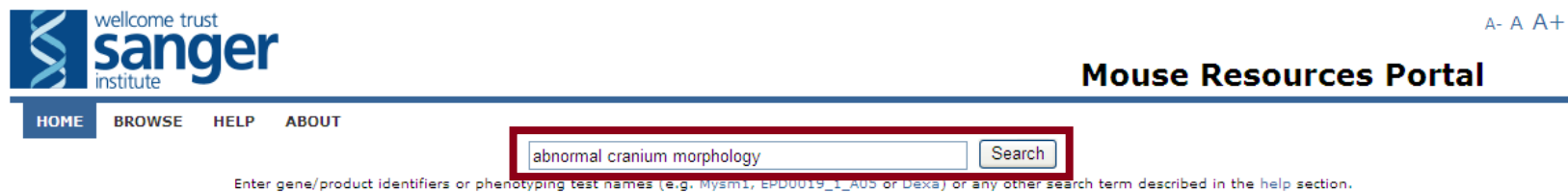


Sanger Mouse Portal “How to” Guide

How to search for lines assigned a particular mammalian phenotype (MP) ontology term or key word

1. From the Sanger Mouse Portal home page (<http://www.sanger.ac.uk/mouseportal/>), enter your mammalian phenotype (MP) ontology term of interest (e.g. abnormal cranium morphology), or key word from that term (e.g. cranium), into the **Search** field and click search:



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Enter gene/product identifiers or phenotyping test names (e.g. Mym1, EP00019_1_A05 or Daxa) 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 C57BL/6J 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.

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2. This returns a list of genes that have been assigned the MP term abnormal cranium morphology or the key word used from that term.

The screenshot shows the Sanger Mouse Resources Portal search results for the query 'abnormal cranium morphology'. The page features the Wellcome Trust Sanger Institute logo, navigation links (HOME, BROWSE, HELP, ABOUT), and a search bar. The search results are displayed as a list of genes, each with a 'Datasets' section containing links to various resources. The gene 'Cenpj' is highlighted with a red box. The 'Datasets' section for 'Cenpj' is also highlighted with a red box, showing links to Gene Details, WTSI Phenotyping, Mice, IKMC Vectors and ES Cells, and DNA Clone Resources. The page includes pagination controls at the top and bottom.

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Search Results for 'abnormal cranium morphology'

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Explain These Search Results

▸ **Cdk5rap2** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Cenpj** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Csrp2bp** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Daam2** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Exoc3l2** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Kdm4b** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Ltbp1** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Mysm1** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Nsun2** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

▸ **Phf20** Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

« Previous 1 2 Next »

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3. This list summarises the available data for each gene split into the following datasets that are populated (pink with white writing) when resources are available and grey when no information is available:

Datasets: Gene Details WTSI Phenotyping Mice IKMC Vectors and ES Cells DNA Clone Resources

- i. Gene Details
 - ii. WTSI Phenotyping
 - iii. Mice
 - iv. IKMC Vectors and ES Cells
 - v. DNA Clone Resources
4. These data can be reviewed one gene at a time as follows. Click on the first gene of interest e.g. *Cenpj*. This rolls down the gene specific information split into the above datasets.

The screenshot shows the Sanger Mouse Resources Portal interface. At the top left is the Wellcome Trust Sanger Institute logo. On the right, there is a search bar with the text "Search Results for 'abnormal cranium morphology'" and a search button. Below the search bar, there are navigation links: "HOME", "BROWSE", "HELP", and "ABOUT". A search bar contains the text "abnormal cranium morphology" and a "search" button. Below the search bar, there are pagination links: "« Previous", "1", "2", "Next »". A button labeled "Explain These Search Results" is visible. The search results are displayed in a list format. The first result is "Cdk5rap2" with a dropdown arrow. To its right, there are dataset filters: "Gene Details", "WTSI Phenotyping", "Mice", "IKMC Vectors and ES Cells", and "DNA Clone Resources". The second result is "Cenpj" with a dropdown arrow. Below "Cenpj", there is a section for "Gene Details" with the text "no data available". Below "Gene Details", there is a section for "WTSI Phenotyping" with a dropdown arrow. Under "WTSI Phenotyping", there is a link for "MP Ontology Based Heatmap".

