

# *Ctsh* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Ctsh*

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**Project type**

**Cas9-KO**

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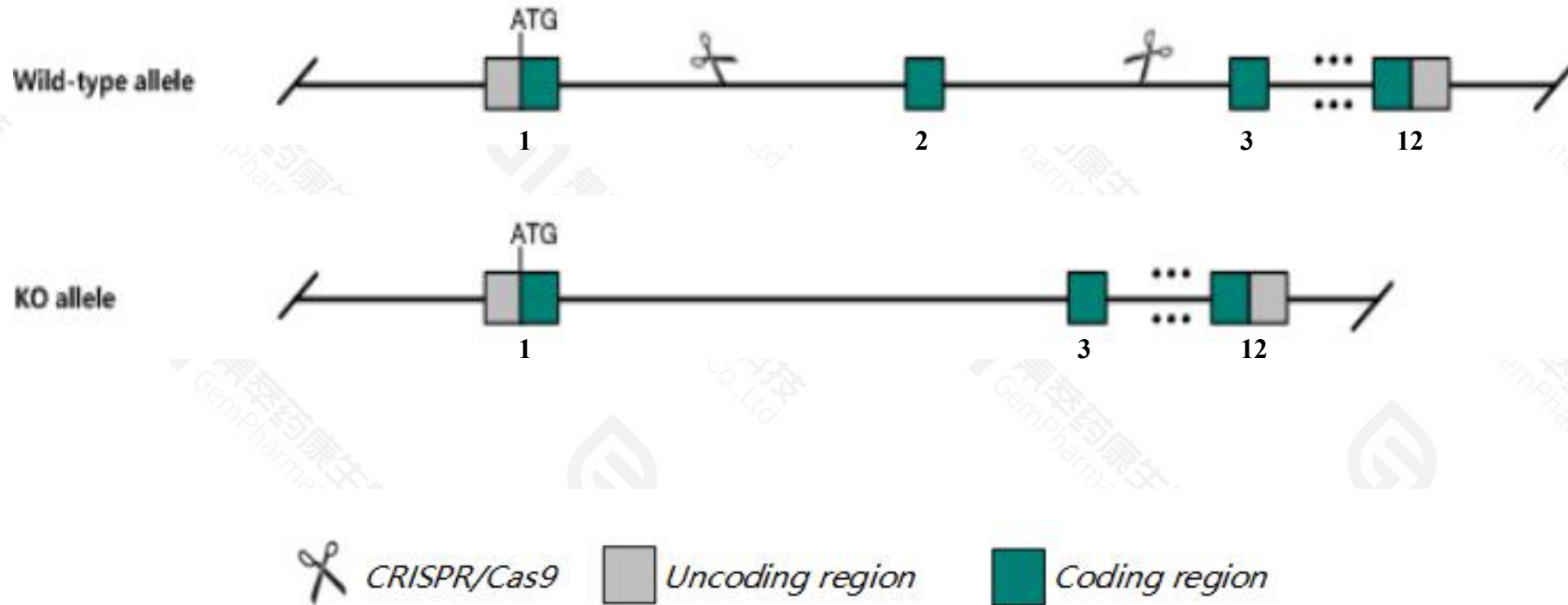
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ctsh* gene. The schematic diagram is as follows:



- The *Ctsh* gene has 11 transcripts. According to the structure of *Ctsh* gene, exon2 of *Ctsh-201*(ENSMUST00000034915.15) transcript is recommended as the knockout region. The region contains 32bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ctsh* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice homozygous for a reporter allele exhibit impaired lung surfactant and an abnormal eye globe with elongated axial length.
- The *Ctsh* gene is located on the Chr9. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)

## Ctsh cathepsin H [Mus musculus (house mouse)]

Gene ID: 13036, updated on 13-Mar-2020

### Summary

**Official Symbol** Ctsh provided by [MGI](#)

**Official Full Name** cathepsin H provided by [MGI](#)

**Primary source** [MGI:MGI:107285](#)

**See related** [Ensembl:ENSMUSG00000032359](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** AL022844

**Summary** This gene encodes a member of the peptidase C1 (papain) family of cysteine proteases. Alternative splicing results in multiple transcript variants, at least one of which encodes a preproprotein that is proteolytically processed to generate multiple protein products. These products include the cathepsin H mini, heavy, and light chains. In rat and human, these three chains can associate to form the mature enzyme, which has both aminopeptidase and endopeptidase activities. Homozygous knockout mice for this gene exhibit impaired lung surfactant processing and reduced tumorigenesis in a pancreatic cancer model. Multiple pseudogenes of this gene have been identified in the genome. [provided by RefSeq, Aug 2015]

