

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

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: 20260829T182233+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 770 mentions in open access literature.

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

Antoniou M, et al. (2026) Predicting peroxisome proliferator-activated receptor gamma potency of small molecules: a synergistic consensus model and deep learning binding affinity approach powered by Enalos Cloud Platform. Molecular diversity, 30(2), 1821.

Farkas Z, et al. (2026) Emerging risk identification in the food chain using text mining-supported monitoring of food safety news: insights from 2022 to 2023. Scientific reports, 16(1).

Carnielli JBT, et al. (2026) Chemical genetics reveals Leishmania KKT2 and CRK9 kinase activity is required for cell cycle progression. PLoS pathogens, 22(5), e1014194.

Shakib SH, et al. (2026) Risk factors for mechanical ventilation and mortality among hospitalized Medicaid patients with COVID-19 in Kentucky, 2020-2021. Scientific reports, 16(1).

Dey S, et al. (2026) Ontogeny independent expression of LPCAT2 in granuloma macrophages during experimental visceral leishmaniasis. Communications biology, 9(1).

Vavougios GD, et al. (2026) The quantified immune-aging dysregulation index: a large-language model-powered method for annotating and quantifying systems-level dysregulation. Frontiers in artificial intelligence, 9, 1732901.

Marín M, et al. (2026) Antimitotic Naphthalene Sulfonamides Are Potent Antitumor Agents Acting Differently from Colchicine. *Pharmaceutics*, 18(6).

Moreno-Villanueva M, et al. (2026) Biologically Younger Individuals, as Identified by MARK-AGE Biological Age Scores, Display a Distinct Favourable Blood Chemistry Profile Regardless of Age. *Aging cell*, 25(3), e70437.

Navarro-Cobos MJ, et al. (2026) Modification of internal RNA domains from the long non-coding RNA XIST refines roles in silencing and heterochromatin recruitment. *Human molecular genetics*, 35(6).

Li R, et al. (2026) Single-molecule dynamics of the TRiC chaperonin system in vivo. *Nature*, 652(8109), 481.

Chen HY, et al. (2026) Tumor size larger than 6.5 cm and microvascular invasion are comparable prognosticators for hepatocellular carcinoma: a multi-institutional observational study. *Clinical & translational oncology : official publication of the Federation of Spanish Oncology Societies and of the National Cancer Institute of Mexico*, 28(1), 215.

Herold NK, et al. (2026) Identification of Neuroactive Chemicals in Crude Oil-Derived Water-Accommodated Fractions. *Environmental science & technology*, 60(1), 181.

Thibaud JL, et al. (2026) Small Molecule Kinase Inhibitors with In Vitro γ -Hematin Formation and Plasmodium falciparum Protein Kinase G Inhibitory Activity Identified Using Machine Learning. *ChemMedChem*, 21(3), e202500756.

Çiçek Y, et al. (2026) A machine learning model for accurate prediction of CMV end-organ disease. *BMC medical informatics and decision making*, 26(1).

Agapiou M, et al. (2026) Held out wings RNA binding activity in the cytoplasm during early spermatogenesis. *Communications biology*, 9(1), 156.

Shakib SH, et al. (2026) Where Inequities Emerge: Racial and Ethnic Differences Across the COVID-19 Hospitalization Continuum. *International journal of environmental research and public health*, 23(2).

Wray C, et al. (2026) Integration of human microbiota (SIHUMIx) and zebrafish models reveals microbiome-mediated host responses to azoxystrobin. *Toxicological sciences : an official journal of the Society of Toxicology*, 209(4).

Isawi IH, et al. (2026) Computational Studies toward the Identification of CB2R-M1R Dual Modulators. *ACS omega*, 11(8), 13121.

Sündermann J, et al. (2026) The nitrovinyl moiety determines the cyto- and genotoxic profiles of γ -nitrostyrene derivatives: evidence from in silico and in vitro evaluation. *Archives of toxicology*, 100(6), 2647.

Jain S, et al. (2026) Integrating AI in Medicinal Chemistry for Accelerated Drug Discovery: A Comprehensive SAR (CSAR) Optimization Strategy and Discovery of Potent ALDH3A1 Inhibitors. *Journal of medicinal chemistry*, 69(11), 13589.