

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, service resource, data or information resource, data repository, data analysis service, database, production 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: 20260729T044136+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 2010 mentions in open access literature.

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

Taheri S, et al. (2026) The role of flour type and feeding schedule on the sourdough microbiome. Microbiology spectrum, 14(1), e0238025.

Vu D, et al. (2026) Advancing Yeast Identification Using High-Throughput DNA Barcode Data From a Curated Culture Collection. Molecular ecology resources, 26(1), e70082.

Qi J, et al. (2026) Integrated genomic and metabolomic analysis reveals the biocontrol potential of endophytic *Bacillus velezensis* NS13 against *Fusarium* species in *Lonicera macranthoides*. BMC microbiology, 26(1), 5.

Han P, et al. (2026) Integrated multi-omics reveals microbial and metabolic mechanisms driving enhanced fermentation quality in cigar tobacco leaves with exogenous additives. Bioresources and bioprocessing, 13(1), 2.

Lankes HFN, et al. (2026) Moss-Accumulated eDNA Is a Promising Source for Terrestrial Biodiversity Surveys Across the Tree of Life and Biomes. Molecular ecology resources, 26(1), e70088.

Liu Q, et al. (2026) Biocontrol efficiency and mechanism of novel *Streptomyces luomodiensis* SCA4-21 against banana *Fusarium* wilt. *Microbiology spectrum*, 14(1), e0296824.

Liu S, et al. (2025) Genetic modification of the shikimate pathway to reduce lignin content in switchgrass (*Panicum virgatum* L.) significantly impacts plant microbiomes. *Microbiology spectrum*, 13(1), e0154624.

Contreras-Negrete G, et al. (2025) Agricultural Practices and Environmental Factors Drive Microbial Communities in the Mezcal-Producing *Agave angustifolia* Haw. *Microbial ecology*, 87(1), 181.

Jara-Servin A, et al. (2025) Microbial Communities in Agave Fermentations Vary by Local Biogeographic Regions. *Environmental microbiology reports*, 17(1), e70057.

Rasuk MC, et al. (2025) Insights into the lemon (*Citrus limon*) epiphytic microbiome: impact of the biocontrol yeast *Clavispora lusitaniae* 146. *BMC research notes*, 18(1), 11.

Emelianova K, et al. (2025) Ecological divergence of sibling allopolyploid marsh orchids is associated with species specific plasticity and distinct fungal communities. *The Plant journal : for cell and molecular biology*, 121(4), e70001.

Daskalopoulos V, et al. (2025) The Diversity of the Genus *Tuber* in Greece-A New Species to Science in the *Maculatum* Clade and Seven First National Records. *Journal of fungi (Basel, Switzerland)*, 11(5).

Bento JT, et al. (2025) Airborne Fungal Spore Diversity Assessment Using Culture-Dependent and Metabarcoding Approaches in Bat-Inhabited Natural and Anthropogenic Roosts in Portugal. *Journal of fungi (Basel, Switzerland)*, 11(5).

Zhang S, et al. (2025) Soil Fungal Diversity, Community Structure, and Network Stability in the Southwestern Tibetan Plateau. *Journal of fungi (Basel, Switzerland)*, 11(5).

Rousseau C, et al. (2025) A Practical Comparison of Short- and Long-Read Metabarcoding Sequencing: Challenges and Solutions for Plastid Read Removal and Microbial Community Exploration of Seaweed Samples. *Molecular ecology resources*, 25(7), e14129.

Zou H, et al. (2025) Community structure of habitat microorganisms and endophytes of narrow-ranged species *Corybas fanjingshanensis* at different ecological niche specificities. *BMC plant biology*, 25(1), 993.

Dai C, et al. (2025) Mechanism study on improving chloropicrin fumigation effect by covering fumigated soil with appropriate thickness film. *Frontiers in microbiology*, 16, 1631869.

Zhou F, et al. (2025) Regional-scale biogeographical patterns of soil- and root-associated microbial communities across nine planted Chinese fir forests. *mSphere*, 10(8), e0045025.

Zhang FQ, et al. (2025) Environmental drivers of fungal community structure: a comparative high-throughput sequencing study of two geothermally distinct hot springs in Hefei, China. *Frontiers in microbiology*, 16, 1477445.

Zhang W, et al. (2025) Microbial Metabolic Limitations and Their Relationships with Sediment Organic Carbon Across Lake Salinity Gradient in Tibetan Plateau. *Microorganisms*, 13(3).