

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

geneXplain

RRID:SCR_005573

Type: Tool

Proper Citation

geneXplain (RRID:SCR_005573)

Resource Information

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

Proper Citation: geneXplain (RRID:SCR_005573)

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 [PRECISE-TBI](#) .

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).