

Gene Expression/Transcriptomics Resources

- [Arabidopsis Next-Gen Sequence Databases](#) —

Resource Link	Arabidopsis Next-Gen Sequence Databases
Description	Small RNA, MetC and PARE data from Blake Meyers' group.
Maintained by	Blake Meyers

- [small_rna](#)
- [arabidopsis](#)
- [gene_expression](#)
- [methylation](#)

- [Arabidopsis Single Cell Developmental Atlas Viewer](#) —

Resource Link	Arabidopsis Single Cell Developmental Atlas Viewer
Description	Browser and visualization of single nuclei transcriptome across development.
Maintained by	Travis Lee

- [transcriptomics](#)
- [single_cell](#)

- [Array Express](#) —

Resource Link	Array Express
Description	Repository for functional genomics data. Access and submit functional genomics data in MIAME compliant format.
Maintained by	EMBL-EBI

- [microarray](#)
- [gene_expression](#)
- [data_repository](#)
- [data_submission](#)

- [ARS-Arabidopsis RNA-seq Database](#) —

Resource Link	Arabidopsis RNA-seq Database (ARS)
Description	ARS is a free, web-accessible, and user-friendly database, contributes to searching, filtering, visualizing, browsing, and downloading the RNA-seq data including over 28,000 publicly available datasets from Arabidopsis.
Maintained by	zhaijx@sustech.edu.cn or zhangh9@mail.sustech.edu.cn .

- [ma_seq](#)
- [gene](#)
- [gene_expression](#)
- [transcriptomics](#)

- [ARVEX-Arabidopsis Root Virtual Expression eXplorer](#) —

Resource Link	Arabidopsis Root Virtual Expression eXplorer
Description	ARVEX is a Shiny app for exploring single cell gene expression of <i>Arabidopsis</i> root
Maintained by	Che-Wei Hsu

- [single_cell](#)
- [gene_expression](#)

- [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](#)

• [Bio-Analytic Resource for Plant Biology \(BAR\)](#) —

Resource Link	Bio-Analytic Resource for Plant Biology (BAR)
	
Description	ePlant tool allows for exploration of Arabidopsis data sets from the kilometre to nanometre scales. eFP Browser provides "gene expression anatograms" for depicting where and when a gene is expressed. Arabidopsis Interactions Viewer taps into the BAR's database of more than 100k protein-protein interactions and 2.8M protein-DNA interactions. Tools for exploring other plant data available too!
Maintained by	Provart Laboratory at the University of Toronto

- [general](#)
- [gene_expression](#)

• [CoNekT](#) —

Resource Link	CoNekt
	
Description	Platform to query and visualize plant co-expression and co-function networks. Compare expression profiles across sets of homologs.
Maintained by	Proost and Mutwil

- [gene_expression](#)
- [gene_ontology](#)
- [homology](#)

• [Diurnal](#) —

Resource Link	Diurnal
Description	Check if your favorite gene is cycling in different environmental conditions, locate orthologs between Arabidopsis, rice, Brachypodium, and check expression of orthologs in diel conditions (and sometimes circadian) in those species as well.
Maintained by	Todd Mockler

- [gene_expression](#)

• [eFP-SEQ Browser](#) —

Resource Link	eFP-Seq Browser
Description	Electronic pictograph browser for visualizing RNA seq data from existing sources or upload your own.
Maintained by	Provant Lab

- [rna_seq](#)
- [gene_expression](#)

• [Eukaryotic Promoter Database](#) —

Resource Link	Eukaryotic Promoter Database
Description	Database of experimentally verified promoters from a variety model organisms including Arabidopsis. Genome annotation version is TAIR 10 not Araport 11
Maintained by	Swiss Institute of Bioinformatics

- [promoter](#)
- [gene_expression](#)
- [genomics](#)

• [GemMaker](#) —

Resource Link	GemMaker
	 GEMmaker
Description	GEMmaker is a Nextflow workflow for large-scale gene expression sample processing, expression-level quantification and Gene Expression Matrix (GEM) construction. Results from GEMmaker are useful for differential gene expression (DGE) and gene co-expression network (GCN) analyses. The GEMmaker workflow currently supports Illumina RNA-seq datasets.
Maintained by	

- [gene_expression](#)
- [software](#)
- [data_analysis](#)

