

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.

sample1 - sampleN: summed normalized intensity (AUC)

medianInt_condition1 - medianInt_conditionN: median intensity of replicate measurements.

cv_condition1 - cv_conditionN: Intensity coefficient of variance across replicate intensities.

log2ratio_conditionX: median log2 intensity ratio (condition X / CTRL)

pValue_conditionX: moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

qValue_conditionX: Multiple-testing correction using Benjamini-Hochberg FDR procedure.

Peptide .tsv

peptide: peptide sequeence

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.

sample1 - sampleN: summed normalized intensity (AUC)

medianInt_condition1 - medianInt_conditionN: median intensity of replicate measurements.

cv_condition1 - cv_conditionN: Intensity coefficient of variance across replicate intensities.

log2ratio_conditionX: median log2 intensity ratio (condition X / CTRL)

pValue_conditionX: moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

qValue_conditionX: Multiple-testing correction using Benjamini-Hochberg FDR procedure.