

Zfat Cas9-KO Strategy

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Project Overview

Project Name

Zfat

Project type

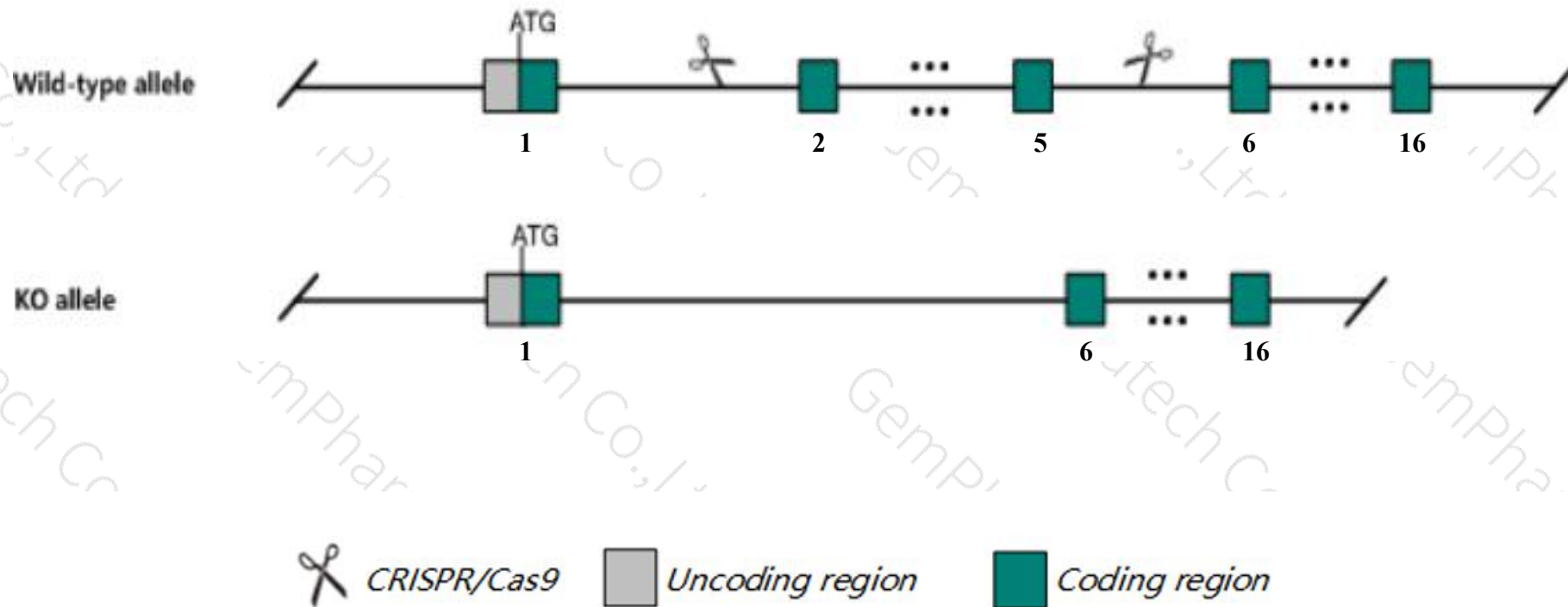
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Zfat* gene has 5 transcripts. According to the structure of *Zfat* gene, exon2-exon5 of *Zfat*-202(ENSMUST00000160248.7) transcript is recommended as the knockout region. The region contains 766bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfat* 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 knock-out allele exhibit complete embryonic lethality associated with failure to initiation of embryo turning, abnormal embryonic hematopoiesis, abnormal spongiotrophoblast layer morphology, abnormal visceral yolk sac blood island morphology and pale yolk sac.
- The *Zfat* gene is located on the Chr15. 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)

Zfat zinc finger and AT hook domain containing [Mus musculus (house mouse)]

Gene ID: 380993, updated on 13-Mar-2020

Summary



Official Symbol [Zfat](#) provided by [MGI](#)

Official Full Name [zinc finger and AT hook domain containing](#) provided by [MGI](#)

