

Resource Summary Report

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[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, data analysis software, software application, software resource

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: 20260801T190430+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 [RRID](#).

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.

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.

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.

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

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.

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).

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.

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

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.

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.