

Resource Summary Report

Generated by T1D on Aug 26, 2026

Bash

RRID:SCR_021268

Type: Tool

Proper Citation

Bash (RRID:SCR_021268)

Resource Information

URL: <https://www.gnu.org/software/bash/>

Proper Citation: Bash (RRID:SCR_021268)

Description: GNU Project shell. Sh-compatible shell that incorporates useful features from Korn shell (ksh) and the C shell (csh). Improvements offered by Bash include command-line editing, unlimited size command history, job control, shell functions and aliases, indexed arrays of unlimited size, integer arithmetic in any base from two to sixty four.

Synonyms: Bourne Again SHell

Resource Type: software resource

Keywords: GNU Project shell, command-line editing, unlimited size command history, job control, shell functions and aliases, indexed arrays of unlimited size, integer arithmetic

Availability: Free, Freely available

Resource Name: Bash

Resource ID: SCR_021268

License: GNU GPL

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260815T182646+0000

Ratings and Alerts

No rating or validation information has been found for Bash.

No alerts have been found for Bash.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Arrigoni A, et al. (2026) Advanced lung segmentation on chest HRCT: comprehensive pipeline for quantification of airways, vessels, and injury patterns. *La Radiologia medica*, 131(4), 634.

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.

Rutz A, et al. (2026) MultiMS2: A curated multi-modal, multi-energy spectral library for metabolomics. *GigaScience*, 15.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Zanella E, et al. (2026) Damage-induced i-loops generate eccDNA from repetitive elements. *Molecular cell*, 86(10), 1856.

Torres LM, et al. (2025) Integrating Genomic Data into Public Health Surveillance for Multidrug-Resistant Organisms, Washington, USA. *Emerging infectious diseases*, 31(13), 25.

Shahbazi M, et al. (2024) Comparison of GWAS results between de novo tinnitus and cancer treatment-related tinnitus suggests distinctive roles for genetic risk factors. *Scientific reports*, 14(1), 27952.

Kalef-Ezra E, et al. (2024) Single-cell somatic copy number variants in brain using different amplification methods and reference genomes. *Communications biology*, 7(1), 1288.

Ray R, et al. (2024) Eliciting a single amino acid change by vaccination generates antibody protection against group 1 and group 2 influenza A viruses. *Immunity*, 57(5), 1141.

Shahbazi M, et al. (2023) Comprehensive association analysis of speech recognition thresholds after cisplatin-based chemotherapy in survivors of adult-onset cancer. *Cancer medicine*, 12(3), 2999.

Ortega-Sanz I, et al. (2023) CamPype: an open-source workflow for automated bacterial whole-genome sequencing analysis focused on *Campylobacter*. *BMC bioinformatics*, 24(1), 291.

Álvarez-Prado ÁF, et al. (2023) Immunogenomic analysis of human brain metastases reveals diverse immune landscapes across genetically distinct tumors. *Cell reports. Medicine*, 4(1), 100900.

Raghavan V, et al. (2022) A simple guide to de novo transcriptome assembly and annotation. *Briefings in bioinformatics*, 23(2).

Zachariou V, et al. (2022) Ironsmith: An automated pipeline for QSM-based data analyses. *NeuroImage*, 249, 118835.

Vuong P, et al. (2022) Ten simple rules for investigating (meta)genomic data from environmental ecosystems. *PLoS computational biology*, 18(12), e1010675.

Biedermannová L, et al. (2022) Knowledge-based prediction of DNA hydration using hydrated dinucleotides as building blocks. *Acta crystallographica. Section D, Structural biology*, 78(Pt 8), 1032.

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.

Vuong P, et al. (2021) Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. *Frontiers in microbiology*, 12, 697309.

Schloss PD, et al. (2018) The Riffomonas Reproducible Research Tutorial Series. *The Journal of open source education*, 1(3).