

Resource Summary Report

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EDAM Ontology

RRID:SCR_006620

Type: Tool

Proper Citation

EDAM Ontology (RRID:SCR_006620)

Resource Information

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

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Description: An ontology of bioinformatics operations (tool, application, or workflow functions), types of data including identifiers, topics (application domains), and data formats. The applications of EDAM are within organizing tools and data, finding suitable tools in catalogues, and integrating them into complex applications or workflows. Semantic annotations with EDAM are applicable to diverse entities such as for example Web services, databases, programmatic libraries, standalone tools and toolkits, interactive applications, data schemas, data sets, or publications within bioinformatics. Annotation with EDAM may also contribute to data provenance, and EDAM terms and synonyms can be used in text mining. EDAM - and in particular the EDAM Data sub-ontology - serves also as a markup vocabulary for bioinformatics data on the Semantic Web.

Abbreviations: EDAM

Synonyms: EMBRACE Data and Methods Ontology, EDAM Ontology - Bioinformatics operations types of data topics and data formats, EMBRACE Data And Methods

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

Keywords: bioinformatics, operation, data, topic, type, identifier, format, semantic annotation, obo format, owl

Availability: Acknowledgement required, Permission required

Resource Name: EDAM Ontology

Resource ID: SCR_006620

Alternate IDs: nlx_151281

Alternate URLs: <http://purl.bioontology.org/ontology/EDAM>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260804T043306+0000

Ratings and Alerts

No rating or validation information has been found for EDAM Ontology.

No alerts have been found for EDAM Ontology.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Gustafsson OJR, et al. (2025) WorkflowHub: a registry for computational workflows. Scientific data, 12(1), 837.

Mortensen HM, et al. (2024) Translating nanoEHS data using EPA NaKnowBase and the resource description framework. F1000Research, 13, 169.

Suetake H, et al. (2022) A workflow reproducibility scale for automatic validation of biological interpretation results. GigaScience, 12.

Gundersen S, et al. (2021) Recommendations for the FAIRification of genomic track metadata. F1000Research, 10.

Kasalica V, et al. (2021) APE in the Wild: Automated Exploration of Proteomics Workflows in the bio.tools Registry. Journal of proteome research, 20(4), 2157.

Rambold G, et al. (2019) Meta-omics data and collection objects (MOD-CO): a conceptual schema and data model for processing sample data in meta-omics research. Database : the journal of biological databases and curation, 2019.

Gnimpieba EZ, et al. (2017) Bio-TDS: bioscience query tool discovery system. Nucleic acids research, 45(D1), D1117.

Rodríguez-Iglesias A, et al. (2016) Publishing FAIR Data: An Exemplar Methodology Utilizing PHI-Base. Frontiers in plant science, 7, 641.

Malladi VS, et al. (2015) Ontology application and use at the ENCODE DCC. Database : the journal of biological databases and curation, 2015.