Resource Summary Report

Generated by dkNET on Aug 13, 2026

Mondo

RRID:SCR_022183
Type: Tool

Proper Citation

Mondo (RRID:SCR_022183)

Resource Information

URL: https://mondo.monarchinitiative.org/

Proper Citation: Mondo (RRID:SCR_022183)

Description: Open, community-driven ontology that integrates key medical and biomedical terminologies, supporting disease data integration to improve diagnosis, treatment, and translational research. Mondo records sources of all data and is continually updated, making it suitable for research and clinical applications that require up-to-date disease knowledge.

Abbreviations: Mondo

Synonyms: Mondo Disease Ontology

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

Defining Citation: DOI:10.1101/2022.04.13.22273750

Keywords: integrates key medical and biomedical terminologies, disease data integration support, disease knowledge

Availability: Free, Freely available

Resource Name: Mondo

Resource ID: SCR_022183

Alternate URLs: https://github.com/monarch-initiative/mondo

Record Creation Time: 20220427T191217+0000

Record Last Update: 20260813T055240+0000

Ratings and Alerts

No rating or validation information has been found for Mondo.

No alerts have been found for Mondo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Vasilevsky NA, et al. (2026) Mondo: integrating disease terminology across communities. Genetics, 232(4).

Reese JT, et al. (2026) Systematic benchmarking demonstrates large language models have not reached the diagnostic accuracy of traditional rare-disease decision support tools. European journal of human genetics : EJHG, 34(4), 498.

Ji X, et al. (2026) ResMicroDb: a comprehensive database and analysis platform for the human respiratory microbiome. Nucleic acids research, 54(D1), D858.

Ross JE, et al. (2025) Clinical validity of congenital myopathy genes determined by the ClinGen Congenital Myopathies Expert Panel. Journal of neuromuscular diseases, 12(6), 778.

Michel É, et al. (2025) Rare diseases load through the study of a regional population. PLoS genetics, 21(10), e1011876.

Qian Q, et al. (2025) CVD Atlas: a multi-omics database of cardiovascular disease. Nucleic acids research, 53(D1), D1348.

Twigg SRF, et al. (2025) The power of mouse models in the diagnostic odyssey of patients with rare congenital anomalies. Mammalian genome : official journal of the International Mammalian Genome Society, 36(2), 354.

Mutai H, et al. (2025) Genetic landscape in undiagnosed patients with syndromic hearing loss revealed by whole exome sequencing and phenotype similarity search. Human genetics, 144(1), 93.

Bertolini E, et al. (2024) MultifacetedProtDB: a database of human proteins with multiple functions. Nucleic acids research, 52(D1), D494.

Qin G, et al. (2024) Generating Biomedical Knowledge Graphs from Knowledge Bases, Registries, and Multiomic Data. bioRxiv : the preprint server for biology.

Gargano MA, et al. (2024) The Human Phenotype Ontology in 2024: phenotypes around the world. Nucleic acids research, 52(D1), D1333.

Mohan S, et al. (2024) Expert Panel Curation of 31 Genes in Relation to Limb Girdle Muscular Dystrophy. bioRxiv : the preprint server for biology.

Menotti L, et al. (2023) Modelling digital health data: The ExaMode ontology for computational pathology. Journal of pathology informatics, 14, 100332.

Domingo-Fernández D, et al. (2023) Modern drug discovery using ethnobotany: A large-scale cross-cultural analysis of traditional medicine reveals common therapeutic uses. iScience, 26(9), 107729.

Babbi G, et al. (2022) Pathogenic variation types in human genes relate to diseases through Pfam and InterPro mapping. Frontiers in molecular biosciences, 9, 966927.