

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

[bio.tools](#)

RRID:SCR_014695

Type: Tool

Proper Citation

bio.tools (RRID:SCR_014695)

Resource Information

URL: <https://bio.tools>

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Description: Community registry of software tools and data resources for life sciences. Tools and data services registry as community effort to document bioinformatics resources. Registry of software and databases, facilitating researchers from across spectrum of biological and biomedical science. When adding tools to registry, information including URL, contact information, resource function, field its relevant in, and its primary publication are required. Development is supported by ELIXIR - the European Infrastructure for Biological Information.

Resource Type: catalog, data or information resource, database, software repository, software resource

Defining Citation: [DOI:10.1186/s13059-019-1772-6](https://doi.org/10.1186/s13059-019-1772-6), [PMID:26538599](https://pubmed.ncbi.nlm.nih.gov/26538599/)

Keywords: Registry, software registry, biological tool, data services registry, services discovery portal, bio.tools

Funding: Danish Ministry of Higher Education and Science ;
European Union Horizon 2020 ELIXIR-EXCELERATE grant 676559

Availability: Free, Freely available

Resource Name: bio.tools

Resource ID: SCR_014695

Alternate IDs: biotools:bio.tools, r3d100013668

Alternate URLs: <https://github.com/bio-tools/biotoolsRegistry/>, <https://bio.tools/bio.tools>,
<https://doi.org/10.17616/R31NJN1G>

Old URLs: <http://bio.tools>

License: CC BY 4.0, GPL 3.0

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260821T194026+0000

Ratings and Alerts

No rating or validation information has been found for bio.tools.

No alerts have been found for bio.tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Di Cosmo R, et al. (2026) CODE beyond FAIR: a roadmap for reusable research software. Scientific data, 13(1).

Park SJ, et al. (2026) Mechanism by which a linoleic acid metabolite suppresses cancer cell growth by inhibiting mTOR. Cell chemical biology, 33(5), 637.

Bergsma P, et al. (2025) Integration of Whole-Genome Sequencing Analysis with Unique Patient-Derived Models Reveals Clinically Relevant Drug Targets in TFCP2 Fusion-Defined Rhabdomyosarcoma. Molecular cancer therapeutics, 24(12), 1989.

Gustafsson OJR, et al. (2025) WorkflowHub: a registry for computational workflows. Scientific data, 12(1), 837.

Tanriver G, et al. (2025) Exploring the multifaceted roles of resuscitation-promoting factors in tuberculosis: Implications for diagnosis, vaccine development, and drug targeting. Biotechnology reports (Amsterdam, Netherlands), 46, e00886.

Luo Y, et al. (2025) BVSim: A benchmarking variation simulator mimicking human variation spectrum. GigaScience, 14.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to Francisella tularensis infection reveals interleukin-17-dependent protection by MAIT cells. iScience, 28(3), 111810.

Martí Del Pico E, et al. (2024) FAIRsoft-a practical implementation of FAIR principles for research software. Bioinformatics (Oxford, England), 40(8).

Darden C, et al. (2024) Distinct structural motifs are necessary for targeting and import of Tim17 in Trypanosoma brucei mitochondrion. mSphere, 9(1), e0055823.

Reed CJ, et al. (2024) Beyond Blast: Enabling Microbiologists to Better Extract Literature, Taxonomic Distributions and Gene Neighborhood Information for Protein Families. bioRxiv : the preprint server for biology.

Nasr E, et al. (2024) microGalaxy: A gateway to tools, workflows, and training for reproducible and FAIR analysis of microbial data. bioRxiv : the preprint server for biology.

Finn RD, et al. (2024) Establishing the ELIXIR Microbiome Community. F1000Research, 13.

Zhang H, et al. (2024) Reviewability and supportability: New complementary principles to empower research software practices. Computational and structural biotechnology journal, 23, 3989.

, et al. (2024) The Galaxy platform for accessible, reproducible, and collaborative data analyses: 2024 update. Nucleic acids research, 52(W1), W83.

Reed CJ, et al. (2024) Beyond blast: enabling microbiologists to better extract literature, taxonomic distributions and gene neighbourhood information for protein families. Microbial genomics, 10(2).

Cowan DA, et al. (2024) Extremophiles in a changing world. Extremophiles : life under extreme conditions, 28(2), 26.

D'Anna F, et al. (2024) A research data management (RDM) community for ELIXIR. F1000Research, 13.

Buchan DWA, et al. (2024) Deep learning for the PSIPRED Protein Analysis Workbench. Nucleic acids research, 52(W1), W287.

Ritsch M, et al. (2023) Navigating the Landscape: A Comprehensive Review of Current Virus Databases. Viruses, 15(9).

Omidi-Shahsavandi M, et al. (2023) Effect of silibinin and trans-chalcone in an Alzheimer's disease-like model generated by insulin amyloids. Brazilian journal of medical and biological research = Revista brasileira de pesquisas medicas e biologicas, 56, e12443.