# Resource Summary Report

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## MONARCH Initiative

RRID:SCR_000824
Type: Tool

### Proper Citation

MONARCH Initiative (RRID:SCR_000824)

### Resource Information

**URL:** https://monarchinitiative.org/

**Proper Citation:** MONARCH Initiative (RRID:SCR_000824)

**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 ability to navigate multi-scale spatial and temporal phenotypes across in vivo and in vitro model systems in context of genetic and genomic data, using semantics and statistics. Discovery system provides basic and clinical science researchers, informaticists, and medical professionals with integrated interface and set of discovery tools to reveal genetic basis of disease, facilitate hypothesis generation, and identify novel candidate drug targets. Database that indexes authoritative information on experimental models of disease from MGI, RGD and ZFIN.

**Abbreviations:** Monarch

**Synonyms:** MONARCH Integrated Disease Model, MONARCH Integrated Disease Models View, MONARCH Disease Models View, The MONARCH Initiative

**Resource Type:** data or information resource, database

**Defining Citation:** PMID:26269093

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

**Funding:** NIH Office of the Director R24 OD011883

**Availability:** Free, Freely available

**Resource Name:** MONARCH Initiative

**Resource ID:** SCR_000824

**Alternate IDs:** r3d100011594, nlx_152525, SCR_001373, nlx_152748

**Alternate URLs:** https://orip.nih.gov/comparative-medicine/programs/genetic-biological-and-information-resources, https://doi.org/10.17616/R31M09

**Record Creation Time:** 20220129T080203+0000

**Record Last Update:** 20260829T182031+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 13 mentions in open access literature.

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

Wei S, et al. (2026) Risk assessment for hydrophobic disinfectants and antiseptics as contaminants in freshwater using risk quotient and network pharmacology approaches. iScience, 29(7), 116339.

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

Harper L, et al. (2018) AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database : the journal of biological databases and curation, 2018.

Cooper L, et al. (2018) The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. Nucleic acids research, 46(D1), D1168.

Balik-Meisner M, et al. (2018) Population genetic diversity in zebrafish lines. Mammalian genome : official journal of the International Mammalian Genome Society, 29(1-2), 90.

Wangler MF, et al. (2017) Model Organisms Facilitate Rare Disease Diagnosis and Therapeutic Research. Genetics, 207(1), 9.

Griffin PC, et al. (2017) Best practice data life cycle approaches for the life sciences. F1000Research, 6, 1618.

Zaman S, et al. (2017) Use of Biomedical Ontologies for Integration of Biological Knowledge for Learning and Prediction of Adverse Drug Reactions. Gene regulation and

systems biology, 11, 1177625017696075.

Wangler MF, et al. (2017) Drosophila and genome-wide association studies: a review and resource for the functional dissection of human complex traits. Disease models & mechanisms, 10(2), 77.

Boycott KM, et al. (2017) International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American journal of human genetics, 100(5), 695.

Meehan TF, et al. (2017) Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature genetics, 49(8), 1231.

Manolio TA, et al. (2017) Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 169(1), 6.

McEwan P, et al. (2015) Estimating the clinical and economic benefit associated with incremental improvements in sustained virologic response in chronic hepatitis C. PloS one, 10(1), e0117334.