDMILTASR,<br>LWDLNTGLTTR |
| 4 | 1 | 44 | gi\|28564107 | SOL1 | 16776.24 | 5.58 | FAGRDSVK |
| 5 | 1 | 67 | gi\|46438514 | ATP/ADPtranslocator | 32754.91 | 9.62 | EFNGLVDVYKK |

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.