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5. 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

▼ WTSI Phenotyping

MP Ontology Based Heatmap

Allele Name	Colony Prefix	Colony Strain	adipose tissue	behavior/neurological	cardiovascular system	cellular	craniofacial	digestive/alimentary	embryogenesis	endocrine/exocrine gland	growth/size	hearing/vestibular/ear	hematopoietic system	homeostasis/metabolism	immune system	integument	limbs/digits/tail	liver/biliary system	mortality/aging	muscle	nervous system	other	pigmentation	renal/urinary system	reproductive system	respiratory system	skeleton	taste/olfaction	tumorigenesis	vision/eye
Cenpj ^{tm1a} (EuCOMM)Wtsi	MBKA																													

Legend: No Raw Data No Significant Annotations Significant Annotation Present Link to a test report page

About This Heatmap

This heatmap is built up of top-level terms from the MP (Mammalian Phenotype) ontology. We have mapped a majority of the parameters in our tests to appropriate MP terms, so when we perform a given test we can say if it should be annotated with the given MP term (if the phenotype is significant). This is what you see in this heatmap - if a significant result has been annotated to a top-level MP term (or any of its children), the cell will be red, if the result was not significant, the cell will be blue.

Please Note: as mentioned above we do not annotate all of our phenotyping tests to the MP ontology. The tests that are excluded are: 'Adult LacZ Expression', 'Brain/Eye/Skin Histopathology', 'Embryo LacZ Expression', 'Fertility', 'Heart Histology', 'Micronuclei', 'MicroCT & Quantitative Faxitron', 'Plasma Immunoglobulins', 'Prepulse Inhibition', 'Recessive Lethal Study', 'Tail Epidermis Wholemount', 'Tissue Biobank' and 'Viability at Weaning'. You can find our results for these tests in the 'Phenotyping Test Based Heatmap' below.

Phenotyping Test Based Heatmap

- 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.

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▼ **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)	Peripheral Blood Lymphocytes	Micronuclei	Tissue Biobank	Heart Weight
Cenp1 ^{tm1a} (EUCOMM)Wtsi	MBKA																														

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

- 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
- 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

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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 Cenpj (MBKA)



Standard Protocol

Grip Strength (week 9) [Mice were fed on High Fat Diet (21.4% crude fat content, Western RD, 829100, Special Diets Services) from 4 weeks of age]: 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	Female Hom	Male Het	Male Hom	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							

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9. 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.








Weight Curves Data for Cenpj (MBKA)






Weight Curves (HFD) - significant parameters


Weight Curves [Mice were fed on High Fat Diet (21.4% crude fat content, Western RD, 829100, Special Diets Services) from 4 weeks of age]: Mice of both genders are weighed at regular intervals between 4 and 16 weeks of age.

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
Weight Curve						 view graph	MP:0001262 - decreased body weight

10. 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.

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Weight Curves Data

Weight Curves (HFD) - significant

Weight Curves [Mice were fed on HFD between 4 and 16 weeks of age]

