Proteomics Resources

Proteomics Resources

- ATHENA (Arabidopsis THaliana ExpressioN Atlas) —

Resource Link	ATHENA
Description	ATHENA is a data exploration tool that provides access to a collection of > 18,000 protein and > 25,000 transcript expression profiles across a set of 30 matching tissues from Arabidopsis thaliana (Col-0). Data represent intensity-based absolute quantifications (iBAQ) for the proteome and transcripts per kilobase million (TPM) for the transcriptome.
Maintained by	Technical University of Munich

  - proteomics
  - gene_expression
  - transcriptomics

- BioGRID —

Resource Link	Biological General Repository for Interaction Datasets (BioGRID)
Description	Data repository for curated protein and genetic interactions.
Maintained by	Tyers Lab

  - proteomics
  - interactome

- Functional Analysis Tools for Post-Translational Modifications (FAT-PTM) —

Resource Link	Functional Analysis Tools for Post-Translational Modifications
Description	Database of post translational modifications (PTMS) for Arabidopsis proteins including quantitative phosphorylation data, ubiquitylation, glycosylation,acetylation and others.Search by proteins, modification and co PTM networks.
Maintained by	Ian Wallace, University of Nevada

  - proteomics
  - post_translational_modification

- IntAct —

Resource Link	IntAct
Description	IntAct provides a freely available, open source database system and analysis tools for molecular interaction data. All interactions are derived from literature curation or direct user submissions and are freely available.
Maintained by	EMBL-EBI

  - proteomics
  - interactome

- MassIVE —

Resource Link	MassIVE

	MassIVE Mass Spectrometry Interactive Virtual Environment
Description	Repository for proteomics data, with tools for searching, reanalyzing, and comparison.
Maintained by	Center for Computational Mass Spectrometry

- data_submission
- proteomics
- metadata
- data_analysis
- data_repository

- Plant Protein Phosphorylation DataBase (P3DB) —

Resource Link	Plant Protein Phosphorylation DataBase (P3DB)
Description	The Plant Protein Phosphorylation DataBase (P3DB) contains several published proteomics datasets listing sites of protein phosphorylation and acetylation for Arabidopsis and other plant species.
Maintained by	Jay Thelen and Dong Xu

- proteomics

- Pride/ProteomeXchange —

Resource Link	Pride/ProteomeXchange
	EMBL-EBI
Description	The PRIDE PRoteomics IDEntifications (PRIDE) database is a centralized, standards compliant, public data repository for proteomics data, including protein and peptide identifications, post-translational modifications and supporting spectral evidence.
Maintained by	EBI-EMBL

- proteomics
- data_repository
- data_submission

- Protein Modification Viewer (PTM Viewer) —

Resource Link	Protein Modification Viewer
Description	Protein modification database, data repository and analysis tools.
Maintained by	VIB

- proteomics
- data_submission
- data_repository

- data_analysis

- ProteomicsDB —

Resource Link	Proteomics DB
Description	Database and repository for quantitative mass spectrometry-based proteomics data and protein turnover data. Now includes data for Arabidopsis.
Maintained by	Prof. Dr. Bernhard Küster

  - proteomics
  - data_analysis
  - data_repository

- Research Collaboratory for Structural Bioinformatics-Protein Data Bank —

Resource Link	Research Collaboratory for Structural Bioinformatics-Protein Data Bank (PDB)
Description	Database of protein and DNA 3-dimensional structures.Search, visualization and analysis tools for structural biology.
Maintained by	Rutgers and UCSD/SDSC

  - proteomics
  - structures
  - data_repository
  - data_analysis
  - data_submission

- Seed Proteome Database —

Resource Link	Seed Proteome Database
Description	Datasets for seed dormancy and germination proteomes.
Maintained by	Institut Jean Pierre Bourgin

  - proteomics
  - dataset

- SUBA4 —

Resource Link	SUBA4
	
Description	SUBA is the central resource for Arabidopsis protein subcellular location data and provides a subcellular data query platform, protein sequence BLAST alignment, a high confidence subcellular locations reference standards and analytic tools.
Maintained by	Harvey Millar

  - proteomics

- The Arabidopsis Protein Phosphorylation Site Database (PhosPhAt) —

Resource Link	The Arabidopsis Protein Phosphorylation Site Database (PhosPhAt)

Description	The Arabidopsis Protein Phosphorylation Site Database contains large scale proteomic based data from both published and unpublished sources. Data is provided as either a searchable list of identified peptides or ions with annotated phosphorylation site (where available) or as a protein summary page with AGI.
Maintained by	University of Hohenheim

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