

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 $-10\lg(p)$, where 13 equals $p=0.05$.
Ratios	Protein area ratios for the different groups, compared to the first group (default)