Resource Summary Report

Generated by dkNET on May 21, 2025

Graph2GO

RRID:SCR_018726
Type: Tool

Proper Citation

Graph2GO (RRID:SCR_018726)

Resource Information

URL: https://github.com/yanzhanglab/Graph2GO

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Description: Software tool as graph based representation learning method for protein function prediction. Multi modal graph based representation learning model that can integrate heterogeneous information including multiple types of interaction networks including sequence similarity network and protein-protein interaction network, and protein features including amino acid sequence, sub cellular location and protein domains, to predict protein functions on Gene Ontology.

Resource Type: software application, software resource, data analysis software, data processing software

Keywords: Protein function prediction, graph neural network, attributed network embedding, representation learning, multi-modal model, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Graph2GO

Resource ID: SCR_018726

Alternate IDs: SCR_018727, biotools:graph2go

Alternate URLs: https://integrativeomics.shinyapps.io/graph2go/, https://bio.tools/graph2go

License: MIT License

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250519T204042+0000

Ratings and Alerts

No rating or validation information has been found for Graph2GO.

No alerts have been found for Graph2GO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Lin B, et al. (2024) A comprehensive review and comparison of existing computational methods for protein function prediction. Briefings in bioinformatics, 25(4).

Fan K, et al. (2020) Graph2GO: a multi-modal attributed network embedding method for inferring protein functions. GigaScience, 9(8).