

**STANDARD DISCOVERY DATA HEADERS**

|                |  |
|----------------|--|
| Protein Groups | Group of identified proteins (can be more than one per group, sequence similar proteins)     |
| Protein ID     | Protein ID number (unique number per single entry).  |
| Accession      | Protein accession number (Uniprot, NCBI) or gene ID (metagenomics data).                     |
| -10lgP         | Protein identification score (results already filtered for high confidence identifications). |
| Coverage %     | % of protein sequence identified in this experiment (usually a broad range of %).            |
| Area Sample    | Area of identified protein.  |
| Peptides       | Number of peptides found for this particular protein.  |
| #Unique        | Number of observed protein unique peptides sequences.  |
| #Spec Sample   | Number of peptide spectra measured for this protein entry.                                   |
| PTM            | Modification(s) used during database search (you can ignore this column).                    |
| Avg. Mass      | Average mass of protein (calculated from amino acid sequence).                               |
| Domain         | Taxonomic annotation (Domain identifier) for protein ID.                                     |
| Phylum         | Taxonomic annotation (Phylum identifier) for protein ID.                                     |
| Genus          | Taxonomic annotation (Genus identifier) for protein ID.                                      |
| Gene name      | Gene name (KEGG database).   |
| Score          | Homology score (BLAST using KEGG database) of closest protein used for annotation.           |
| Orthology      | KEGG Orthology.  |
| Functions      | Potential protein function as annotated by BLAST (KEGG database).                            |

**ADDITIONAL QUANTITATIVE PROTEOMICS HEADERS**

|              |   |
|--------------|---|
| Significance | Statistical sign of fold change (ANOVA). Expressed as -10lg(p), where 13 equals p=0.05. |
| Ratios       | Protein area ratios for the different groups, compared to the first group (default)     |