

Ptprm Cas9-CKO Strategy

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Project Overview

Project Name

Ptprm

Project type

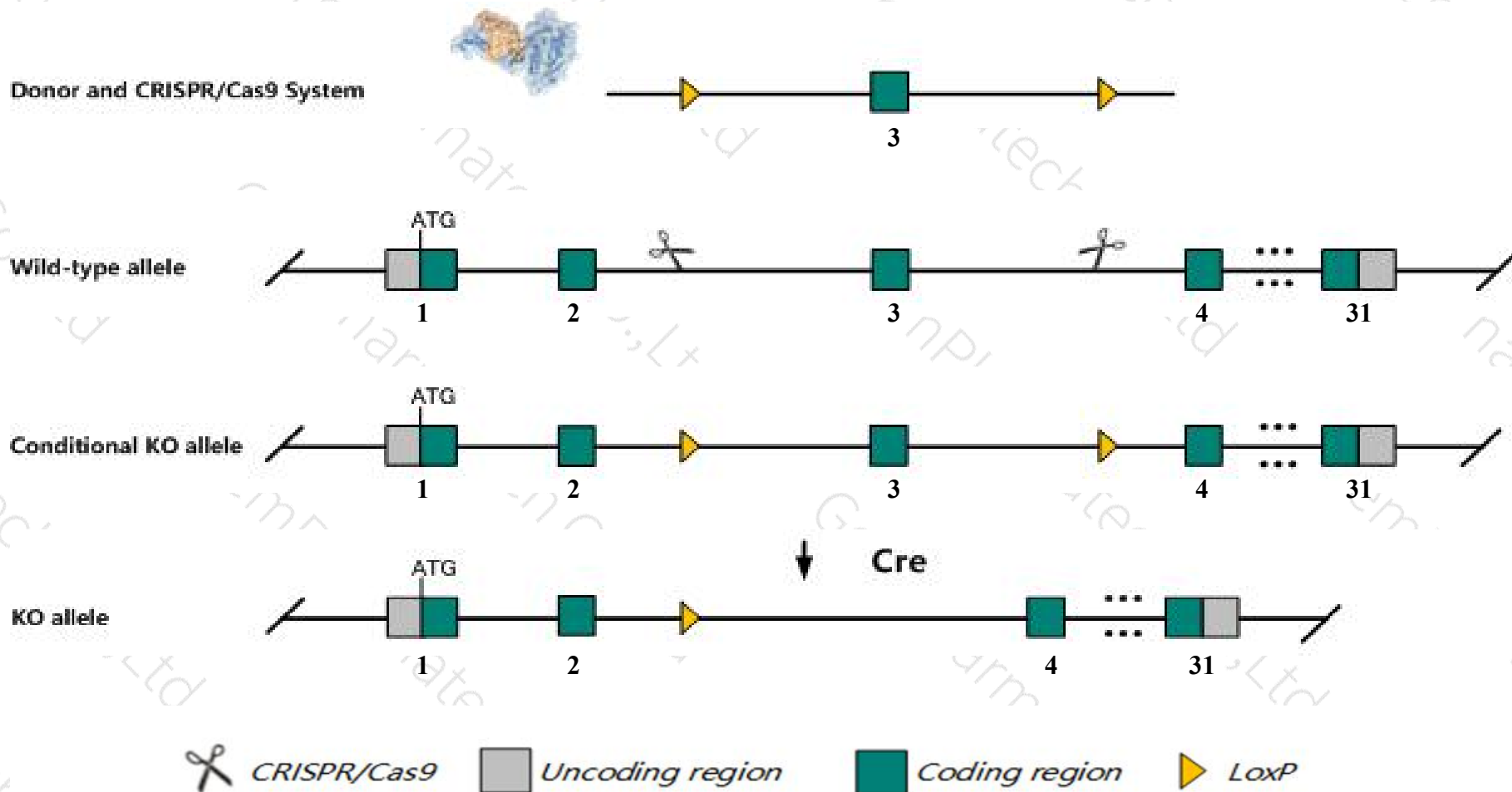
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Ptprm* gene has 7 transcripts. According to the structure of *Ptprm* gene, exon3 of *Ptprm-202* (ENSMUST00000223982.1) transcript is recommended as the knockout region. The region contains 272bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptprm* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data, Homozygous mutation of this gene results in impaired flow-induced dilation in mesenteric resistance arteries.
- The effect on transcript *Ptprm*-204 is unknown.
- Transcript *Ptprm*-205&206&207 may not be affected.
- The *Ptprm* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ptpm protein tyrosine phosphatase, receptor type, M [*Mus musculus* (house mouse)]

