

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: service resource, data repository, data analysis service, data or information resource, database, storage service resource, analysis service resource, production 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: 20260731T042725+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 [kravitz2](#) .

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.

Chou M-Y, et al. (2025) Fungicide use intensity influences the soil microbiome and links to fungal disease suppressiveness in amenity turfgrass. *Applied and environmental microbiology*, 91(3), e0177124.

Adouane E, et al. (2025) Multi-omics analysis of the correlation between surface microbiome and metabolome in *Saccharina latissima* (Laminariales, Phaeophyceae). *FEMS microbiology ecology*, 101(3).

Zhao H, et al. (2025) Effects and health risk assessments of different spray disinfectants on microbial aerosols in chicken houses. *Poultry science*, 104(5), 105083.

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).

Hou Z, et al. (2025) Differentiated response mechanisms of soil microbial communities to nitrogen deposition driven by tree species variations in subtropical planted forests. *Frontiers in microbiology*, 16, 1534028.

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.

Jia Y, et al. (2025) Effects of different fermentation temperatures on microbiomes of cigar tobacco leaves. *Frontiers in bioengineering and biotechnology*, 13, 1550383.

Cui P, et al. (2025) Fungal community composition and function in different Chinese post-fermented teas. *Scientific reports*, 15(1), 8514.

Jones AL, et al. (2025) Foliar Fungal Endophyte Communities of Scottish Plantation Pines. *Journal of fungi* (Basel, Switzerland), 11(2).

Shen Y, et al. (2025) Microbial proliferation deteriorates the corrosion inhibition capability, lubricity, and stability of cutting fluid. *Frontiers in microbiology*, 16, 1522265.

Schreiner VC, et al. (2025) Timing Matters: Viticultural Land Use Determines Responses in Structure and Function of Fungal Stream Communities Across One Growing Season. *Global change biology*, 31(2), e70085.

Kampouris ID, et al. (2025) Selective recruitment of beneficial microbes in the rhizosphere of maize affected by microbial inoculants, farming practice, and seasonal variations. *Environmental microbiome*, 20(1), 69.

Bogati KA, et al. (2025) Unraveling the Effect of Soil Moisture on Microbial Diversity and Enzymatic Activity in Agricultural Soils. *Microorganisms*, 13(6).

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