|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Ssp****2702** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q6FTS0 | Similar to uniprot|P15703 Saccharomyces cerevisiae YGR282c BGL2 GN=CAGL0G00220g - [Q6FTS0\_CANGA] | 2888394 | 21.95 | 26.62 | 8 | 21 | catalytic activity; hydrolase activity, hydrolyzing O-glycosyl compounds | cellwallsecreted | carbohydra-te metabolic process metabolic process | 308 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | SSTIAGFLVGSEALYR | 3 |  | 2.48 | 835.94 | 2 | 1670.88 | 2.44 | 41.90 | 0 |
| High | DDLTASQLADK | 3 |  | 2.21 | 588.79 | 2 | 1176.58 | 2.95 | 22.81 | 0 |
| High | TTNDYENDLK | 3 |  | 2.04 | 606.77 | 2 | 1212.54 | 2.89 | 21.37 | 0 |
| High | NALSSFLPNLK | 5 |  | 1.93 | 602.34 | 2 | 1203.68 | 3.05 | 40.30 | 0 |
| High | NYVSNIKDSQGNSYSGK | 3 |  | 1.91 | 930.94 | 2 | 1860.88 | 2.86 | 22.79 | 1 |
| High | DDLTASQLADKINDIR | 2 |  | 1.90 | 894.46 | 2 | 1787.92 | 2.54 | 33.98 | 1 |
| High | HWGVWTSGDNLK | 1 |  | 1.52 | 700.34 | 2 | 1399.68 | 1.98 | 32.25 | 0 |
| High | NYVSNIK | 1 |  | 1.32 | 419.23 | 2 | 837.45 | 2.93 | 21.03 | 0 |
| **Ssp****3902** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q8TG07 | Lysophospholipase 1 GN=PLB1 - [PLB1\_CANGA] | 2889465 | 90.56 | 20.49 | 10 | 36 | catalytic activity; lysophospholi-pase activity | extracellularregion | metabolic process; phospholi-pid catabolic process | 659 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | KPTFFGcDAR | 7 | C7(Carbamidomethyl) | 4.04 | 400.19 | 3 | 1198.57 | 2.24 | 21.86 | 0 |
| High | SLSESEYLFLVDGGEDGQNVPLVPLIQQER | 8 |  | 3.81 | 833.68 | 4 | 3331.68 | 4.31 | 40.76 | 0 |
| High | QFGFQGQGVTFPSVPGTDTFVNLGLNK | 5 |  | 2.90 | 952.49 | 3 | 2855.45 | 4.16 | 40.60 | 0 |
| High | RQFGFQGQGVTFPSVPGTDTFVNLGLNK | 3 |  | 2.76 | 1004.52 | 3 | 3011.55 | 3.99 | 38.64 | 1 |
| High | IGIAASGGGYR | 2 |  | 2.56 | 511.28 | 2 | 1021.55 | 3.30 | 19.62 | 0 |
| High | WDHISDAVEDK | 3 |  | 2.52 | 438.87 | 3 | 1314.60 | 4.20 | 21.30 | 0 |
| High | NLATHFLK | 4 |  | 2.51 | 472.27 | 2 | 943.54 | 3.80 | 24.30 | 0 |
| High | GGVAYLWSDLR | 1 |  | 2.06 | 618.82 | 2 | 1236.64 | 3.50 | 35.03 | 0 |
| Medium | DLSEDYDDIAVYAPNPFR | 2 |  | 1.73 | 1050.48 | 2 | 2099.96 | 3.32 | 37.79 | 0 |
| Medium | LSYSEKER | 1 |  | 1.67 | 506.26 | 2 | 1011.51 | 3.77 | 13.16 | 1 |
| **Ssp****6404** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q6FUX8 | Strain CBS138 chromosome E complete sequence GN=CAGL0E06358g - [Q6FUX8\_CANGA] | 2887384 | 319.63 | 19.84 | 7 | 117 | catalytic activity; phosphoglyce-rate mutase activity | cytoplasm; cytosol | metabolicprocess; glycolyticprocess | 247 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | RSFDVPPPVIEADSPYSQK | 19 |  | 4.82 | 711.36 | 3 | 2132.07 | 3.52 | 28.14 | 1 |
