Explanation of the Display options (out put parameters) in PPDB (http://ppdb.tc.cornell.edu). Updated August 2008.

PPDB Help (?)

Output Format: The option allows you to specify the columns in the search result table:

Accession: Accession number

STD Annot: Standard gene annotation according to sequence source database

Lab Annot: Gene annotation curated by our laboratory – based on experimental evidence mostly obtained from primary literature

Curated Loc.: Subcellular localization curated by our laboratory

Tair Loc. Subcellular localization suggested by TAIR (with PubMed reference)

MapManBin: Gene function 'bin' used by MapMan, a user driving tool for displaying large datasets (Pubmed Link). Each 'bin' assignment has been reviewed for PPDB and where needed bin assignment has been changed.

Sep.MapManBin. Similar as MapManBin, but the bin number and text are in two different cells

Aramemnon: Consensus Prediction of transmembrane proteins. (http://aramemnon.botanik.uni-koeln.de). Predicted transmembrane domains that overlap with N-terminal transit or signal peptides are ignored.

TMHMM: Prediction of transmembrane proteins. (http://www.cbs.dtu.dk/services/TMHMM/). Predicted transmembrane domains that overlap with an cTP or lTP are ignored.

TargetP: The location predicted by TargetP in combination with LumenP and TMHMM (L: lumen; S: Stroma; M: Membrane; A: ambiguous). Prediction strategies are discussed in Qi et al. (2004) Plant Physiology 135, 723-734.

Predotar: Predicted subcellular location according to Predotar (v1.03) (see Small et al. (2004) Proteomics 4(6), 1581-1590) C = chloroplast; M = mitochondria

PFAM: Predicted domain(s) in a protein sequence using the software Pfam. (http://www.sanger.ac.uk/Software/Pfam/)

Cys: Cysteine residue content in a protein as a percentage of the content of all amino acid residues. Cys-cTP is without cTP region.

Calc. gravy: Grand average of hydropathicity index indicates the solubility of the proteins: positive GRAVY (hydrophobic), negative GRAVY (hydrophilic) (Kyte and Doolittle, 1982). expr . gravy-cTP is without cTP region.

Calc. MW: The calculated molecular weight (kDA). MW-cTP and MW-lTP are without cTP and lTP regions.

Calc. PI: The calculated pI value. PI-cTP and PI-lTP are without cTP regions.

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exp . MW: The experimentally determined molecular weight (kDA). MW D is based on denaturing gel. MW N is based on the native gel.

exp . pI: The experimentally determined molecular weight (kDA). pI D is based on denaturing gel. pI N is based on the native gel.

Exp. Volume: Normalized volume of protein spot (from 2-D gels only; normalization based on total spot volume)

exp. ambiguity: Match of Mass Spectrometry data to additional protein(s) – this is quite often a closely related paralogue

exp.amb_gmodel. Match of Mass Spectrometry data to a different gene model

exp. MS_type. Type of mass spectrometry platform used for the identification. M= MALDI-TOF; Q – LC-ESI/MS/MS by Q-TOF; L – LC-ESI/MS/MS by LTQ-Orbitrap

exp. Mascot score: MOWSE score from the MASCOT search engine (MS using peptide mass finger printing or MS/MS)

exp. #peptides: Number of matching peptides used for identification (MS using peptide mass finger printing or MS/MS)

exp. ID*: The experiment identification number of the experiment in which the protein is identified.

exp. spot: The sample number (within the experiment) in which the protein is identified. Sample can be a spot from a 2-D gel, a band from a 1-D gel, a chromatography fraction or a more complex protein sample.

exp. Queries. The number of times a spectral can be matched to the accession. Only those matched peptides that pass our in-house filters are counted.

exp. uniq. Queries The number of times a spectral can be matched to the accession. Only those matched peptides that pass our in-house filters are counted and that are not shared with other identified accessions are counted.

exp . Tissue: The plant tissue that served as the starting point for purification of the sample

exp . Fraction: This refers to %B in case of off-line chromatography

exp. Genotype: The genotype of the plant material analyzed.

exp . Sep. Steps: The experimental steps for isolating the proteins.

Cell type: For Maize only. Sample obtained from leaf proteins strongly enriched for Bundle sheath (BunSh) or Mesophyll chloroplasts (Meso)

ProteomicsPub: Published data sets from high throughput proteomics studies. Each data set name has a reference to the subcellular compartment and the Medline Reference number.

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GFP/YFP loc.: Localization data based on GFP/YFP experiments. (obtained from SUBA and other databases)

Best AT hit: The highest scoring BLAST hit in the Arabidopsis predicted proteome

Best Rice hit: The highest scoring BLAST hit in the rice predicted proteome

Best Maize hit: The highest scoring BLAST hit in the maize predicted proteome

Coverage: The proportion of aminoacid residues in the primary sequence that are identified by mass spectrometry

Top3pep: The three most frequently observed peptides for a protein

Top3pep(-MetCys): The three most frequently observed peptides for a protein, but excluding peptides that contain cystein and/or methionine

#Tryptic Frag. : The maximal theoretical number of full tryptic fragments that can be obtained from the primary sequence (no missed cleavages allowed)

#Tryptic Frag.(-ctp): The maximal theoretical number of full tryptic fragments that can be obtained from the primary sequence minus the predicted cTP (no missed cleavages allowed)

#Tryptic Frag.(-ltp): The maximal theoretical number of full tryptic fragments that can be obtained from the primary sequence minus the predicted cTP and lTP (no missed cleavages allowed)