Gene ID: 19274, updated on 24-Dec-2019

Summary

Official Symbol Ptpm provided by [MGI](#)
Official Full Name protein tyrosine phosphatase, receptor type, M provided by [MGI](#)
Primary source [MGI:MGI:102694](#)
See related [Ensembl:ENSMUSG00000033278](#)
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 RPTPmu; mKIAA4044
Expression Broad expression in lung adult (RPKM 20.9), heart adult (RPKM 9.9) and 19 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 17 E1.1; 17 37.88 cM

See Ptpm in [Genome Data Viewer](#)

Exon count: 33

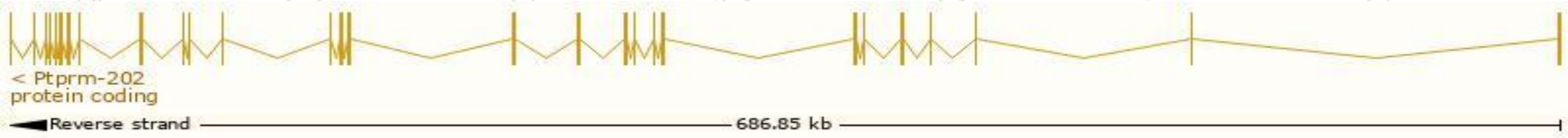
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (66666848..67354491, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (67016188..67703799, complement)

Transcript information (Ensembl)

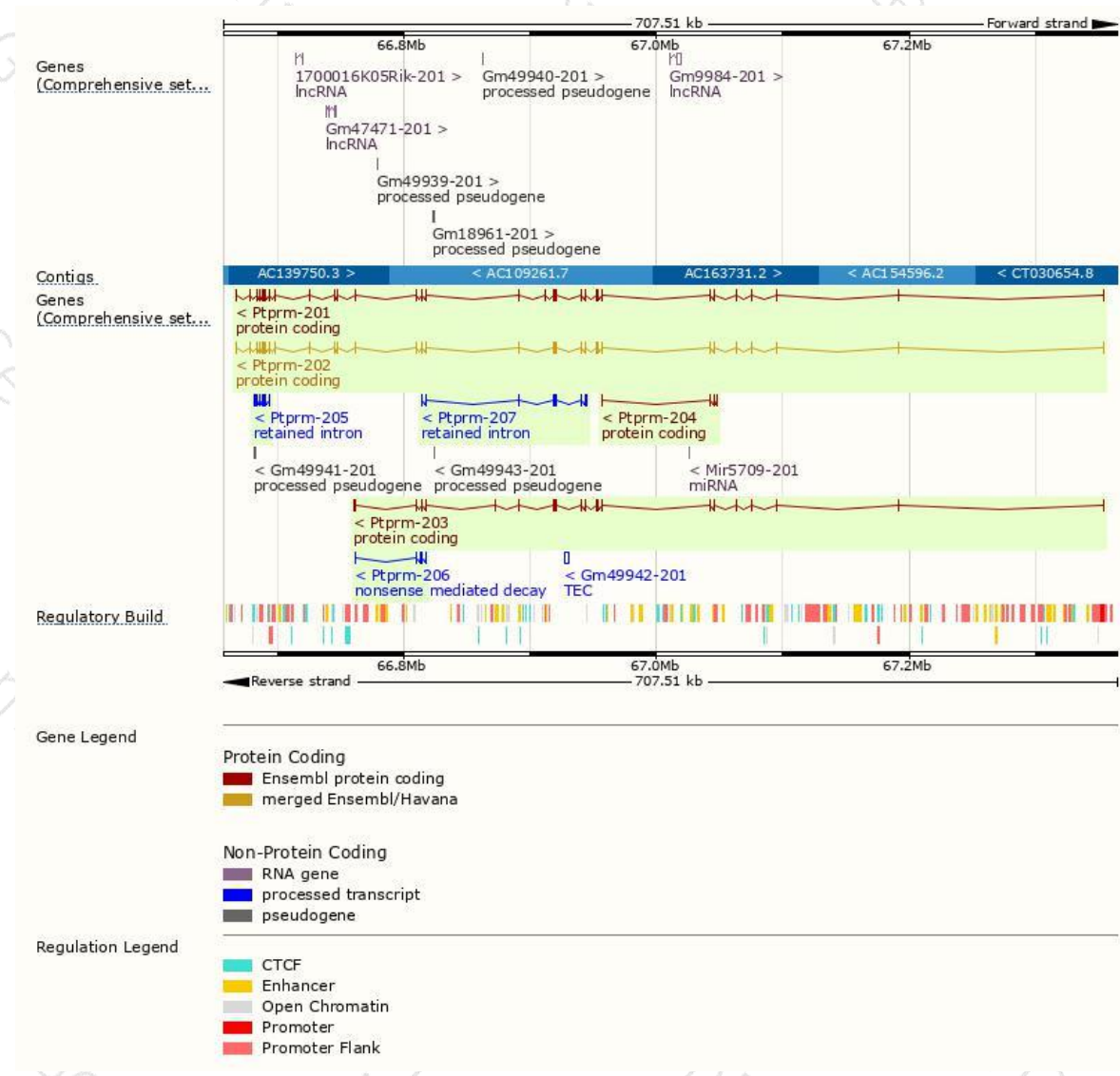
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptpm-202	ENSMUST00000223982.1	4802	1452aa	Protein coding	CCDS28948	P28828	GENCODE basic APPRIS P2
Ptpm-201	ENSMUST00000037974.9	5186	1486aa	Protein coding	-	Q68FM4	TSL:1 GENCODE basic APPRIS ALT 1
Ptpm-203	ENSMUST00000224091.1	3773	990aa	Protein coding	-	A0A286YDL1	GENCODE basic
Ptpm-204	ENSMUST00000224862.1	754	160aa	Protein coding	-	A0A286YCW9	CDS 3' incomplete
Ptpm-206	ENSMUST00000225554.1	590	77aa	Nonsense mediated decay	-	A0A286YCL1	CDS 5' incomplete
Ptpm-205	ENSMUST00000225074.1	2713	No protein	Retained intron	-	-	
Ptpm-207	ENSMUST00000225688.1	1674	No protein	Retained intron	-	-	

