

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.