# Gene Expression/Transcriptomics Resources

- Arabidopsis Next-Gen Sequence Databases —

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| **Resource Link** | Arabidopsis Next-Gen Sequence Databases |
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| **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 —

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

  - transcriptomics
  - single_cell

- Array Express —

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| **Resource Link** | Array Express |
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| **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 —

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| **Resource Link** | Arabidopsis RNA-seq Database (ARS) |
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| **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. |

  - rna_seq
  - gene
  - gene_expression
  - transcriptomics

- ARVEX-Arabidopsis Root Virtual Expression eXplorer —

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

  - single_cell
  - gene_expression

- ATHENA (Arabidopsis THaliana ExpressioN Atlas) —

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| **Resource Link** | ATHENA |
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| **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) —

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| **Resource Link** | Bio-Analytic Resource for Plant Biology (BAR) |
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| **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 —

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| **Resource Link** | CoNekt |
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| **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 —

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| **Resource Link** | Diurnal |
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| **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 —

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

  - rna_seq
  - gene_expression

- Eukaryotic Promoter Database —

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| **Resource Link** | Eukaryotic Promoter Database |
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| **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 Bioinformatcs |

  - promoter
  - gene_expression
  - genomics

- GemMaker —

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| **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

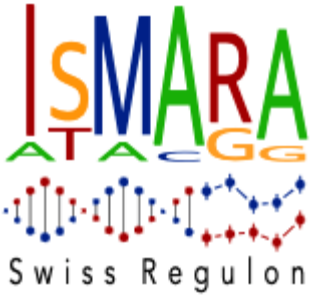
- Gene Expression Omnibus (GEO) —

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| **Resource Link** | Gene Expression Omnibus (GEO) |
| | 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) —

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

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| **Description** | The Integrated System for Motif Actitivity 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
- rna_seq

- Jacobsen Epigenomics Browser —

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| **Resource Link** | Jacobsen Epigenomics Browser |
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| **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 —

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| **Resource Link** | Medicinal Plants Genomics Resource |
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| **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) —

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| **Resource Link** | MetaOmGraph (MOG) |
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| **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 —

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| **Resource Link** | MiROOT Browser |

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| | 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 —

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| **Resource Link** | NCBI Bioinformatics Workshops |
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| **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 —

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| **Resource Link** | PlaNet |
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| **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) —

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|---|---|
| **Resource Link** | Plant/Eukaryotic and Microbial Systems Resource (PMR) |
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| **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 —

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| **Resource Link** | Root Cell Atlas |
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| **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 —

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

- transcriptomics
- interactome
- data_analysis
- gene_expression