

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

GeneMANIA

RRID:SCR_005709

Type: Tool

Proper Citation

GeneMANIA (RRID:SCR_005709)

Resource Information

URL: <http://genemania.org/>

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Description: Data analysis service to predict the function of your favorite genes and gene sets. Indexing 1,421 association networks containing 266,984,699 interactions mapped to 155,238 genes from 7 organisms. GeneMANIA interaction networks are available for download in plain text format. GeneMANIA finds other genes that are related to a set of input genes, using a very large set of functional association data. Association data include protein and genetic interactions, pathways, co-expression, co-localization and protein domain similarity. You can use GeneMANIA to find new members of a pathway or complex, find additional genes you may have missed in your screen or find new genes with a specific function, such as protein kinases. Your question is defined by the set of genes you input. If members of your gene list make up a protein complex, GeneMANIA will return more potential members of the protein complex. If you enter a gene list, GeneMANIA will return connections between your genes, within the selected datasets. GeneMANIA suggests annotations for genes based on Gene Ontology term enrichment of highly interacting genes with the gene of interest. GeneMANIA is also a gene recommendation system. GeneMANIA is also accessible via a Cytoscape plugin, designed for power users. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GeneMANIA

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource, software resource

Defining Citation: [PMID:20576703](#), [PMID:18613948](#), [PMID:20926419](#)

Keywords: gene, association data, protein interaction, genetic interaction, pathway, co-expression, co-localization, protein, software library, statistical analysis, term enrichment, analysis, browser, gene ontology, gene predicting, gene prioritization, database or data warehouse, other analysis, interaction browser, protein-protein interaction, interaction,

FASEB list

Funding: Genome Canada ;
Ontario Ministry of Research and Innovation 2007-OGI-TD-05

Availability: Open unspecified license, Free for academic use

Resource Name: GeneMANIA

Resource ID: SCR_005709

Alternate IDs: nlx_149159, r3d100013978

Alternate URLs: <https://doi.org/10.17616/R31NJNA2>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260821T193737+0000

Ratings and Alerts

No rating or validation information has been found for GeneMANIA.

No alerts have been found for GeneMANIA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4535 mentions in open access literature.

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

Dwead AM, et al. (2026) The YAP1-NPM1 nuclear complex regulates MYC and reveals a targetable oncogenic node. iScience, 29(5), 115588.

Liu L, et al. (2026) Serine/threonine kinase 32 family proteins: The potential multifaceted regulators in cancer. Translational oncology, 63, 102608.

Huang J, et al. (2026) Redistribution of super-enhancers promotes malignancy in human hepatocellular carcinoma. Journal of advanced research, 82, 803.

Chen Y, et al. (2026) Expression of PSTPIP1 in Renal Cell Carcinoma and Its Prognostic Value. Biochemical genetics, 64(2), 2836.

Yao D, et al. (2026) Single-cell Transcriptomic Profiling Reveals Diagnostic of T Cell-platelet Aggregates in Peripheral Blood for Coronary Vulnerable Plaques. Journal of cardiovascular translational research, 19(1), 6.

Zhu X, et al. (2026) Elevated IGF1R and abnormal methylated IGF1R in immune thrombocytopenia. *Annals of hematology*, 105(1), 34.

Ke J, et al. (2026) The ANGPTL3-integrin $\alpha 5$ axis drives retinal vascular leakage in diabetic retinopathy. *Journal of translational medicine*, 24(1), 183.

Lin Y, et al. (2026) Intermittent fasting inhibits Tp53-driven glioma through gut microbiota-mediated methionine-m6A regulation. *Nature communications*, 17(1), 1804.

Hatakeyama K, et al. (2026) Translating spatial transcriptomic signatures in adenosquamous carcinoma into bulk prognostic biomarkers in lung adenocarcinoma: a bottom-up approach. *NPJ precision oncology*, 10(1).

Liang Y, et al. (2026) Integrative multi-omics reveal a CD4⁺ T cell-derived six-gene signature linking the immune-stromal ecosystem to prognosis and immunotherapy selection in pancreatic cancer. *BMC cancer*, 26(1), 262.

Huang Z, et al. (2026) Integrating single-cell and spatial transcriptomics with pan-cancer bulk sequencing identifies OSR2 as a multifaceted biomarker for prognosis and tumor immunity. *Discover oncology*, 17(1).

Deng Y, et al. (2026) MiR-21-5p regulates biological malignancy in esophageal squamous cell carcinoma via targeting CNTFR. *BMC gastroenterology*, 26(1).

Wang X, et al. (2026) *Coptis chinensis* extracellular vesicles loaded with CA1-siRNA promote endothelial repair and stent restenosis therapy by regulating the PADI2 and NF- κ B pathway. *Journal of nanobiotechnology*, 24(1), 157.

Rao Y, et al. (2026) TRPA1 promotes overactive bladder progression by activating the NLRP3 inflammasome and driving pyroptosis. *Cell death & disease*, 17(1), 226.

Li A, et al. (2026) Transcriptome and single-cell RNA sequencing analysis with 101 machine learning combinations and experimental verification reveals the mechanism of action of mannose metabolism in bladder cancer. *Frontiers in immunology*, 17, 1710823.

Chen J, et al. (2026) Machine-learning-guided transcriptomic integration identifies GFM1 as a lactylation-related candidate biomarker in aortic dissection. *Scientific reports*, 16(1).

Yi L, et al. (2026) Expression and association of HNRNPA2B1 with clinical prognosis in breast cancer: An evaluation based on the TCGA and GEO databases. *Medicine*, 105(2), e46875.

Yang S, et al. (2026) Identification of Notch pathway-related biomarkers in patients with idiopathic pulmonary fibrosis. *PloS one*, 21(1), e0339287.

Tang S, et al. (2026) Mechanistic Insights into Threonine Tyrosine Kinase Mediated Cell Cycle Regulation in Triple-negative Breast Cancer. *Cancer genomics & proteomics*, 23(1), 93.

Mahemuti M, et al. (2026) Exploring hub genes related to adipocytokines in keloids: a combined analysis integrating single-cell, Mendelian randomization and bulk transcriptome data with experimental verification. *Frontiers in molecular biosciences*, 13, 1740876.