

Resource Summary Report

Generated by SPARC SAWG on Sep 13, 2026

VSEARCH

RRID:SCR_024494

Type: Tool

Proper Citation

VSEARCH (RRID:SCR_024494)

Resource Information

URL: <https://github.com/torognes/vsearch>

Proper Citation: VSEARCH (RRID:SCR_024494)

Description: Software versatile open source tool for metagenomics. Used for processing and preparing metagenomics, genomics and population genomics nucleotide sequence data.

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

Defining Citation: [PMID:27781170](https://pubmed.ncbi.nlm.nih.gov/27781170/)

Keywords: processing and preparing metagenomics, genomics and population genomics, nucleotide sequence data,

Availability: Free, Available for download, Freely available

Resource Name: VSEARCH

Resource ID: SCR_024494

Record Creation Time: 20231002T161336+0000

Record Last Update: 20260912T200048+0000

Ratings and Alerts

No rating or validation information has been found for VSEARCH.

No alerts have been found for VSEARCH.

Data and Source Information

Usage and Citation Metrics

We found 1553 mentions in open access literature.

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

Huang W, et al. (2026) Core gastric microbiota linked to pathogenesis and preserved across age-stratified cohorts. *Cell reports. Medicine*, 7(7), 102905.

Deng S, et al. (2026) Repurposing of the Macrolide Antibiotic Clarithromycin for the Prevention of Lung Cancer. *Molecular cancer therapeutics*, 25(2), 283.

New JS, et al. (2026) Human anti-glycan reactivity emerges from B cells utilizing private gene rearrangements that are affinity matured in germinal centers. *Immunity*, 59(3), 651.

Lobel L, et al. (2026) Dietary sulfur amino acids enhance anti-tumor immunity in colon cancer via an NKT cell-XCL1-cDC1 circuit. *Immunity*, 59(6), 1708.

Kong JY, et al. (2026) Cross-site oral and esophageal microbiome signatures define diagnostic patterns and reveal mechanistic drivers of ESCC. *iScience*, 29(8), 116667.

Brício DG, et al. (2026) Metagenomic and biogenic amine changes in cassava fermentation for tucupi production using *Pediococcus acidilactici* starter culture. *Journal of the science of food and agriculture*, 106(4), 2424.

Richardson RT, et al. (2026) Sensitive Environmental DNA Methods for Low-Risk Surveillance of At-Risk Bumble Bees. *Molecular ecology resources*, 26(1), e70073.

Rodríguez MM, et al. (2026) Assessment of water quality and microbial contamination in Santa Marta's major rivers using conventional methods and next-generation sequencing. *Environmental science and pollution research international*, 33(17), 8335.

Tharapan W, et al. (2026) Impact of Biofloc on Life Characteristics, Fecundity, and Innate Immunity of Fairy Shrimp (*Branchinella thailandensis*, Sanoamuang, Saengphan and Murugan, 2002). *Biology*, 15(8).

Motivans Švara E, et al. (2026) Method comparison of microscopy, metabarcoding, and multispectral imaging flow cytometry for identification and relative abundance analysis of insect-dispersed pollen. *Scientific reports*, 16(1).

Yagi N, et al. (2026) Species identification and genotyping of *Citrobacter* spp. using genes with high nucleotide diversity. *Microbiology spectrum*, 14(6), e0364625.

Marchesini G, et al. (2026) Unveiling Diet Preferences and Their Nutritional Drivers Through Metabarcoding: The Case of Alpine Marmot (*Marmota marmota* L.) in High Altitude Grazed Pastures. *Ecology and evolution*, 16(3), e73309.

Pieters J, et al. (2026) Hidden Partners in Diversity: Acidobacteriota and Their Distribution in the Cape Floristic Region. *MicrobiologyOpen*, 15(1), e70192.

Seo J, et al. (2026) Standardizing vaginal microbial profiling: evaluating swab materials, storage conditions, and host DNA depletion strategies. *BMC microbiology*, 26(1), 2.

Kato NN, et al. (2026) Microbial Chemical Diversity and Cytotoxic Potential From Brazilian Ferruginous Caves: A Pioneering Metabolomic Survey. *Chemistry & biodiversity*, 23(1), e02912.

Wang B, et al. (2026) Mineral substrates as evolutionary drivers of soil microbial diversity through the rare biosphere. *Applied and environmental microbiology*, 92(1), e0201125.

Li T, et al. (2026) Rearing systems shape the successional dynamics of the gut microbiota, resistome, and mobilome in Lueyang Black-boned chickens. *Poultry science*, 105(10), 107322.

De Corte D, et al. (2026) Nanopore sequencing dataset of marine rocky shoreline microbial communities from the UK's first marine citizen science week event. *Data in brief*, 67, 112966.

Aldasoro M, et al. (2026) Pest consumption by common bats in diverse landscapes. *PloS one*, 21(6), e0347853.

Ding Y, et al. (2026) Integrative Multi-Omics Reveals Microbiome and Genome Streamlining Underlie Ecological Divergence in Chinese and Xinjiang Cordyceps: A Preliminary Study. *International journal of molecular sciences*, 27(12).