

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

EnvO

RRID:SCR_000182

Type: Tool

Proper Citation

EnvO (RRID:SCR_000182)

Resource Information

URL: <http://environmentontology.org/>

Proper Citation: EnvO (RRID:SCR_000182)

Description: Community ontology for the concise, controlled description of environmental features and habitats. It provides a structured vocabulary that is designed to support the annotation of any organism or biological sample with environment descriptors. EnvO contains terms for biomes, environmental features, and environmental material.

Abbreviations: EnvO

Synonyms: Environment Ontology

Resource Type: controlled vocabulary, data or information resource, ontology

Keywords: biome, environmental feature, environmental material, environment, habitat

Availability: The community can contribute to this resource

Resource Name: EnvO

Resource ID: SCR_000182

Alternate IDs: nlx_153832

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260912T195504+0000

Ratings and Alerts

No rating or validation information has been found for EnvO.

No alerts have been found for EnvO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Klemetsen T, et al. (2018) The MAR databases: development and implementation of databases specific for marine metagenomics. Nucleic acids research, 46(D1), D692.

Gibson R, et al. (2016) Biocuration of functional annotation at the European nucleotide archive. Nucleic acids research, 44(D1), D58.

Pafilis E, et al. (2016) EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. Database : the journal of biological databases and curation, 2016.

Sinclair L, et al. (2016) Seqenv: linking sequences to environments through text mining. PeerJ, 4, e2690.

Buttigieg PL, et al. (2016) The environment ontology in 2016: bridging domains with increased scope, semantic density, and interoperation. Journal of biomedical semantics, 7(1), 57.

La Salle J, et al. (2016) Biodiversity analysis in the digital era. Philosophical transactions of the Royal Society of London. Series B, Biological sciences, 371(1702).

Costello MJ, et al. (2015) Biological and ecological traits of marine species. PeerJ, 3, e1201.

Appels R, et al. (2015) Discoveries and advances in plant and animal genomics. Functional & integrative genomics, 15(2), 121.

Thessen AE, et al. (2015) Emerging semantics to link phenotype and environment. PeerJ, 3, e1470.

Pesant S, et al. (2015) Open science resources for the discovery and analysis of Tara Oceans data. Scientific data, 2, 150023.

Faust K, et al. (2015) Cross-biome comparison of microbial association networks. Frontiers in microbiology, 6, 1200.

Couto JM, et al. (2015) Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O₂-Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment. Current microbiology, 71(2), 296.

Thessen AE, et al. (2014) Knowledge extraction and semantic annotation of text from the encyclopedia of life. PloS one, 9(3), e89550.

Walls RL, et al. (2014) Semantics in support of biodiversity knowledge discovery: an introduction to the biological collections ontology and related ontologies. PLoS one, 9(3), e89606.

Schmidt TS, et al. (2014) Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. PLoS computational biology, 10(4), e1003594.

Buttigieg PL, et al. (2013) The environment ontology: contextualising biological and biomedical entities. Journal of biomedical semantics, 4(1), 43.

Fernández-Guerra A, et al. (2012) Habitat-associated phylogenetic community patterns of microbial ammonia oxidizers. PLoS one, 7(10), e47330.

Ferry-Dumazet H, et al. (2011) MeRy-B: a web knowledgebase for the storage, visualization, analysis and annotation of plant NMR metabolomic profiles. BMC plant biology, 11, 104.

Thessen AE, et al. (2011) Data issues in the life sciences. ZooKeys(150), 15.

Jensen LJ, et al. (2010) Ontologies in quantitative biology: a basis for comparison, integration, and discovery. PLoS biology, 8(5), e1000374.