

Resource Summary Report

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Experimental Factor Ontology

RRID:SCR_003574

Type: Tool

Proper Citation

Experimental Factor Ontology (RRID:SCR_003574)

Resource Information

URL: <http://www.ebi.ac.uk/efo/>

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Description: An application focused ontology modelling the experimental factors in ArrayExpress and Gene Expression Atlas. It has been developed to increase the richness of the annotations that are currently made in the ArrayExpress repository, to promote consistent annotation, to facilitate automatic annotation and to integrate external data. The ontology describes cross-product classes from reference ontologies in area such as disease, cell line, cell type and anatomy. The methodology employed in the development of EFO involves construction of mappings to multiple existing domain specific ontologies, such as the Disease Ontology and Cell Type Ontology. This is achieved using a combination of automated and manual curation steps and the use of a phonetic matching algorithm. The ontology is evaluated with use cases from the ArrayExpress repository and ArrayExpress Atlas. You may also browse the EFO in the NCBO Bioportal. Term submissions are welcome.

Abbreviations: EFO

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

Defining Citation: [PMID:20200009](#)

Keywords: gene expression, owl, experimental factor, disease, cell line, cell type, anatomy, gold standard

Funding: European Molecular Biology Laboratory ;
European Union FELICS contract 021902;
European Union EMERALD LSHG-CT-2006-037686;
European Union Gen2Phen contract 200754

Availability: The community can contribute to this resource

Resource Name: Experimental Factor Ontology

Resource ID: SCR_003574

Alternate IDs: nlx_11363

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260801T190223+0000

Ratings and Alerts

No rating or validation information has been found for Experimental Factor Ontology.

No alerts have been found for Experimental Factor Ontology.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Kyoda K, et al. (2024) SSBD: an ecosystem for enhanced sharing and reuse of bioimaging data. Nucleic acids research.

van Rijn JPM, et al. (2024) From papers to RDF-based integration of physicochemical data and adverse outcome pathways for nanomaterials. Journal of cheminformatics, 16(1), 49.

Sun Y, et al. (2023) MACdb: A curated knowledgebase for metabolic associations across human cancers. Molecular cancer research : MCR.

Barrio-Hernandez I, et al. (2023) Network expansion of genetic associations defines a pleiotropy map of human cell biology. Nature genetics, 55(3), 389.

Laisk T, et al. (2021) Genome-wide association study identifies five risk loci for pernicious anemia. Nature communications, 12(1), 3761.

Bucher E, et al. (2019) Annot: a Django-based sample, reagent, and experiment metadata tracking system. BMC bioinformatics, 20(1), 542.

Harper L, et al. (2018) AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database : the journal of biological databases and curation, 2018.

Kafkas ??, et al. (2017) Literature evidence in open targets - a target validation platform. Journal of biomedical semantics, 8(1), 20.

Sarntivijai S, et al. (2016) Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. *Journal of biomedical semantics*, 7, 8.

Waagmeester A, et al. (2016) Using the Semantic Web for Rapid Integration of WikiPathways with Other Biological Online Data Resources. *PLoS computational biology*, 12(6), e1004989.

Sloan CA, et al. (2016) ENCODE data at the ENCODE portal. *Nucleic acids research*, 44(D1), D726.

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

Kibbe WA, et al. (2015) Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. *Nucleic acids research*, 43(Database issue), D1071.

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

Merrill E, et al. (2014) Semantic Web repositories for genomics data using the eXframe platform. *Journal of biomedical semantics*, 5(Suppl 1 Proceedings of the Bio-Ontologies Spec Interest G), S3.

Ganzinger M, et al. (2012) On the ontology based representation of cell lines. *PloS one*, 7(11), e48584.