Resource Summary Report

Generated by RRID on May 18, 2025

MPO

RRID:SCR_004855
Type: Tool

Proper Citation

MPO (RRID:SCR_004855)

Resource Information

URL: http://www.informatics.jax.org/searches/MP_form.shtml

Proper Citation: MPO (RRID:SCR_004855)

Description: Community ontology to provide standard terms for annotating mammalian phenotypic data. It has a hierarchical structure that permits a range of detail from high-level, broadly descriptive terms to very low-level, highly specific terms. This range is useful for annotating phenotypic data to the level of detail known and for searching for this information using either broad or specific terms as search criteria. Your input is welcome.

Abbreviations: MPO, MP

Synonyms: Mammalian Phenotype Ontology

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

Defining Citation: PMID:17989687

Keywords: mus, phenotype, obo

Funding:

Availability: The community can contribute to this resource

Resource Name: MPO

Resource ID: SCR_004855

Alternate IDs: nlx_83784

Alternate URLs: http://obofoundry.org/cgi-bin/detail.cgi?id=mammalian_phenotype,

http://purl.bioontology.org/ontology/MP

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250516T053747+0000

Ratings and Alerts

No rating or validation information has been found for MPO.

No alerts have been found for MPO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Fisher ME, et al. (2022) The Xenopus phenotype ontology: bridging model organism phenotype data to human health and development. BMC bioinformatics, 23(1), 99.

Bubier JA, et al. (2020) Discovery of a Role for Rab3b in Habituation and Cocaine Induced Locomotor Activation in Mice Using Heterogeneous Functional Genomic Analysis. Frontiers in neuroscience, 14, 721.

Block A, et al. (2018) The GABAA?5-selective Modulator, RO4938581, Rescues Protein Anomalies in the Ts65Dn Mouse Model of Down Syndrome. Neuroscience, 372, 192.

Schumacher J, et al. (2017) Effects of different kinds of essentiality on sequence evolution of human testis proteins. Scientific reports, 7, 43534.

Eppig JT, et al. (2017) Mouse Genome Informatics (MGI) Resource: Genetic, Genomic, and Biological Knowledgebase for the Laboratory Mouse. ILAR journal, 58(1), 17.

Irizarry KJ, et al. (2016) Leveraging Comparative Genomics to Identify and Functionally Characterize Genes Associated with Sperm Phenotypes in Python bivittatus (Burmese Python). Genetics research international, 2016, 7505268.

Chylíková B, et al. (2016) Recurrent Microdeletions at Xq27.3-Xq28 and Male Infertility: A Study in the Czech Population. PloS one, 11(6), e0156102.

Hoppmann AS, et al. (2016) GenToS: Use of Orthologous Gene Information to Prioritize Signals from Human GWAS. PloS one, 11(9), e0162466.

Ohno Y, et al. (2015) Hcn1 is a tremorgenic genetic component in a rat model of essential tremor. PloS one, 10(5), e0123529.

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

Janssens J, et al. (2015) Investigating the role of filamin C in Belgian patients with frontotemporal dementia linked to GRN deficiency in FTLD-TDP brains. Acta neuropathologica communications, 3, 68.

Daimon CM, et al. (2015) Hippocampal Transcriptomic and Proteomic Alterations in the BTBR Mouse Model of Autism Spectrum Disorder. Frontiers in physiology, 6, 324.

Su Z, et al. (2014) Effect of duplicate genes on mouse genetic robustness: an update. BioMed research international, 2014, 758672.

Smemo S, et al. (2014) Obesity-associated variants within FTO form long-range functional connections with IRX3. Nature, 507(7492), 371.

Weninger WJ, et al. (2014) Phenotyping structural abnormalities in mouse embryos using high-resolution episcopic microscopy. Disease models & mechanisms, 7(10), 1143.

DiTommaso T, et al. (2014) Identification of genes important for cutaneous function revealed by a large scale reverse genetic screen in the mouse. PLoS genetics, 10(10), e1004705.

Collier N, et al. (2013) Toward knowledge support for analysis and interpretation of complex traits. Genome biology, 14(9), 214.

Bandrowski AE, et al. (2012) A hybrid human and machine resource curation pipeline for the Neuroscience Information Framework. Database : the journal of biological databases and curation, 2012, bas005.

Xiong Q, et al. (2009) Quantitative trait loci, genes, and polymorphisms that regulate bone mineral density in mouse. Genomics, 93(5), 401.