

Resource Summary Report

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UBERON

RRID:SCR_010668

Type: Tool

Proper Citation

UBERON (RRID:SCR_010668)

Resource Information

URL: <http://uberon.org>

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Description: An integrated cross-species anatomy ontology representing a variety of entities classified according to traditional anatomical criteria such as structure, function and developmental lineage. The ontology includes comprehensive relationships to taxon-specific anatomical ontologies, allowing integration of functional, phenotype and expression data. Uberon consists of over 10000 classes (March 2014) representing structures that are shared across a variety of metazoans. The majority of these classes are chordate specific, and there is large bias towards model organisms and human.

Abbreviations: UBERON

Synonyms: Uber anatomy ontology, Uber-anatomy ontology

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

Defining Citation: [PMID:22293552](#)

Keywords: anatomy, comparative, evolution, organ system, anatomical structure, body part, organ, tissue, body, vertebrate, function, phenotype, expression, model organism, obo

Funding: ARRA ;
NSF ;
NHGRI 5R01HG004838;
NHGRI P41HG002273;
DOE DE-AC02-05CH11231;
NCRR 1U24RR029825-01;
NHGRI P41HG002273-09S1

Resource Name: UBERON

Resource ID: SCR_010668

Alternate IDs: nlx_74404

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260728T043349+0000

Ratings and Alerts

No rating or validation information has been found for UBERON.

No alerts have been found for UBERON.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Bueckle A, et al. (2025) Construction, Deployment, and Usage of the Human Reference Atlas Knowledge Graph. Scientific data, 12(1), 1100.

Mouhou E, et al. (2025) High tissue specificity of lncRNAs maximises the prediction of tissue of origin of circulating DNA. Scientific reports, 15(1), 12941.

Bastian FB, et al. (2025) Bgee in 2024: focus on curated single-cell RNA-seq datasets, and query tools. Nucleic acids research, 53(D1), D878.

Rueda M, et al. (2025) ClarID: A Human-Readable and Compact Identifier Specification for Biomedical Metadata Integration. medRxiv : the preprint server for health sciences.

Matentzoglou N, et al. (2025) The Unified Phenotype Ontology : a framework for cross-species integrative phenomics. Genetics, 229(3).

Riquelme-García A, et al. (2025) Annotation of biological samples data to standard ontologies with support from large language models. Computational and structural biotechnology journal, 27, 2155.

Imam FT, et al. (2025) Developing a multiscale neural connectivity knowledgebase of the autonomic nervous system. Frontiers in neuroinformatics, 19, 1541184.

Matentzoglou N, et al. (2024) The Unified Phenotype Ontology (uPheno): A framework for cross-species integrative phenomics. bioRxiv : the preprint server for biology.

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

Althagafi A, et al. (2024) Prioritizing genomic variants through neuro-symbolic, knowledge-enhanced learning. *Bioinformatics* (Oxford, England), 40(5).

Stefancsik R, et al. (2023) The Ontology of Biological Attributes (OBA)-computational traits for the life sciences. *Mammalian genome : official journal of the International Mammalian Genome Society*, 34(3), 364.

Herr BW, et al. (2023) Specimen, biological structure, and spatial ontologies in support of a Human Reference Atlas. *Scientific data*, 10(1), 171.

Triant DA, et al. (2023) AgAnimalGenomes: browsers for viewing and manually annotating farm animal genomes. *Mammalian genome : official journal of the International Mammalian Genome Society*, 34(3), 418.

Stefancsik R, et al. (2023) The Ontology of Biological Attributes (OBA) - Computational Traits for the Life Sciences. *bioRxiv : the preprint server for biology*.

Morris JH, et al. (2023) The scalable precision medicine open knowledge engine (SPOKE): a massive knowledge graph of biomedical information. *Bioinformatics* (Oxford, England), 39(2).

Burger A, et al. (2023) Towards a clinically-based common coordinate framework for the human gut cell atlas: the gut models. *BMC medical informatics and decision making*, 23(1), 36.

Boppana A, et al. (2023) Anatomical structures, cell types, and biomarkers of the healthy human blood vasculature. *Scientific data*, 10(1), 452.

Althagafi A, et al. (2022) DeepSVP: integration of genotype and phenotype for structural variant prioritization using deep learning. *Bioinformatics* (Oxford, England), 38(6), 1677.

Hawkins NT, et al. (2022) Systematic tissue annotations of genomics samples by modeling unstructured metadata. *Nature communications*, 13(1), 6736.

Surles-Zeigler MC, et al. (2022) Extending and using anatomical vocabularies in the stimulating peripheral activity to relieve conditions project. *Frontiers in neuroinformatics*, 16, 819198.