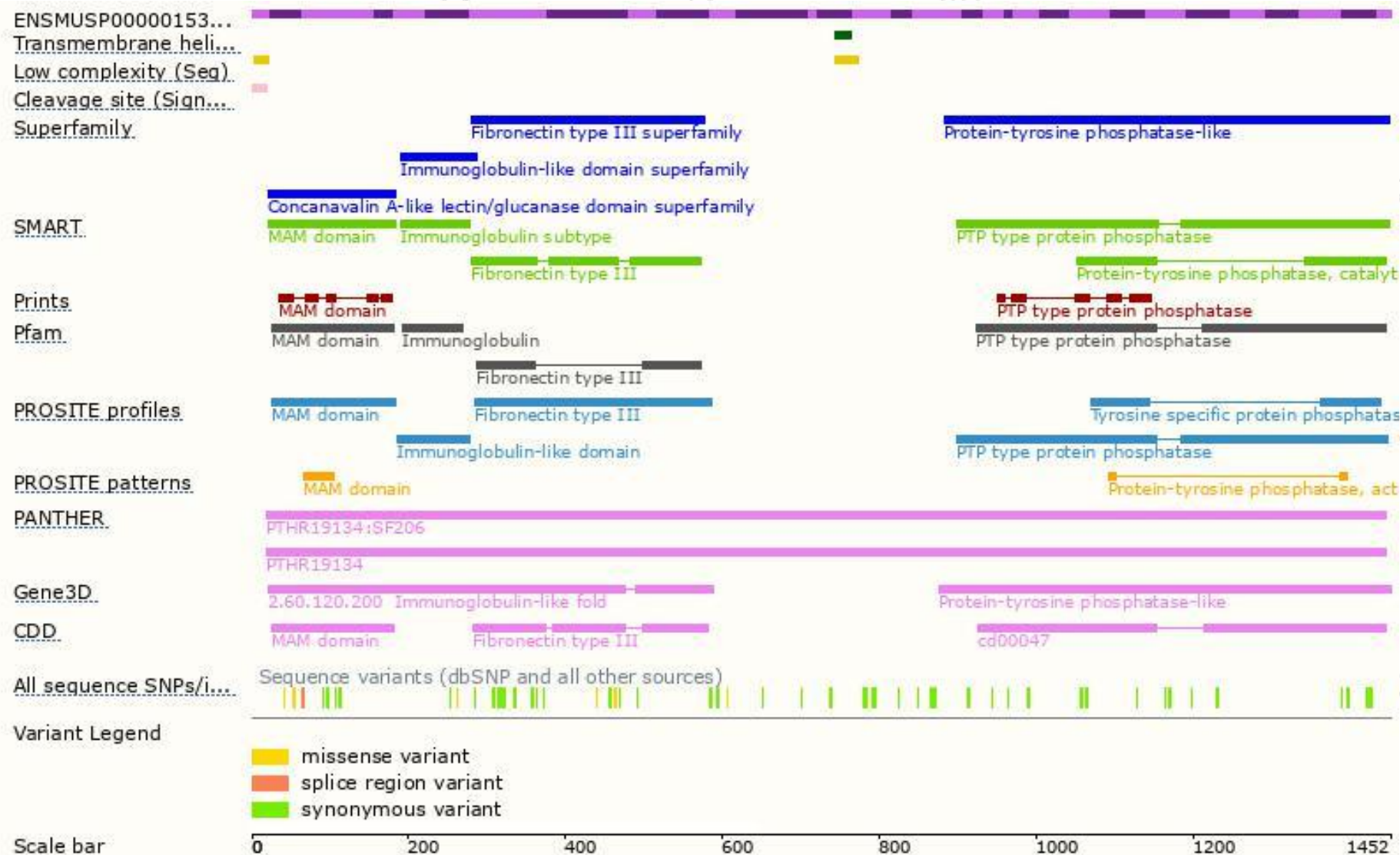
The strategy is based on the design of *Ptpm-202* transcript,The transcription is shown below



