

Resource Summary Report

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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: 20260905T132540+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 [PRECISE-TBI](#) .

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

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

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

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

Yang Y, et al. (2026) Integrative proteogenomic and observational analysis identifies potential biomarkers for latent autoimmune diabetes in adults. Cardiovascular diabetology, 25(1).

Zhao J, et al. (2026) Identification and Validation of Mitophagy-Related Biomarkers in Colorectal Cancer: An Integrated Analysis of Single-Cell Transcriptome and Mendelian Randomization. *Genetics research*, 2026(1), e5579542.

Liu Y, et al. (2026) MYC promotes myocardial fibrosis via METTL1-mediated m7G modification of HILPDA. *Biology direct*, 21(1).

Wang J, et al. (2026) Identification of shared biomarkers in obesity and non-alcoholic fatty liver disease: a comprehensive analysis of Mendelian randomization and transcriptomic data. *Frontiers in nutrition*, 13, 1780686.

Mou L, et al. (2026) Advancing lupus nephritis research through multi-omics and predictive modeling. *Innate immunity*, 32, 17534259261426818.

Xie C, et al. (2026) LRP1 as a potential diagnostic and immunomodulatory target in endometriosis: evidence from multi-omics and single-cell analyses. *Frontiers in immunology*, 17, 1735221.

Xue C, et al. (2026) Genetic and Molecular Interconnections Between Chronic Obstructive Pulmonary Disease and Osteoporosis: Insights from Single-Cell and Mendelian Randomization Analyses. *International journal of chronic obstructive pulmonary disease*, 21, 602067.

Zhang B, et al. (2026) SYTL2 and DENND2B as shared drivers in mouse abdominal aortic aneurysm and lung cancer. *iScience*, 29(6), 115783.

Zhang S, et al. (2026) APOA2-mediated endothelial mesenchymal transition and cancer lipid metabolism reprogramming confers antiangiogenic drug resistance through TGF- β . *Cell death discovery*, 12(1).

Wu S, et al. (2026) Single-cell hdWGCNA and experimental validation identify an innovative T-cell-associated prognostic model and immune microenvironment in lung adenocarcinoma with lymph node metastasis. *BMC cancer*, 26(1).

Zha J, et al. (2026) Inhibition of TRPC6 channel suppresses bladder cancer proliferation by disrupting store-operated calcium entry. *Scientific reports*, 16(1).

Khaled R, et al. (2026) RNA biomarker signatures for prediction of acute kidney injury in acute coronary syndrome patients undergoing PCI. *BMC nephrology*, 27(1).

Dustin A, et al. (2026) Suicide risk genes impact evolutionarily conserved survival strategies. *Translational psychiatry*, 16(1).

Wu J, et al. (2026) Discovery of serum APOD as an early sarcopenia biomarker in older adults with low muscle mass: a cross-sectional proteomic and transcriptomic investigation. *PeerJ*, 14, e21058.

Wang Z, et al. (2026) A pseudouridine-related prognostic model of colorectal cancer based on single-cell sequencing analysis and transcriptome analysis. *Scientific reports*, 16(1), 4735.

Daniel MM, et al. (2026) Integrative Bioinformatics Reveals Novel Molecular Mechanisms and Therapeutic Targets in Acute Myeloid Leukaemia. *Journal of cellular and molecular*

medicine, 30(1), e71007.