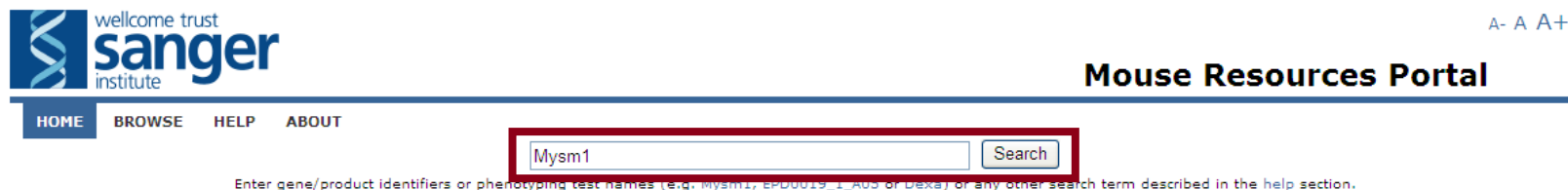


# Sanger Mouse Portal “How to” Guide

## How to search for phenotyping data on a gene of interest?

1. From the Sanger Mouse Portal home page (<http://www.sanger.ac.uk/mouseportal/>), enter your gene of interest e.g. *Mysm1* into the **Search** field and click search:



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**sanger**  
institute

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### Mouse Resources Portal

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Enter gene/product identifiers or phenotyping test names (e.g. Mysm1, EP00019\_1\_A03 or D6x4) or any other search term described in the help section.

### About This Portal

The Wellcome Trust Sanger Institute generates, characterises, and uses a variety of reagents for mouse genetics research. It also aims to facilitate the distribution of these resources to the external scientific community. Here, you will find unified access to the different resources available from the Institute or its collaborators. The resources include: 129S7 and C57BL6/J bacterial artificial chromosomes (BACs), MICER gene targeting vectors, knock-out first conditional-ready gene targeting vectors, embryonic stem (ES) cells with gene targeted mutations or with retroviral gene trap insertions, mutant mouse lines, and phenotypic data generated from the Institute’s primary screen.

### Phenotyping Summary

The table below displays the **number of alleles** that have completed different stages of the MGP Phenotyping pipeline (funded by WTSI & EUMODIC)

Comprehensive Phenotyping Substantively Complete	564
Infection Challenge (Salmonella and Citrobacter)	495
LacZ Expression (Adult and E14.5)	339

### Other Data Summary

The table below displays the **number of unique genes** with each individual product type produced at the Wellcome Trust Sanger Institute.

Funding:	WTSI EUMODIC	KOMP EUCOMM	KOMP EUCOMM	WT	WT	WT
Products:	Mice	Targeted ES Cells	Gene Targeting Vectors	MICER	C57Bl/6J BACs	129S7 BACs
	904	13011	15105	6719	12037	11874

### Phenotyping Overview



Download a heat map of phenotyping results by assay. This spreadsheet also links to the detailed phenotyping data on this portal.

You can also access (and search) the same data via the MGP Phenotyping BioMart.

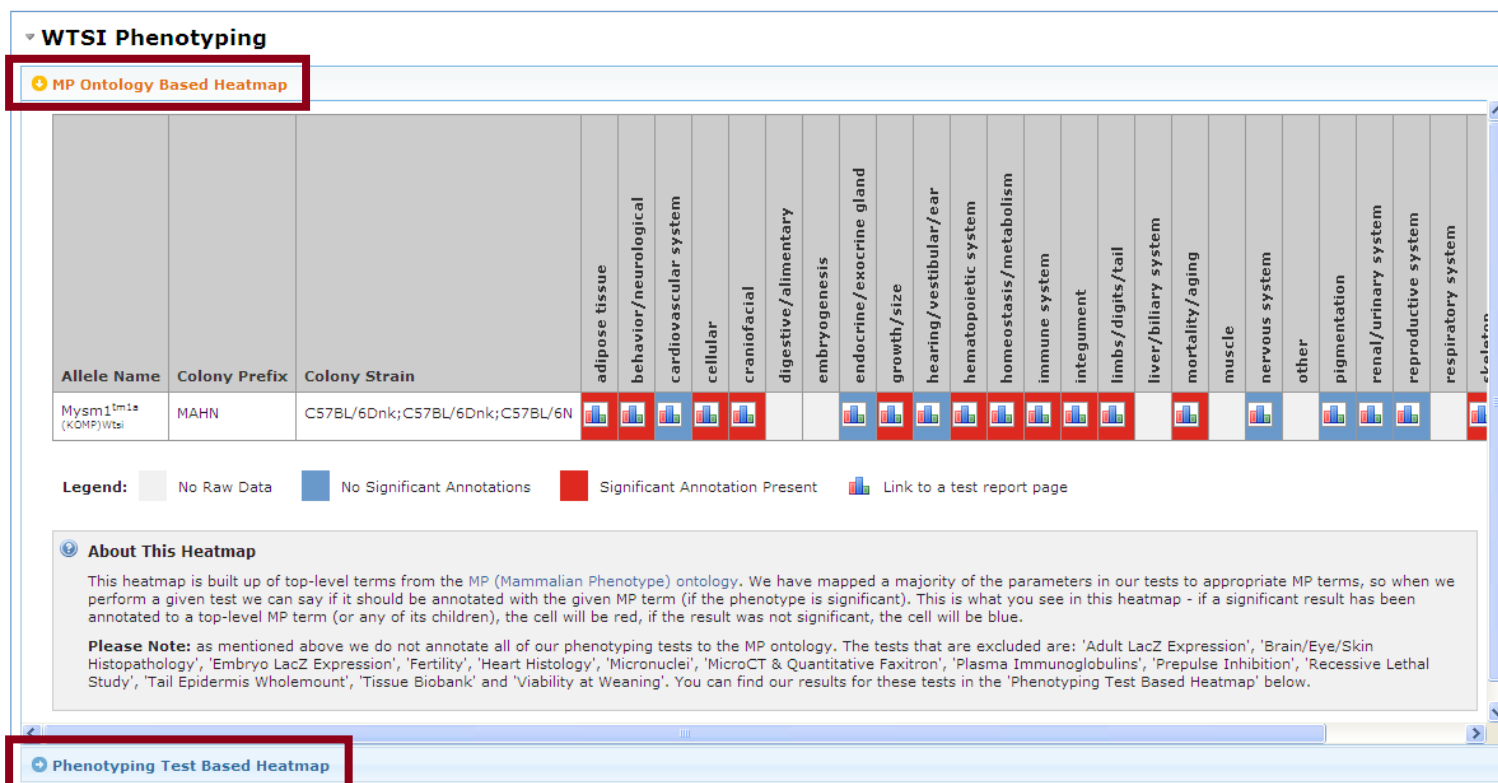
**NEW** - Disease predictions based on semantic similarity between OMIM disorder clinical features and model organism phenotypes.



