

# Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

## Datamash

RRID:SCR\_016067

Type: Tool

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### Proper Citation

Datamash (RRID:SCR\_016067)

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### Resource Information

**URL:** <https://savannah.gnu.org/projects/datamash/>

**Proper Citation:** Datamash (RRID:SCR\_016067)

**Description:** Software for a command-line interface which performs basic numeric, textual and statistical operations on input textual data files. It is designed to aid researchers in automating analysis pipelines, without writing code or short scripts.

**Synonyms:** GNU Datamash

**Resource Type:** data analysis software, data processing software, software application, software resource

**Keywords:** command-line, interface, basic, numerical, textual, statistical, operation, input, data, files, automate, analysis, pipelines

**Funding:** Free Software Foundation (FSF)

**Availability:** Free, Available for download

**Resource Name:** Datamash

**Resource ID:** SCR\_016067

**Alternate URLs:** <https://sources.debian.org/src/datamash/>

**License:** GNU General Public License v3

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20260912T195834+0000

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### Ratings and Alerts

No rating or validation information has been found for Datamash.

No alerts have been found for Datamash.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Guimar??es LO, et al. (2026) Wyeomyia confusa Lispivirus (WcLispV-SP): a novel neotropical mosquito virus in the Lispiviridae family. Archives of virology, 171(6).

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. Microbial genomics, 12(4).

Patel AP, et al. (2023) A multi-ancestry polygenic risk score improves risk prediction for coronary artery disease. Nature medicine, 29(7), 1793.

Selvarajan I, et al. (2021) Integrative analysis of liver-specific non-coding regulatory SNPs associated with the risk of coronary artery disease. American journal of human genetics, 108(3), 411.