

Kcnj15 Cas9-CKO Strategy

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Project Overview

Project Name

Kcnj15

Project type

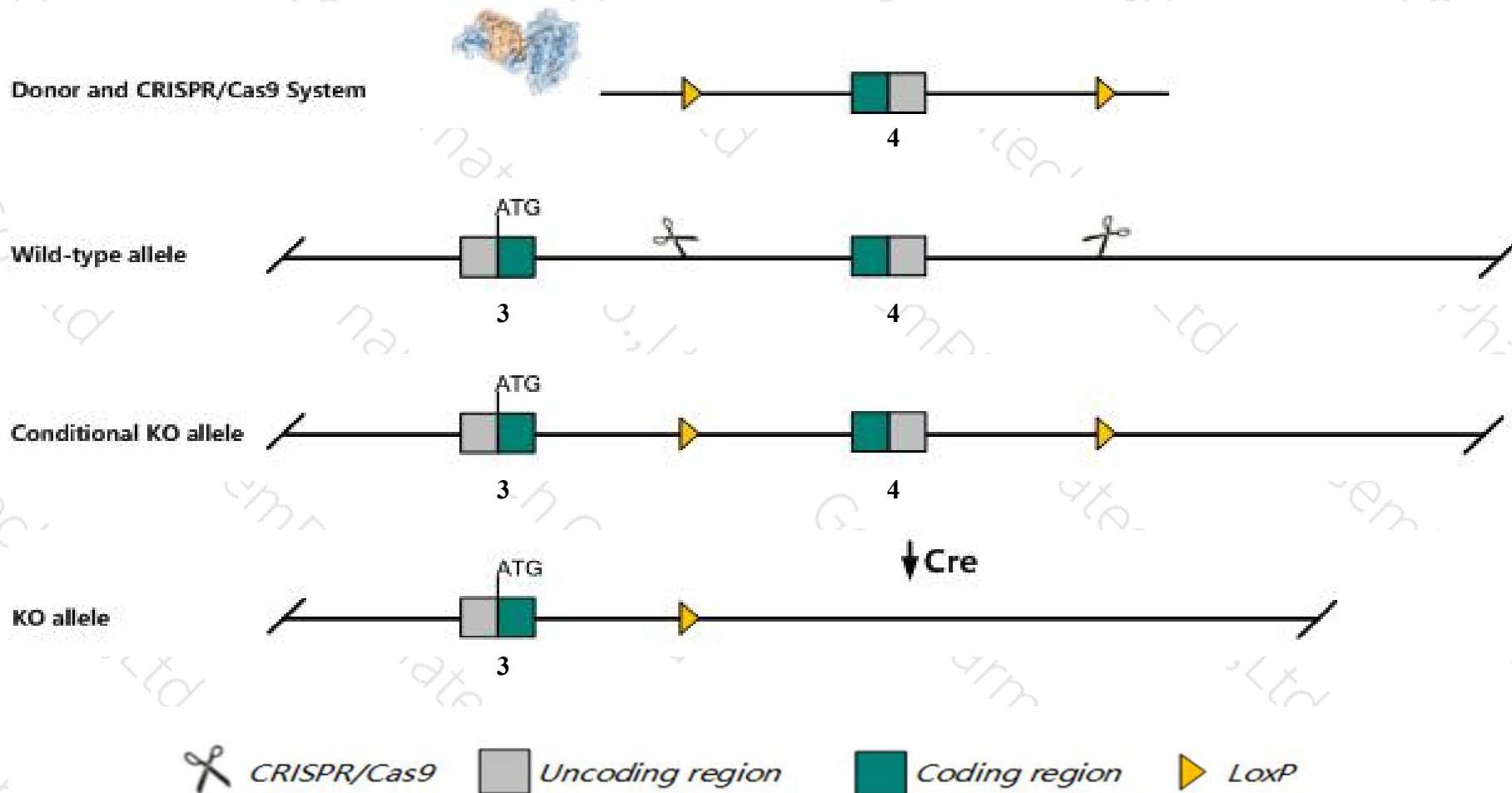
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnj15* gene. The schematic diagram is as follows:



- The *Kcnj15* gene has 13 transcripts. According to the structure of *Kcnj15* gene, exon4 of *Kcnj15*-208 (ENSMUST00000113862.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnj15* 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.

