

Resource Summary Report

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Knime

RRID:SCR_006164

Type: Tool

Proper Citation

Knime (RRID:SCR_006164)

Resource Information

URL: <http://knime.org/>

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Description: KNIME (Konstanz Information Miner) is a user-friendly and comprehensive Open-Source data integration, processing, analysis, and exploration platform. KNIME (naim) is a user-friendly graphical workbench for the entire analysis process: data access, data transformation, initial investigation, powerful predictive analytics, visualization and reporting. The open integration platform provides over 1000 modules (nodes), including those of the KNIME community and its extensive partner network. KNIME can be downloaded onto the desktop and used free of charge. KNIME products include additional functionalities such as shared repositories, authentication, remote execution, scheduling, SOA integration and a web user interface as well as world-class support. Robust big data extensions are available for distributed frameworks such as Hadoop. KNIME is used by over 3000 organizations in more than 60 countries. The modular data exploration platform, initially developed at the University of Konstanz, Germany, enables the user to visually create data flows, execute selected analysis steps, and later investigate the results through interactive views on data and models. KNIME is a proven integration platform for tools of numerous vendors due to its open and modular API. The KNIME.com product pipeline includes an Enterprise Server, Cluster Execution, Reporting solutions, and professional KNIME support subscriptions. KNIME.com also offer services such as data analysis, hands-on training and the development of customized components for KNIME.

Abbreviations: KNIME

Synonyms: Konstanz Information Miner

Resource Type: workflow software, data processing software, software toolkit, text-mining software, software resource, software application

Defining Citation: [PMID:23110532](#), [PMID:22644661](#), [PMID:22607449](#), [PMID:21984761](#), [PMID:21873641](#)

Keywords: platform, next-generation sequencing, data analysis, visualization, selection, analysis, high-throughput screening, data mining, drug discovery

Resource Name: Knime

Resource ID: SCR_006164

Alternate IDs: nlx_151666

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260731T042719+0000

Ratings and Alerts

No rating or validation information has been found for Knime.

No alerts have been found for Knime.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 717 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Shumanska M, et al. (2025) Mitochondrial calcium uniporter complex controls T-cell-mediated immune responses. EMBO reports, 26(2), 407.

McSwiggen DT, et al. (2025) A high-throughput platform for single-molecule tracking identifies drug interaction and cellular mechanisms. eLife, 12.

Cervantes Recalde MF, et al. (2025) Role of homovanillic acid esters in the regulation of skin inflammatory pathways and their effect on tight junction protein expression. Frontiers in pharmacology, 16, 1629941.

Mueller L, et al. (2025) Safety and Efficacy of Repeated Low-Dose LSD for ADHD Treatment in Adults: A Randomized Clinical Trial. JAMA psychiatry, 82(6), 555.

Moen EL, et al. (2025) Cross-State Travel for Cancer Care and Implications for Telehealth Reciprocity. JAMA network open, 8(2), e2461021.

Dudášová S, et al. (2025) Retrospective Identification of Novel and Legacy Per- and Polyfluoroalkyl Substances in German Archived Fish Livers Using a Combined High-Resolution Mass Spectrometry Approach. Environmental science & technology, 59(25), 12865.

- Willems S, et al. (2025) Comparative Profiling and Chemogenomics Application of Chemical Tools for NR4A Nuclear Receptors. *Journal of medicinal chemistry*, 68(19), 19955.
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- Hinkle TB, et al. (2025) Comprehensive Protein Inference Analysis with PyProteinInference Elucidates Biological Understanding of Tandem Mass Spectrometry Data. *Journal of proteome research*, 24(4), 2135.
- Pauwels J, et al. (2025) A 96-Well Ultrafiltration Approach for the High-Throughput Proteome Analysis of Extracellular Vesicles Isolated From Conditioned Medium. *Journal of extracellular vesicles*, 14(7), e70103.
- Pabba MK, et al. (2025) Super-Resolution Compatible DNA Labeling Technique Reveals Chromatin Mobility and Organization Changes During Differentiation. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(45), e05955.
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- Thiel Z, et al. (2025) Development of a p62 biodegrader for autophagy targeted degradation. *Nature communications*, 16(1), 10858.
- Schieszl T, et al. (2025) Fumonisin Intake from Consumption of Wheat- and Corn-Based Products in Hungary. *Toxins*, 17(12).
- Zhao Y, et al. (2025) Harnessing Risk Assessment for Thrombosis and Bleeding to Optimize Anticoagulation Strategy in Nonvalvular Atrial Fibrillation. *Thrombosis and haemostasis*, 125(5), 492.
- Ahn B, et al. (2025) Categorizing high-grade serous ovarian carcinoma into clinically relevant subgroups using deep learning-based histomic clusters. *Journal of pathology and translational medicine*, 59(2), 91.
- Adamczyk J, et al. (2025) ApisTox: a new benchmark dataset for the classification of small molecules toxicity on honey bees. *Scientific data*, 12(1), 5.
- Woo K, et al. (2025) Understanding Gender-Specific Daily Care Preferences: Topic Modeling Study. *Journal of medical Internet research*, 27, e64160.
- Wintermans SEL, et al. (2025) High-throughput competitive binding assay for targeting RNA tertiary structures with small molecules: application to pseudoknots and G-quadruplexes. *Nucleic acids research*, 53(16).