

Resource Summary Report

Generated by [NIF](#) on Jul 30, 2026

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

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: 20260731T043004+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 [NIF](#) .

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.

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.

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.

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.

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.

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

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.

He L, et al. (2025) Identification of hub genes related to DNA damage response in asthma via combinative bioinformatics strategy. *The Journal of international medical research*, 53(4), 3000605251332204.

Li B, et al. (2025) Machine Learning and Experiments Revealed Key Genes Related to PANoptosis Linked to Drug Prediction and Immune Landscape in Spinal Cord Injury. *Molecular neurobiology*, 62(6), 7364.

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.

Su G, et al. (2025) Klf5-adjacent super-enhancer functions as a 3D genome structure-dependent transcriptional driver to safeguard ESC identity. Nature communications, 16(1), 5540.

Dai X, et al. (2025) Identification and validation of parthanatos-related genes in end-stage renal disease. Renal failure, 47(1), 2519834.

Sun M, et al. (2025) Transcriptome combined with Mendelian randomization to identify key genes related to polyamine metabolism in childhood obesity and elucidate their molecular regulatory mechanisms. Scientific reports, 15(1), 17799.

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 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.

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.

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.