

Resource Summary Report

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USEARCH

RRID:SCR_027438

Type: Tool

Proper Citation

USEARCH (RRID:SCR_027438)

Resource Information

URL: <http://www.drive5.com>

Proper Citation: USEARCH (RRID:SCR_027438)

Description: Software application that provides search and clustering functionality, typically used with amplicon sequence data. Used to assign sequences to clusters.

Synonyms: USEARCH12

Resource Type: software application, source code, software resource

Defining Citation: [PMID:20709691](#)

Keywords: assign sequences to clusters, search and clustering functionality, amplicon sequence data,

Availability: Free, Available for download, Freely available

Resource Name: USEARCH

Resource ID: SCR_027438

Alternate URLs: <https://github.com/rcedgar/usearch12>

License: GNU GPL-3.0

Record Creation Time: 20250917T060928+0000

Record Last Update: 20260806T054842+0000

Ratings and Alerts

No rating or validation information has been found for USEARCH.

No alerts have been found for USEARCH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2967 mentions in open access literature.

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

Chen Z, et al. (2026) Ryegrass improves carcass trait of meat geese effects of dietary ryegrass supplementation on growth performance, carcass traits, and gut microbiota in meat geese. *Poultry science*, 105(1), 106035.

Yu YH, et al. (2026) Transcriptome and microbiota analysis reveal differences in the cecum of weaning pigs in response to different dietary crude protein levels. *Animal bioscience*, 39(1), 250135.

Fay JC, et al. (2026) Distribution of yeast species and their resistance to copper and sulfite across arboreal and viticulture habitats. *FEMS yeast research*, 26.

Zhu J, et al. (2026) The potential immunological mechanisms of gut microbiota dysbiosis caused by antibiotics exacerbate the lethality of influenza viruses. *Gut microbes*, 18(1), 2609451.

Wang Z, et al. (2026) Rotation-driven changes in physicochemical properties modulate soil microbial diversity and community complexity in tobacco-woad soils. *Microbiology spectrum*, 14(1), e0301624.

Huang M, et al. (2026) The application of *Rhizobium subbaroonis* TY15 increased soybean growth and disease resistance by modifying rhizosphere microbial communities. *Microbiology spectrum*, 14(1), e0115525.

Pronozin AY, et al. (2026) Diversity of lncRNAs in the pan-transcriptome of maize inbred lines. *BMC genomics*, 27(1), 1.

Alvarenga L, et al. (2026) Impact of *Curcuma longa* L. extract supplementation on the gut microbiota of hemodialysis patients. *Jornal brasileiro de nefrologia*, 48(1), e20250032.

Wu W, et al. (2026) Protist diversity and community structure around the Xianbei Seamount in the South China Sea. *Microbiology spectrum*, 14(1), e0273425.

Zhao M, et al. (2026) *Prevotella copri* facilitates wound healing in mice through the sphingosine-CerS1-ceramide metabolic pathway. *Microbiology spectrum*, 14(1), e0158725.

Villegas-Rodríguez SB, et al. (2025) Influence of pH and temperature on the performance and microbial community during the production of medium-chain carboxylic acids using winery effluents as substrate. *Environmental science and pollution research international*,

32(28), 16617.

Zhang J, et al. (2025) Astragalus polysaccharide alleviates asthma by modulating gut microbiota and serum metabolomics. *Biomedical reports*, 22(1), 12.

Almási ÉDH, et al. (2025) *Klebsiella oxytoca* facilitates microbiome recovery via antibiotic degradation and restores colonization resistance in a diet-dependent manner. *Nature communications*, 16(1), 551.

Lin Z, et al. (2025) Comparison of diet and exercise on cardiometabolic factors in young adults with overweight/obesity: multiomics analysis and gut microbiota prediction, a randomized controlled trial. *MedComm*, 6(1), e70044.

Nichols RG, et al. (2025) Clade-specific long-read sequencing increases the accuracy and specificity of the *gyrB* phylogenetic marker gene. *mSystems*, 10(1), e0148024.

Spinck M, et al. (2025) Automated orthogonal tRNA generation. *Nature chemical biology*, 21(5), 657.

Marzouk NH, et al. (2025) Proinflammatory and GABA eating bacteria in Parkinson's disease gut microbiome from a meta-analysis prospective. *NPJ Parkinson's disease*, 11(1), 145.

Correa JS, et al. (2025) Conservative evolution of genetic and genomic features in *Caenorhabditis becei*, an experimentally tractable gonochoristic worm. *bioRxiv : the preprint server for biology*.

Dissanayake DC, et al. (2025) Multi-metal-resistant *Staphylococcus warneri* strain TWSL_1: revealing heavy metal-resistant genomic features by whole-genome sequencing and analysis. *Access microbiology*, 7(5).

Wang ??? Z, et al. (2025) Unveiling Neonatal Pneumonia Microbiome by High-throughput Sequencing and Droplet Culturomics. *Genomics, proteomics & bioinformatics*, 23(6).