

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/>

Proper Citation: ArrayExpress (RRID:SCR_002964)

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

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

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

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

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: 20260729T044042+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 7529 mentions in open access literature.

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

Ryu S, et al. (2026) Transcriptional regulation of neuropeptide receptors underlies context-dependent adaptation in *Drosophila melanogaster*. *FEBS open bio*, 16(1), 90.

Abplanalp WT, et al. (2026) Clonal hematopoiesis activates procalcific pathways in macrophages and promotes aortic valve stenosis. *The Journal of clinical investigation*, 136(1).

Lin J, et al. (2026) Enhancing cancer susceptibility to disulfidptosis by inducing cell cycle arrest and impairing DNA repair. *Theranostics*, 16(2), 637.

Rotem A, et al. (2026) Differentiation between regulated and disrupted growth arrests allows tailoring of effective treatments for antibiotic persistence. *Science advances*, 12(1), eadt6577.

Li H, et al. (2026) Single-cell and spatial transcriptomics reveal P4HA2-mediated radiotherapy resistance mechanisms in breast cancer. *Theranostics*, 16(5), 2192.

Silva RA, et al. (2026) The unfolded protein response in progeria arteries originates from non-endothelial cell types. *Life science alliance*, 9(2).

Pu L, et al. (2025) Avoidance of hydrogen sulfide is modulated by external and internal states in *Caenorhabditis elegans*. *eLife*, 12.

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in T-ALL. *Clinical epigenetics*, 17(1), 114.

Buermann LE, et al. (2025) CD27 Agonist Antibodies Mediate Clinical Responses through Intratumoral Stimulation in B-cell Malignancies: Multicenter RiVa Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(22), 4664.

Ma T, et al. (2025) Pan-Cancer Analyses Refine the Single-Cell Portrait of Tumor-Infiltrating Dendritic Cells. *Cancer research*, 85(19), 3596.

Caruso A, et al. (2025) Adipocyte/Tumor cell crosstalk via IGF-1/TXNIP axis promotes malignancy and endocrine resistance in breast cancer. *Cell communication and signaling : CCS*, 23(1), 262.

Anastasia A, et al. (2025) Stroma gene signature predicts responsiveness to chemotherapy in pancreatic ductal adenocarcinoma patient-derived xenograft models. *Molecular oncology*, 19(4), 1075.

Mou Z, et al. (2025) Integration of single-cell and bulk RNA-sequencing data reveals the prognostic potential of epithelial gene markers for prostate cancer. *Molecular oncology*, 19(6), 1811.

Flynn A, et al. (2025) Multi-omic analysis of SDHB-deficient pheochromocytomas and paragangliomas identifies metastasis and treatment-related molecular profiles. *Nature communications*, 16(1), 2632.

Qin K, et al. (2025) Kinesin family member 14 expression and its clinical implications in colorectal cancer. *World journal of gastrointestinal oncology*, 17(3), 102696.

He X, et al. (2025) Integrative multi-omics analysis and machine learning refine global histone modification features in prostate cancer. *Frontiers in molecular biosciences*, 12, 1557843.

Volat F, et al. (2025) Pancreatic CAF-Derived Autotaxin Drives Autocrine CTGF Expression to Modulate Protumorigenic Signaling. *Molecular cancer therapeutics*, 24(2), 230.

Yin M, et al. (2025) sc2GWAS: a comprehensive platform linking single cell and GWAS traits of human. *Nucleic acids research*, 53(D1), D1151.

Yin J, et al. (2025) Disulfidptosis: a novel gene-based signature predicts prognosis and immunotherapy efficacy of pancreatic adenocarcinoma. *Discover oncology*, 16(1), 308.

Wyles SP, et al. (2025) SenSkin???: a human skin-specific cellular senescence gene set. *GeroScience*, 47(3), 2631.