

# Resource Summary Report

Generated by [ASWG](#) on Aug 23, 2026

## GraphWeb

RRID:SCR\_005746

Type: Tool

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### Proper Citation

GraphWeb (RRID:SCR\_005746)

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### Resource Information

**URL:** <http://biit.cs.ut.ee/graphweb/>

**Proper Citation:** GraphWeb (RRID:SCR\_005746)

**Description:** GraphWeb allows the detection of modules from biological, heterogeneous and multi-species networks, and the interpretation of detected modules using Gene Ontology, cis-regulatory motifs and biological pathways. GraphWeb is a public web server for graph-based analysis of biological networks that: \* analyses directed and undirected, weighted and unweighted heterogeneous networks of genes, proteins and microarray probesets for many eukaryotic genomes; \* integrates multiple diverse datasets into global networks; \* incorporates multispecies data using gene orthology mapping; \* filters nodes and edges based on dataset support, edge weight and node annotation; \* detects gene modules from networks using a collection of algorithms; \* interprets discovered modules using Gene Ontology, pathways, and cis-regulatory motifs. Platform: Online tool

**Abbreviations:** GraphWeb

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Defining Citation:** [PMID:18460544](#)

**Keywords:** analysis, biological network, ontology or annotation visualization, protein interaction, gene id conversion, orthology mapping, network visualization, graph clustering, gene ontology, cis-regulatory motif, module, network, pathway, biological pathway, motif, visualization, protein interaction, orthology mapping, network visualization, graph clustering, analysis, statistical analysis, term enrichment

**Funding:** European Union FP6 ENFIN LSHG-CT-2005-518254;  
European Union FP6 COBRED LSHB-CT-2007-037730;  
Estonian Science Foundation ETF7437

**Availability:** Open unspecified license - Free for academic use

**Resource Name:** GraphWeb

**Resource ID:** SCR\_005746

**Alternate IDs:** nlx\_149205

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260821T042659+0000

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## Ratings and Alerts

No rating or validation information has been found for GraphWeb.

No alerts have been found for GraphWeb.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Guan L, et al. (2019) A prognostic prediction system for hepatocellular carcinoma based on gene co-expression network. *Experimental and therapeutic medicine*, 17(6), 4506.

Zhang X, et al. (2019) Inferring immune-associated signatures based on a co-expression network in Guillain-Barré syndrome. *Cell proliferation*, 52(4), e12634.

Wang Y, et al. (2018) A 44-gene set constructed for predicting the prognosis of clear cell renal cell carcinoma. *International journal of molecular medicine*, 42(6), 3105.

Zhang Y, et al. (2018) A 63 signature genes prediction system is effective for glioblastoma prognosis. *International journal of molecular medicine*, 41(4), 2070.

Wang H, et al. (2018) Detection of dysregulated competing endogenous RNA modules associated with clear cell kidney carcinoma. *Molecular medicine reports*, 18(2), 1963.

Zheng B, et al. (2018) Construction of a prognostic prediction system for pancreatic ductal adenocarcinoma to investigate the key prognostic genes. *Molecular medicine reports*, 17(1), 216.

Jiang H, et al. (2018) A 65?gene signature for prognostic prediction in colon adenocarcinoma. *International journal of molecular medicine*, 41(4), 2021.

Li Y, et al. (2017) Immunoglobulin superfamily genes are novel prognostic biomarkers for breast cancer. *Oncotarget*, 8(2), 2444.

Zhao L, et al. (2017) Identification of potential prognostic ceRNA module biomarkers in patients with pancreatic adenocarcinoma. *Oncotarget*, 8(55), 94493.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. *GigaScience*, 4, 38.

Jia X, et al. (2014) Cancer-risk module identification and module-based disease risk evaluation: a case study on lung cancer. *PloS one*, 9(3), e92395.

Qu X, et al. (2014) Identifying colon cancer risk modules with better classification performance based on human signaling network. *Genomics*, 104(4), 242.