| High | SFDVPPPVIEADSPYSQK | 51 |  | 4.10 | 659.33 | 3 | 1975.97 | 3.92 | 30.46 | 0 |
| High | DKAETLETYGEEK | 18 |  | 3.52 | 756.86 | 2 | 1512.71 | 2.98 | 19.14 | 1 |
| High | HYGALQGK | 12 |  | 3.10 | 437.23 | 2 | 873.46 | 2.51 | 11.19 | 0 |
| High | AETLETYGEEK | 6 |  | 2.99 | 635.30 | 2 | 1269.59 | 3.44 | 19.37 | 0 |
| High | ADRLWIPVK | 4 |  | 2.32 | 366.56 | 3 | 1097.65 | 3.52 | 27.49 | 1 |
| High | LWIPVK | 7 |  | 1.91 | 378.25 | 2 | 755.48 | 3.52 | 28.66 | 0 |
| **Ssp****7401** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q6FWL5 | Superoxidedismutase [Cu-Zn] GN=SOD1 - [SODC\_CANGA] | 2886862 | 99.15 | 87.66 | 10 | 52 | antioxidant activity; catalytic activity; metal ion binding | cytoplasm; cytosol | metabolicprocess | 154 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | GFHIHEFGDVTNGcVSAGPHFNPFK | 7 | C14(Carbamidomethyl) | 3.28 | 693.58 | 4 | 2771.29 | 3.53 | 40.87 | 0 |
| High | SVVVHAGTDDLGK | 6 |  | 3.12 | 649.34 | 2 | 1297.68 | 3.30 | 19.87 | 0 |
| High | GSAGVSGVVTLEQASEQDPTTITYEIAGNDPNAER | 4 |  | 2.93 | 894.93 | 4 | 3576.71 | 3.68 | 37.84 | 0 |
| High | HVGDLGNIK | 3 |  | 2.90 | 476.77 | 2 | 952.52 | 2.89 | 19.10 | 0 |
| High | HVGDLGNIKTDAQGVAK | 9 |  | 2.83 | 574.98 | 3 | 1722.92 | 3.02 | 23.54 | 1 |
| High | LIGPTSVVGR | 5 |  | 2.80 | 499.80 | 2 | 998.60 | 3.29 | 25.27 | 0 |
| High | TGNAGPRPAcGVIGLTN | 7 | C10(Carbamidomethyl) | 2.72 | 827.92 | 2 | 1654.84 | 3.47 | 26.35 | 0 |
| High | GFHIHEFGDVTNGcVSAGPHFNPFKK | 2 | C14(Carbamidomethyl) | 2.65 | 725.60 | 4 | 2899.38 | 3.54 | 40.86 | 1 |
| High | GVITDSLVK | 1 |  | 1.83 | 466.28 | 2 | 931.55 | 2.84 | 25.58 | 0 |
| **Ssp****7502** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q6FTZ7 | Strain CBS138 chromosome F complete sequence GN=CAGL0F07579g - [Q6FTZ7\_CANGA] | 2887779 | 1048.88 | 40.09 | 10 | 512 | structural molecule activity; structural constituent of cell wall | fungal-typecellwall |  | 212 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | LKFSDNTYAVVNSDGSIK | 15 |  | 4.89 | 979.50 | 2 | 1958.00 | 6.86 | 32.61 | 1 |
| High | TGSESEGTSGFALSGSHLTYK | 127 |  | 4.31 | 706.00 | 3 | 2116.00 | 7.56 | 31.81 | 0 |
| High | FSDNTYAVVNSDGSIK | 88 |  | 3.85 | 858.91 | 2 | 1716.82 | 6.95 | 29.26 | 0 |
| High | FSDNTYAVVNSDGSIKTGSESEGTSGFALSGSHLTYK | 8 |  | 3.58 | 954.21 | 4 | 3813.80 | 6.88 | 35.97 | 1 |
| High | TGSESEGTSGFALSGSHLTYKGNSGFFAIPSGSEYK | 3 |  | 3.45 | 1219.91 | 3 | 3657.72 | 6.27 | 40.51 | 1 |
| High | SGGSFAGTVTDAGK | 102 |  | 3.44 | 627.81 | 2 | 1254.60 | 5.62 | 23.86 | 0 |
| High | FSTAQGTGAIDIVISPR | 97 |  | 3.27 | 866.97 | 2 | 1732.94 | 7.04 | 36.90 | 0 |