**Expression** Broad expression in placenta adult (RPKM 82.3), bladder adult (RPKM 57.4) and 21 other tissues [See more](#)

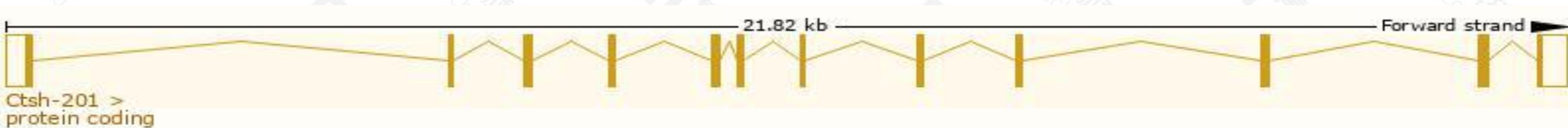
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

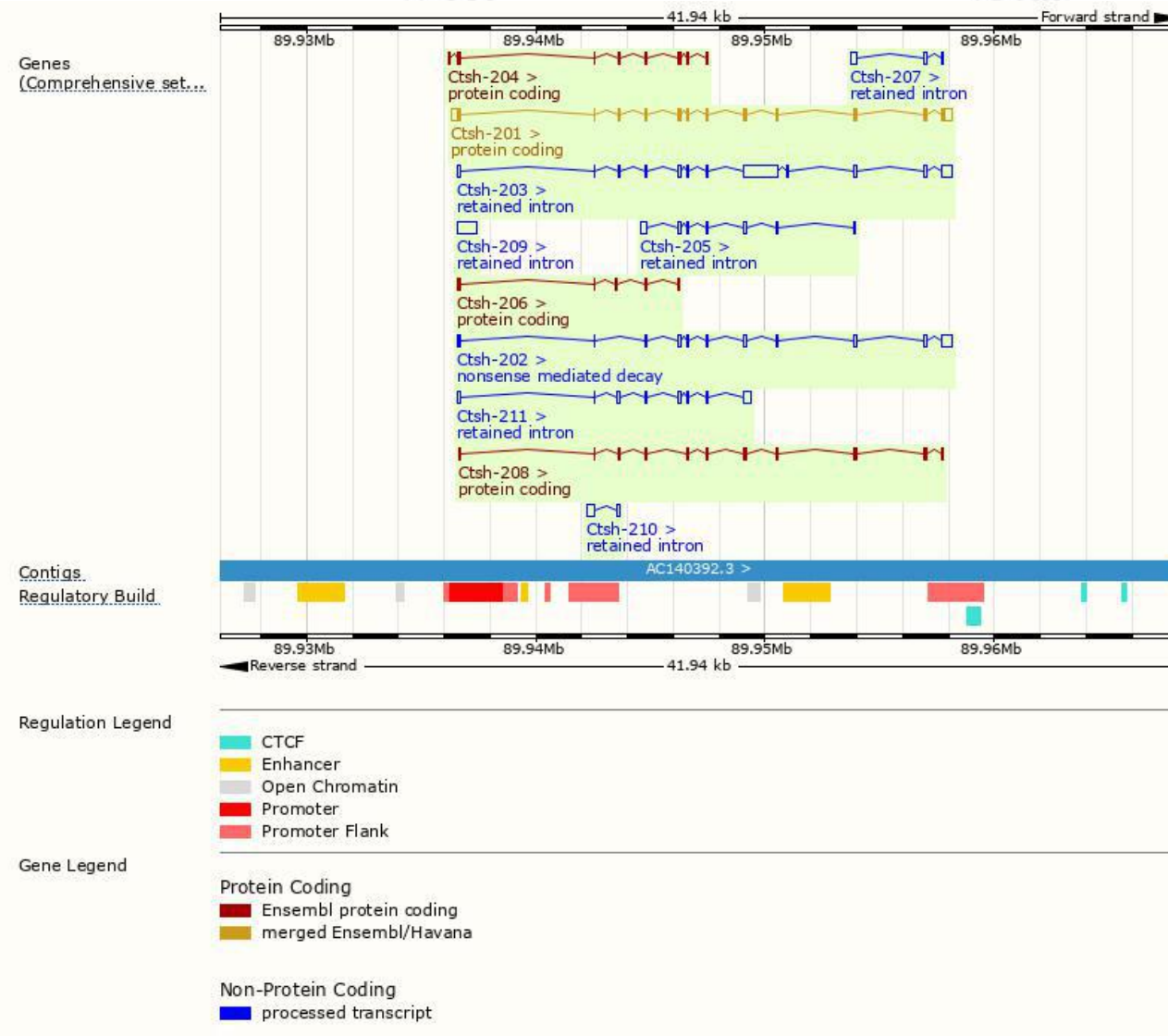
The gene has 11 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ctsh-201	<a href="#">ENSMUST0000034915.14</a>	1617	<a href="#">333aa</a>	Protein coding	<a href="#">CCDS23399</a>	<a href="#">P49935</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Ctsh-208	<a href="#">ENSMUST00000185459.1</a>	872	<a href="#">290aa</a>	Protein coding	-	<a href="#">A0A087WR20</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Ctsh-204	<a href="#">ENSMUST00000132718.7</a>	631	<a href="#">198aa</a>	Protein coding	-	<a href="#">D3Z437</a>	CDS 3' incomplete TSL:3
Ctsh-206	<a href="#">ENSMUST00000143172.7</a>	370	<a href="#">119aa</a>	Protein coding	-	<a href="#">D3YVI3</a>	CDS 3' incomplete TSL:3
Ctsh-202	<a href="#">ENSMUST00000123320.7</a>	1238	<a href="#">41aa</a>	Nonsense mediated decay	-	<a href="#">D7UJQ9</a>	TSL:1
Ctsh-203	<a href="#">ENSMUST00000127842.7</a>	2743	No protein	Retained intron	-	-	TSL:2
Ctsh-211	<a href="#">ENSMUST00000190338.6</a>	873	No protein	Retained intron	-	-	TSL:3
Ctsh-209	<a href="#">ENSMUST00000186126.1</a>	818	No protein	Retained intron	-	-	TSL:NA
Ctsh-205	<a href="#">ENSMUST00000142750.1</a>	732	No protein	Retained intron	-	-	TSL:3
Ctsh-210	<a href="#">ENSMUST00000187437.1</a>	480	No protein	Retained intron	-	-	TSL:3
Ctsh-207	<a href="#">ENSMUST00000151219.1</a>	424	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Ctsh-201* transcript, the transcription is shown below:

