

Resources



These pages include a curated set of bioinformatics and data resources that have been compiled by members of the International Arabidopsis Informatics Consortium (IAIC) and curators at TAIR. This is not a comprehensive list; if you know of a resource that you think should be included, please [send us an email](#).

Search within these pages for Arabidopsis community bioinformatics tools and data resources. You can use labels for data types such as 'proteomics' or 'gene_expression' or actions such as data submission or data analysis.

Browse by subject portals

[Epigenomics Resources](#)

[Education and Outreach Resources](#)

[General Databases](#)

[Gene Expression/Transcriptomics Resources](#)

[Metabolomics Resources](#)

[Mutant and Mapping Resources](#)

[Proteomics Resources](#)

[Stock Centers \(DNA, Seeds, other Physical Resources\)](#)

Or you can **browse** the list of resources **based on tags**.

A-C	D-E	F-G	H-L	M-N
advocacy analytics arabidopsis bioinformatics brassicaceae chip-seq cis_elements clones comparative_genomics covid_19	data_analysis data_management data_repository data_sets data_submission data_visualization dataset dna_methylation dna_stocks education_outreach epigenomics	fair functional_annotation gene gene_annotation gene_expression gene_function gene_ontology general genomics governance gwas	help_documents homologs homology illustrations interactome	mapping meeting-notes metabolomics metadata methylation microarray mirna mutants natural_variation nomenclature
O	P	Q-R	S	T-Z
ontologies organization	phasirna phenotypes phylogenetics phylogenomics plant_transformation plasmids polymorphisms post_translational_modification promoter proteomics protocols publications	reagents rna_seq	seed_stocks seeds sequence single_cell small_rna software standards stock_center structures synteny	term_enrichment tf_binding_sites transcription_factor_binding_sites transcriptomics variants



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