

Resource Summary Report

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BioXpress

RRID:SCR_014191

Type: Tool

Proper Citation

BioXpress (RRID:SCR_014191)

Resource Information

URL: <https://hive.biochemistry.gwu.edu/tools/bioxpress/>

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Description: BioXpress is a gene expression and cancer association database in which the expression levels are mapped to genes using RNA-seq data obtained from The Cancer Genome Atlas, International Cancer Genome Consortium, Expression Atlas and publications. BioXpress can be searched by gene name or cancer type. To search the database by gene name, select the appropriate identifier type from the dropdown menu and type in the corresponding identifier in the adjacent text box. The results are computed and presented to the user with information such as variable expression levels and tumor expression. To search by cancer type, select the desired type from the dropdown menu, such as "Cancer Type", "Significant", "Expression", "Adjusted p-value" and "p-value". Results are shown in a graph displaying the top 10 differentially expressed genes for the specified cancer type in terms of the frequency of significant altered expression between the tumor and normal pairs.

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1093/database/bav019](https://doi.org/10.1093/database/bav019)

Keywords: rnaseq, differential expression, pan-cancer analysis, database

Funding: NCI EDRN Associate Member contract 156620

Availability: Public

Resource Name: BioXpress

Resource ID: SCR_014191

License: GNU General Public License version 3

License URLs: <https://hive.biochemistry.gwu.edu/hive.cgi?cmd=privacy>

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260905T133209+0000

Ratings and Alerts

No rating or validation information has been found for BioXpress.

No alerts have been found for BioXpress.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Khoshandam M, et al. (2026) Expression Analysis of VEGF-Related Hub Genes and Pathways in Breast Cancer: A Comprehensive Bioinformatics Analysis. Iranian journal of medical sciences, 51(2), 126.

Basova LV, et al. (2023) MRP8/14 Is a Molecular Signature Triggered by Dopamine in HIV Latent Myeloid Targets That Increases HIV Transcription and Distinguishes HIV+ Methamphetamine Users with Detectable CSF Viral Load and Brain Pathology. Viruses, 15(6).

Vyas B, et al. (2023) Predicting the molecular mechanism-driven progression of breast cancer through comprehensive network pharmacology and molecular docking approach. Scientific reports, 13(1), 13729.

Garcia KA, et al. (2022) Fatty acid binding protein 5 regulates lipogenesis and tumor growth in lung adenocarcinoma. Life sciences, 301, 120621.

Ullah S, et al. (2022) The Cancer Research Database (CRDB): Integrated Platform to Gain Statistical Insight Into the Correlation Between Cancer and COVID-19. JMIR cancer, 8(2), e35020.

Lakshmi Ch NP, et al. (2021) Molecular basis for RASSF10/NPM/RNF2 feedback cascade-mediated regulation of gastric cancer cell proliferation. The Journal of biological chemistry, 297(2), 100935.

Patel JA, et al. (2021) Bioinformatics tools developed to support BioCompute Objects. Database : the journal of biological databases and curation, 2021.

Fiorito V, et al. (2021) The heme synthesis-export system regulates the tricarboxylic acid cycle flux and oxidative phosphorylation. Cell reports, 35(11), 109252.

Chang TC, et al. (2019) Investigation of somatic single nucleotide variations in human endogenous retrovirus elements and their potential association with cancer. PloS one, 14(4), e0213770.

Peeney D, et al. (2019) Matrisome-Associated Gene Expression Patterns Correlating with TIMP2 in Cancer. Scientific reports, 9(1), 20142.

Xu H, et al. (2019) Identification of ESM1 overexpressed in head and neck squamous cell carcinoma. Cancer cell international, 19, 118.

Pawar G, et al. (2019) In Silico Toxicology Data Resources to Support Read-Across and (Q)SAR. Frontiers in pharmacology, 10, 561.

Mangangcha IR, et al. (2019) Identification of key regulators in prostate cancer from gene expression datasets of patients. Scientific reports, 9(1), 16420.

Fleischer LM, et al. (2018) Review and Meta-Analyses of TAAR1 Expression in the Immune System and Cancers. Frontiers in pharmacology, 9, 683.

Gupta S, et al. (2018) DEXTER: Disease-Expression Relation Extraction from Text. Database : the journal of biological databases and curation, 2018.

Dingerdissen HM, et al. (2018) BioMuta and BioXpress: mutation and expression knowledgebases for cancer biomarker discovery. Nucleic acids research, 46(D1), D1128.

Ananthi S, et al. (2018) Global Quantitative Proteomics reveal Deregulation of Cytoskeletal and Apoptotic Signalling Proteins in Oral Tongue Squamous Cell Carcinoma. Scientific reports, 8(1), 1567.

Krishnan R, et al. (2018) Interplay between human nucleolar GNL1 and RPS20 is critical to modulate cell proliferation. Scientific reports, 8(1), 11421.

Awasthi S, et al. (2018) DDX49 is an RNA helicase that affects translation by regulating mRNA export and the levels of pre-ribosomal RNA. Nucleic acids research, 46(12), 6304.

Shaul YD, et al. (2016) MERAV: a tool for comparing gene expression across human tissues and cell types. Nucleic acids research, 44(D1), D560.