

Resource Summary Report

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BOLD

RRID:SCR_004278

Type: Tool

Proper Citation

BOLD (RRID:SCR_004278)

Resource Information

URL: <http://www.barcodinglife.com/>

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Description: DNA barcode data with an online workbench that supports data validation, annotation, and publication for specimen, distributional, and molecular data. The data platform consists of three main modules, a data portal, a database of barcode clusters, and data collection workbench. The Public Data Portal provides access to all public barcode data which consists of data generated using the Workbench module as well as data mined from other sources. The Barcode Index Number (BIN) system assigns a unique identifier to each sequence cluster of COI, providing an interim taxonomic system for species in the animal kingdom. The workbench module integrates secure databases with analytical tools to provide a private collaborative environment for researchers to collect, analyze, and publish barcode data and ancillary DNA sequences. This platform also provides an annotation framework that supports tagging and commenting on records and their components (i.e. taxonomy, images, and sequences), allowing for community-based validation of barcode data. By providing specialized services, it aids in the assembly of records that meet the standards needed to gain BARCODE designation in the global sequence databases. Because of its web-based delivery and flexible data security model, it is also well positioned to support projects that involve broad research alliances. Public data records include record identifiers, taxonomy, specimen details, collection information and sequence data. Data that has been publicly released through BOLD can be retrieved manually through the BOLD public interface or automatically through BOLD web services. BOLD analytical tools are available for any data set that exists in BOLD (including publicly available data). Analytical tools can be accessed through the BOLD Project Console under the headings Sequences Analysis or Specimen Aggregates. Some examples include Taxon ID Tree, Alignment Viewer, Distribution Maps, and Image Library.

Abbreviations: BOLD

Synonyms: BOLD Systems, Barcode of Life Database Systems, Barcode of Life Database, Barcode of Life Data Systems, BOLD : The Barcode of Life Data System

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

Defining Citation: [PMID:18784790](#)

Keywords: protists, taxonomy, dna, barcode, dna barcode, gene sequence, primer, publication, barcode index number, unique identifier, annotation, platform, data management, data sharing, dna sequence, bioinformatics, molecular biology, biology, geography, species, sequence cluster, map, web service, image collection, FASEB list

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Availability: Free, Public

Resource Name: BOLD

Resource ID: SCR_004278

Alternate IDs: DOI:10.17616/R3PP7J, nlx_29236, DOI:10.25504/FAIRsharing.en9nnp, DOI:10.5883, r3d100010129

Alternate URLs: <http://www.boldsystems.org/>, <https://doi.org/10.17616/R3PP7J>, <https://doi.org/10.17616/r3pp7j>, <https://doi.org/10.5883/>, <https://dx.doi.org/10.5883/>, <https://fairsharing.org/10.25504/FAIRsharing.en9nnp>, <https://doi.org/10.17616/R3KG65>

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260812T044058+0000

Ratings and Alerts

No rating or validation information has been found for BOLD.

No alerts have been found for BOLD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 499 mentions in open access literature.

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

Decker O, et al. (2026) Distance-decay reveals contrasting effects of land-use types on arthropod community homogenisation. *Nature communications*, 17(1), 763.

Rubio-Palis Y, et al. (2026) Anopheles species complexes from Guyana and Venezuela malaria endemic areas using COI sequences. *Malaria journal*, 25(1), 95.

Wang JX, et al. (2026) Re-Examination: No True *Tabidia* Snellen, 1880 (Lepidoptera: Crambidae) in China, with Descriptions of Two New Genera and Three New Species. *Insects*, 17(2).

Al Shaye NA, et al. (2026) Chemical and Molecular Insights into the Arid Wild Plant Diversity of Saudi Arabia. *Plants (Basel, Switzerland)*, 15(2).

Qin M, et al. (2026) Characterization and evolutionary insights into complete mitochondrial genome of *Sedum sarmentosum* within the family Crassulaceae. *Frontiers in plant science*, 17, 1710625.

Horton T, et al. (2026) A new superfamily and family of the infraorder Hadziida (Amphipoda, Senticaudata) based on a new genus and species from the Clarion-Clipperton Zone, Pacific Ocean. *ZooKeys*, 1274, 271.

Jaśdewska AM, et al. (2026) New deep-sea Amphipoda from the Clarion-Clipperton Zone: 24 new species described under the Sustainable Seabed Knowledge Initiative: One Thousand Reasons campaign. *ZooKeys*, 1274, 1.

Tandberg AHS, et al. (2026) Stilipedidae Holmes, 1908 (Crustacea, Amphipoda) of the Clarion-Clipperton Zone. *ZooKeys*, 1274, 17.

Miller J, et al. (2026) Description of a new Andean species of widow spider (Araneae, Theridiidae, *Latrodectus*). *ZooKeys*, 1281, 49.

Ontaneda-Gallegos R, et al. (2026) Carpenter bees (Apidae: Xylocopa) of Ecuador: distribution, DNA barcodes and plant interactions. *PeerJ*, 14, e21345.

Smith S, et al. (2026) Global COI meta-analysis reveals ocean-basin genetic structure in *Sphyrna lewini*. *PloS one*, 21(3), e0344911.

Cao H, et al. (2026) Geographical diet variations and microbial diversity: insights into François' langur's adaptive strategies. *mSphere*, 11(3), e0059425.

Ivanova NV, et al. (2026) Rapid assessment of phytoplankton assemblages using Next Generation Sequencing and Barcode of Life Data System: a widely applicable HAB-ID toolkit for detecting and monitoring biodiversity loss and harmful algal blooms. *PeerJ*, 14, e20747.

Torres-Cambas Y, et al. (2026) The Danube Fish Database: documenting species distributions across a major European river basin. *Scientific data*, 13(1).

Wu L, et al. (2026) Comparative Analysis of Lepidopteran Community Structure Using DNA Metabarcoding: Warm-Temperate Forest Versus Grass-Shrub Ecotones in Pangquangou National Nature Reserve. *Ecology and evolution*, 16(6), e73738.

Boza BR, et al. (2026) Evaluation of the occurrence of multiple paternity in *Squalus acanthias* in the South Atlantic region using nuclear markers. *Genetics and molecular biology*, 49(2), e20260013.

Mintara R, et al. (2026) Diversity and Host Blood Meal Analysis of *Culicoides* (Diptera: Ceratopogonidae) from Laos. *Insects*, 17(6).

Savran MJ, et al. (2026) Evaluation of the safety and insecticidal efficacy of ivermectin-treated bird feed formulations in different avian species. *Parasites & vectors*, 19(1).

González-Toral C, et al. (2026) Extending Specimens to Save Plant DNA: Structuring Department DNA Collections in Times of Biodiversity Loss. *Ecology and evolution*, 16(4), e73211.

Tagliabue A, et al. (2026) Comparative Multi-Marker Environmental DNA Metabarcoding of Marine Metazoan Communities: Water vs. Sediment. *Molecular ecology resources*, 26(3), e70126.