Primary source [MGI:MGI:2681865](#)

See related [Ensembl:ENSMUSG00000022335](#)

Gene type [protein coding](#)

RefSeq status [VALIDATED](#)

Organism [Mus musculus](#)

Lineage [Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Glires](#); [Rodentia](#); [Myomorpha](#); [Muroidea](#); [Muridae](#); [Murinae](#); [Mus](#); [Mus](#)

Also known as [Gm922](#), [Zfat1](#), [Zfp406](#)

Expression Ubiquitous expression in ovary adult (RPKM 1.9), placenta adult (RPKM 1.6) and 28 other tissues [See more](#)

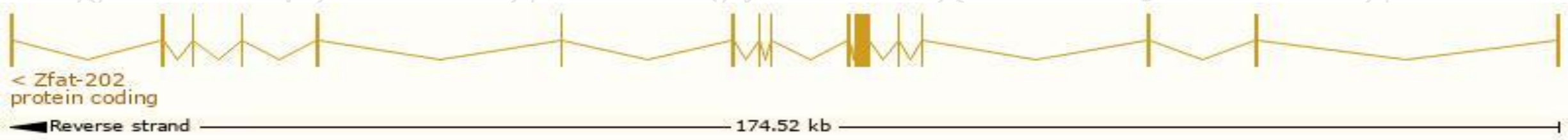
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

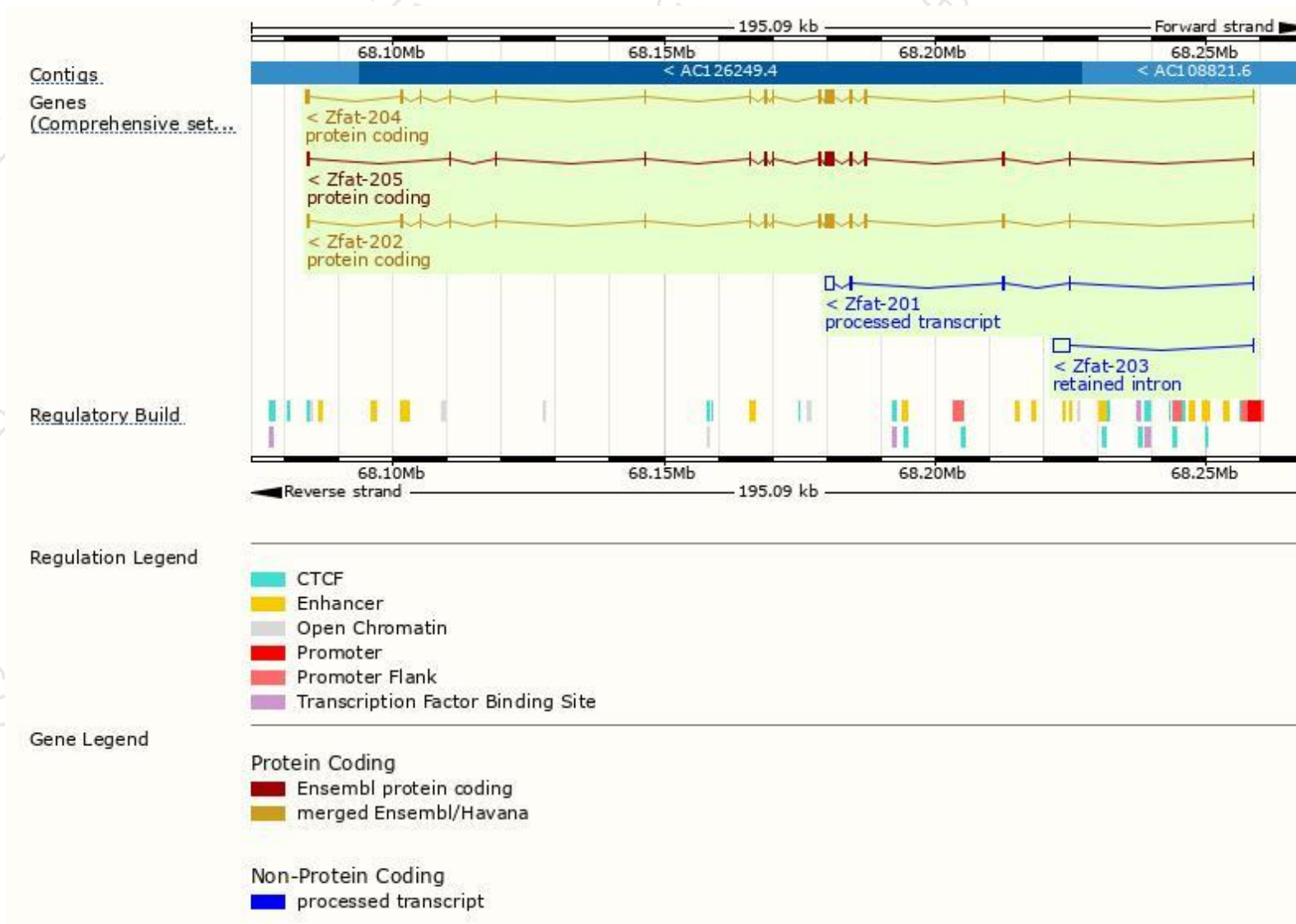
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfat-204	ENSMUST00000162054.8	4388	1219aa	Protein coding	CCDS49624	Q7TS63	TSL:1 GENCODE basic APPRIS ALT2
Zfat-202	ENSMUST00000160248.7	3866	1237aa	Protein coding	CCDS49623	Q7TS63	TSL:1 GENCODE basic APPRIS P4
Zfat-205	ENSMUST00000162173.7	3561	1152aa	Protein coding	-	E0CX30	TSL:5 GENCODE basic APPRIS ALT2
Zfat-201	ENSMUST00000159430.1	2021	No protein	Processed transcript	-	-	TSL:5
Zfat-203	ENSMUST00000161139.1	3240	No protein	Retained intron	-	-	TSL:3

