

Resource Summary Report

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UNITE

RRID:SCR_006518

Type: Tool

Proper Citation

UNITE (RRID:SCR_006518)

Resource Information

URL: <http://unite.ut.ee/index.php>

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Description: A fungal rDNA internal transcribed spacer (ITS) sequence database (although additional genes and genetic markers are also welcome) to facilitate identification of environmental samples of fungal DNA. Additional important features include user annotation of INSD sequences to add metadata on, e.g., locality, habitat, soil, climate, and interacting taxa. The user can furthermore annotate INSD sequences with additional species identifications that will appear in the results of any analyses done. UNITE focuses on high-quality ITS sequences generated from fruiting bodies collected and identified by experts and deposited in public herbaria. In addition, it also holds all fungal ITS sequences in the International Nucleotide Sequence Databases (INSD: NCBI, EMBL, DDBJ). Both sets of sequences may be used in any analyses carried out. UNITE is accompanied by a project management system called PlutoF, where users can store field data, document the sequencing lab procedures, manage sequences, and make analyses. PlutoF intends to make it possible for taxonomists, ecologists, and biogeographers to use a common platform for data storage, handling, and analyses, with the intent of facilitating an integration of these disciplines. A user can have an unlimited number of projects but still make analyses across any project data available to him.

Abbreviations: UNITE

Synonyms: unite: A molecular database for the identification of fungi

Resource Type: analysis service resource, data analysis service, data or information resource, data repository, database, production service resource, service resource, storage service resource

Defining Citation: [PMID:20409185](#), [PMID:15869663](#)

Keywords: sequence, barcoding sequence, internal transcribed spacer sequence, rdna, gene, genetic marker, internal transcribed spacer, dna, FASEB list

Availability: Creative Commons Attribution-ShareAlike License, v3 Unported, The community can contribute to this resource

Resource Name: UNITE

Resource ID: SCR_006518

Alternate IDs: nlx_61947, r3d100011316

Alternate URLs: <https://doi.org/10.17616/R37635>

Old URLs: <http://unite.zbi.ee>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T132555+0000

Ratings and Alerts

No rating or validation information has been found for UNITE.

No alerts have been found for UNITE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2291 mentions in open access literature.

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

Hussain U, et al. (2026) Microbial communities in semi-mature oak trees are resilient to drought, nutrient limitation, and pathogen challenge. *Cell host & microbe*, 34(2), 344.

Fan Y, et al. (2026) Spatiotemporal Dynamics and Co-Occurrence Patterns of Marine Fungal Communities Along Nutrient Gradients in the Leizhou Peninsula, China. *Journal of fungi (Basel, Switzerland)*, 12(4).

Porter KLJ, et al. (2026) Pilliga Ghosts: The Novel Fungi of the Rivers, Creeks, Lakes, and Dams of the Narrabri Region, Australia. *Environmental microbiology reports*, 18(3), e70348.

Liu F, et al. (2026) Differential Enhancement of Cigar Tobacco Leaf Aroma by Single-Strain Inoculation with *Alcaligenes phenolicus* and *Bacillus subtilis*. *Journal of microbiology and biotechnology*, 36, e2601012.

Wang M, et al. (2026) Characteristics of the rhizosphere microbial communities of different mulberry varieties in saline soil. *Scientific reports*, 16(1).

Sui J, et al. (2026) Soil-Nutrient Depletion and Microbial Community Restructuring in Continuous Celery Cropping: Opposing Responses of Bacteria and Fungi. *Biology*, 15(10).

Mena CJ, et al. (2026) Gut Mycobiota Dysbiosis in People Living with HIV/AIDS: Insights from an Argentine Cohort with Severe Immunosuppression. *Journal of fungi (Basel, Switzerland)*, 12(5).

Laurent-Webb L, et al. (2026) Endophytic and ectomycorrhizal, an overlooked dual ecological niche? Insights from natural environments and *Russula* species. *The New phytologist*, 250(6), 3946.

Pinheiro LM, et al. (2026) Salt marsh zonation and substrate type modulation for plastisphere: an experimental assessment in the Lagoon Patos estuary in extreme south of Brazil. *Archives of microbiology*, 208(5).

Zhang J, et al. (2026) Terracing influences soil microbial assembly in citrus orchards: stochastic processes dominate community dynamics in a karst sloping land. *BMC microbiology*, 26(1).

Zhou X, et al. (2026) Multi-kingdom profiling reveals altered gut phage-bacteria-metabolite interactions in MASLD. *Nature communications*, 17(1).

Long L, et al. (2026) Unveiling microbial risks in Chinese household dust: a comprehensive analysis from absolute abundance to virulence unit. *Microbiome*, 14(1).

Pe??a-Valencia MF, et al. (2026) Lignocellulose-mediated selection of potential halophilic PET-degrading enzymes from mangrove soil. *Nature communications*, 17(1).

Arriagada V, et al. (2026) Functional Diversity and Community Composition of Soil Fungi Associated With Canopy Dieback in *Araucaria araucana* Forests of Contrasting Edaphic Conditions. *Environmental microbiology reports*, 18(3), e70361.

Benaud N, et al. (2026) Integrating novel culturing and culture-independent methods to unveil soil fungal dark matter, functional guilds and environmental drivers across Robinson Ridge, East Antarctica. *Mycology*, 17(2), 635.

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).

Liu Z, et al. (2026) Dynamic Changes and Correlations of Physicochemical Parameters, Flavor Compounds and Microbial Communities During Soy Sauce Koji Production. *Foods (Basel, Switzerland)*, 15(12).

Quah RJ, et al. (2026) Sporadic Appetites: Unearthing the Fungal Diets of Two Mycophagous Mammals Across an Australian Climate Gradient. *Ecology and evolution*, 16(6), e73839.

Wang Q, et al. (2026) Interaction and Flavor Metabolic Function of Microbiota During Fermentation of Pigskin Through Bioaugmentation with *Latilactobacillus sakei*. *Molecules (Basel, Switzerland)*, 31(11).

Ostrowska M, et al. (2026) Oral Mycobiome Alterations in Children with Phenylketonuria: Associations with Dietary Intake and Metabolic Context-A Pilot Study. *Nutrients*, 18(11).