• [Gene Expression Omnibus \(GEO\)](#) —

Resource Link	Gene Expression Omnibus (GEO)
	 Gene Expression Omnibus
Description	GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.
Maintained by	NCBI

- [gene_expression](#)
- [data_repository](#)
- [data_submission](#)
- [microarray](#)

• [Integrated System for Motif Activity Response Analysis \(ISMARA\)](#) —

Resource Link	Integrated System for Motif Activity Response Analysis (ISMARA)
----------------------	---

	
Description	The Integrated System for Motif Activity Response Analysis is an online tool for automatically inferring regulatory networks from gene expression (RNA-seq/ micro-array) or chromatin state (ChIP-seq) data.
Maintained by	van Nimwegen group of the Biozentrum, University of Basel and Swiss Institute of Bioinformatics.

- [gene_expression](#)
- [chip-seq](#)
- [ma_seq](#)

• [Jacobsen Epigenomics Browser](#) —

Resource Link	Jacobsen Epigenomics Browser
Description	DNA methylation, small RNA, ChIP data from Jacobsen lab publications, in searchable browser/
Maintained by	Steve Jacobsen

- [epigenomics](#)
- [dna_methylation](#)
- [small_rna](#)
- [gene_expression](#)

• [Medicinal Plants Genomics Resource](#) —

Resource Link	Medicinal Plants Genomics Resource
Description	Medicinal plant genome databases, genome browsers and genome annotation for 12 species.
Maintained by	Buell Lab

- [gene_annotation](#)
- [genomics](#)
- [gene_expression](#)
- [metabolomics](#)
- [data_sets](#)

• [MetaOmGraph \(MOG\)](#) —

Resource Link	MetaOmGraph (MOG)
Description	Java platform for rapid, interactive correlations and visualization of large data sets. Species and data-type agnostic; preformatted data supplied, or format your own.
Maintained by	Eve Wurtele

- [transcriptomics](#)
- [data_visualization](#)
- [data_analysis](#)

• [miROOT Browser](#) —

Resource Link	MiROOT Browser
----------------------	--------------------------------

	https://doi.org/10.15252/embj.2018100754
Description	Browser for examining root specific single cell miRNA expression and loading data from https://doi.org/10.15252/embj.2018100754
Maintained by	Olivier Vionnet

- [mirna](#)
- [single_cell](#)
- [gene_expression](#)
- [transcriptomics](#)

• [NCBI Bioinformatics Workshop Lessons](#) —

Resource Link	NCBI Bioinformatics Workshops
Description	Recorded from Wash U/NCBI workshop. Lessons include: NCBI Resources for Animal and Plant Genomics Research, Update on NCBI BLAST and Other Sequence Analysis Tools and NCBI Resources for Gene Expression and Genetic Variation Research
Maintained by	NLM, NCBI

- [education_outreach](#)
- [bioinformatics](#)
- [analytics](#)
- [gene_expression](#)
- [genomics](#)

• [PlaNet](#) —

Resource Link	PlaNet
Description	Co-expression network analysis across multiple plant species including Arabidopsis
Maintained by	Marek Mutwil

- [interactome](#)
- [data_analysis](#)
- [transcriptomics](#)

• [Plant/Eukaryotic and Microbial Systems Resource \(PMR\)](#) —

Resource Link	Plant/Eukaryotic and Microbial Systems Resource (PMR)
Description	Database with web-based visualization and analysis of processed metabolomics data and its metadata. Combined with transcriptomic and/or Mass Spec Imaging (MSI) data/metabolite imaging data from the same samples as the metabolomic data (as available).
Maintained by	Eve Wurtele

- [metabolomics](#)
- [transcriptomics](#)

• [Root Cell Atlas](#) —

Resource Link	Root Cell Atlas
Description	Web service for visualizing single cell transcriptomic data in an AI model of a plant root.
Maintained by	Dr. Maria Savina, Department of Plant Systems Physiology, RIBES, Radboud University

- [single_cell](#)
- [transcriptomics](#)
- [gene_expression](#)

• [TF2Network](#) —

Resource Link	TF2Network
	
Description	Predict gene regulatory networks in Arabidopsis using published TF binding sites.
Maintained by	Klaas Vandepoele

- [transcriptomics](#)
- [interactome](#)
- [data_analysis](#)
- [gene_expression](#)