IMPC

International Mouse Phenotyping Consortium

What is IMPC?

An emerging challenge for precision medicine is the lack of experimental evidence for biological function in two-thirds of the mammalian genome. The **International Mouse Phenotyping Consortium** (IMPC) is addressing this challenge by generating and characterizing a knockout mouse strain for every protein-coding gene within the next 10 years. IMPC will transform medicine by providing an encyclopedia of gene-phenotype associations that will inform precision medicine and will catalyse further research by making all mouse strains available for functional and therapeutic studies into human disease. IMPC partners come over a dozen countries that are supported by a number of national and international funding sources including the NIH Common Fund mechanism KOMP2.

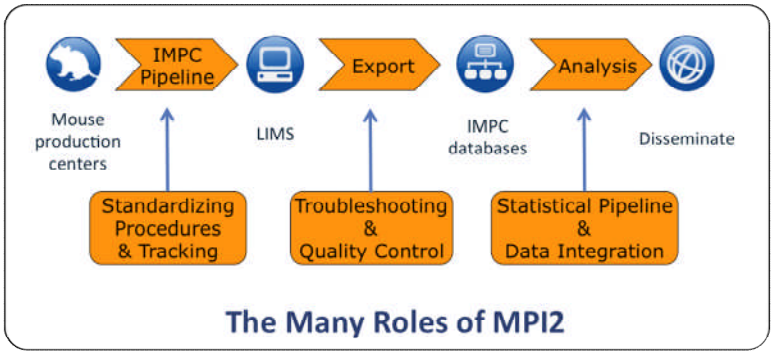
Who provides informatics support?

MPI2

Mouse Phenotyping Informatics Infrastructure

A global project requires a team of experts to coordinate activities, ensure data generated is of high quality, and provide an intuitive web portal that integrates phenotype data with other resources to find insights into human disease. The Mouse Phenotyping Informatics Infrastructure (MPI2) - a group of specialists from EMBL-EBI, MRC Harwell and the Wellcome Trust Sanger Institute, provides informatics for IMPC. We are biologists, bioinformaticians, software engineers and data integration experts. Our team builds the IMPC data resource, mousephenotype.org , and is supported by the NIH KOMP2 informatics grant.

What services does MPI2 perform?



MPI2 is involved throughout the IMPC pipeline. We coordinate production of mice, harmonize protocols and data export across centers, associate genes to phenotypes, and perform data integration to gain new insights into human disease. All data is freely available via multiple resources.

MRC Harwell

wellcome trust sanger institute

EMBL-EBI

www.mousephenotype.org

IMPC Partners

What resources can I access via the IMPC web portal?

The IMPC web portal is under a rapid development cycle with features being added after user testing. You can now:

- **NEW!** Observe preliminary phenotype data for dozens of genes with no known biological function
- Track production of knockout mouse strains online and via e-mail
- Search our database of protocols, developed by an international forum
- View gene detail pages that include an interactive browser, links to phenotype data, and access to the Ensembl Compara viewer to compare mouse and human gene structure

What new features are planned?

- Up-to-date phenotype summaries as mouse strains are characterised
- Detailed phenotype data on demand by web and API resources
- Pre-computed statistical analysis with ability for user to do their own analysis
- Zoomable images of histological and LacZ data
- Mapping between mouse phenotypes and human disease traits
- Gene discovery by shared phenotype and transcription characteristics

How will phenotype data be integrated?

The IMPC database combines gene, allele and strain nomenclature with biomedical ontologies to create an enriched resource to help you quickly find the data you want. We are leveraging EBI resources to put phenotype data into a genomic, epigenomic and transcriptomic context and are actively involved with groups mapping human disease traits to the ontologies we use in our databases.

How can I get involved?

- Registering interest in a gene is an important way to get involved. Anonymized information is used to help prioritize knockout mouse strain production
- User feedback is a critical component in how we develop our web portal. To test our beta site please contact us: www.mousephenotype.org/contact-us

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www.mousephenotype.org