

Resource Summary Report

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UCHIME

RRID:SCR_008057

Type: Tool

Proper Citation

UCHIME (RRID:SCR_008057)

Resource Information

URL: http://drive5.com/usearch/manual/uchime_algo.html

Proper Citation: UCHIME (RRID:SCR_008057)

Description: An algorithm for detecting chimeric sequences.

Abbreviations: UCHIME

Resource Type: software resource

Resource Name: UCHIME

Resource ID: SCR_008057

Alternate IDs: OMICS_01115

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260725T190645+0000

Ratings and Alerts

No rating or validation information has been found for UCHIME.

No alerts have been found for UCHIME.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1777 mentions in open access literature.

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

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.

Kim CW, et al. (2025) Gut dysbiosis from high-salt diet promotes glioma via propionate-mediated TGF- β activation. *The Journal of experimental medicine*, 222(8).

Ouyang P, et al. (2025) Butyrate Ameliorates Graves' Orbitopathy Through Regulating Orbital Fibroblast Phenotypes and Gut Microbiota. *Investigative ophthalmology & visual science*, 66(3), 5.

Yin H, et al. (2025) Response of Soil Bacteria to Short-Term Nitrogen Addition in Nutrient-Poor Areas. *Microorganisms*, 13(1).

Ji K, et al. (2025) Distribution patterns of fungal community diversity in the dominant tree species *Dacrydium pectinatum* and *Vatica mangachapoi* in tropical rainforests. *Microbiology spectrum*, 13(6), e0309224.

Moya Uribe IA, et al. (2025) Fecal microbiota transplants (FMT) of three distinct human communities to germ-free mice exacerbated inflammation and decreased lung function in their offspring. *mBio*, 16(5), e0376424.

Lei Y, et al. (2025) Comparative analysis of the human microbiome from four different regions of China and machine learning-based geographical inference. *mSphere*, 10(1), e0067224.

Yuan W, et al. (2025) Weather parameters and biotic factors synergistically shape the phyllosphere microbiome of pomelo (*Citrus maxima* (Burm.) Merr.) across annual cycle. *Frontiers in plant science*, 16, 1532188.

Li Y, et al. (2025) Characteristics and dynamic changes of gut microbiota in Mongolian horses and Guizhou horses. *Frontiers in microbiology*, 16, 1582821.

He K, et al. (2025) Diversity and Composition of Gut Microbiota in Different Developmental Stages of the Tibetan Toad (*Bufo tibetanus*). *Animals : an open access journal from MDPI*, 15(12).

Li WJ, et al. (2025) Overlapping and specific bacterial communities in the gut and reproductive system of *Bactrocera dorsalis* (Hendel) (Diptera: Tephritidae) adults. *Frontiers in microbiology*, 16, 1567154.

Chen M, et al. (2025) Diversity analysis of oral and gut microbiota in osteoporotic rats. *PloS one*, 20(6), e0320063.

Guo Y, et al. (2025) The intratumoral microbiota heterogeneity is related to the prognosis and tumorigenesis of cervical cancer. *Frontiers in cellular and infection microbiology*, 15, 1574511.

Li J, et al. (2025) Soil microorganism distributions depend on habitat partitioning of topography in a temperate mountain forest. *Microbiology spectrum*, 13(7), e0205624.

Gao Y, et al. (2025) Influence of highway construction of alpine grassland area in Gannan on soil properties and microbiota. *Scientific reports*, 15(1), 22964.

Liu Y, et al. (2025) Exploring the role of the vaginal microbiome in HPV infection dynamics: A prospective cohort study. *iScience*, 28(5), 112476.

Chen J, et al. (2025) Responses of soil fertility indicators and fungi community diversity to fertilization strategies in legume-grass mixtures. *Frontiers in plant science*, 16, 1579011.

Cui P, et al. (2025) Diversity, antibacterial and antioxidant activities of fungi associated with *Apis cerana*. *PeerJ*, 13, e19762.

Yu X, et al. (2025) Lower respiratory tract co-infection of *Streptococcus pneumoniae* and respiratory syncytial virus shapes microbial landscape and clinical outcomes in children. *Frontiers in cellular and infection microbiology*, 15, 1593053.

Han X, et al. (2025) IgA Dysfunction Induced by Early-Lifetime Low-Dose Antibiotics Exposure Aggravates Diet-Induced Metabolic Syndrome. *Antibiotics (Basel, Switzerland)*, 14(6).