Resource Summary Report

Generated by NIF on Apr 25, 2025

bio.tools

RRID:SCR_014695
Type: Tool

Proper Citation

bio.tools (RRID:SCR_014695)

Resource Information

URL: https://bio.tools

Proper Citation: bio.tools (RRID:SCR_014695)

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

Defining Citation: DOI:10.1186/s13059-019-1772-6, PMID:26538599

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

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

Availability: Free, Freely available

Resource Name: bio.tools

Resource ID: SCR_014695

Alternate IDs: biotools:bio.tools

Alternate URLs: https://github.com/bio-tools/biotoolsRegistry/, https://bio.tools/bio.tools

Old URLs: http://bio.tools

License: CC BY 4.0, GPL 3.0

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250425T060027+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 18 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

, 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).

Buchan DWA, et al. (2024) Deep learning for the PSIPRED Protein Analysis Workbench.

Nucleic acids research, 52(W1), W287.

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.

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.

Patel B, et al. (2023) Making Biomedical Research Software FAIR: Actionable Step-by-step Guidelines with a User-support Tool. Scientific data, 10(1), 557.

Goel P, et al. (2022) In silico functional and structural characterization revealed virulent proteins of Francisella tularensis strain SCHU4. Molecular biology research communications, 11(2), 73.

Eneva R, et al. (2022) Safe Sialidase Production by the Saprophyte Oerskovia paurometabola: Gene Sequence and Enzyme Purification. Molecules (Basel, Switzerland), 27(24).

Luo X, et al. (2022) The freezability of Mediterranean buffalo sperm is associated with lysine succinylation and lipid metabolism. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 36(12), e22635.

Choi WY, et al. (2021) SdhA blocks disruption of the Legionella-containing vacuole by hijacking the OCRL phosphatase. Cell reports, 37(5), 109894.

Jiménez RC, et al. (2017) Four simple recommendations to encourage best practices in research software. F1000Research, 6.

Vizcaíno JA, et al. (2017) A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 6.

Moreews F, et al. (2015) BioShaDock: a community driven bioinformatics shared Docker-based tools registry. F1000Research, 4, 1443.