

Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

TOPPAS

RRID:SCR_000533

Type: Tool

Proper Citation

TOPPAS (RRID:SCR_000533)

Resource Information

URL: <http://open-ms.sourceforge.net/documentation/knime-integration/>

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Description: A graphical user interface (GUI) for rapid composition of HPLC-MS analysis workflows. Workflow construction is reduced to drag-and-drop of analysis tools and adding connections in between.

Synonyms: The OpenMS Proteomics Pipeline Assistant, TOPP Pipeline Assistant

Resource Type: software resource

Defining Citation: [PMID:22583024](https://pubmed.ncbi.nlm.nih.gov/22583024/)

Keywords: gui, graphical user interface, analysis, hplc-ms, workflow

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TOPPAS

Resource ID: SCR_000533

Alternate IDs: OMICS_02640

Old URLs: <http://open-ms.sourceforge.net/workflow-integration/toppasworkflows/>

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260912T195511+0000

Ratings and Alerts

No rating or validation information has been found for TOPPAS.

No alerts have been found for TOPPAS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Junker J, et al. (2012) TOPPAS: a graphical workflow editor for the analysis of high-throughput proteomics data. Journal of proteome research, 11(7), 3914.