

Resource Summary Report

Generated by NIF on Sep 3, 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: data processing software, software application, software resource, software toolkit, workflow software

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 73 mentions in open access literature.

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

Vazquez-Munoz R, et al. (2026) Enterococcus faecalis induces H₂O₂-mediated epithelial cell death and enhances Candida albicans virulence in oropharyngeal candidiasis. mSphere, 11(1), e0082225.

Suzuki K, et al. (2026) Hepatocyte growth factor in biosheets promotes autonomous regeneration of cutaneous tissue after transplantation onto a full-thickness skin defect. Materials today. Bio, 37, 102969.

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.

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.

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.

Özdemir M, et al. (2025) RNA-Seq of Chicken Embryo Liver Reveals Transcriptional Pathways Influenced by Egg Formaldehyde Treatment. Genes, 16(5).

Nishida S, et al. (2025) Trans-Omic Analysis Identifies the 'PRMT1-STAT3-Integrin α 6 Axis' as a Novel Therapeutic Target in Tacrolimus-Induced Chronic Nephrotoxicity. International journal of molecular sciences, 26(21).

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.

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.

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.

Borlak J, et al. (2024) The Abl1 tyrosine kinase is a key player in doxorubicin-induced cardiomyopathy and its p53/p73 cell death mediated signaling differs in atrial and ventricular cardiomyocytes. *Journal of translational medicine*, 22(1), 845.

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.

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 Mice for 28 Days. *International journal of molecular sciences*, 24(2).

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.

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.