Resource Summary Report

Generated by RRID on May 19, 2025

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

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

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

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250519T203226+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 7192 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Meng X, et al. (2025) GTO: a comprehensive gene therapy omnibus. Nucleic acids research, 53(D1), D1393.

Wu L, et al. (2025) RNALocate v3.0: Advancing the Repository of RNA Subcellular Localization with Dynamic Analysis and Prediction. Nucleic acids research, 53(D1), D284.

Tian Y, et al. (2025) CCR5 and IL-12 co-expression in CAR T cells improves antitumor efficacy by reprogramming tumor microenvironment in solid tumors. Cancer immunology, immunotherapy : CII, 74(2), 55.

Liu H, et al. (2025) A Comprehensive Analysis of Sex-Biased Gene Expression in the Aging Human Retina Through a Combination of Single-Cell and Bulk RNA Sequencing. Investigative ophthalmology & visual science, 66(1), 28.

Yang Y, et al. (2025) Tumor-associated-fibrosis and active collagen-CD44 axis characterize a poor-prognosis subtype of gastric cancer and contribute to tumor immunosuppression. Journal of translational medicine, 23(1), 123.

Xiong Y, et al. (2025) Highly proliferating cancer cells function as novel prognostic biomarkers for lung adenocarcinoma with particular usefulness for stage IA risk stratification. BMC cancer, 25(1), 25.

Liu L, et al. (2025) Revealing the role of cancer-associated fibroblast senescence in prognosis and immune landscape in pancreatic cancer. iScience, 28(1), 111612.

Fenn J, et al. (2025) An ultra-early, transient interferon-associated innate immune response associates with protection from SARS-CoV-2 infection despite exposure. EBioMedicine, 111, 105475.

Zheng X, et al. (2025) Mitochondrial dysfunction-driven AMPK-p53 axis activation underpins the anti-hepatocellular carcinoma effects of sulfane sulfur. Scientific reports, 15(1), 3708.

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

Karathanasis N, et al. (2025) Predicting the Progression from Asymptomatic to Symptomatic Multiple Myeloma and Stage Classification Using Gene Expression Data. Cancers, 17(2).

Cao D, et al. (2025) Time-series single-cell transcriptomic profiling of luteal-phase endometrium uncovers dynamic characteristics and its dysregulation in recurrent implantation failures. Nature communications, 16(1), 137.

Huang H, et al. (2025) Comprehensive analyses reveal the promising value of gasdermins as prognostic biomarkers and immunotherapeutic targets in head and neck squamous cell carcinoma. Heliyon, 11(1), e41213.

Song W, et al. (2025) Abundant repressor binding sites in human enhancers are associated with the fine-tuning of gene regulation. iScience, 28(1), 111658.

Liu Q, et al. (2025) Inhibition of Retinal Neovascularization by BEZ235: Targeting the Akt/4EBP1/Cyclin D1 Pathway in Endothelial Cells. Investigative ophthalmology & visual science, 66(1), 66.

Cheng W, et al. (2025) scMMO-atlas: a single cell multimodal omics atlas and portal for exploring fine cell heterogeneity and cell dynamics. Nucleic acids research, 53(D1), D1186.

Xu Y, et al. (2025) ScDrugAct: a comprehensive database to dissect tumor microenvironment cell heterogeneity contributing to drug action and resistance across

human cancers. Nucleic acids research, 53(D1), D1536.

Zheng X, et al. (2025) Integrative analyses of mendelian randomization and bioinformatics reveal casual relationship and genetic links between COVID-19 and knee osteoarthritis. BMC medical genomics, 18(1), 2.

Ye Z, et al. (2025) Comprehensive analysis of telomere and aging-related signature for predicting prognosis and immunotherapy response in lung adenocarcinoma. Journal of cardiothoracic surgery, 20(1), 31.

Hu K, et al. (2025) Annotation-free deep learning algorithm trained on hematoxylin & eosin images predicts epithelial-to-mesenchymal transition phenotype and endocrine response in estrogen receptor-positive breast cancer. Breast cancer research : BCR, 27(1), 6.