- According to the existing MGI data, Homozygous knockout mice exhibited impaired balance/coordination in a high-throughput screen.
- The KO region contains functional region of the *Gm49643* and *Gm31641* gene. Knockout the region may affect the function of *Gm49643* and *Gm31641* gene.
- The *Kcnj15* gene is located on the Chr16. 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)

Kcnj15 potassium inwardly-rectifying channel, subfamily J, member 15 [Mus musculus (house mouse)]

Gene ID: 16516, updated on 13-Mar-2020

Summary



Official Symbol Kcnj15 provided by [MGI](#)

Official Full Name potassium inwardly-rectifying channel, subfamily J, member 15 provided by [MGI](#)

Primary source [MGI:MGI:1310000](#)

See related [Ensembl:ENSMUSG00000062609](#)

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 4930414N08Rik, AI182284, AI267127, IRKK, Kir4.2

Expression Biased expression in kidney adult (RPKM 32.3), lung adult (RPKM 4.3) and 2 other tissues [See more](#)

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

Transcript information (Ensembl)

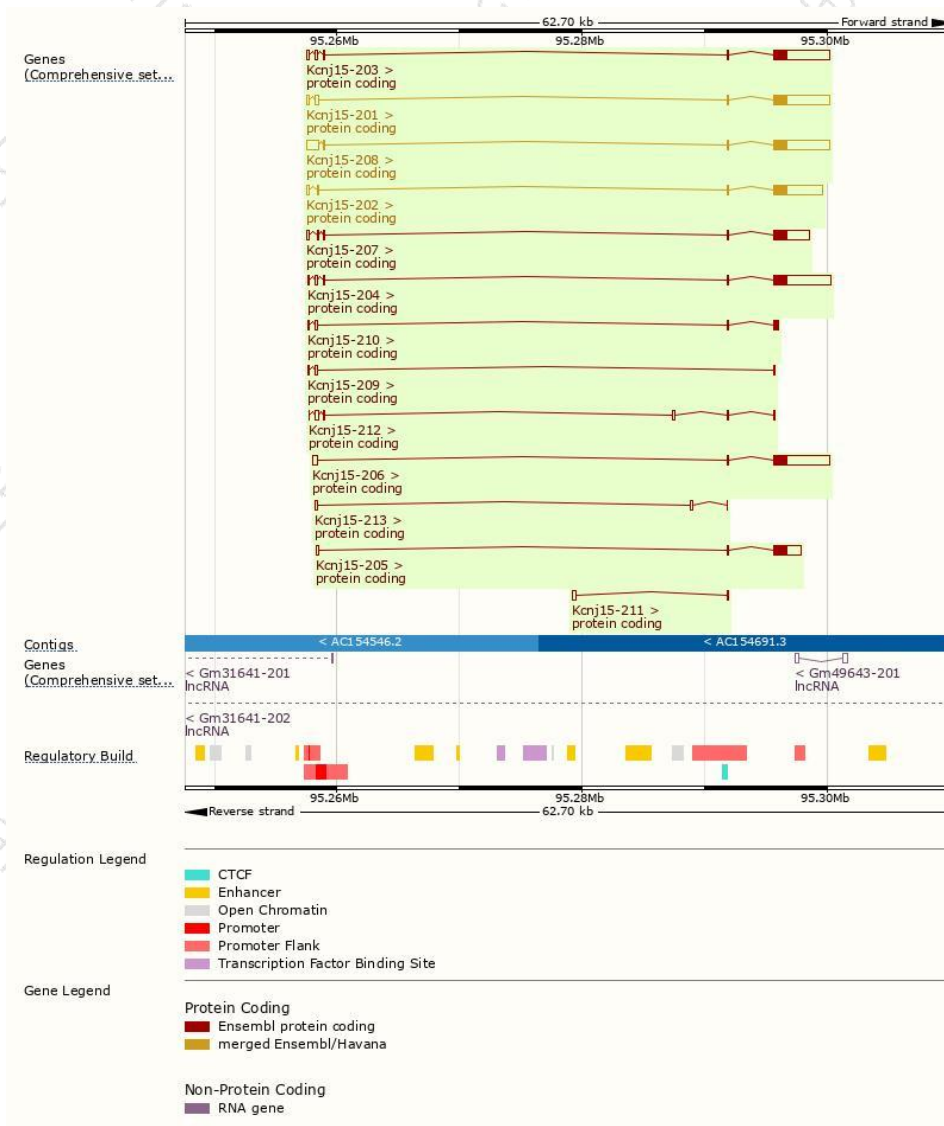
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnj15-208	ENSMUST00000113862.7	5705	402aa	Protein coding	CCDS28351	Q3TNE6	TSL:1 GENCODE basic
Kcnj15-204	ENSMUST00000113856.7	5129	375aa	Protein coding	CCDS37410	O88932 Q53Z04	TSL:3 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 P1
Kcnj15-203	ENSMUST00000113855.7	5128	375aa	Protein coding	CCDS37410	O88932 Q53Z04	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 P1
Kcnj15-201	ENSMUST00000037154.13	5089	402aa	Protein coding	CCDS28351	Q3TNE6	TSL:1 GENCODE basic
Kcnj15-206	ENSMUST00000113859.7	5046	402aa	Protein coding	CCDS28351	Q3TNE6	TSL:1 GENCODE basic
Kcnj15-202	ENSMUST00000113854.7	4409	375aa	Protein coding	CCDS37410	O88932 Q53Z04	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 P1
Kcnj15-207	ENSMUST00000113861.7	3385	402aa	Protein coding	CCDS28351	Q3TNE6	TSL:1 GENCODE basic
Kcnj15-205	ENSMUST00000113858.2	2576	375aa	Protein coding	CCDS37410	O88932 Q3TNE6 Q53Z04	TSL:5 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 P1
Kcnj15-210	ENSMUST00000134166.7	784	173aa	Protein coding	-	D3YXQ3	CDS 3' incomplete TSL:3
Kcnj15-212	ENSMUST00000140222.7	751	53aa	Protein coding	-	D3YVH1	CDS 3' incomplete TSL:5
Kcnj15-209	ENSMUST00000125847.1	363	34aa	Protein coding	-	D3YV68	CDS 3' incomplete TSL:3
Kcnj15-211	ENSMUST00000138329.1	356	23aa	Protein coding	-	D3Z370	CDS 3' incomplete TSL:2
Kcnj15-213	ENSMUST00000152516.1	318	2aa	Protein coding	-	-	CDS 3' incomplete TSL:3

