

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 14, 2026

## NetPathMiner

RRID:SCR\_002757

Type: Tool

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### Proper Citation

NetPathMiner (RRID:SCR\_002757)

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### Resource Information

**URL:** <https://github.com/ahmohamed/NetPathMiner>

**Proper Citation:** NetPathMiner (RRID:SCR\_002757)

**Description:** Software that implements a flexible module-based process flow for network path mining and visualization, which can be fully integrated with user-customized functions. It supports construction of various types of genome scale networks from three different pathway file formats (KGML, SBML and BioPAX), enabling its utility to most common pathway databases. In addition, it provides different visualization techniques to facilitate the analysis of even thousands of output paths.

**Synonyms:** NetPathMiner: R package for network path mining through gene expression

**Resource Type:** software resource

**Defining Citation:** [PMID:25075120](#)

**Keywords:** software package, mac os x, unix/linux, windows, r, bio.tools

**Availability:** Free, Freely available, Available for download

**Resource Name:** NetPathMiner

**Resource ID:** SCR\_002757

**Alternate IDs:** biotools:netpathminer, OMICS\_05210

**Alternate URLs:** <https://bio.tools/netpathminer>

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260912T195546+0000

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### Ratings and Alerts

No rating or validation information has been found for NetPathMiner.

No alerts have been found for NetPathMiner.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Ustjanzew A, et al. (2024) Unraveling the glycosphingolipid metabolism by leveraging transcriptome-weighted network analysis on neuroblastic tumors. Cancer & metabolism, 12(1), 29.

Derbyshire MC, et al. (2023) Surface frustration re-patterning underlies the structural landscape and evolvability of fungal orphan candidate effectors. Nature communications, 14(1), 5244.

Mohamed A, et al. (2020) Concurrent lipidomics and proteomics on malignant plasma cells from multiple myeloma patients: Probing the lipid metabolome. PloS one, 15(1), e0227455.