Resource Summary Report

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HumanNet

RRID:SCR_016146
Type: Tool

Proper Citation

HumanNet (RRID:SCR_016146)

Resource Information

URL: http://www.functionalnet.org/humannet/about.html

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Description: Database of human protein-encoding genes that is constructed by a modified Bayesian integration of 'omics' data from multiple organisms. Each data type is weighted according to how well it links genes that are known to function together in humans, and each interaction has an associated log-likelihood score (LLS) that measures the probability of an interaction representing a true functional linkage between two genes.

Resource Type: database, data analysis software, software resource, software application, data processing software, web application, data or information resource

Keywords: probability, gene, protein, encode, statistic, likelihood, network, bayesian, omic, pathway, guilt by association, FASEB list

Funding: National Research Foundation of Korea (NRF) ;
Korean government (MEST) 2010-0017649;
POSCO TJ ;
U.S. Army Research 58343-MA;
Welch F1515;
Packard Foundations ;
Wellcome Trust 076113;
Wellcome Trust 085475

Availability: Freely available

Resource Name: HumanNet

Resource ID: SCR_016146

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260728T043514+0000

Ratings and Alerts

No rating or validation information has been found for HumanNet.

No alerts have been found for HumanNet.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 132 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Wright SN, et al. (2025) Common and rare genetic variants show network convergence for a majority of human traits. medRxiv : the preprint server for health sciences.

Buzzao D, et al. (2025) FunCoup 6: advancing functional association networks across species with directed links and improved user experience. Nucleic acids research, 53(D1), D658.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Wen H, et al. (2025) EssSubgraph improves performance and generalizability of mammalian essential gene prediction with large networks. GigaScience, 14.

Yu J, et al. (2025) HCNetlas: A reference database of human cell type-specific gene networks to aid disease genetic analyses. PLoS biology, 23(2), e3002702.

Li X, et al. (2025) A cell type and state specific gene regulation network inference method for immune regulatory analysis. NPJ systems biology and applications, 11(1), 94.

Alwadi D, et al. (2025) RNA-Seq Uncovers Association of Endocrine-Disrupting Chemicals with Hub Genes and Transcription Factors in Aggressive Prostate Cancer. International journal of molecular sciences, 26(12).

Wu J, et al. (2025) Dual graph-embedded fusion network for predicting potential microbe-disease associations with sequence learning. Frontiers in genetics, 16, 1511521.

Le DH, et al. (2025) Improving computational drug repositioning through multi-source disease similarity networks. Scientific reports, 15(1), 30773.

A J, et al. (2025) DyNDG: Identifying Leukemia-related Genes Based on Time-series Dynamic Network by Integrating Differential Genes. Genomics, proteomics & bioinformatics, 23(2).

Buzzao D, et al. (2024) Benchmarking enrichment analysis methods with the disease pathway network. Briefings in bioinformatics, 25(2).

Li Z, et al. (2024) An atlas of cell-type-specific interactome networks across 44 human tumor types. Genome medicine, 16(1), 30.

Shi K, et al. (2024) Predicting microbe-disease association based on graph autoencoder and inductive matrix completion with multi-similarities fusion. Frontiers in microbiology, 15, 1438942.

Sullivan KA, et al. (2024) Analyses of GWAS signal using GRIN identify additional genes contributing to suicidal behavior. Communications biology, 7(1), 1360.

Wei H, et al. (2024) DiSMVC: a multi-view graph collaborative learning framework for measuring disease similarity. Bioinformatics (Oxford, England), 40(5).

Pudjihartono M, et al. (2024) Links between melanoma germline risk loci, driver genes and comorbidities: insight from a tissue-specific multi-omic analysis. Molecular oncology, 18(4), 1031.

Visonà G, et al. (2024) Network propagation for GWAS analysis: a practical guide to leveraging molecular networks for disease gene discovery. Briefings in bioinformatics, 25(2).

Niemira M, et al. (2024) Circulating serum miR-362-3p and miR-6721-5p as potential biomarkers for classification patients with adult-type diffuse glioma. Frontiers in molecular biosciences, 11, 1368372.

Ma Y, et al. (2024) Kernel Bayesian logistic tensor decomposition with automatic rank determination for predicting multiple types of miRNA-disease associations. PLoS computational biology, 20(7), e1012287.

Sullivan KA, et al. (2024) MENTOR: Multiplex Embedding of Networks for Team-Based Omics Research. bioRxiv : the preprint server for biology.