



CEPLAS

Cluster of Excellence on Plant Sciences

Seeking <Data> | {Tools} | ?Help?





# Sources for data – Reference genomes

## Phytozome

<https://phytozome-next.jgi.doe.gov/>

## Ensembl

<https://www.ensembl.org/>

## UCSC genome browser

<https://genome.ucsc.edu/>

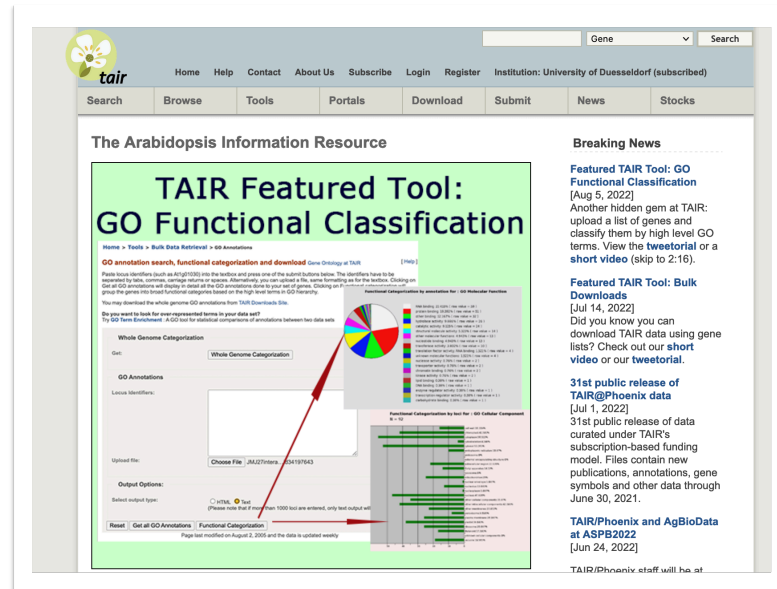
## RefSeq

<https://www.ncbi.nlm.nih.gov/refseq/>

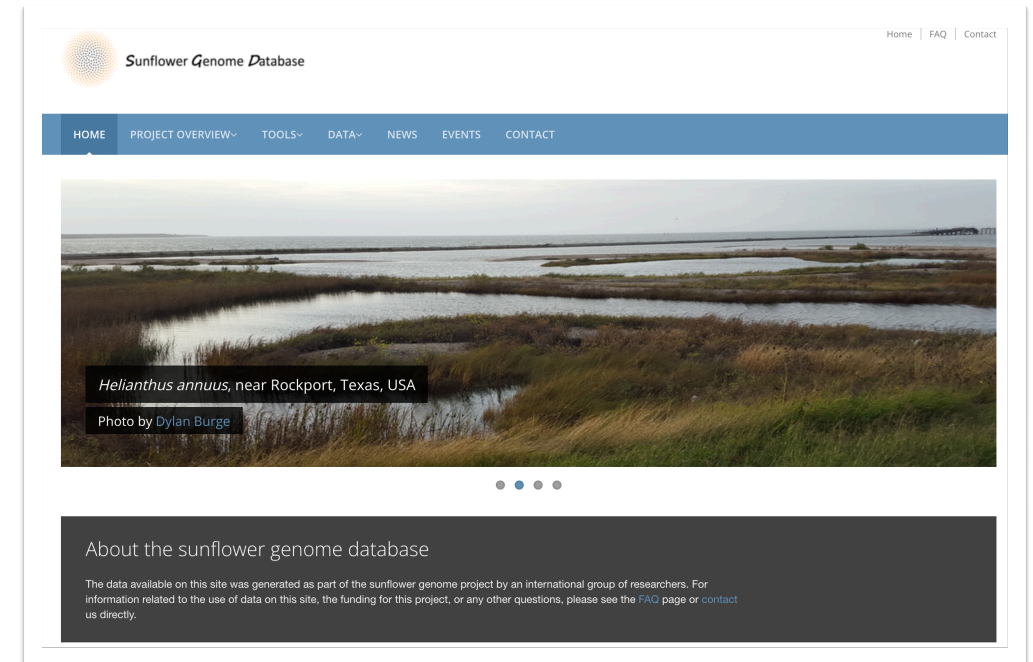




# Sources for data – Reference genomes



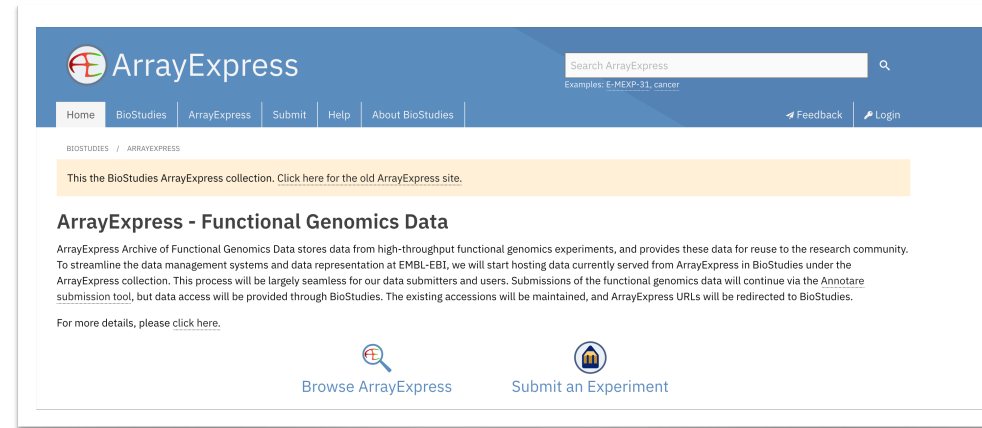
**The Arabidopsis Information Resource (TAIR)**  
<https://arabidopsis.org/>



**Sunflower Genome Database**  
<https://www.sunflowergenome.org/>

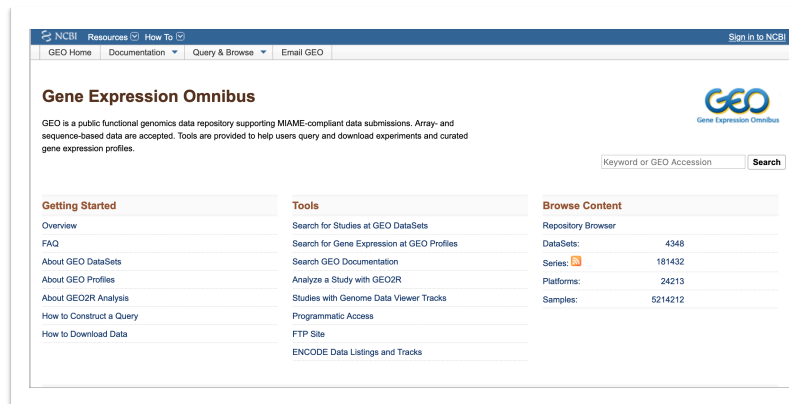


# Sources for data – RNA-Seq datasets



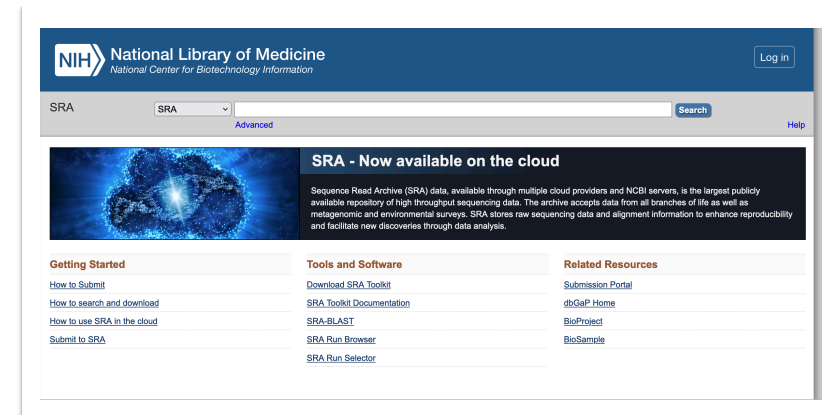
## ArrayExpress

<https://www.ebi.ac.uk/biostudies/arrayexpress>



## Gene Expression Omnibus

<https://www.ncbi.nlm.nih.gov/geo/>



## Short Read Archive

<https://www.ncbi.nlm.nih.gov/sra/>



# Finding the “right” tool

- Sources
  - GitHub
- Check “maintenance”
  - Last updates (commits, releases)
  - Issues and active forum
- Check for docs / manuals / tutorials
  - bad docs ~ bad tool (?)
- Play around with sample data first
- Check (literature) for what other people have done using that tool



# Finding the “right” tool – Example Kallisto

Issues

The screenshot shows the GitHub repository page for `pachterlab/kallisto`. The repository is public and has 123 issues, 9 pull requests, 22 branches, and 16 tags. The repository structure is listed on the left, including files like `.github/workflows`, `ext`, `func_tests`, `src`, `test`, `unit_tests`, `.gitignore`, `.gitmodules`, `.ycm_extra_conf.py`, `CMakeLists.txt`, `INSTALL.md`, `README.md`, `astyle.txt`, `gen_release.sh`, `gulpfile.js`, and `license.txt`. The right sidebar shows the repository's description, badges for `rna-seq`, `kallisto`, and `pseudoalignment`, and a list of releases. The latest release is `Increase in generalizability of...` on Jan 17, marked as `Latest`. The repository has 499 stars, 51 watchers, and 154 forks.

Commits

Latest release

<https://github.com/pachterlab/kallisto>



- Google (or stackoverflow-search) your question, error, etc.
- Read manuals and walk through tutorials first.
- Better question => better help
  - Check if (similar) question was asked before
  - Supply as much (useful) info as possible
    - Version numbers of package / tool
    - Operating system and version
  - Supply a minimal example

