

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: 20260801T190528+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 12 mentions in open access literature.

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

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).

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.

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

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.

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.