

Resource Summary Report

Generated by [dkNET](#) on Aug 4, 2026

[geneXplain](#)

RRID:SCR_005573

Type: Tool

Proper Citation

geneXplain (RRID:SCR_005573)

Resource Information

URL: <http://www.genexplain.com/>

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Description: An online toolbox and workflow management system for a broad range of bioinformatic and systems biology applications. The individual modules, or Bricks, are unified under a standardized interface, with a consistent look-and-feel and can flexibly be put together to comprehensive workflows. The workflow management is intuitively handled through a simple drag-and-drop system. With this system, you can edit the predefined workflows or compose your own workflows from scratch. Your own Bricks can easily be added as scripts or plug-ins and can be used in combination with pre-existing analyses. GeneXplain GmbH provides a number of state-of-the-art bricks; some of them can be obtained free of charge, while others require licensing for small fee in order to guarantee active maintenance and dynamic adaptation to the rapidly developing know-how in this field.

Abbreviations: GeneXplain

Synonyms: geneXplain GmbH

Resource Type: software toolkit, workflow software, software application, data processing software, software resource

Keywords: scientific workflow, bioinformatics, systems biology, network modeling, microarray, proteomics, mirna, chip-chip, sequence, biomarker, gene expression

Resource Name: geneXplain

Resource ID: SCR_005573

Alternate IDs: nlx_146199

Record Creation Time: 20220129T080231+0000

Ratings and Alerts

No rating or validation information has been found for geneXplain.

No alerts have been found for geneXplain.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

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

Padam KSR, et al. (2025) Multifaceted regulation of the HOX cluster and its implications in oral cancer. *Clinical epigenetics*, 17(1), 126.

Patton ME, et al. (2025) Sex differences in bile acid homeostasis and excretion underlie the disparity in liver cancer incidence between males and females. *eLife*, 13.

Umrigar A, et al. (2025) CFTR Gene Regulation in Human Pancreatic Duct, Bile Duct and Sweat Gland Epithelial Cells. *Journal of cellular and molecular medicine*, 29(15), e70751.

Rodriguez-Sosa A, et al. (2025) Multiomic Sequencing Reveals Distinctive Gene Expression and Epigenetic Alterations Associated With Primary Sclerosing Cholangitis Development in Treatment-Naïve Pediatric Ulcerative Colitis. *Gastro hep advances*, 4(3), 100586.

Al-Janabi SAA, et al. (2025) High throughput transcriptomics analysis of ovine mammary epithelial cells stimulated with *Staphylococcus aureus* in vitro. *PloS one*, 20(9), e0333355.

Kurochkina NS, et al. (2024) Age-related changes in human skeletal muscle transcriptome and proteome are more affected by chronic inflammation and physical inactivity than primary aging. *Aging cell*, 23(4), e14098.

Tang S, et al. (2024) Genomics of human NAFLD: Lack of data reproducibility and high interpatient variability in drug target expression as major causes of drug failures. *Hepatology (Baltimore, Md.)*, 80(4), 901.

Kisakol B, et al. (2024) Identification of unique rectal cancer-specific subtypes. *British journal of cancer*, 130(11), 1809.

Finnegan E, et al. (2024) Complexation of histone deacetylase inhibitor belinostat to Cu(II) prevents premature metabolic inactivation in vitro and demonstrates potent anti-cancer activity in vitro and ex vivo in colon cancer. *Cellular oncology (Dordrecht, Netherlands)*, 47(2), 533.

Saberi F, et al. (2023) Identification of Renal Transplantation Rejection Biomarkers in Blood Using the Systems Biology Approach. *Iranian biomedical journal*, 27(6), 375.

Zhong S, et al. (2023) Sex disparities in non-small cell lung cancer: mechanistic insights from a cRaf transgenic disease model. *EBioMedicine*, 95, 104763.

Tang Z, et al. (2023) Combined inhibition of histone deacetylase and cytidine deaminase improves epigenetic potency of decitabine in colorectal adenocarcinomas. *Clinical epigenetics*, 15(1), 89.

Kato M, et al. (2023) Long non-coding RNA lncMGC mediates the expression of TGF- β -induced genes in renal cells via nucleosome remodelers. *Frontiers in molecular biosciences*, 10, 1204124.

Selvaraj S, et al. (2023) Diclofenac Disrupts the Circadian Clock and through Complex Cross-Talks Aggravates Immune-Mediated Liver Injury-A Repeated Dose Study in Minipigs for 28 Days. *International journal of molecular sciences*, 24(2).

Audouard E, et al. (2022) Bioelectronic cell-based device provides a strategy for the treatment of the experimental model of multiple sclerosis. *Journal of controlled release : official journal of the Controlled Release Society*, 352, 994.

Meier T, et al. (2021) Gene networks and transcriptional regulators associated with liver cancer development and progression. *BMC medical genomics*, 14(1), 41.

Donato L, et al. (2021) Impairments of Photoreceptor Outer Segments Renewal and Phototransduction Due to a Peripherin Rare Haplotype Variant: Insights from Molecular Modeling. *International journal of molecular sciences*, 22(7).

Tenesaca S, et al. (2021) Statins act as transient type I interferon inhibitors to enable the antitumor activity of modified vaccinia Ankara viral vectors. *Journal for immunotherapy of cancer*, 9(7).

Chereda H, et al. (2021) Explaining decisions of graph convolutional neural networks: patient-specific molecular subnetworks responsible for metastasis prediction in breast cancer. *Genome medicine*, 13(1), 42.

Basova L, et al. (2021) Detection of H3K4me3 Identifies NeuroHIV Signatures, Genomic Effects of Methamphetamine and Addiction Pathways in Postmortem HIV+ Brain Specimens that Are Not Amenable to Transcriptome Analysis. *Viruses*, 13(4).