

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

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: 20260905T132815+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 975 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.

Wang G, et al. (2026) Development of a prognostic model for thyroid cancer based on mitochondrial metabolism-related genes and immune profiling. *World journal of surgical oncology*, 24(1), 67.

Zhu X, et al. (2026) Investigating the therapeutic mechanism of Asarum for oral ulcer from a network pharmacology perspective. *Medicine*, 105(1), e46880.

Liao D, et al. (2026) Targeting CXCL8 in post-traumatic stress disorder and Alzheimer's disease: insights from cross-disorder molecular analysis. *Annals of medicine*, 58(1), 2610559.

Zhang T, et al. (2026) Identification of key genes in the pathogenesis of hepatic ischemia-reperfusion injury based on bioinformatics and experimental verification. *Scientific reports*, 16(1).

Wang J, et al. (2026) Cuproptosis of endothelial cells in a hypoxic environment: from molecular classification to PMAIP1-targeted intervention. *Hereditas*, 163(1).

Wang Y, et al. (2026) Ozone Exposure Induces Anemia via Immune-Inflammatory Disruption of Erythroid Homeostasis. *Environment & health (Washington, D.C.)*, 4(2), 301.

Bokhari BT, et al. (2026) System biology and network-based approach to identify the therapeutic signatures and potential inhibitors against polycystic lipomembranous osteodysplasia with Sclerosing Leukoencephalopathy. *PloS one*, 21(2), e0343274.

Ling S, et al. (2026) Integrative omics and experimental validation reveal METTL17 and SLC27A1 as biomarkers and potential therapeutic targets in chronic kidney disease. *Frontiers in immunology*, 17, 1724740.

Guan H, et al. (2026) Shared immune dysregulation in systemic lupus erythematosus and colorectal cancer: a multi-omics guided discovery of DNASE1L3-centric efferocytosis deficiency. *Frontiers in immunology*, 17, 1775776.

Ruan F, et al. (2026) Comprehensive machine learning for identifying platelet-associated diagnostic biomarkers and immune landscape in Kawasaki disease. *Translational pediatrics*, 15(2), 34.

Bai M, et al. (2026) Comprehensive Analysis of the Expression and Prognostic Significance of NPAS1 in Patients with Colorectal Adenocarcinoma Based on Bioinformatics. *International journal of general medicine*, 19, 556875.

Gu Z, et al. (2026) Mature tertiary lymphoid structures tumor microenvironment-based risk model to assess patients with pancreatic ductal adenocarcinoma. *Translational cancer research*, 15(2), 128.

Shan B, et al. (2026) Identification of the biomarkers associated with lipid metabolism and endoplasmic reticulum stress in pediatric sepsis through bioinformatics analysis and quantitative reverse transcriptase PCR (qRT-PCR) assay. *European journal of medical research*, 31(1).

Liu X, et al. (2026) Comprehensive analysis of m6A RNA methylation regulators and the immune microenvironment in spinal cord injury. *Frontiers in neurology*, 17, 1759661.

Kampmann S, et al. (2026) Inhibition of Fibroblast Growth Factor Receptor 3 Signaling by Ponatinib Reduces Growth and Cytokine Production of Multiple Myeloma Cells. *International journal of molecular sciences*, 27(12).

Yu A, et al. (2026) A novel diagnostic model for HIV-HTN comorbidity: genomic discovery, clinical validation, and mechanistic elucidation. *Frontiers in medicine*, 13, 1781646.

Zhang X, et al. (2026) Identification and Analysis of Biomarkers Associated With Lipid Metabolism and Ferroptosis in Ulcerative Colitis. *Journal of immunology research*, 2026(1), e9283449.

Liu X, et al. (2026) Comparative transcriptome profiling of leg muscle development from the embryonic to growth stages in Huanglang chickens. *Poultry science*, 105(9), 107190.

Zhang S, et al. (2026) Exploring the common ferroptosis-related genes and molecular mechanisms in periodontitis and systemic sclerosis via integrated bioinformatics and experimental analysis. *Frontiers in cell and developmental biology*, 14, 1803091.