

# Resource Summary Report

Generated by [NIF](#) on Aug 28, 2026

## Git

RRID:SCR\_003932

Type: Tool

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### Proper Citation

Git (RRID:SCR\_003932)

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### 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 application, software development tool, software resource, version source control system

**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:** 20260821T193712+0000

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### 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 73 mentions in open access literature.

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

Luo S, et al. (2026) Protocol for an interpretable self-attention artificial neural network framework to predict cancer risk in oral potentially malignant disorders. STAR protocols, 7(2), 104490.

Moretti S, et al. (2026) MetaNetX: a bridge between metabolic resources for enhanced curation and multi-omics data harmonization. Nucleic acids research, 54(D1), D617.

Gupta A, et al. (2026) NaP-TRAP: A versatile and accessible workflow to dissect principles of translational regulation and mRNA stability. bioRxiv : the preprint server for biology.

Apgar M, et al. (2026) Dietary fiber reduces mortality from secondary sepsis in a murine model of Clostridioides difficile infection. iScience, 29(4), 115258.

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.

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.

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

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.

Mastropietro A, et al. (2024) Protocol to explain support vector machine predictions via exact Shapley value computation. STAR protocols, 5(2), 103010.

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.

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.

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

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.

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

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.

Marchezan L, et al. (2023) Generating repairs for inconsistent models. Software and systems modeling, 22(1), 297.