If you would like to be kept updated with information on our phenotyping data, please subscribe to our mailing list.

## Sanger Mouse Portal “How to” Guide

2. This opens a gene specific page containing information split into the following panels that are populated when resources are available:
  - i. Gene Details
  - ii. WTSI Phenotyping
  - iii. Mice
  - iv. IKMC Vectors and ES Cells
  - v. DNA Clone Resources
  
3. The WTSI Phenotyping panel presents the primary phenotyping data as a colour coded heat map style summary of all phenotyping data for that gene. Data are grouped for presentation in two ways:
  - i. As a Mammalian Phenotype (MP) Ontology Based Heatmap



## Sanger Mouse Portal “How to” Guide

- ii. As a Phenotyping Test Based Heatmap, opened by clicking the bar of the same name. Note this action causes the MP Ontology Based Heatmap to roll up.

▼ **WTSI Phenotyping**

MP Ontology Based Heatmap

**Phenotyping Test Based Heatmap**

Allele Name	Colony Prefix	Colony Strain	Viability at weaning	Recessive Lethal Study	Fertility	Embryo LacZ Expression	Adult LacZ Expression	General Observations	Weight Curves	Open Field	Modified SHIRPA	Grip Strength	Hot Plate	Dysmorphology	Rotarod	Non-Invasive Blood Pressure	Prepulse Inhibition	Indirect Calorimetry	Glucose Tolerance (ip)	Auditory Brainstem Response	Body Composition (DEXA)	X-ray Imaging	Stress Induced Hyperthermia	Eye Morphology	Plasma Chemistry	Plasma Immunoglobulins	Haematology (CBC)
Mysm1 <sup>tm1a</sup> (KOMP)Wtsi	MAHN	C57BL/6Dnk;C57BL/6Dnk;C57BL/6N																									


download a spreadsheet containing all WTSI phenotyping data

**Legend** - hover over each heading to get a more complete description

- Test complete and data/resources are available
- Test is complete but the data are not considered interesting
- Test not performed or applicable
- Test is complete and the data are considered interesting
- Preliminary indication of an interesting phenotype
- Test abandoned
- Test pending
- Link to a test report page
- Link to a pdf report

4. Both heatmaps list details of each mutant mouse line that has been phenotyped by the Sanger MGP for that gene, one row representing one unique allele:
  - Allele Name (column A): Full allele name carried by the mutant mouse line
  - Colony Prefix (column B): Unique identifier for the mutant mouse line
  - Colony Strain (column C): Genetic background upon which the mutant mouse line was phenotyped

## Sanger Mouse Portal “How to” Guide

- The remaining columns present a summary of the phenotyping data collected by the Sanger Mouse Genetics Project split either based on top level Mammalian Phenotype ontology terms (for details of the MP Ontology see [http://www.informatics.jax.org/searches/MP\\_form.shtml](http://www.informatics.jax.org/searches/MP_form.shtml)) or by the phenotyping test. The legend for each presentation is inserted below each heatmap. Note you may need to scroll to the right of the heatmap to see all its contents.
- From the Phenotyping Test Based Heatmap, clicking on any graph symbol  opens the web page on the Sanger Mouse Portal describing the standard protocol and parameters collected for that mutant mouse line/phenotypic test combination.



