Resource Summary Report

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Europhenome Mouse Phenotyping Resource

RRID:SCR_006935
Type: Tool

Proper Citation

Europhenome Mouse Phenotyping Resource (RRID:SCR_006935)

Resource Information

URL: http://www.europhenome.org

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Description: Open source software system for capturing, storing and analyzing raw phenotyping data from SOPs contained in EMPReSS, it provides access to raw and annotated mouse phenotyping data generated from primary pipelines such as EMPReSSlim and secondary procedures from specialist centers. Mutants of interest can be identified by searching the gene or the predicted phenotype. You can also access phenotype data from the EMPReSSlim Pipeline for inbred mouse strains. Initially EuroPhenome was developed within the EUMORPHIA programme to capture and store pilot phenotyping data obtained on four background strains (C57BL/6J, C3H/HeBFeJ, BALB/cByJ and 129/SvPas). EUMORPHIA (European Union Mouse Research for Public Health and Industrial Applications) was a large project comprising of 18 research centers in 8 European countries, with the main focus of the project being the development of novel approaches in phenotyping, mutagenesis and informatics to improve the characterization of mouse models for understanding human molecular physiology and pathology. The current version of EuroPhenome is capturing data from the EUMODIC project as well as the WTSI MGP, HMGU GMC pipeline and the CMHD. EUMODIC is undertaking a primary phenotype assessment of up to 500 mouse mutant lines derived from ES cells developed in the EUCOMM project as well as other lines. Lines showing an interesting phenotype will be subject to a more in depth assessment. EUMODIC is building upon the comprehensive database of standardized phenotyping protocols, called EMPReSS, developed by the EUMORPHIA project. EUMODIC has developed a selection of these screens, called EMPReSSslim, to enable comprehensive, high throughput, primary phenotyping of large numbers of mice. Phenovariants are annotated using a automated pipeline, which assigns a MP term if the mutant data is statistically different to the baseline data. This data is shown in the Phenomap and the mine for a mutant tool. Please note that a statistically significant result and the subsequent MP annotation does not necessarily mean a true phenovariant.

There are other factors that could cause this result that have not been accounted for in the analysis. It is the responsibility of the user to download the data and use their expert knowledge or further analysis to decide whether they agree or not. EuroPhenome is primarily based in the bioinformatics group at MRC Harwell. The development of EuroPhenome is in collaboration with the Helmholtz Zentrum Munchen, Germany, the Wellcome Trust Sanger Institute, UK and the Institut Clinique de la Souris, France.

Abbreviations: EuroPhenome

Resource Type: data analysis service, analysis service resource, database, production service resource, service resource, data or information resource

Defining Citation: PMID:19933761, PMID:17905814

Keywords: phenotype, gene, mutant mouse strain, inbred mouse strain, annotation, ortholog, high-throughput, phenovariant, disorder, c57bl/6j, c3h/hebfej, balb/cbyj, 129/svpas

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MRC ;
National Genome Research Network

Availability: Open unspecified license, Acknowledgement requested

Resource Name: Europhenome Mouse Phenotyping Resource

Resource ID: SCR_006935

Alternate IDs: nif-0000-30535

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250420T014349+0000

Ratings and Alerts

No rating or validation information has been found for Europhenome Mouse Phenotyping Resource.

No alerts have been found for Europhenome Mouse Phenotyping Resource.

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 NIF.

Prokic I, et al. (2020) Differential physiological roles for BIN1 isoforms in skeletal muscle development, function and regeneration. Disease models & mechanisms, 13(11).

de Angelis MH, et al. (2015) Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. Nature genetics, 47(9), 969.

Kirov JV, et al. (2015) Reporter Gene Silencing in Targeted Mouse Mutants Is Associated with Promoter CpG Island Methylation. PloS one, 10(8), e0134155.

Karp NA, et al. (2014) Impact of temporal variation on design and analysis of mouse knockout phenotyping studies. PloS one, 9(10), e111239.

Lopez-Delisle L, et al. (2014) Hyperactivation of Alk induces neonatal lethality in knock-in AlkF1178L mice. Oncotarget, 5(9), 2703.

Zimprich A, et al. (2014) A robust and reliable non-invasive test for stress responsivity in mice. Frontiers in behavioral neuroscience, 8, 125.

Mandillo S, et al. (2014) Early motor deficits in mouse disease models are reliably uncovered using an automated home-cage wheel-running system: a cross-laboratory validation. Disease models & mechanisms, 7(3), 397.

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

Cheeseman MT, et al. (2012) A mouse model for osseous heteroplasia. PloS one, 7(12), e51835.

Smith CL, et al. (2012) The Mammalian Phenotype Ontology as a unifying standard for experimental and high-throughput phenotyping data. Mammalian genome : official journal of the International Mammalian Genome Society, 23(9-10), 653.

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.

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

Eisener-Dorman AF, et al. (2010) The 23rd International Mammalian Genome Conference meeting report. Mammalian genome : official journal of the International Mammalian Genome Society, 21(5-6), 217.

Rubio-Aliaga I, et al. (2009) Dll1 haploinsufficiency in adult mice leads to a complex phenotype affecting metabolic and immunological processes. PloS one, 4(6), e6054.

Hancock JM, et al. (2009) Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian genome : official journal of the International Mammalian Genome Society, 20(8), 457.

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