Resource Summary Report

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Monarch Initiative

RRID:SCR_001373
Type: Tool

Proper Citation

Monarch Initiative (RRID:SCR_001373)

Resource Information

URL: http://monarchinitiative.org/

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Description: Repository of information about model organisms, in vitro models, genes, pathways, gene expression, protein and genetic interactions, orthology, disease, phenotypes, publications, and authors, and the the ability to navigate multi-scale spatial and temporal phenotypes across in vivo and in vitro model systems in the context of genetic and genomic data, using semantics and statistics. The discovery system provides basic and clinical science researchers, informaticists, and medical professionals with an integrated interface and set of discovery tools to reveal the genetic basis of disease, facilitate hypothesis generation, and identify novel candidate drug targets. The aim for this system is to promote true translational research, in that clinicians can connect with model systems researchers with expertise in related phenotypes, assays, or models. In addition to providing easy-to-use tools to navigate the model-disease data landscape, it also provides services for other resources, and educational outreach regarding the production of structured data for biomedical discovery. Model systems are the cornerstone of biomedical research to investigate biological processes, test gene-based disease hypotheses, and develop and test disease treatments. The vast knowledge about model systems can be better utilized if semantically aggregated and made queryable based on any number of facets, such as phenotypic similarity, network analysis, gene expression and function, and genomics.

Abbreviations: Monarch

Resource Type: database, data or information resource

Keywords: phenotype, model organism, in vitro model, gene, pathway, gene expression, protein interaction, genetic interaction, orthology, disease, publication, author, genetic, genomic, model system, genotype, disease, drug, in vivo model

Funding: NIH Office of the Director 1R24OD011883-01

Availability: Free, Public

Resource Name: Monarch Initiative

Resource ID: SCR_001373

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260903T234435+0000

Ratings and Alerts

No rating or validation information has been found for Monarch Initiative.

No alerts have been found for Monarch Initiative.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Thaxton C, et al. (2022) Lumping versus splitting: How to approach defining a disease to enable accurate genomic curation. Cell genomics, 2(5).

Edwards NA, et al. (2021) Developmental basis of trachea-esophageal birth defects. Developmental biology, 477, 85.

Marmon P, et al. (2021) Pharmacology-informed prediction of the risk posed to fish by mixtures of non-steroidal anti-inflammatory drugs (NSAIDs) in the environment. Environment international, 146, 106222.

Lloyd KCK, et al. (2020) The Deep Genome Project. Genome biology, 21(1), 18.

Motch Perrine SM, et al. (2020) Phenotypes, Developmental Basis, and Genetics of Pierre Robin Complex. Journal of developmental biology, 8(4).

Gourdine JF, et al. (2019) Representing glycophenotypes: semantic unification of glycobiology resources for disease discovery. Database : the journal of biological databases and curation, 2019.

Galperin MY, et al. (2017) The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes. Nucleic acids research, 45(D1), D1.

Mungall CJ, et al. (2017) The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic acids research, 45(D1), D712.

Bandrowski A, et al. (2016) The Resource Identification Initiative: a cultural shift in publishing. Brain and behavior, 6(1), e00417.

Smedley D, et al. (2016) A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. American journal of human genetics, 99(3), 595.

Bandrowski A, et al. (2016) The Resource Identification Initiative: A Cultural Shift in Publishing. The Journal of comparative neurology, 524(1), 8.

Hoehndorf R, et al. (2015) Analysis of the human diseasome using phenotype similarity between common, genetic, and infectious diseases. Scientific reports, 5, 10888.

Ring N, et al. (2015) A mouse informatics platform for phenotypic and translational discovery. Mammalian genome : official journal of the International Mammalian Genome Society, 26(9-10), 413.

Groza T, et al. (2015) The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American journal of human genetics, 97(1), 111.

Bandrowski A, et al. (2015) The Resource Identification Initiative: A cultural shift in publishing. F1000Research, 4, 134.

Schriml LM, et al. (2015) The Disease Ontology: fostering interoperability between biological and clinical human disease-related data. Mammalian genome : official journal of the International Mammalian Genome Society, 26(9-10), 584.

Kibbe WA, et al. (2015) Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. Nucleic acids research, 43(Database issue), D1071.

Smedley D, et al. (2015) Phenotype-driven strategies for exome prioritization of human Mendelian disease genes. Genome medicine, 7(1), 81.

Bello SM, et al. (2015) Allele, phenotype and disease data at Mouse Genome Informatics: improving access and analysis. Mammalian genome : official journal of the International Mammalian Genome Society, 26(7-8), 285.

Haendel MA, et al. (2015) Disease insights through cross-species phenotype comparisons. Mammalian genome : official journal of the International Mammalian Genome Society, 26(9-10), 548.