

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 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, production service resource, 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:** 20260912T200129+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 59 mentions in open access literature.

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

Dalantai M, et al. (2026) Draft genome sequence of the plastic-degrading fungus *Fusicolla acetilerea* strain NIBRFGC000505922. *BMC genomic data*, 27(1).

Heydarabadipour A, et al. (2026) Antimony 3: Extending human-readable model definitions for SBML Level 3 Core and Packages. *bioRxiv : the preprint server for biology*.

Mostolizadeh R, et al. (2026) MCC: automated mass and charge curation at the genome scale applied to *C. tuberculostearicum*. *Microbiology spectrum*, 14(2), e0320024.

Neumann S, et al. (2026) MassBank: an open and FAIR mass spectral data resource. *Nucleic acids research*, 54(D1), D601.

Li LX, et al. (2026) TabularQual: A spreadsheet-based format for annotating and curating logical models in SBML-qual. *bioRxiv : the preprint server for biology*.

Babb L, et al. (2025) Improving the FAIRness and Sustainability of the NHGRI Resources Ecosystem. *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.

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

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

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.

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 fumariolicum* under auto-, hetero- and methanotrophic conditions. *Frontiers in systems biology*, 4, 1291612.

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

Bauerle F, et al. (2023) Genome-scale metabolic models consistently predict in vitro characteristics of *Corynebacterium striatum*. *Frontiers in bioinformatics*, 3, 1214074.

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

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

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.

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.

D'Ambrosio V, et al. (2022) A FAIR-compliant parts catalogue for genome engineering and expression control in *Saccharomyces cerevisiae*. *Synthetic and systems biotechnology*, 7(2), 657.