

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 16, 2024

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

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

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

Funding Agency: European Union , SLING , European Commission , Gen2Phen , NHGRI

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

Alternate URLs: <http://www.ebi.ac.uk/microarray-as/ae>

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 6837 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Saggese P, et al. (2024) Glucose Deprivation Promotes Pseudohypoxia and Dedifferentiation in Lung Adenocarcinoma. *Cancer research*, 84(2), 305.

Liang J, et al. (2024) Mechanistic study of transcription factor Sox18 during heart development. *General and comparative endocrinology*, 350, 114472.

Bitzenhofer NL, et al. (2024) Exploring engineered vesiculation by *Pseudomonas putida* KT2440 for natural product biosynthesis. *Microbial biotechnology*, 17(1), e14312.

Ding H, et al. (2024) Comprehensive analysis of single cell and bulk data develops a promising prognostic signature for improving immunotherapy responses in ovarian cancer. *PloS one*, 19(2), e0298125.

Yin SY, et al. (2024) Overexpression of FERM Domain Containing Kindlin 2 (FERMT2) in Fibroblasts Correlates with EMT and Immunosuppression in Gastric Cancer. *International journal of genomics*, 2024, 4123737.

Lu YW, et al. (2024) Identification of gene signatures and molecular mechanisms underlying the mutual exclusion between psoriasis and leprosy. *Scientific reports*, 14(1), 2199.

Zi Z, et al. (2024) Discoveries of GPR39 as an evolutionarily conserved receptor for bile

acids and of its involvement in biliary acute pancreatitis. *Science advances*, 10(5), eadj0146.

Li C, et al. (2024) Outcomes of intermediate or high-risk CMML patients treated with hypomethylating agents combined with venetoclax: A single center experience. *Clinical and translational science*, 17(1), e13711.

Goldmann K, et al. (2024) Expression quantitative trait loci analysis in rheumatoid arthritis identifies tissue specific variants associated with severity and outcome. *Annals of the rheumatic diseases*, 83(3), 288.

Pilcher L, et al. (2024) The Neural Progenitor Cell-Associated Transcription Factor FoxG1 Regulates Cardiac Epicardial Cell Proliferation. *Stem cells international*, 2024, 8601360.

Saha B, et al. (2024) In-depth transcriptomic analysis of *Anopheles gambiae* hemocytes uncovers novel genes and the oenocytoid developmental lineage. *BMC genomics*, 25(1), 80.

Hansen MS, et al. (2024) Transcriptional reprogramming during human osteoclast differentiation identifies regulators of osteoclast activity. *Bone research*, 12(1), 5.

Rinaldi L, et al. (2024) Downregulation of praja2 restrains endocytosis and boosts tyrosine kinase receptors in kidney cancer. *Communications biology*, 7(1), 208.

Liu Z, et al. (2024) CDS-DB, an omnibus for patient-derived gene expression signatures induced by cancer treatment. *Nucleic acids research*, 52(D1), D1163.

Gavriil M, et al. (2024) 2-Hydroxyglutarate modulates histone methylation at specific loci and alters gene expression via Rph1 inhibition. *Life science alliance*, 7(2).

Hijazo-Pechero S, et al. (2024) Transcriptional analysis of landmark molecular pathways in lung adenocarcinoma results in a clinically relevant classification with potential therapeutic implications. *Molecular oncology*, 18(2), 453.

Dean I, et al. (2024) Rapid functional impairment of natural killer cells following tumor entry limits anti-tumor immunity. *Nature communications*, 15(1), 683.

Talbot EJ, et al. (2024) cGAS-STING signalling regulates microglial chemotaxis in genome instability. *Nucleic acids research*, 52(3), 1188.

Bei Y, et al. (2024) Passenger Gene Coamplifications Create Collateral Therapeutic Vulnerabilities in Cancer. *Cancer discovery*, 14(3), 492.

Li Y, et al. (2024) Integrative Analyses of Pyrimidine Salvage Pathway-Related Genes Revealing the Associations Between UPP1 and Tumor Microenvironment. *Journal of inflammation research*, 17, 101.