view legend

legend - hover over each heading

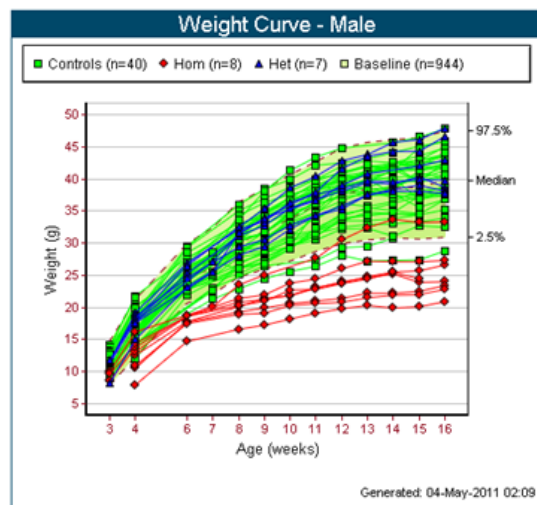
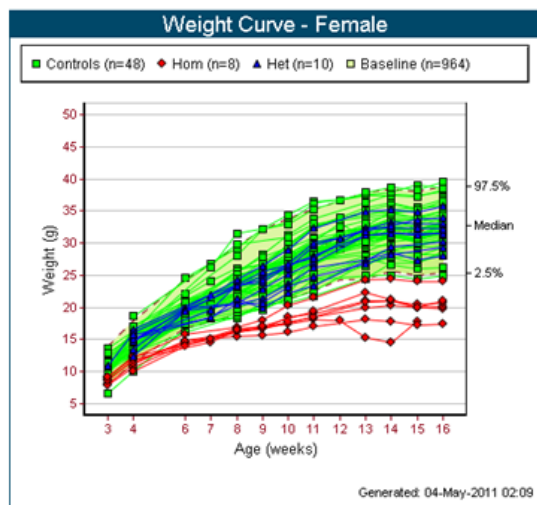
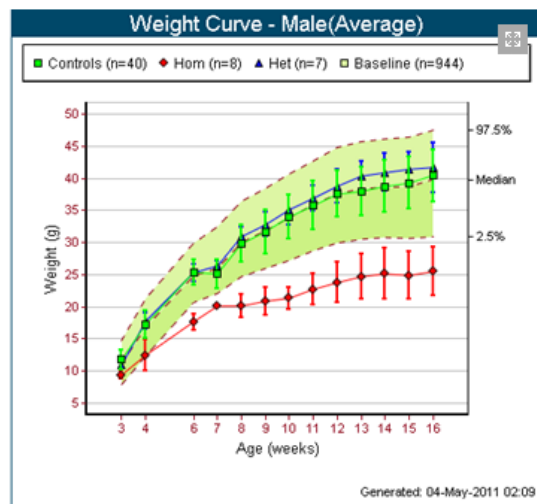
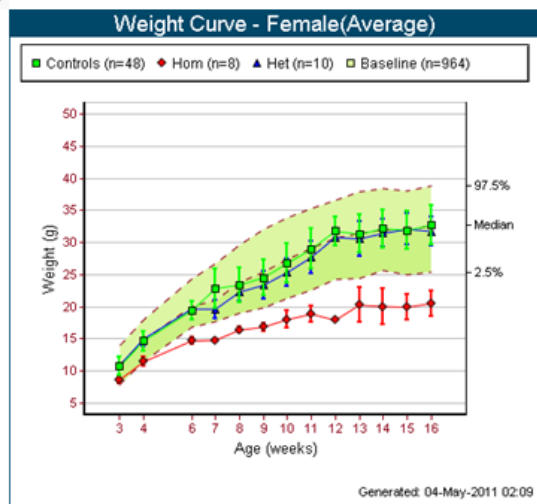
Test complete and data/responses available

Test is complete but the data is not available

Test abandoned

Parameter	Female Het	Female Hom
Weight Curve		




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[view data](#) [download data](#)

Protocol	Parameter	Female Het	Female Hom	Male Het	Male Hom	population parameter	MP Annotation
Weight Curves (HFD)	Weight Curve						MP:0001262 - decreased body weight

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11. 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.
12. 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.
13. 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.



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Phenotyping Data for Cenpj (MBKA) Associated with 'limbs/digits/tail' (MP:0005371)

[Dysmorphology: Dysmorphology - significant parameters](#)

[X-ray Imaging: Standard Protocol - significant parameters](#)

[MicroCT & Quantitative Faxitron: Standard Protocol](#)

14. Data from each of these phenotyping tests can be accessed as described above (steps 8-12) simply by clicking the standard protocol of interest.