

Resource Summary Report

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NetworkAnalyst

RRID:SCR_016909

Type: Tool

Proper Citation

NetworkAnalyst (RRID:SCR_016909)

Resource Information

URL: <https://www.networkanalyst.ca/>

Proper Citation: NetworkAnalyst (RRID:SCR_016909)

Description: Web tool for gene expression profiling, meta-analysis and systems understanding. Used for statistical, visual and network-based meta-analysis of gene expression data.

Resource Type: software application, analysis service resource, service resource, data analysis software, data analysis service, data access protocol, data processing software, software resource, production service resource, web service, network analysis software

Defining Citation: [PMID:25950236](#)

Keywords: gene, expression, profiling, meta, data, analysis, statistical, visual, bio.tools

Availability: Free, Freely available, Tutorial available

Resource Name: NetworkAnalyst

Resource ID: SCR_016909

Alternate IDs: biotools:networkanalyst

Alternate URLs: <https://bio.tools/networkanalyst>

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260729T044425+0000

Ratings and Alerts

No rating or validation information has been found for NetworkAnalyst.

No alerts have been found for NetworkAnalyst.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 635 mentions in open access literature.

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

Cai S, et al. (2026) Identification and validation of novel inflammatory response-related diagnostic biomarkers in diabetic foot ulcers. *Journal of diabetes investigation*, 17(1), 103.

Luan R, et al. (2026) Pan-cancer multi-omics reveals DCAF7 as an immune-modulating prognostic driver and Wnt/??-catenin activator in hepatocellular carcinoma. *Clinical and translational medicine*, 16(1), e70572.

Xu HR, et al. (2025) Identification of potential hub genes associated with recurrent miscarriage through combined transcriptomic and proteomic analysis. *Biomolecules & biomedicine*, 25(6), 1259.

Li G, et al. (2025) Identification of key genes associated with oxidative stress in ischemic stroke via bioinformatics integrated analysis. *BMC neuroscience*, 26(1), 3.

Zhao N, et al. (2025) Identification of critical endoplasmic reticulum stress-related genes in advanced atherosclerotic plaque. *Scientific reports*, 15(1), 2107.

Li X, et al. (2025) Identifying Common Diagnostic Biomarkers and Therapeutic Targets between COPD and Sepsis: A Bioinformatics and Machine Learning Approach. *International journal of chronic obstructive pulmonary disease*, 20, 1761.

Li S, et al. (2025) Exploring shared pathogenic mechanisms and biomarkers in hepatic fibrosis and inflammatory bowel disease through bioinformatics and machine learning. *Frontiers in immunology*, 16, 1533246.

Li Z, et al. (2025) Exploring the Potential Regulatory Mechanisms of Mitophagy in Ischemic Cardiomyopathy. *International journal of general medicine*, 18, 2881.

Zhang Y, et al. (2025) Single-cell spatial atlas of smoking-induced changes in human gingival tissues. *International journal of oral science*, 17(1), 60.

Wu Y, et al. (2025) Study on identification and analysis of biomarkers related to neutrophils extracellular traps in childhood asthma. *Medicine*, 104(31), e43489.

Sun L, et al. (2025) Identification and validation of ANXA3 and SOCS3 as biomarkers for acute myocardial infarction related to sphingolipid metabolism. *Hereditas*, 162(1), 150.

Borgonio-Cuadra VM, et al. (2025) In Silico Analysis of miRNA-Regulated Pathways in Spinocerebellar Ataxia Type 7. *Current issues in molecular biology*, 47(3).

Li J, et al. (2025) Identification and verification of biomarkers associated with arachidonic acid metabolism in non-alcoholic fatty liver disease. *Scientific reports*, 15(1), 8521.

He W, et al. (2025) The role of senescence-related hub genes correlating with immune infiltration in type A aortic dissection: Novel insights based on bioinformatic analysis. *PloS one*, 20(6), e0326939.

Ye H, et al. (2025) Text Mining Strategy Identifies Gene Networks Under Control of miR-21 in Breast Cancer Development. *Cancer medicine*, 14(13), e70986.

Chen Y, et al. (2025) Single-cell RNA-seq uncovers lineage-specific regulatory alterations of fibroblasts and endothelial cells in ligamentum flavum hypertrophy. *Frontiers in immunology*, 16, 1569296.

Wang H, et al. (2025) Identification of prognostic genes associated with phase separation in lung adenocarcinoma and construction of prognostic models. *Scientific reports*, 15(1), 34547.

Li ZF, et al. (2025) Cellular and molecular features of acute myeloid leukemia investigation based on single-cell RNA sequencing. *Cancer cell international*, 25(1), 326.

Huang X, et al. (2025) Identification of lipid metabolism-related genes in dapagliflozin treated rats with diabetic cardiomyopathy by bioinformatics. *Frontiers in endocrinology*, 16, 1525831.

Xu Y, et al. (2025) Integrated analysis of DNA methylation and transcriptome profiles to identify oxidative stress-related placenta-specific molecules for preeclampsia. *The journal of obstetrics and gynaecology research*, 51(3), e16209.