

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

ECO

RRID:SCR_002477

Type: Tool

Proper Citation

ECO (RRID:SCR_002477)

Resource Information

URL: <http://www.evidenceontology.org>

Proper Citation: ECO (RRID:SCR_002477)

Description: A controlled vocabulary that describes types of scientific evidence within the realm of biological research that can arise from laboratory experiments, computational methods, manual literature curation, and other means. Researchers can use these types of evidence to support assertions about research subjects that result from scientific research, such as scientific conclusions, gene annotations, or other statements of fact. ECO comprises two high-level classes, evidence and assertion method, where evidence is defined as a type of information that is used to support an assertion, and assertion method is defined as a means by which a statement is made about an entity. Together evidence and assertion method can be combined to describe both the support for an assertion and whether that assertion was made by a human being or a computer. However, ECO can not be used to make the assertion itself; for that, one would use another ontology, free text description, or other means. ECO was originally created around the year 2000 to support gene product annotation by the Gene Ontology. Today ECO is used by many groups concerned with provenance in scientific research. ECO is used in AmiGO 2

Abbreviations: ECO

Synonyms: Evidence Codes Ontology, Evidence Ontology, evidenceontology, The Evidence Ontology

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

Keywords: evidence, assertion, assertion method, gene product, obo, evidence code, experiment, similarity, provenance

Funding: NIGMS GM089636

Availability: Free, Available for download, Freely available

Resource Name: ECO

Resource ID: SCR_002477

Alternate IDs: nlx_155860

Alternate URLs: <http://code.google.com/p/evidenceontology/>,
<http://bioportal.bioontology.org/ontologies/ECO>

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Record Creation Time: 20220129T080213+0000

Record Last Update: 20260801T042517+0000

Ratings and Alerts

No rating or validation information has been found for ECO.

No alerts have been found for ECO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Nadendla S, et al. (2022) ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic acids research, 50(D1), D1515.

Giachelle F, et al. (2021) Search, access, and explore life science nanopublications on the Web. PeerJ. Computer science, 7, e335.

Díaz-Rodríguez M, et al. (2021) Lisen&Curate: A platform to facilitate gathering textual evidence for curation of regulation of transcription initiation in bacteria. Biochimica et biophysica acta. Gene regulatory mechanisms, 1864(11-12), 194753.

Hobbs ET, et al. (2021) ECO-CollecTF: A Corpus of Annotated Evidence-Based Assertions in Biomedical Manuscripts. Frontiers in research metrics and analytics, 6, 674205.

Yuan J, et al. (2020) Evolutionary conservation and functional impact of dopamine D2 receptor. Neuroscience letters, 733, 135081.

Chen Q, et al. (2020) Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases. Genomics, proteomics &

bioinformatics, 18(2), 91.

Nash RS, et al. (2020) Incorporation of a unified protein abundance dataset into the Saccharomyces genome database. Database : the journal of biological databases and curation, 2020.

Wong ED, et al. (2019) Integration of macromolecular complex data into the Saccharomyces Genome Database. Database : the journal of biological databases and curation, 2019.

Giglio M, et al. (2019) ECO, the Evidence & Conclusion Ontology: community standard for evidence information. Nucleic acids research, 47(D1), D1186.

Tang YA, et al. (2019) Ten quick tips for biocuration. PLoS computational biology, 15(5), e1006906.

Kanavy DM, et al. (2019) Comparative analysis of functional assay evidence use by ClinGen Variant Curation Expert Panels. Genome medicine, 11(1), 77.

Cooper L, et al. (2018) The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. Nucleic acids research, 46(D1), D1168.

Cusin I, et al. (2018) A new bioinformatics tool to help assess the significance of BRCA1 variants. Human genomics, 12(1), 36.

Aksoy BA, et al. (2017) CTD2 Dashboard: a searchable web interface to connect validated results from the Cancer Target Discovery and Development Network. Database : the journal of biological databases and curation, 2017.

Torto-Alalibo T, et al. (2014) Genetic resources for advanced biofuel production described with the Gene Ontology. Frontiers in microbiology, 5, 528.

Pruitt KD, et al. (2014) RefSeq: an update on mammalian reference sequences. Nucleic acids research, 42(Database issue), D756.

Costanzo MC, et al. (2014) Saccharomyces genome database provides new regulation data. Nucleic acids research, 42(Database issue), D717.

Vihinen M, et al. (2014) Variation Ontology for annotation of variation effects and mechanisms. Genome research, 24(2), 356.

Chibucos MC, et al. (2014) Standardized description of scientific evidence using the Evidence Ontology (ECO). Database : the journal of biological databases and curation, 2014.