

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 [Kravitz](#) .

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.

Aliyat FZ, et al. (2026) Argan fruit microbiomes: influence of biogeographic and soil driven environmental factors. *BMC plant biology*, 26(1), 314.

L??pez-Garc??a CM, et al. (2026) The microbiota of avocado floral nectar inhibits pathogens and improves plant fitness. *Journal of experimental botany*, 77(8), 2549.

Lu Y, et al. (2026) Landscape effects on global soil pathogenic fungal diversity across spatial scales. *Nature communications*, 17(1), 1164.

Magosch S, et al. (2026) Microbial allies against drought stress: an optimized screening method to improve seedling survival for forest restorations. *Environmental microbiome*, 21(1).

Montes-Carretero LM, et al. (2026) Comparative fecal microbiome analysis of the endangered Volcano rabbit (*Romerolagus diazi*) reveals a microbial core in contrasting

habitats of Central Mexico. *PloS one*, 21(3), e0343260.

Lee YI, et al. (2026) Mycorrhizal specificity of fully mycoheterotrophic *Yuania* in Taiwan and China and novel natural abundance stable isotope patterns. *Plant biology (Stuttgart, Germany)*, 28(4), 1159.

Martins GL, et al. (2026) Connectivity and Age of Restored Atlantic Forest Fragments Drives Composition and Functionality of the Fungal Community in the Leaf Litter Layer. *Molecular ecology*, 35(6), e70325.

Wang X, et al. (2026) Multi-omics integration unveils fungal succession and volatile metabolite dynamics in spontaneous fermentation of Beibinghong icewine: Identifying yeast strains critical for flavor development. *Food chemistry: X*, 33, 103442.

Yu Z, et al. (2026) Responses of Restored Vegetation Communities, Soil Properties, and Microbial Composition to Different Fertilization Treatments in an Alpine Mining Area. *Plants (Basel, Switzerland)*, 15(4).

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).

Ivester K, et al. (2026) Genomic Epidemiology of Fungi Identified in Bronchoalveolar Lavage Fluid from Asthmatic Horses in the US. *Animals : an open access journal from MDPI*, 16(4).

Eskildsen J, et al. (2026) Novel CRISPR/Cas9-Derived *mlo* Alleles in Barley: Resistance to Powdery Mildew and Microbiome Implications. *International journal of molecular sciences*, 27(4).

Steindorff AS, et al. (2026) Phenogenomics reveals the ecology and evolution of *Trichoderma* fungi for sustainable agriculture. *Nature microbiology*, 11(3), 815.

Li X, et al. (2026) Surfactin-Producing *Bacillus velezensis* A1 Inhibits Lactic Acid Bacteria in Jiang-Flavor Baijiu Fermentation. *Foods (Basel, Switzerland)*, 15(7).

Li W, et al. (2026) Tissue-specific assembly of endophytic microbiota in *Agriophyllum squarrosum* (L.) Moq. *BMC microbiology*, 26(1).

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.

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).

Cheng Q, et al. (2026) Gut proteome and microbiome alterations: Analysis of transverse colon samples from pathologically confirmed Alzheimer's disease patients. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(1), e71021.