

Resource Summary Report

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Understanding Human Disease Through Mouse Genetics

RRID:SCR_000785

Type: Tool

Proper Citation

Understanding Human Disease Through Mouse Genetics (RRID:SCR_000785)

Resource Information

URL: <http://eumorphia.publicwebserver3.har.mrc.ac.uk/>

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Description: A portal documenting a project for the development of novel approaches in phenotyping, mutagenesis and informatics to improve the characterization of mouse models for understanding human molecular physiology and pathology. EUMORPHIA has developed a new robust primary screening platform for determining the phenotype of mice: EMPReSS - European Mouse Phenotyping Resource for Standardised Screens. The project is also focused on training new young scientists by funding them to work in a variety of laboratories to gain a broader swathe of techniques. The project has also identified the need for more trained mouse pathologists. To address this, they are setting up training courses in pathology and working at a European level to establish more training.

Abbreviations: EUMORPHIA

Synonyms: European Union Mouse Research for Public Health and Industrial Applications

Resource Type: data or information resource, group, training resource, portal

Keywords: european, european union, mouse, gene, phenotype, model, physiology, molecular, informatics, mutagenesis

Funding: European Union under FP5 from October 2002 until March 2006

Resource Name: Understanding Human Disease Through Mouse Genetics

Resource ID: SCR_000785

Alternate IDs: nif-0000-30502

Old URLs: <http://www.eumorphia.org>

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250426T055425+0000

Ratings and Alerts

No rating or validation information has been found for Understanding Human Disease Through Mouse Genetics.

No alerts have been found for Understanding Human Disease Through Mouse Genetics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Brault V, et al. (2015) Opposite phenotypes of muscle strength and locomotor function in mouse models of partial trisomy and monosomy 21 for the proximal Hspa13-App region. PLoS genetics, 11(3), e1005062.

Traboulsi H, et al. (2014) Dynamic partnership between TFIIF, PGC-1 β and SIRT1 is impaired in trichothiodystrophy. PLoS genetics, 10(10), e1004732.

McMurray F, et al. (2012) From mice to humans. Current diabetes reports, 12(6), 651.

Ayadi A, et al. (2012) Mouse large-scale phenotyping initiatives: overview of the European Mouse Disease Clinic (EUMODIC) and of the Wellcome Trust Sanger Institute Mouse Genetics Project. Mammalian genome : official journal of the International Mammalian Genome Society, 23(9-10), 600.

Brown SD, et al. (2012) Towards an encyclopaedia of mammalian gene function: the International Mouse Phenotyping Consortium. Disease models & mechanisms, 5(3), 289.

Fuchs H, et al. (2012) Innovations in phenotyping of mouse models in the German Mouse Clinic. Mammalian genome : official journal of the International Mammalian Genome Society,

23(9-10), 611.

van der Weyden L, et al. (2011) The mouse genetics toolkit: revealing function and mechanism. *Genome biology*, 12(6), 224.

Pereira PL, et al. (2009) A new mouse model for the trisomy of the Abcg1-U2af1 region reveals the complexity of the combinatorial genetic code of down syndrome. *Human molecular genetics*, 18(24), 4756.

Andrieu D, et al. (2006) Sensory defects in Necdin deficient mice result from a loss of sensory neurons correlated within an increase of developmental programmed cell death. *BMC developmental biology*, 6, 56.

Brown SD, et al. (2006) Understanding mammalian genetic systems: the challenge of phenotyping in the mouse. *PLoS genetics*, 2(8), e118.

Argmann CA, et al. (2006) Minimizing variation due to genotype and environment. *Current protocols in molecular biology*, Chapter 29.

Gkoutos GV, et al. (2005) Using ontologies to describe mouse phenotypes. *Genome biology*, 6(1), R8.