

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

Digital Expression Explorer 2 Project

RRID:SCR_016929

Type: Tool

Proper Citation

Digital Expression Explorer 2 Project (RRID:SCR_016929)

Resource Information

URL: <http://dee2.io/>

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Description: Software tool as a repository of uniformly processed RNA-seq data mined from public data obtained from NCBI Short Read Archive . DEE2 consists of three parts: Webserver where end-users can search for and obtain data-sets of interest, Pipeline that can download and process SRA data as well as users own fastq files, Back-end that collects, filters and organises data provided by contributing worker nodes.

Abbreviations: DEE2

Synonyms: DEE2 Project

Resource Type: service resource, data or information resource, data repository, project portal, database, storage service resource, portal

Defining Citation: [DOI:10.5281/zenodo.1561840](https://doi.org/10.5281/zenodo.1561840)

Keywords: transcriptome, database, RNA-seq, sequencing, processed, data

Availability: Free, Freely available

Resource Name: Digital Expression Explorer 2 Project

Resource ID: SCR_016929

License: GNU General Public License v3.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260729T044429+0000

Ratings and Alerts

No rating or validation information has been found for Digital Expression Explorer 2 Project.

No alerts have been found for Digital Expression Explorer 2 Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Alexandre CM, et al. (2023) LTP2 hypomorphs show genotype-by-environment interaction in early seedling traits in *Arabidopsis thaliana*. bioRxiv : the preprint server for biology.

Tang YM, et al. (2022) Comparing the Characteristics of Microglia Preparations Generated Using Different Human iPSC-Based Differentiation Methods to Model Neurodegenerative Diseases. ASN neuro, 14, 17590914221145105.

Tierrafr??a VH, et al. (2022) RegulonDB 11.0: Comprehensive high-throughput datasets on transcriptional regulation in *Escherichia coli* K-12. Microbial genomics, 8(5).

Ziemann M, et al. (2019) Digital expression explorer 2: a repository of uniformly processed RNA sequencing data. GigaScience, 8(4).