

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

SNP-sites

RRID:SCR_022265

Type: Tool

Proper Citation

SNP-sites (RRID:SCR_022265)

Resource Information

URL: <http://sanger-pathogens.github.io/snp-sites/>

Proper Citation: SNP-sites (RRID:SCR_022265)

Description: Software tool to find SNP sites from multi-FASTA alignment file. Can output results in multiple formats for downstream analysis.

Synonyms: Single Nucleotide Polymorphisms-sites

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

Keywords: find SNP sites, Single Nucleotide Polymorphisms, single nucleotide polymorphisms extracting, large whole genome alignment,

Availability: Free, Available for download, Freely available

Resource Name: SNP-sites

Resource ID: SCR_022265

Alternate IDs: <https://github.com/sanger-pathogens/snp-sites>

License: GNU GPL v3

Record Creation Time: 20220507T050148+0000

Record Last Update: 20260812T044419+0000

Ratings and Alerts

No rating or validation information has been found for SNP-sites.

No alerts have been found for SNP-sites.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Froschauer K, et al. (2025) Complementary Ribo-seq approaches map the translome and provide a small protein census in the foodborne pathogen *Campylobacter jejuni*. *Nature communications*, 16(1), 3078.

Koncz M, et al. (2024) Genomic surveillance as a scalable framework for precision phage therapy against antibiotic-resistant pathogens. *Cell*, 187(21), 5901.

Lin Y, et al. (2023) Comparative Genomic Analyses of *Lactococcus garvieae* Isolated from Bovine Mastitis in China. *Microbiology spectrum*, 11(3), e0299522.