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### Grip Strength Data for Mysm1 (MAHN)



#### Standard Protocol

Grip Strength (week 9) (Mice were fed on Mouse Breeder Diet (5021, Labdiet) from weaning): Neuromuscular function and muscle strength are assessed with a Bioseb grip strength meter. Three trials each of fore paws and all paws are performed immediately following each other.

[view legend](#)

Parameter	Female Het	Male Het	population parameter	Graph	MP Annotation
Grip Strength Fore Paws Trial 1					
Grip Strength Fore Paws Trial 2					
Grip Strength Fore Paws Trial 3					
Grip Strength All Paws Trial 1					
Grip Strength All Paws Trial 2					
Grip Strength All Paws Trial 3					

# Sanger Mouse Portal “How to” Guide

7. Where the test is complete and the data are considered interesting  (red cells), the  link opens the web page on the Sanger Mouse Portal describing the standard protocol, listing the parameters collected and the Mammalian Phenotype (MP) annotations assigned to describe each observed phenotype, and providing a link to view the graph for each parameter considered significant.



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## Mouse Resources Portal

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### X-ray Imaging Data for Mysm1 (MAHN)



**Standard Protocol - significant parameters**

X-Ray Morphology (week 14) [Mice were fed on High Fat Diet (21.4% crude fat content, Western RD, 829100, Special Diets Services) from 4 weeks of age]: Digital X-Ray images are acquired using a Faxitron system MX20 (Faxitron X-ray Corporation). Mice are anaesthetised and up to five standard images are taken for each mouse. The images are annotated using a standardised protocol

view legend


**Legend** - hover over each heading to get a more complete description

- Test complete and data/resources are available
- Test is complete and the data are considered interesting
- Preliminary indication of an interesting phenotype
- Test is complete but the data are not considered interesting
- Test not performed or applicable
- Test pending
- Test abandoned

Parameter	Female Het	Female Hom	Male Het	Male Hom	population parameter	Graph	MP Annotation
Skull Shape						 view graph	MP:0000438 - abnormal cranium morphology
Zygomatic Bone							
Maxilla							
Mandible							
Teeth							
Scapula							
Clavicle							
Number of Ribs Right							
Number of Ribs Left							
Shape of Ribs						 view graph	MP:0000150 - abnormal rib morphology



## Sanger Mouse Portal “How to” Guide

- Click on the  [view graph](#) icon to open a window that allows you to scroll through graphs of data from both sexes for each significant parameter.



The screenshot displays the Sanger Mouse Resources Portal interface. The main content area shows two bar charts comparing Skull Shape parameters for Female and Male mice across four groups: Controls, Hom (Homozygous), Het (Heterozygous), and Baseline. The y-axis represents the Amount (%).

**Skull Shape - Female**

Group	Abnormal (%)	Normal (%)	Count
Controls	0	100.0	10
Hom	100.0	0	5
Het	0	100.0	11
Baseline	0	100.0	120




**Skull Shape - Male**

Group	Abnormal (%)	Normal (%)	Count
Controls	0	100.0	10
Hom	100.0	0	8
Het	0	100.0	11
Baseline	3.4	96.6	115

Below the charts is a data table with columns: Protocol, Parameter, Female Het, Female Hom, Male Het, Male Hom, population parameter, and MP Annotation. The 'view data' and 'download data' buttons are highlighted with a red box.

Protocol	Parameter	Female Het	Female Hom	Male Het	Male Hom	population parameter	MP Annotation
Standard Protocol	Skull Shape	Normal	Abnormal	Normal	Abnormal		MP:0000438 - abnormal cranium morphology

## Sanger Mouse Portal “How to” Guide

- The raw data from mutant mice (Subjects), wildtype mice run on the same week as the mutants (Controls) and, where appropriate, all age, sex, genetic background and pipeline matched wildtype mice (Baseline) are viewable by clicking the  [view data](#) icon.
- The raw data from mutant mice (Subjects), wildtype mice run on the same week as the mutants (Controls) and, where appropriate, all age, sex, genetic background and pipeline matched wildtype mice (Baseline) can be downloaded as an XML document by clicking the  [download data](#) icon.
- From the MP Ontology Based Heatmap, clicking on a graph symbol  may open the web page on the Sanger Mouse Portal describing one standard protocol or a collection of standard protocols grouped under a single MP term. For example, the MP term “limbs/digits/tail” groups data from Dysmorphology, X-ray imaging, MicroCT & Quantitative Faxitron and, where related MP terms have been assigned, Recessive Lethality.



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#### Phenotyping Data for Mym1 (MAHN) Associated with 'limbs/digits/tail' (MP:0005371)

- [Dysmorphology: Dysmorphology - significant parameters](#)
- [X-ray Imaging: Standard Protocol - significant parameters](#)
- [Recessive Lethal Study: Standard Protocol - significant parameters](#)
- [MicroCT & Quantitative Faxitron: Standard Protocol](#)

- Data from each of these phenotyping tests can be accessed as described above (steps 6-10) simply by clicking the standard protocol of interest.