

# Resource Summary Report

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## MultiNet

RRID:SCR\_016149

Type: Tool

### Proper Citation

MultiNet (RRID:SCR\_016149)

### Resource Information

**URL:** <http://homes.gersteinlab.org/Khurana-PLoSCompBio-2013/>

**Proper Citation:** MultiNet (RRID:SCR\_016149)

**Description:** Software for an integrated network combining multiple biological network database sources into a single human protein interactome. The software package contains gene interaction pairs corresponding to the unified global network.

**Resource Type:** software resource

**Defining Citation:** [PMID:23505346](#)

**Keywords:** network, integration, human, protein, interactome, gene, interaction

**Availability:** Free, Available for download

**Resource Name:** MultiNet

**Resource ID:** SCR\_016149

**Record Creation Time:** 20220129T080329+0000

**Record Last Update:** 20260912T195836+0000

### Ratings and Alerts

No rating or validation information has been found for MultiNet.

No alerts have been found for MultiNet.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Duan J, et al. (2026) Discovering proteo-transcriptomic networks via biologically informed heterogeneous graph learning. *Nucleic acids research*, 54(8).

Eini P, et al. (2025) Machine learning-based classification of carotid plaques via ultrasound: a systematic review and meta-analysis of diagnostic performance. *International journal of emergency medicine*, 18(1), 247.

Diogoul N, et al. (2024) Estimating the copepod biomass in the North West African upwelling system using a bi-frequency acoustic approach. *PloS one*, 19(9), e0308083.

Li X, et al. (2024) Towards simplified graph neural networks for identifying cancer driver genes in heterophilic networks. *Briefings in bioinformatics*, 26(1).

Cui Y, et al. (2023) SMG: self-supervised masked graph learning for cancer gene identification. *Briefings in bioinformatics*, 24(6).

Tao Z, et al. (2022) The diel vertical distribution and carbon biomass of the zooplankton community in the Caroline Seamount area of the western tropical Pacific Ocean. *Scientific reports*, 12(1), 18908.

Jagtap S, et al. (2022) BRANENet: embedding multilayer networks for omics data integration. *BMC bioinformatics*, 23(1), 429.

Ma Q, et al. (2022) m6Acancer-Net: Identification of m6A-mediated cancer driver genes from gene-site heterogeneous network. *Methods (San Diego, Calif.)*, 203, 125.

Majaneva S, et al. (2021) Hiding in plain sight-Euplokamis dunlapae (Ctenophora) in Norwegian waters. *Journal of plankton research*, 43(2), 257.

Yu H, et al. (2021) Genome-wide discovery of hidden genes mediating known drug-disease association using KDDANet. *NPJ genomic medicine*, 6(1), 50.

Li Z, et al. (2020) Multi-omics characterization of molecular features of gastric cancer correlated with response to neoadjuvant chemotherapy. *Science advances*, 6(9), eaay4211.

Zhang SY, et al. (2019) Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. *PLoS computational biology*, 15(1), e1006663.

Lv BM, et al. (2018) Drug Repurposing for Japanese Encephalitis Virus Infection by Systems Biology Methods. *Molecules (Basel, Switzerland)*, 23(12).

Zhang F, et al. (2016) Identification of novel prognostic indicators for triple-negative breast cancer patients through integrative analysis of cancer genomics data and protein interactome data. *Oncotarget*, 7(44), 71620.