

Resource Summary Report

Generated by [ASWG](#) on Aug 5, 2026

sabre

RRID:SCR_011843

Type: Tool

Proper Citation

sabre (RRID:SCR_011843)

Resource Information

URL: <https://github.com/najoshi/sabre>

Proper Citation: sabre (RRID:SCR_011843)

Description: Software tool to demultiplex barcoded reads into separate files. Works on both single-end and paired-end data in fastq format. Used in next generation sequencing to analyze a broad range of data.

Abbreviations: sabre

Synonyms: Systems Approach to Biomarker Research

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

Keywords: demultiplex, barcode, separate, fastq, format, data, next, generation, sequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: sabre

Resource ID: SCR_011843

Alternate IDs: biotools:sabre, OMICS_01090

Alternate URLs: <https://bio.tools/sabre>

License: MIT License

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260805T044252+0000

Ratings and Alerts

No rating or validation information has been found for sabre.

No alerts have been found for sabre.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 199 mentions in open access literature.

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

Boyd A, et al. (2025) UK Longitudinal Linkage Collaboration (UK LLC): The National Trusted Research Environment for Longitudinal Research. International journal of population data science, 10(1), 2468.

de Kort FAS, et al. (2025) Cerebral white matter hyperintensity volumes: Normative age- and sex-specific values from 15 population-based cohorts comprising 14,876 individuals. Neurobiology of aging, 146, 38.

Jia M, et al. (2025) Identification of late blight resistance QTLs in an interspecific RIL population of tomato via genotyping-by-sequencing. Molecular breeding : new strategies in plant improvement, 45(4), 43.

Olah B, et al. (2025) The flexibility of SABRE, a new quantitative receptor function model, when fitting challenging concentration-effect data. Frontiers in pharmacology, 16, 1591761.

Li J, et al. (2025) Effects of traditional Chinese medicine Zuo-Gui-Wan on gut microbiota in an osteoporotic mouse model. Journal of orthopaedic surgery and research, 20(1), 128.

Elsafy M, et al. (2025) Genome-wide association scan and candidate gene analysis for seed coat color in sesame (*Sesamum indicum* L.). Frontiers in plant science, 16, 1541656.

Park J, et al. (2025) Iron Fortification and Inulin Supplementation in Early Infancy: Evaluating the Impact on Gut Microbiome in a Piglet Model. Current developments in nutrition, 9(4), 104587.

Sharapov S, et al. (2025) A genome-wide association study in 10,000 individuals links plasma N-glycome to liver disease and anti-inflammatory proteins. Nature communications, 16(1), 5525.

Lin CP, et al. (2025) Spatiotemporal dynamics reveal high turnover and contrasting assembly processes in fungal communities across contiguous habitats of tropical forests. Environmental microbiome, 20(1), 23.

Chaudhuri E, et al. (2025) CPSF6 promotes HIV-1 preintegration complex function. Journal of virology, 99(5), e0049025.

McBride SJ, et al. (2025) Carbon-13 Hyperpolarization of ??-Ketocarboxylates with Parahydrogen in Reversible Exchange. *ChemMedChem*, 20(5), e202400378.

Buchwald P, et al. (2025) Quantification of signal amplification for receptors: the K_d/EC_{50} ratio of full agonists as a gain parameter. *Frontiers in pharmacology*, 16, 1541872.

Kireta D, et al. (2025) A Novel Approach for Pollen Identification and Quantification Using Hybrid Capture-Based DNA Metabarcoding. *Ecology and evolution*, 15(4), e71311.

Lartey I, et al. (2025) The Composition and Function of Bacterial Communities Associated with the Northern Root-Knot Nematode (*Meloidogyne hapla*) Populations Showing Parasitic Variability. *Microorganisms*, 13(3).

Kim K, et al. (2025) Impact of dietary supplementation of *Bacillus subtilis* on the metabolic profiles and microbial ecology of weanling pigs experimentally infected with a pathogenic *Escherichia coli*. *Journal of animal science and biotechnology*, 16(1), 167.

Rohlfes N, et al. (2025) The nuclear localization signal of CPSF6 governs post-nuclear import steps of HIV-1 infection. *PLoS pathogens*, 21(1), e1012354.

Talukder S, et al. (2025) Effect of conventional grain-fed and grass-fed feeding systems on fecal microbiota and shiga toxin-producing *Escherichia coli* in beef cattle. *BMC microbiology*, 25(1), 351.

Zhai Y, et al. (2025) ReAlign-P: a vertical iterative realignment method for protein multiple sequence alignment. *Bioinformatics (Oxford, England)*, 41(8).

Wolf B, et al. (2025) Rational engineering of allosteric protein switches by in silico prediction of domain insertion sites. *Nature methods*, 22(8), 1698.

Dirvin B, et al. (2025) Identification and targeting of regulators of SARS-CoV-2-host interactions in the airway epithelium. *Science advances*, 11(20), eadu2079.