# **Resource Summary Report**

Generated by dkNET on Apr 17, 2025

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

Keywords: version control, distributed, bio.tools

**Funding:** 

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: 20250416T063336+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 60 mentions in open access literature.

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

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.

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.

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.

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.

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

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.

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

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 Al-based tools for hospitals of tomorrow. Open research Europe, 2, 33.

Domander R, et al. (2021) BoneJ2 - refactoring established research software. Wellcome open research, 6, 37.

Leaf AT, et al. (2021) SFRmaker and Linesink-Maker: Rapid Construction of Streamflow Routing Networks from Hydrography Data. Ground water, 59(5), 761.

Halchenko YO, et al. (2021) DataLad: distributed system for joint management of code, data, and their relationship. Journal of open source software, 6(63).

Li F, et al. (2021) A protocol for transposon insertion sequencing in Schizosaccharomyces pombe to identify factors that maintain heterochromatin. STAR protocols, 2(2), 100392.

Grothausmann R, et al. (2021) Combination of  $\mu$ CT and light microscopy for generation-specific stereological analysis of pulmonary arterial branches: a proof-of-concept study. Histochemistry and cell biology, 155(2), 227.

Schölzel C, et al. (2021) Characteristics of mathematical modeling languages that facilitate model reuse in systems biology: a software engineering perspective. NPJ systems biology and applications, 7(1), 27.