

Resource Summary Report

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SOAPBarcode

RRID:SCR_015776

Type: Tool

Proper Citation

SOAPBarcode (RRID:SCR_015776)

Resource Information

URL: <https://sourceforge.net/projects/metabarcoding/>

Proper Citation: SOAPBarcode (RRID:SCR_015776)

Description: Software for metabarcoding of DNA. SOAPBarcode takes advantage of high throughput capacity of next-generation-sequencing (NGS) platforms and can characterize the biodiversity of large volumes of eukaryote samples.

Synonyms: metabarcoding

Resource Type: sequencing analysis software

Keywords: metabarcoding, metabarcode, bgi, soap, ngs, next generation sequencing, eukaryote

Funding: National High-tech Research and Development Project (863) of China 2012AA021601;
Yunnan Province 20080A001;
Chinese Academy of Sciences 0902281081;
Chinese Academy of Sciences KSCX2-YW-Z-1027;
National Natural Science Foundation of China 31170498;
Ministry of Science and Technology of China 2012FY110800;
University of East Anglia

Availability: Free, Available for download

Resource Name: SOAPBarcode

Resource ID: SCR_015776

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T190520+0000

Ratings and Alerts

No rating or validation information has been found for SOAPBarcode.

No alerts have been found for SOAPBarcode.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 193 mentions in open access literature.

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

Wu W, et al. (2026) Protist diversity and community structure around the Xianbei Seamount in the South China Sea. *Microbiology spectrum*, 14(1), e0273425.

Blanco-Bercial L, et al. (2026) MetaZooGene Intercalibration Experiment (MZG-ICE): Metabarcoding Marine Zooplankton Diversity of the Global Ocean. *Molecular ecology resources*, 26(1), e70090.

Lemonnier C, et al. (2026) Comparison of Metabarcoding and Shotgun Sequencing Confirms the Relevance of Chloroplastic rRNA Genes to Assess Community Structure of Lake Phytoplankton. *Molecular ecology resources*, 26(1), e70077.

Saccaram C, et al. (2025) Elucidating the interplay between metabolites and microorganisms in the spermosphere of common bean (*Phaseolus vulgaris* L.) seeds. *mSystems*, 10(8), e0070725.

Crevecoeur S, et al. (2025) Spatio-Temporal Resolution of Microbial Functions and Taxa Associated With Cyanobacterial Harmful Algae Blooms Along a 500-Km Aquatic Continuum in the Lake Erie Watershed. *Environmental microbiology*, 27(10), e70183.

Dodd S, et al. (2025) Tracing the botanical origins of UK heather honey by relative quantification of plant DNA. *NPJ science of food*, 9(1), 196.

Yeo IC, et al. (2025) Vertical Structure and Functional Diversity of Microbial Communities in the Ross Sea, Antarctica. *Microbial ecology*, 88(1), 99.

Holman LE, et al. (2025) Navigating Past Oceans: Comparing Metabarcoding and Metagenomics of Marine Ancient Sediment Environmental DNA. *Molecular ecology resources*, 25(6), e14086.

Kim SY, et al. (2025) Integrating DNA metabarcoding and morphological analysis improves marine zooplankton biodiversity assessment. *Scientific reports*, 15(1), 7283.

Gygax D, et al. (2025) Evaluation of nanopore sequencing for increasing accessibility of eDNA studies in biodiverse countries. *PloS one*, 20(10), e0333994.

Camilla P, et al. (2025) *Shewanella oneidensis* and *Methanosarcina barkerii* augmentation and conductive material effects on long-term anaerobic digestion performance. *Biotechnology for biofuels and bioproducts*, 18(1), 10.

Pierella Karlusich JJ, et al. (2025) Patterns and drivers of diatom diversity and abundance in the global ocean. *Nature communications*, 16(1), 3452.

Ezzat L, et al. (2025) Diversity and biogeography of the bacterial microbiome in glacier-fed streams. *Nature*, 637(8046), 622.

Casas-Monroy O, et al. (2025) Effectiveness of ballast water management systems in the Great Lakes based on a paired uptake-discharge sample design. *Environmental monitoring and assessment*, 197(6), 618.

Tan SH, et al. (2025) Using eDNA tools to examine the impact of kelp farming on underlying sediments. *PloS one*, 20(9), e0331416.

Oliveira J, et al. (2025) Genetic and Metabolic Diversity of Cyanobacteria on the Rock-Water Interface in Mountainous Ecosystems. *Environmental science & technology*, 59(38), 20595.

Van Nynatten A, et al. (2025) Marine Heatwaves Transform Coral Symbioses With Enduring Effects. *Ecology letters*, 28(11), e70263.

Mack JM, et al. (2025) From Mud to Meat: Comparative Metabarcoding Reveals Two Different Evolutionary Paths to Carnivory in a Group of Meiofaunal Annelids. *Molecular ecology*, 34(22), e70151.

Masaki HI, et al. (2025) Biodiversity and Biological Interactions of Actinobacteria Associated with Deep Sea and Intertidal Marine Invertebrates. *Marine drugs*, 23(10).

Richards-Perhatch V M, et al. (2025) Forage preference in two geographically co-occurring fungus gardening ants: A dietary DNA approach. *PloS one*, 20(12), e0336150.