

Resource Summary Report

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Gene Expression Atlas

RRID:SCR_007989

Type: Tool

Proper Citation

Gene Expression Atlas (RRID:SCR_007989)

Resource Information

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

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Description: Gene Expression Atlas is a semantically enriched database of meta-analysis based summary statistics over a curated subset of ArrayExpress Archive, servicing queries for condition-specific gene expression patterns as well as broader exploratory searches for biologically interesting genes/samples. The EBI Gene Expression Atlas Blog discusses ideas, features and problems of creating a large scale meta-analytical atlas of gene expression from publicly available microarray data. Atlas REST API provides all the results available in the main web application in a pragmatic, easy to use form - simple HTTP GET queries as input and either JSON or XML formats as output. Gene Expression Atlas goals: 1. Provision of a statistically robust framework for integration of gene expression experiment results across different platforms at a meta-analytical level 2. A simple interface for identifying strong differential expression candidate genes in conditions of interest 3. Integration of ontologies for high quality annotation of gene and sample attributes 4. Construction of new gene expression summarized views, with a view to analysis of putative signaling pathway targets, discovery of correlated gene expression patterns and the identification of condition/tissue-specific patterns of gene expression.

Resource Type: data or information resource, expression atlas, database, atlas

Keywords: expression, gene, annotation, assay, molecular neuroanatomy resource, gold standard, bio.tools

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Resource Name: Gene Expression Atlas

Resource ID: SCR_007989

Alternate IDs: nif-0000-06686, biotools:gxa_expt, r3d100010223, biotools:gene_expression_atlas

Alternate URLs: https://bio.tools/gxa_expt, https://bio.tools/gene_expression_atlas, <https://doi.org/10.17616/R3Z888>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260729T044200+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Atlas.

No alerts have been found for Gene Expression Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 127 mentions in open access literature.

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

Poovitha S, et al. (2025) Srebf and Runx3 regulate hepatic HMG-CoA reductase and intracellular cholesterol under hypoxia. Cellular and molecular life sciences : CMLS, 82(1), 222.

Al-Harbi S, et al. (2025) Eugenol Promotes Apoptosis in Leukemia Cells via Targeting the Mitochondrial Biogenesis PPRC1 Gene. Cells, 14(4).

Salmerón C, et al. (2025) Histamine H1 Receptor: A potential therapeutic target for pancreatic ductal adenocarcinoma. The Journal of pharmacology and experimental therapeutics, 392(5), 103573.

Majewska AM, et al. (2024) Secreted novel AID/APOBEC-like deaminase 1 (SNAD1) - a new important player in fish immunology. Frontiers in immunology, 15, 1340273.

Tang W, et al. (2024) The RNA helicase DDX21 activates YAP to promote tumorigenesis and is transcriptionally upregulated by β -catenin in colorectal cancer. Oncogene, 43(44), 3227.

Nakamoto K, et al. (2024) Effect of Functional Inhibition of BACE1 on Sensitization to γ -Irradiation in Cancer Cells. Current issues in molecular biology, 46(1), 450.

George N, et al. (2024) Expression Atlas update: insights from sequencing data at both bulk and single cell level. Nucleic acids research, 52(D1), D107.

Lim K, et al. (2023) A novel human fetal lung-derived alveolar organoid model reveals mechanisms of surfactant protein C maturation relevant to interstitial lung disease. *bioRxiv* : the preprint server for biology.

Leng D, et al. (2023) Comprehensive Analysis of Tumor Microenvironment Reveals Prognostic ceRNA Network Related to Immune Infiltration in Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(19), 3986.

Soutar MPM, et al. (2022) Regulation of mitophagy by the NSL complex underlies genetic risk for Parkinson's disease at 16q11.2 and MAPT H1 loci. *Brain : a journal of neurology*, 145(12), 4349.

Jayadev R, et al. (2022) A basement membrane discovery pipeline uncovers network complexity, regulators, and human disease associations. *Science advances*, 8(20), eabn2265.

Lirussi L, et al. (2022) A regulatory network comprising let-7 miRNA and SMUG1 is associated with good prognosis in ER+ breast tumours. *Nucleic acids research*, 50(18), 10449.

Indrischek H, et al. (2022) Vision-related convergent gene losses reveal SERPINE3's unknown role in the eye. *eLife*, 11.

Santamaria ME, et al. (2021) Comparative transcriptomics reveals hidden issues in the plant response to arthropod herbivores. *Journal of integrative plant biology*, 63(2), 312.

Dorotea D, et al. (2021) KF-1607, a Novel Pan Src Kinase Inhibitor, Attenuates Obstruction-Induced Tubulointerstitial Fibrosis in Mice. *Biomolecules & therapeutics*, 29(1), 41.

Muyle A, et al. (2021) Gene capture by transposable elements leads to epigenetic conflict in maize. *Molecular plant*, 14(2), 237.

Peluso JJ, et al. (2021) Progesterone Receptor Membrane Component (PGRMC)1 and PGRMC2 and Their Roles in Ovarian and Endometrial Cancer. *Cancers*, 13(23).

Borgese N, et al. (2021) Mutant VAPB: Culprit or Innocent Bystander of Amyotrophic Lateral Sclerosis? *Contact (Thousand Oaks (Ventura County, Calif.))*, 4, 25152564211022515.

De Palma FDE, et al. (2020) The abundance of the long intergenic non-coding RNA 01087 differentiates between luminal and triple-negative breast cancers and predicts patient outcome. *Pharmacological research*, 161, 105249.

Howe KL, et al. (2020) Ensembl Genomes 2020-enabling non-vertebrate genomic research. *Nucleic acids research*, 48(D1), D689.