Resource Summary Report

Generated by dkNET on Apr 24, 2025

PiNGO

RRID:SCR_000692
Type: Tool

Proper Citation

PiNGO (RRID:SCR_000692)

Resource Information

URL: http://www.psb.ugent.be/esb/PiNGO/

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Description: A Java-based tool to easily find unknown genes in a network that are significantly associated with user-defined target Gene Ontology (GO) categories. PiNGO is implemented as a plugin for Cytoscape, a popular open source software platform for visualizing and integrating molecular interaction networks. PiNGO predicts the categorization of a gene based on the annotations of its neighbors, using the enrichment statistics of its sister tool BiNGO. Networks can either be selected from the Cytoscape interface or uploaded from file. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: PiNGO

Resource Type: software resource

Defining Citation: PMID:21278188

Keywords: gene, annotation, network, candidate gene, biological network, ontology or annotation search engine, statistical analysis, term enrichment, functional similarity, functional prediction, search engine, windows, mac os x, linux, unix

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: PiNGO

Resource ID: SCR_000692

Alternate IDs: nlx_149330, OMICS_02281

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250420T014002+0000

Ratings and Alerts

No rating or validation information has been found for PiNGO.

No alerts have been found for PiNGO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.