

## Protein .tsv

**proteinName:** protein identifier

**proteinDescription:** protein description

**idScore:** protein identification score. Calculated as the summed PSM identification score.

**idQValue:** protein identification score q-value. Ratio of the number of decoy and target database identifications at given idScore threshold.

**nbPeptides:** the number of confidently identified peptides for a give protein.

**allAccessions:** accession numbers of proteins sharing a peptide with this protein.

**sample\_S:** summed normalized intensity (AUC)

**medianInt\_condition\_C:** median intensity of replicate measurements.

**cv\_condition\_C:** Intensity coefficient of variance across replicate intensities.

**log2ratio\_condition\_C:** median log2 intensity ratio (condition X / CTRL)

**pValue\_condition\_C:** moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

**qValue\_condition\_C:** Multiple-testing correction using Benjamini-Hochberg FDR procedure.

**log2\_pairedRatio\_sample\_S:** Ratios of all paired samples. Only exported when Correlated Samples (--EC option) experimental design is specified.

## Peptide .tsv

**peptide:** peptide sequece

**proteinName:** protein identifier

**proteinDescription:** protein description

**idScore:** peptide identification score. Calculated as the summed PSM identification score.

**idQValue:** peptide identification score q-value. Ratio of the number of decoy and target database identifications at given idScore threshold.

**retentionTime:** retention time (min)

**ptm:** post-translational modification

**nbPtmsPerPeptide:** number of PTMs per peptide

**motifX:** amino acid sequence surrounding PTM site.

**modifCoord:** distance (number of residues) from n-term of PTM site.

**allAccessions:** accession numbers of proteins sharing a peptide with this protein.

**sample\_S:** summed normalized intensity (AUC)

**medianInt\_condition\_C:** median intensity of replicate measurements.

**cv\_condition\_C:** Intensity coefficient of variance across replicate intensities.

**log2ratio\_condition\_C:** median log2 intensity ratio (condition X / CTRL)

**pValue\_condition\_C:** moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

**qValue\_condition\_C:** Multiple-testing correction using Benjamini-Hochberg FDR procedure.

**log2\_pairedRatio\_sample\_S:** Ratios of all paired samples. Only exported when Correlated Samples (--EC option) experimental design is specified.