

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, data repository, data analysis service, storage service resource, data or information resource, database, production service resource, analysis service resource

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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Genome Canada ;
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NSERC ;
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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: 20260731T042702+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 298 mentions in open access literature.

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

- Lopez Y, et al. (2025) Insights into the transmission cycle of cutaneous leishmaniasis from an endemic community in rural Guatemala. *Current research in parasitology & vector-borne diseases*, 7, 100244.
- Uquillas A, et al. (2025) Climate drives the long-term ant male production in a tropical community. *Scientific reports*, 15(1), 428.
- Bignotto TS, et al. (2025) Integrative morphometric and molecular analyses reveal possible genetic contamination of silver catfish populations of the genus *Rhamdia* in Neotropical River basins. *Journal of fish biology*, 107(2), 535.
- Perez-Mon C, et al. (2025) Hide and seek with falsified medicines: Current challenges and physico-chemical and biological approaches for tracing the origin of trafficked products. *Forensic science international*, 370, 112474.
- Ramanan A, et al. (2025) In Troubled Waters: Applying DNA Barcoding to Monitor Singapore's Shark Fin Trade. *Ecology and evolution*, 15(6), e71607.
- Festa F, et al. (2025) A multi-disciplinary approach to identify spillover interfaces of bat coronaviruses to pig farms in Italy. *PloS one*, 20(10), e0332117.
- Le Roy C, et al. (2025) Adaptations in wing morphology rather than wingbeat kinematics enable flight in small hoverfly species. *eLife*, 13.
- Hebert PDN, et al. (2025) Barcode 100K Specimens: In a Single Nanopore Run. *Molecular ecology resources*, 25(1), e14028.
- Villa S, et al. (2025) Elevational shifts in reproductive ecology indicate the climate response of a model chasmophyte, Rainer's bellflower (*Campanula raineri*). *Annals of botany*, 135(1-2), 181.
- Orkun Ö, et al. (2025) Population genetic structure and demographic history of *Dermacentor marginatus* Sulzer, 1776 in Anatolia. *Scientific reports*, 15(1), 12570.
- Hu X, et al. (2025) Genome assembly of Hawaiian flower thrips *Thrips hawaiiensis* (Thysanoptera: Thripidae). *Scientific data*, 12(1), 225.
- Jiménez-Segura LF, et al. (2025) Fish databases for improving their conservation in Colombia. *Scientific data*, 12(1), 262.
- Marín A, et al. (2025) Development and validation of versatile species-specific primer assays for eDNA monitoring and authentication of 10 commercially important Peruvian marine species. *PloS one*, 20(7), e0313181.
- Christodoulou M, et al. (2025) A taxonomically reliable DNA barcode reference library for North Sea macrobenthos. *Scientific data*, 12(1), 1198.
- Moulin N, et al. (2025) MANGF: a reference library of DNA barcodes for Mantodea from French Guiana (Insecta, Dictyoptera). *Biodiversity data journal*, 13, e149486.
- Del Sambro L, et al. (2025) A retail market survey on fish fraud from Southern Italy using DNA barcoding. *Italian journal of food safety*, 14(4).

Prudente ALC, et al. (2025) Unraveling the herpetofauna diversity in canga and forest ecosystems of the Eastern Amazon. PloS one, 20(11), e0332753.

Kilian IC, et al. (2025) Maximizing Identification Precision of Hymenoptera and Brachycera (Diptera) With a Non-Destructive DNA Metabarcoding Approach. Ecology and evolution, 15(1), e70770.

Dong LN, et al. (2025) Identification of herbal medicine species of *Lysimachia* L. (Primulaceae) in Southern China using genome skimming. BMC plant biology, 25(1), 953.

Kim S, et al. (2025) ?Three new species and a new record of the genus *Lipolexis* (Hymenoptera, Braconidae, Aphidiinae) from South Korea. ZooKeys, 1245, 323.