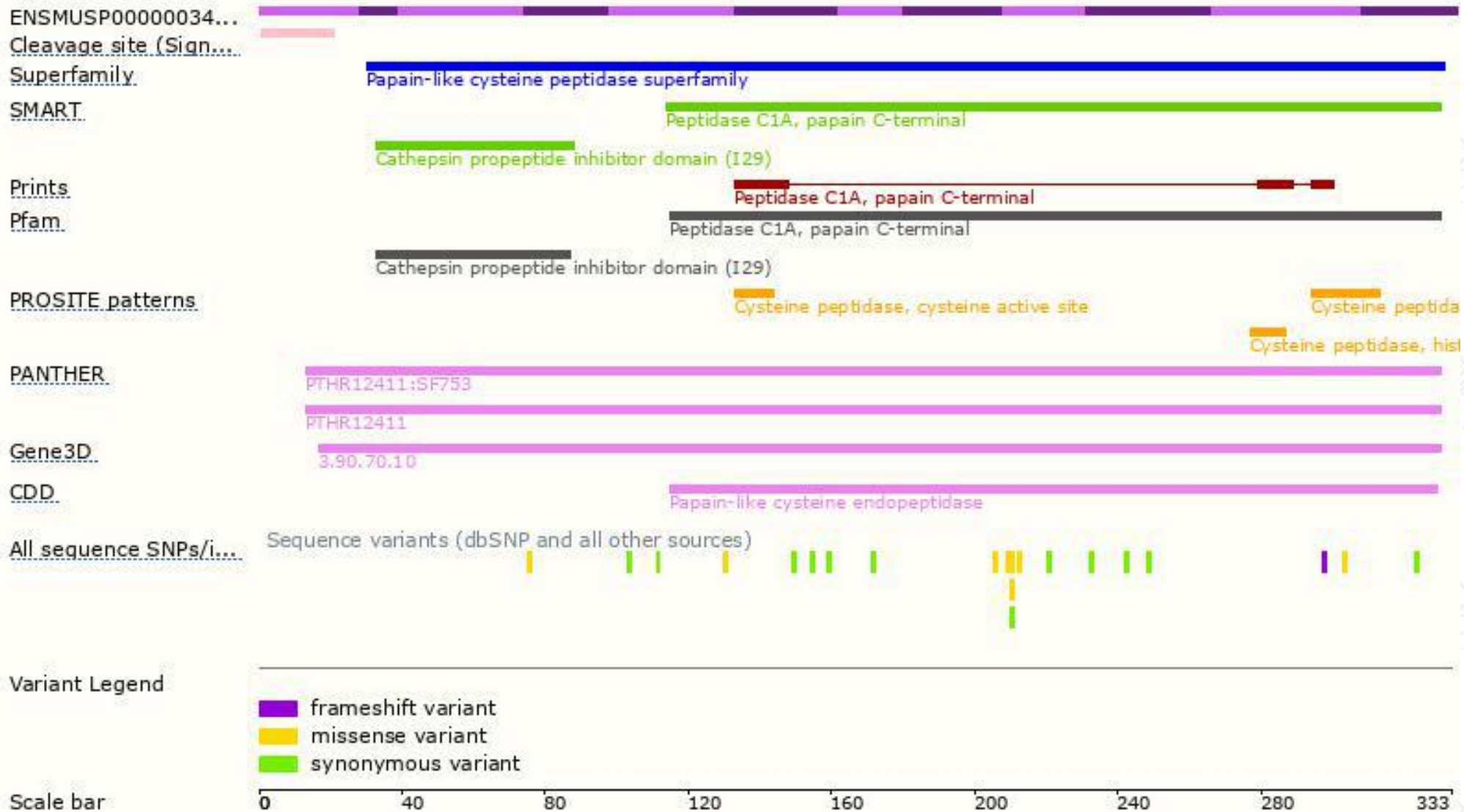


# Genomic location distribution

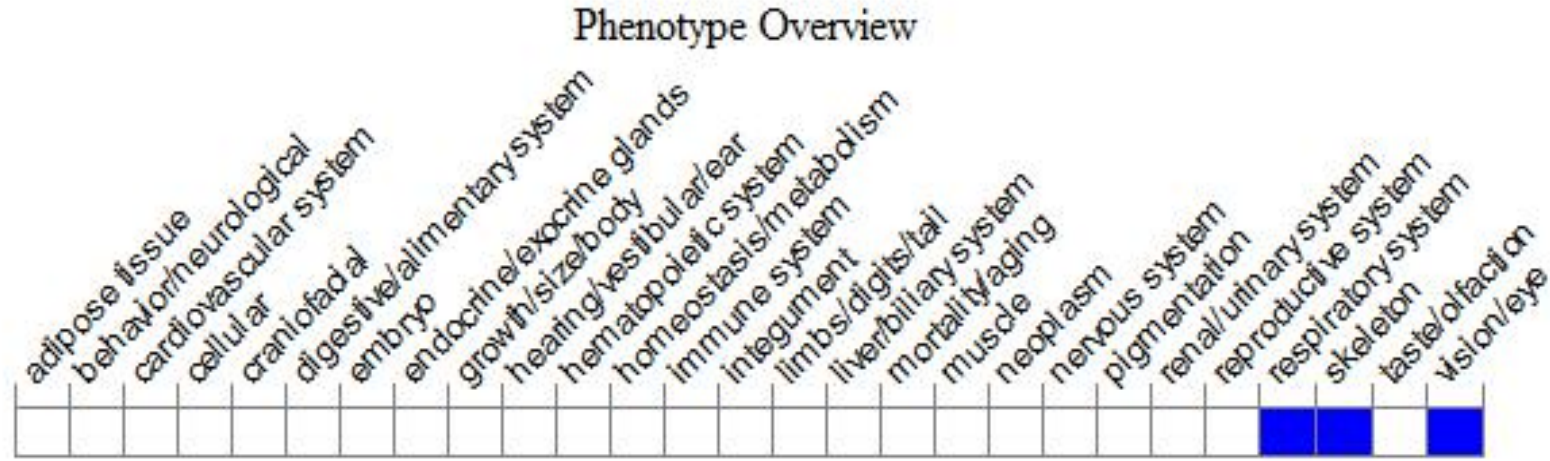




# Protein domain



# Mouse phenotype description(MGI)



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, mice homozygous for a reporter allele exhibit impaired lung surfactant and an abnormal eye globe with elongated axial length.

If you have any questions, you are welcome to inquire.

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