

# 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:** data analysis service, data analysis software, data access protocol, service resource, software application, production service resource, software resource, network analysis software, data processing software, web service, 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:** 20260801T190556+0000

### Ratings and Alerts

No rating or validation information has been found for NetworkAnalyst.

No alerts have been found for NetworkAnalyst.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 635 mentions in open access literature.

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

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.