| High | SGGSFAGTVTDAGKLK | 3 |  | 3.06 | 748.40 | 2 | 1495.79 | 6.86 | 28.79 | 1 |
| High | GNSGFFAIPSGSEYK | 67 |  | 2.98 | 780.88 | 2 | 1560.74 | 7.51 | 36.34 | 0 |
| High | GNSGFFAIPSGSEYKFSTAQGTGAIDIVISPR | 2 |  | 2.21 | 1092.23 | 3 | 3274.66 | 7.27 | 44.52 | 1 |
| **Ssp****7802** | **Accession** | **Description GN=gene name - [Entry name]** | **Gene ID** | **Score** | **Coverage** | **# Peptides** | **# PSMs** | **MolecularFunction** | **Cellular Component** | **BiologicalProcess** | **# AAs** |
| Q6FUQ9 | Strain CBS138 chromosome F complete sequence GN=CAGL0F01463g - [Q6FUQ9\_CANGA] | 2887624 | 80.37 | 9.05 | 2 | 40 | structural molecule activity; structural constituent of cell wall | fungal-typecellwall | response to stimulus; response to stress | 221 |
| **Peptide Confidence** | **Sequence** | **# PSMs** | **Modifications** | **XCorr** | **m/z [Da]** | **Charge** | **MH+ [Da]** | **ΔM [ppm]** | **RT [min]** | **# MissedCleavages** |
| High | SYTSLYPSVDFK | 7 |  | 2.82 | 703.85 | 2 | 1406.69 | 4.80 | 28.12 | 0 |
| High | GIEALLPK | 33 |  | 2.42 | 420.76 | 2 | 840.52 | 4.41 | 30.36 | 0 |

**Supplementary Table 1.**Detailed information about proteins identified by LC-ESI-MS/MS analysis. In the table are listed for each spot number A. protein following parameters:proteinalphanumeric unique protein sequence identifier (Accession), protein name (Description), protein identifier characters with a naming convention [Entry name] provided by UniProtKB/Swiss-Prot protein knowledgebase; gene name and numeric unique gene sequence identifier (Gene ID) provided by NCBI; protein identification’s SEQUEST HT Score;percentage of protein sequence covered by identified peptides (Coverage); number of the identified peptides matching to the protein (# Peptides), total number of identified peptide sequences (peptide spectrum matches) (# PSMs), Gene Ontology Function and length of the protein sequence (number of AminoAcids); B. peptides following parameters: Confidence level associated with the peptide sequence, high confidence is associated to a FDR< 0.01, medium confidence to <0.05; the identified amino acidic peptide Sequence; total number of identified peptide sequences (peptide spectrum matches) (# PSMs); peptides Modification (Carbamidomethyl = + 57.02) at the reported amino acids position; the cross-correlation score (XCorr) for all candidate peptides queried from the database; mass-to-charge ratio (m/z) of the precursor ion and its Charge state; the calculated protonated monoisotopic peptide mass, in daltons [MH+ (Da)]; the calculated peptide mass error in parts per million (ppm); retention time of the precursor ion, in minutes (RT); number of Missed Cleavages.