

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## [Identifiers.org](#)

RRID:SCR\_003735

Type: Tool

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### Proper Citation

Identifiers.org (RRID:SCR\_003735)

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### Resource Information

**URL:** <http://identifiers.org/>

**Proper Citation:** Identifiers.org (RRID:SCR\_003735)

**Description:** A system providing resolvable persistent Uniform Resource Identifiers (URIs) used to identify data for the scientific community, with a current focus on the Life Sciences domain. The provision of resolvable identifiers (URLs) fits well with the Semantic Web vision, and the Linked Data initiative. It provides direct access to the identified data using one chosen physical location (or resource). If more than one physical locations providing the data are recorded in the Registry, then you can access them via the top banner or by using a profile.

**Abbreviations:** Identifiers.org

**Resource Type:** identifier resolution, service resource, production service resource

**Keywords:** identifier, life sciences, bio.tools

**Availability:** Free

**Resource Name:** Identifiers.org

**Resource ID:** SCR\_003735

**Alternate IDs:** nlx\_157931, biotools:identifiers.org

**Alternate URLs:** <https://bio.tools/identifiers.org>

**Record Creation Time:** 20220129T080220+0000

**Record Last Update:** 20260801T190916+0000

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### Ratings and Alerts

No rating or validation information has been found for Identifiers.org.

No alerts have been found for Identifiers.org.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Gao Y, et al. (2024) BioBricks.ai: A Versioned Data Registry for Life Sciences Data Assets. ArXiv.

Leonidou N, et al. (2024) Exploring the metabolic profile of *A. baumannii* for antimicrobial development using genome-scale modeling. PLoS pathogens, 20(9), e1012528.

Ross KE, et al. (2024) Perspectives on tracking data reuse across biodata resources. Bioinformatics advances, 4(1), vbae057.

Saldivar A, et al. (2024) Genome-scale flux balance analysis reveals redox trade-offs in the metabolism of the thermoacidophile *Methylophilum thermophilum* under auto-, hetero- and methanotrophic conditions. Frontiers in systems biology, 4, 1291612.

Bleker C, et al. (2024) Stress Knowledge Map: A knowledge graph resource for systems biology analysis of plant stress responses. Plant communications, 5(6), 100920.

D'Anna F, et al. (2024) A research data management (RDM) community for ELIXIR. F1000Research, 13.

Wright A, et al. (2023) DATA RESOURCES AND ANALYSES FAIR Header Reference genome: A TRUSTworthy standard. bioRxiv : the preprint server for biology.

Arakawa K, et al. (2023) Development of an integrated and inferenceable RDF database of glycan, pathogen and disease resources. Scientific data, 10(1), 582.

Zeng Z, et al. (2023) MantaID: a machine learning-based tool to automate the identification of biological database IDs. Database : the journal of biological databases and curation, 2023.

Ferrence GM, et al. (2023) CSD Communications of the Cambridge Structural Database. IUCrJ, 10(Pt 1), 6.

Menke J, et al. (2022) Establishing Institutional Scores With the Rigor and Transparency Index: Large-scale Analysis of Scientific Reporting Quality. Journal of medical Internet research, 24(6), e37324.

Cernava T, et al. (2022) Metadata harmonization-Standards are the key for a better usage of omics data for integrative microbiome analysis. *Environmental microbiome*, 17(1), 33.

Devaraju A, et al. (2021) An automated solution for measuring the progress toward FAIR research data. *Patterns (New York, N.Y.)*, 2(11), 100370.

Hanspers K, et al. (2021) Ten simple rules for creating reusable pathway models for computational analysis and visualization. *PLoS computational biology*, 17(8), e1009226.

Langenstein M, et al. (2021) A decoupled, modular and scriptable architecture for tools to curate data platforms. *Bioinformatics (Oxford, England)*, 37(20), 3693.

Yates B, et al. (2021) Updates to HCOP: the HGNC comparison of orthology predictions tool. *Briefings in bioinformatics*, 22(6).

Renz A, et al. (2021) First Genome-Scale Metabolic Model of *Dolosigranulum pigrum* Confirms Multiple Auxotrophies. *Metabolites*, 11(4).

Bernal-Llinares M, et al. (2021) Identifiers.org: Compact Identifier services in the cloud. *Bioinformatics (Oxford, England)*, 37(12), 1781.

Rando HM, et al. (2021) An Open-Publishing Response to the COVID-19 Infodemic. *ArXiv*.

Waagmeester A, et al. (2020) Wikidata as a knowledge graph for the life sciences. *eLife*, 9.