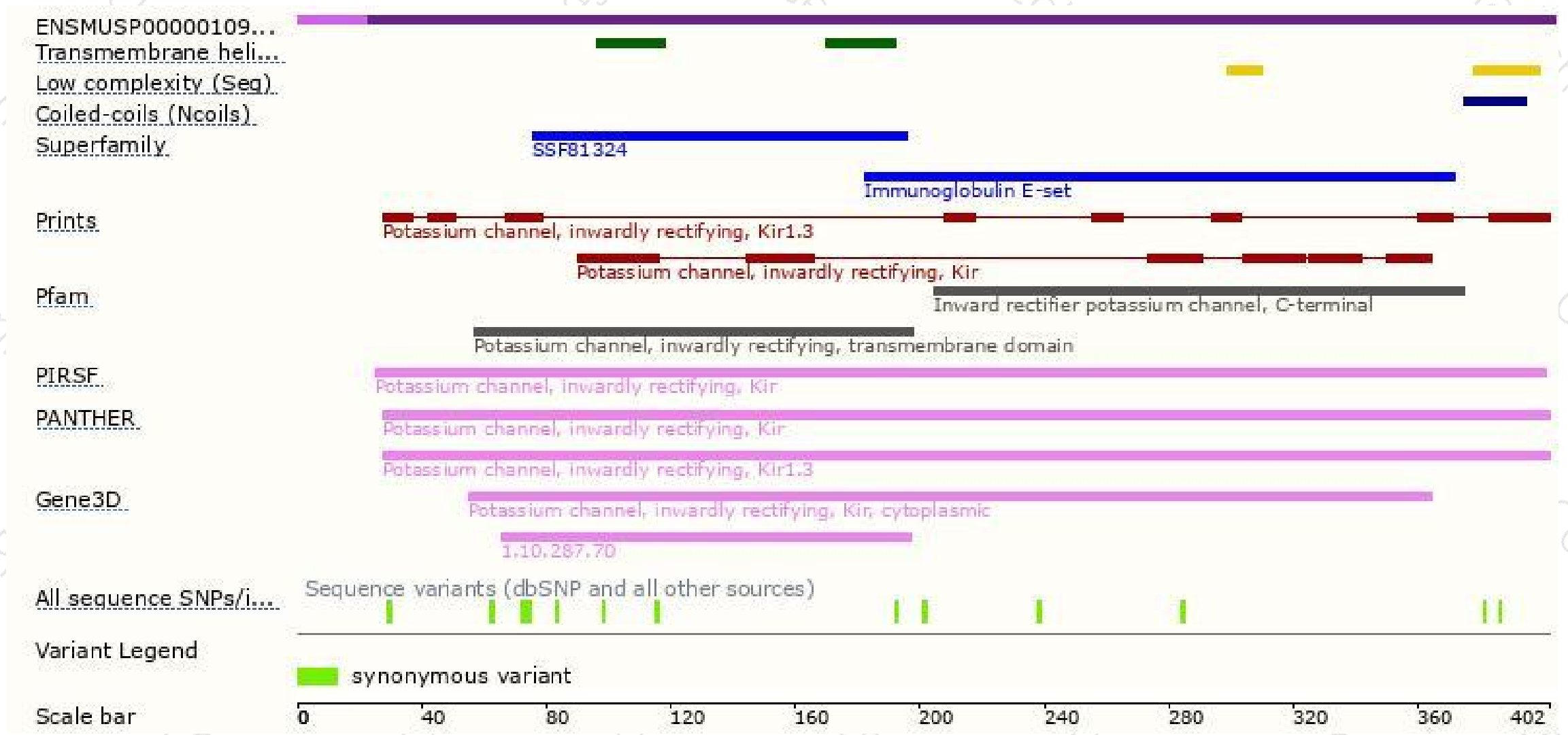
The strategy is based on the design of *Kcnj15-208* transcript,The transcription is shown below



