

# Proteomics Resources

## Proteomics Resources

- [ATHENA \(Arabidopsis THaliana ExpressioN Atlas\)](#) —

<b>Resource Link</b>	<a href="#">ATHENA</a>
<b>Description</b>	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.
<b>Maintained by</b>	<a href="#">Technical University of Munich</a>

- [proteomics](#)
- [gene\\_expression](#)
- [transcriptomics](#)

- [BioGRID](#) —

<b>Resource Link</b>	<a href="#">Biological General Repository for Interaction Datasets (BioGRID)</a>
<b>Description</b>	Data repository for curated protein and genetic interactions.
<b>Maintained by</b>	<a href="#">Tyers Lab</a>

- [proteomics](#)
- [interactome](#)

- [Functional Analysis Tools for Post-Translational Modifications \(FAT-PTM\)](#) —

<b>Resource Link</b>	<a href="#">Functional Analysis Tools for Post-Translational Modifications</a>
<b>Description</b>	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.
<b>Maintained by</b>	<a href="#">Ian Wallace, University of Nevada</a>

- [proteomics](#)
- [post\\_translational\\_modification](#)

- [IntAct](#) —

<b>Resource Link</b>	<a href="#">IntAct</a>
<b>Description</b>	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.
<b>Maintained by</b>	<a href="#">EMBL-EBI</a>

- [proteomics](#)
- [interactome](#)

- [MassIVE](#) —

<b>Resource Link</b>	<a href="#">MassIVE</a>
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	 <p><b>MassIVE</b> Mass Spectrometry Interactive Virtual Environment</p>
<b>Description</b>	Repository for proteomics data, with tools for searching, reanalyzing, and comparison.
<b>Maintained by</b>	Center for Computational Mass Spectrometry

- [data\\_submission](#)
- [proteomics](#)
- [metadata](#)
- [data\\_analysis](#)
- [data\\_repository](#)

• [Plant Protein Phosphorylation DataBase \(P3DB\)](#) —

<b>Resource Link</b>	<a href="#">Plant Protein Phosphorylation DataBase (P3DB)</a>
<b>Description</b>	The Plant Protein Phosphorylation DataBase (P3DB) contains several published proteomics datasets listing sites of protein phosphorylation and acetylation for Arabidopsis and other plant species.
<b>Maintained by</b>	Jay Thelen and Dong Xu

- [proteomics](#)

• [Pride/ProteomeXchange](#) —

<b>Resource Link</b>	<a href="#">Pride/ProteomeXchange</a>
	
<b>Description</b>	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.
<b>Maintained by</b>	EBI-EMBL

- [proteomics](#)
- [data\\_repository](#)
- [data\\_submission](#)

• [Protein Modification Viewer \(PTM Viewer\)](#) —

<b>Resource Link</b>	<a href="#">Protein Modification Viewer</a>
<b>Description</b>	Protein modification database, data repository and analysis tools.
<b>Maintained by</b>	VIB

- [proteomics](#)
- [data\\_submission](#)
- [data\\_repository](#)

- [data\\_analysis](#)

• [ProteomicsDB](#) —

<b>Resource Link</b>	<a href="#">Proteomics DB</a>
<b>Description</b>	Database and repository for quantitative mass spectrometry-based proteomics data and protein turnover data. Now includes data for Arabidopsis.
<b>Maintained by</b>	<a href="#">Prof. Dr. Bernhard Küster</a>

- [proteomics](#)
- [data\\_analysis](#)
- [data\\_repository](#)

• [Research Collaboratory for Structural Bioinformatics-Protein Data Bank](#) —

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

- [proteomics](#)
- [structures](#)
- [data\\_repository](#)
- [data\\_analysis](#)
- [data\\_submission](#)

• [Seed Proteome Database](#) —

<b>Resource Link</b>	<a href="#">Seed Proteome Database</a>
<b>Description</b>	Datasets for seed dormancy and germination proteomes.
<b>Maintained by</b>	Institut Jean Pierre Bourgin

- [proteomics](#)
- [dataset](#)

• [SUBA4](#) —

<b>Resource Link</b>	<a href="#">SUBA4</a>
<b>Description</b>	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.
<b>Maintained by</b>	Harvey Millar

- [proteomics](#)

• [The Arabidopsis Protein Phosphorylation Site Database \(PhosPhAt\)](#) —

<b>Resource Link</b>	<a href="#">The Arabidopsis Protein Phosphorylation Site Database (PhosPhAt)</a>
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<b>Description</b>	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.
<b>Maintained by</b>	University of Hohenheim

- [proteomics](#)