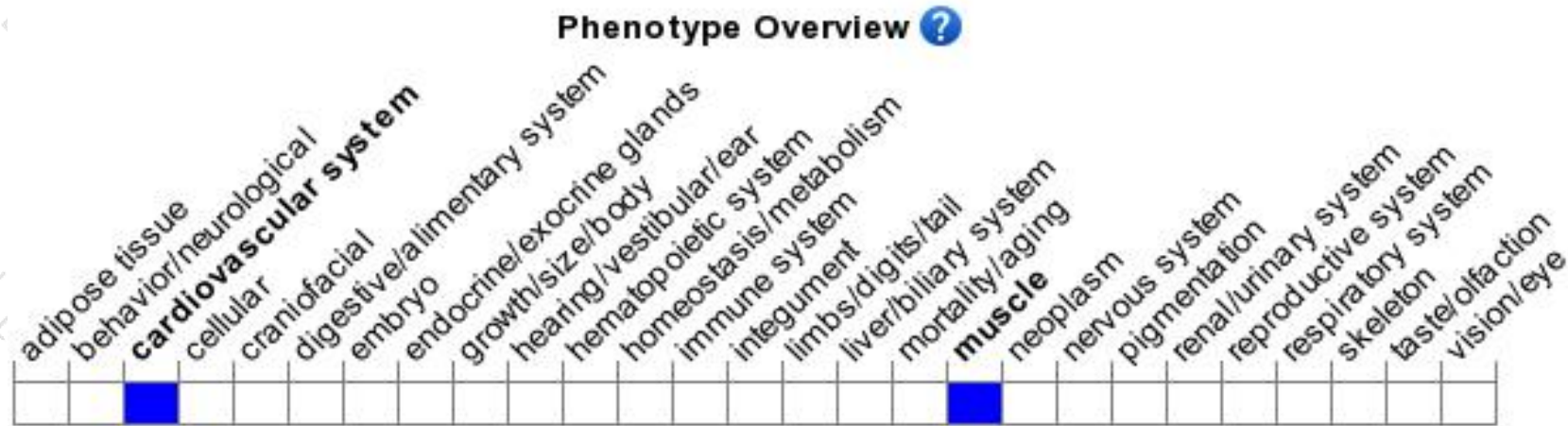
Genomic location distribution



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/>).

According to the existing MGI data, Homozygous mutation of this gene results in impaired flow-induced dilation in mesenteric resistance arteries.

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

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