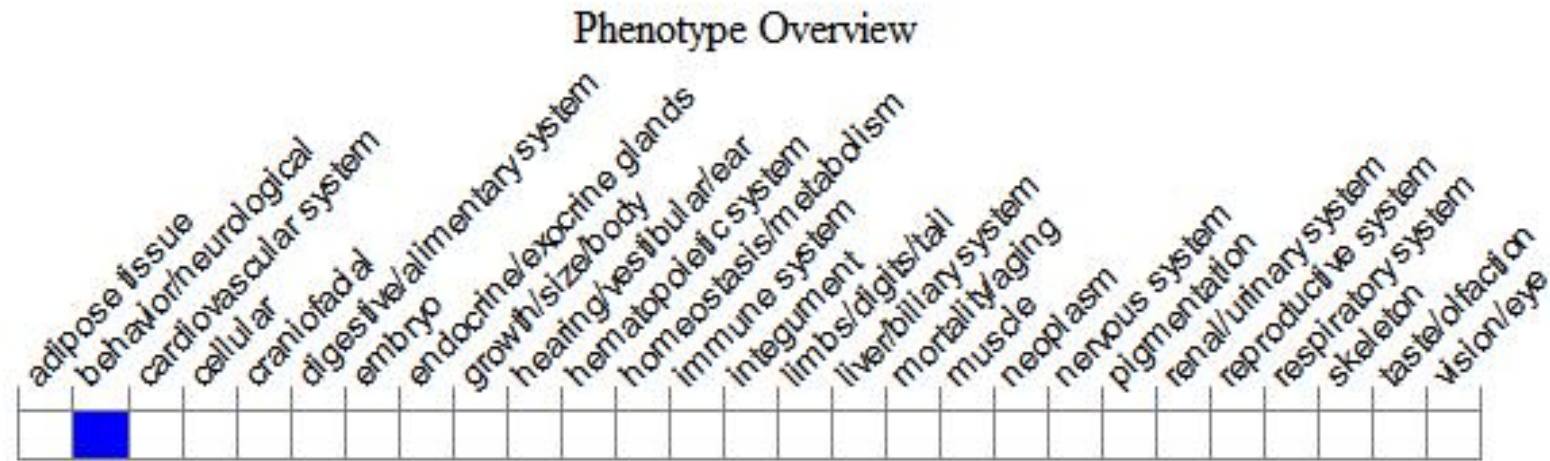
Genomic location distribution



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 knockout mice exhibited impaired balance/coordination in a high-throughput screen.

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

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