

Resource Summary Report

Generated by [nidm-terms](#) on Aug 15, 2026

OMA Orthology database

RRID:SCR_016425

Type: Tool

Proper Citation

OMA Orthology database (RRID:SCR_016425)

Resource Information

URL: <https://omabrowser.org/oma/>

Proper Citation: OMA Orthology database (RRID:SCR_016425)

Description: Web based database interface for orthology prediction for the inference of orthologs among complete genomes. Used to relate genes across many species., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: OMA

Synonyms: Orthologous MAtrix

Resource Type: database, standalone software, web service, data or information resource, data access protocol, software application, software resource

Defining Citation: [PMID:29106550](#)

Keywords: interface, orthology, prediction, inference, complete, genome, species, data

Funding: Swiss Institute of Bioinformatics ;
UK Biotechnology and Biological Sciences Research Council ;
University College London ;
Bayer Crop Science NV

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: OMA Orthology database

Resource ID: SCR_016425

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260815T042734+0000

Ratings and Alerts

No rating or validation information has been found for OMA Orthology database.

No alerts have been found for OMA Orthology database.

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 [nidm-terms](#) .

Vergunov EG, et al. (2025) Computer reconstruction of gene networks controlling anxiety levels in humans and laboratory mice. *Vavilovskii zhurnal genetiki i selektsii*, 29(1), 162.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. *The Journal of physiology*, 603(15), 4383.

Podlesny-Drabiniok A, et al. (2024) Cytokine-induced reprogramming of human macrophages toward Alzheimer's disease-relevant molecular and cellular phenotypes in vitro. *bioRxiv : the preprint server for biology*.

Acevedo A, et al. (2023) Metabolic switch in the aging astrocyte supported via integrative approach comprising network and transcriptome analyses. *Aging*, 15(19), 9896.

Wang S, et al. (2022) Integrated view and comparative analysis of baseline protein expression in mouse and rat tissues. *PLoS computational biology*, 18(6), e1010174.

Deák G, et al. (2022) Missense Variants Reveal Functional Insights Into the Human ARID Family of Gene Regulators. *Journal of molecular biology*, 434(9), 167529.

Valdez L, et al. (2021) Genetic Diversity and Demographic History of the Shaggy Soft-Haired Mouse *Abrothrix hirta* (Cricetidae; Abrotrichini). *Frontiers in genetics*, 12, 642504.

Heger P, et al. (2020) The genetic factors of bilaterian evolution. *eLife*, 9.

Sánchez-Osuna M, et al. (2018) Origin of the Mobile Di-Hydro-Pterate Synthase Gene Determining Sulfonamide Resistance in Clinical Isolates. *Frontiers in microbiology*, 9, 3332.