

Resource Summary Report

Generated by T1D on Aug 2, 2026

Git

RRID:SCR_003932

Type: Tool

Proper Citation

Git (RRID:SCR_003932)

Resource Information

URL: <http://git-scm.com/>

Proper Citation: Git (RRID:SCR_003932)

Description: A free and open source distributed version control system designed to handle everything from small to very large projects with speed and efficiency. Git is easy to learn and has a tiny footprint with lightning fast performance. It outclasses SCM tools like Subversion, CVS, Perforce, and ClearCase with features like cheap local branching, convenient staging areas, and multiple workflows.

Resource Type: software resource, software application, version source control system, software development tool

Keywords: version control, distributed, bio.tools

Availability: GNU General Public License, v2

Resource Name: Git

Resource ID: SCR_003932

Alternate IDs: nlx_158301, biotools:Git

Alternate URLs: <https://bio.tools/Git>

Record Creation Time: 20220129T080221+0000

Record Last Update: 20260801T190235+0000

Ratings and Alerts

No rating or validation information has been found for Git.

No alerts have been found for Git.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Fraga-González G, et al. (2025) Affording reusable data: recommendations for researchers from a data-intensive project. *Scientific data*, 12(1), 258.

Visentin L, et al. (2025) Structuring data analysis projects in the Open Science era with Kerblam! *F1000Research*, 14, 88.

Rodés-Bachs C, et al. (2025) Open Science Practices in Integrated Assessment Models. *Open research Europe*, 5, 12.

Zuliani M, et al. (2025) Using Open Science Tools to Teach Environmental Sciences. *Ecology and evolution*, 15(7), e71837.

Streiber AM, et al. (2025) Improving reproducibility of data analysis and code in medical research: 5 recommendations to get started. *BMJ open*, 15(10), e104691.

Zhao C, et al. (2024) A reproducible and generalizable software workflow for analysis of large-scale neuroimaging data collections using BIDS Apps. *Imaging neuroscience (Cambridge, Mass.)*, 2.

Cougnaud L, et al. (2024) Interactive medical and safety monitoring in clinical trials with clinDataReview: a validated and open-source reporting tool. *Frontiers in medicine*, 11, 1356323.

Hoyt CT, et al. (2024) The O3 guidelines: open data, open code, and open infrastructure for sustainable curated scientific resources. *Scientific data*, 11(1), 547.

Bravo JE, et al. (2024) The TELCoMB Protocol for High-Sensitivity Detection of ARG-MGE Colocalizations in Complex Microbial Communities. *Current protocols*, 4(10), e70031.

Akdeniz BC, et al. (2024) COSGAP: Containerized Statistical Genetics Analysis Pipelines. *Bioinformatics advances*, 4(1), vbae067.

Bai W, et al. (2024) Protocol to develop a chemotherapy drug screening process by constructing a cancer prognostic model using public databases. *STAR protocols*, 5(3), 103158.

Kaushal P, et al. (2024) Protocol for mapping differential protein-protein interaction networks using affinity purification-mass spectrometry. *STAR protocols*, 5(4), 103286.

Bai W, et al. (2024) Protocol to detect immune levels, abnormal metabolism, and signaling pathways in tumor tissue based on scRNA-seq obtained from patient databases. STAR protocols, 5(2), 103065.

Zhao C, et al. (2023) A reproducible and generalizable software workflow for analysis of large-scale neuroimaging data collections using BIDS Apps. bioRxiv : the preprint server for biology.

Liu X, et al. (2023) Applying FAIR4RS principles to develop an integrated modeling environment for the magnetic confinement fusion. Scientific data, 10(1), 592.

Stobbe MD, et al. (2022) Ten simple rules for a successful international consortium in big data omics. PLoS computational biology, 18(10), e1010546.

Li J, et al. (2022) RecombineX: A generalized computational framework for automatic high-throughput gamete genotyping and tetrad-based recombination analysis. PLoS genetics, 18(5), e1010047.

Kulman E, et al. (2022) Reconstructing cancer phylogenies using Pairtree, a clone tree reconstruction algorithm. STAR protocols, 3(4), 101706.

Kolpakov F, et al. (2022) BioUML-towards a universal research platform. Nucleic acids research, 50(W1), W124.

Amram D, et al. (2022) From P4 medicine to P5 medicine: transitional times for a more human-centric approach to AI-based tools for hospitals of tomorrow. Open research Europe, 2, 33.