Resource Summary Report

Generated by NIF on May 24, 2025

Biomine

RRID:SCR_003552
Type: Tool

Proper Citation

Biomine (RRID:SCR_003552)

Resource Information

URL: http://biomine.cs.helsinki.fi/

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Description: Service that integrates cross-references from several biological databases into a graph model with multiple types of edges, such as protein interactions, gene-disease associations and gene ontology annotations. Edges are weighted based on their type, reliability, and informativeness. In particular, it formulates protein interaction prediction and disease gene prioritization tasks as instances of link prediction. The predictions are based on a proximity measure computed on the integrated graph.

Abbreviations: Biomine

Resource Type: service resource, data or information resource, database

Defining Citation: PMID:22672646

Keywords: gene, protein, genetics, visualization, connection, biological entity, protein interaction, disease gene, link prediction

Funding:

Resource Name: Biomine

Resource ID: SCR_003552

Alternate IDs: nlx_157687

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250523T054332+0000

Ratings and Alerts

No rating or validation information has been found for Biomine.

No alerts have been found for Biomine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Guo Y, et al. (2022) Integrative COVID-19 biological network inference with probabilistic core decomposition. Briefings in bioinformatics, 23(1).

Boži? J, et al. (2022) Interactome screening of C9orf72 dipeptide repeats reveals VCP sequestration and functional impairment by polyGA. Brain : a journal of neurology, 145(2), 684.

Herman A, et al. (2015) Analysis of Glioblastoma Patients' Plasma Revealed the Presence of MicroRNAs with a Prognostic Impact on Survival and Those of Viral Origin. PloS one, 10(5), e0125791.

Motaln H, et al. (2015) Heterogeneous glioblastoma cell cross-talk promotes phenotype alterations and enhanced drug resistance. Oncotarget, 6(38), 40998.