

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: service resource, data analysis service, software resource, data or information resource, database, production service resource, analysis service 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: 20260731T042712+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 3358 mentions in open access literature.

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

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.

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.

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

Gulbey O, et al. (2026) Integrated Bioinformatics and Experimental Analysis of Argonaute Family Members in Pancreatic Adenocarcinoma. In vivo (Athens, Greece), 40(1), 123.

Yang R, et al. (2026) Exploring and Validating the Molecular Mechanisms Linking Fatty Acid Metabolism and Sarcopenia. *IET systems biology*, 20(1), e70052.

Liu X, et al. (2026) Mapping protein-protein interactions by mass spectrometry. *Mass spectrometry reviews*, 45(1), 69.

Chen Y, et al. (2026) A non-invasive urinary diagnostic signature for diabetic kidney disease revealed by machine learning and single-cell analysis. *PloS one*, 21(1), e0340096.

Xu Z, et al. (2025) A Prognostic Risk Signature Based on Myeloid-Derived Suppressor Cells and Regulatory T Cells in Clear Cell Renal Cell Carcinoma. *Technology in cancer research & treatment*, 24, 15330338251382839.

Respekta-Dugosz N, et al. (2025) Integrated Transcriptomic and Proteomic Analysis of Omentin-1 Effects on Primary Anterior Pituitary Cells From Different Pig Breeds: An In Vitro Study. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(19), e71081.

Easwaran S, et al. (2025) A genome-wide association study implicates the olfactory system in *Drosophila melanogaster* diapause-associated lifespan extension and fecundity. *eLife*, 13.

Mehta V, et al. (2025) Database analysis reveals endophilin A expression as a marker of metastasis and prognosis in breast cancer. *Discover oncology*, 16(1), 1832.

Ding M, et al. (2025) Identification of a Novel Gene ARNT2 for Osteogenic Differentiation of Mesenchymal Stem Cells. *Calcified tissue international*, 116(1), 100.

He L, et al. (2025) Increased SLC7A3 Expression Inhibits Tumor Cell Proliferation and Predicts a Favorable Prognosis in Breast Cancer. *Recent patents on anti-cancer drug discovery*, 20(1), 55.

Huang F, et al. (2025) Comprehensive bioinformatics analysis of metabolism-related microRNAs in high myopia in young and old adults with age-related cataracts. *Molecular medicine reports*, 31(2).

Wei M, et al. (2025) Identification of a novel disulfidptosis-related gene signature in osteoarthritis using bioinformatics analysis and experimental validation. *Scientific reports*, 15(1), 1339.

Bouزيد A, et al. (2025) Whole exome sequencing identifies ABHD14A and MRNIP as novel candidate genes for developmental language disorder. *Scientific reports*, 15(1), 367.

Shuang L, et al. (2025) Downregulation of Gldc attenuates myocardial ischemia reperfusion injury in vitro by modulating Akt and NF- κ B signalings. *Scientific reports*, 15(1), 268.

Husami SF, et al. (2025) Corporate genome screening India (CoGSI) identified genetic variants association with T2D in young Indian professionals. *Scientific reports*, 15(1), 506.

Wang C, et al. (2025) Unveiling novel biomarkers for platinum chemoresistance in ovarian cancer. *Open medicine (Warsaw, Poland)*, 20(1), 20241084.