

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

## UBERON

RRID:SCR\_010668

Type: Tool

---

### Proper Citation

UBERON (RRID:SCR\_010668)

---

### Resource Information

**URL:** <http://uberon.org>

**Proper Citation:** UBERON (RRID:SCR\_010668)

**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:** ontology, data or information resource, controlled vocabulary

**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:** 20260808T185923+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 62 mentions in open access literature.

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

Kim M, et al. (2026) Ontology-aware DNA methylation classification with a curated atlas of human tissues and cell types. Cell reports methods, 6(3), 101328.

Tandon D, et al. (2026) METRIN-KG: A knowledge graph integrating plant metabolites, traits, and biotic interactions. GigaScience, 15.

Gaio D, et al. (2026) Enhanced semantic classification of microbiome sample origins using large language models (LLMs). GigaScience, 15.

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

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

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.

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

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

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.

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.

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

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

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

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

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.

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.

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).

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

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.