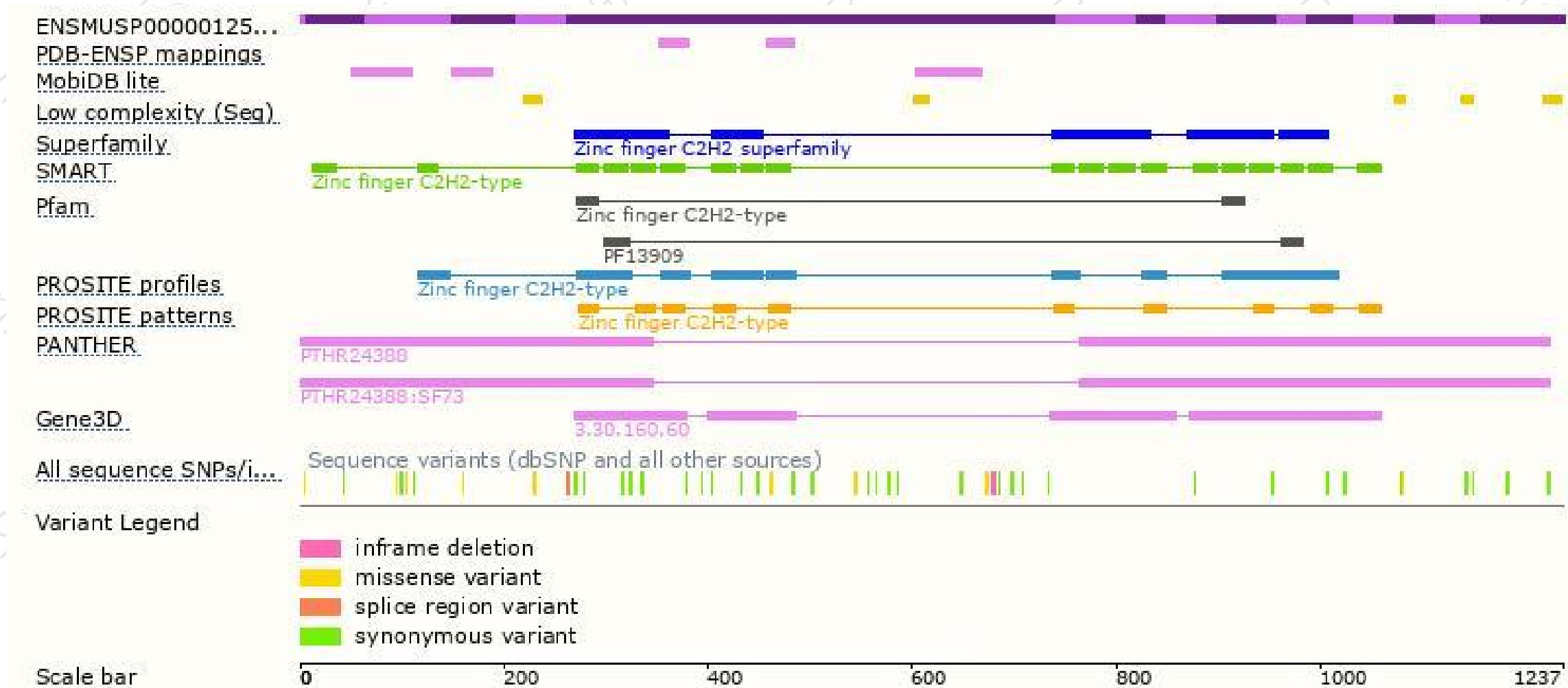
The strategy is based on the design of *Zfat-202* transcript,the transcription is shown below:



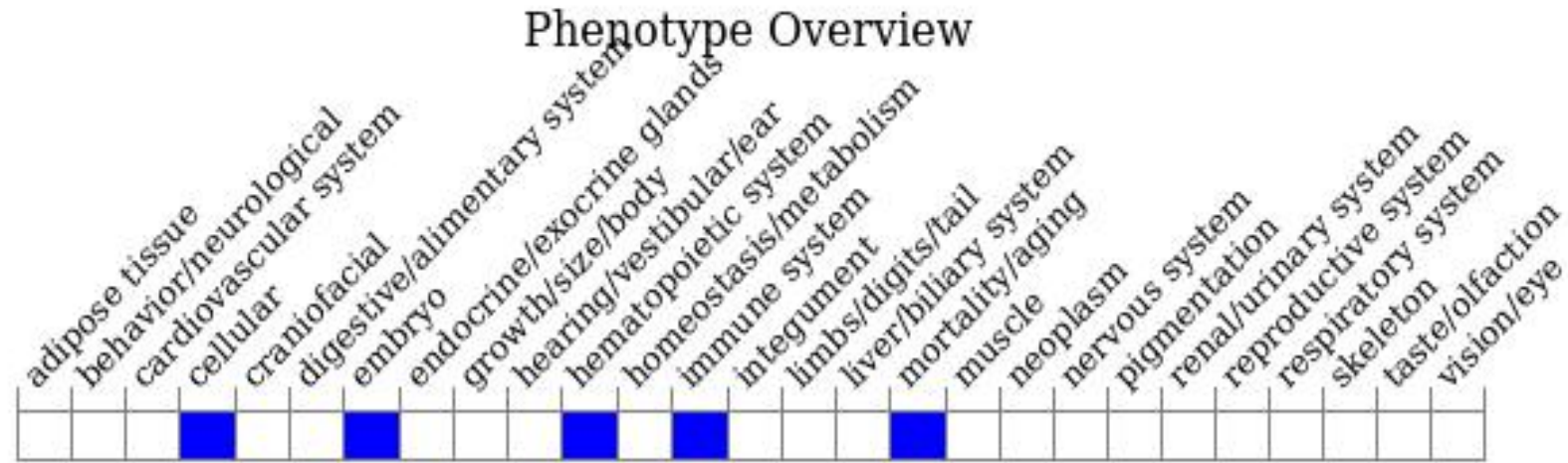
Genomic location distribution



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/>).

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

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