

Resource Summary Report

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ArrayExpress

RRID:SCR_002964

Type: Tool

Proper Citation

ArrayExpress (RRID:SCR_002964)

Resource Information

URL: <http://www.ebi.ac.uk/arrayexpress/>

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Description: International functional genomics data collection generated from microarray or next-generation sequencing (NGS) platforms. Repository of functional genomics data supporting publications. Provides genes expression data for reuse to the research community where they can be queried and downloaded. Integrated with the Gene Expression Atlas and the sequence databases at the European Bioinformatics Institute. Contains a subset of curated and re-annotated Archive data which can be queried for individual gene expression under different biological conditions across experiments. Data collected to MIAME and MINSEQE standards. Data are submitted by users or are imported directly from the NCBI Gene Expression Omnibus.

Abbreviations: ArrayExpress

Synonyms: , ArrayExpress, ArrayExpress - functional genomics data, ArrayExpress Archive

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

Defining Citation: [PMID:23193272](#), [PMID:21071405](#)

Keywords: gold, standard, functional, genomics, data, collection, microarray, next, generation, sequencing, NGS, repository

Funding: European Commission ;
European Union ;
Gen2Phen 200754;
NHGRI P41 HG003619;
SLING 226073

Availability: Available Public or Private, Free, Available for download, The community can contribute to this resource, Acknowledgement requested, to access private data registration required

Resource Name: ArrayExpress

Resource ID: SCR_002964

Alternate IDs: OMICS_01023, nif-0000-30123, r3d100010222

Alternate URLs: <http://www.ebi.ac.uk/microarray-as/ae>, <https://doi.org/10.17616/R3302G>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T195549+0000

Ratings and Alerts

No rating or validation information has been found for ArrayExpress.

No alerts have been found for ArrayExpress.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7814 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hofvander J, et al. (2026) Transcriptomic Subgroups in Soft Tissue Tumors Correlate with Morphologic Subtype, Genomic Features, and Outcome. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1825.

Kobayashi H, et al. (2026) A self-amplifying nerve-fibroblast circuit drives colorectal cancer progression. Cancer cell.

Lesire L, et al. (2026) Enhancing antitumour response to proteasome inhibitors with inhibitors of insulin-degrading enzyme, a new molecular vulnerability in multiple myeloma. British journal of pharmacology, 183(12), 3355.

M Naeini M, et al. (2026) Convergent genomic and molecular features predict risk of metachronous metastasis in clear cell renal cell carcinoma. Communications medicine, 6(1).

Wang Z, et al. (2026) Clonally expanded HSP-specific T cells contribute to glaucomatous neurodegeneration via the mTORC1 pathway. Journal of neuroinflammation, 23(1).

- Pirritano M, et al. (2026) Exogenous dsRNA made accessible to Dicer by two eukaryotic RNA-dependent RNA polymerases in *Paramecium tetraurelia*. *Communications biology*, 9(1), 167.
- Tan J, et al. (2026) Integrated spatial and single-cell transcriptomics reveals RPL8 as a prognostic biomarker and therapeutic target in hepatocellular carcinoma. *Translational oncology*, 64, 102663.
- Eufrásio A, et al. (2026) A conserved 3'UTR short motif regulates gene expression in vertebrates. *Nucleic acids research*, 54(1).
- Abplanalp WT, et al. (2026) Clonal hematopoiesis activates procalcific pathways in macrophages and promotes aortic valve stenosis. *The Journal of clinical investigation*, 136(1).
- Fujikura K, et al. (2026) Genome-wide analysis of somatic noncoding mutation patterns and mitochondrial heteroplasmic shift in type B1 and B2 thymomas. *The Journal of pathology*, 268(2), 135.
- Schwabe J, et al. (2026) A single-domain response regulator activates exopolysaccharide biosynthesis by interaction with the initiating phosphoglycosyl transferase. *mBio*, 17(1), e0298625.
- Griffin A, et al. (2026) Transport of the abundant intestinal amino acid glutamine by the enteric pathogen *Campylobacter jejuni* occurs via GutA (Cj0903), an AGCS family transporter. *Microbiology (Reading, England)*, 172(1).
- Chen CH, et al. (2026) A prognostic 19-gene signature and LBP-mediated immune dysregulation define the tumor microenvironment in poor-prognosis KIRC. *International journal of medical sciences*, 23(3), 824.
- Mierzejewski B, et al. (2026) CD146 + interstitial cells contribute to the dystrophic skeletal muscle phenotype in vitro. *Scientific reports*, 16(1).
- Hong J, et al. (2026) Proximity-based proteomic profiling uncovers distinct interactome of human RAG1 and RAG2. *Acta biochimica et biophysica Sinica*, 58(4), 756.
- Liu D, et al. (2026) In-silico study of machine learning discovers de novo lipogenesis for predicting prognosis and immunotherapy responses in kidney renal clear cell carcinoma. *Biology direct*, 21(1).
- Abroudi AS, et al. (2026) Analysis of microarray and single-cell RNA-seq finds gene co-expression, cell-cell communication, and tumor environment associated with cytoskeleton protein in epithelial-mesenchymal transition in ovarian cancer. *Discover oncology*, 17(1).
- Fang C, et al. (2026) A machine learning-based epigenetic signature reveals YTHDC1 stabilizes POU5F1 to oppose tumor progression. *Journal of translational medicine*, 24(1).
- Dermitzaki E, et al. (2026) Exploring Gene Expression Patterns in Alzheimer's Disease Using a Human Microarray Data Meta-Analysis. *Biology*, 15(4).
- Tavallaie M, et al. (2026) Interleukin-18 Inhibition Aggravates Atherosclerosis in Jak2V617F Clonal Hematopoiesis. *JACC. Basic to translational science*, 11(3), 101463.