

# *Ptp4a3* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Ptp4a3*

**Project type**

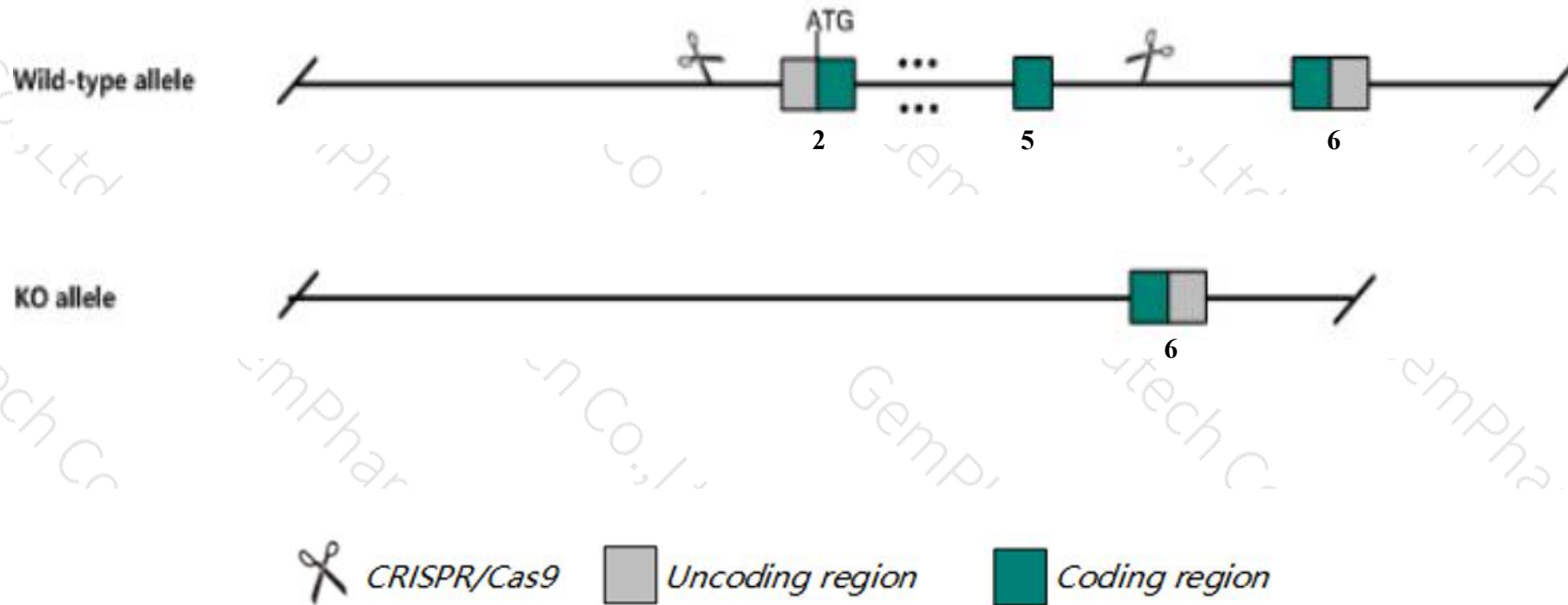
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptp4a3* gene. The schematic diagram is as follows:



- The *Ptp4a3* gene has 10 transcripts. According to the structure of *Ptp4a3* gene, exon2-exon5 of *Ptp4a3*-203 (ENSMUST00000165541.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptp4a3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit partial preweaning lethality and decreased incidence of aom-dds induced tumors. mice homozygous for a different targeted allele exhibit decreased circulating glucose levels in an intraperitoneal glucose tolerance test.
- The *Ptp4a3* 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)

## Ptp4a3 protein tyrosine phosphatase 4a3 [Mus musculus (house mouse)]

Gene ID: 19245, updated on 13-Mar-2020

### Summary



**Official Symbol** Ptp4a3 provided by [MGI](#)

**Official Full Name** protein tyrosine phosphatase 4a3 provided by [MGI](#)

**Primary source** [MGI:MGI:1277098](#)

**See related** [Ensembl:ENSMUSG00000059895](#)

**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** AV088979, Prl-3, pPtp4a3

**Expression** Broad expression in spleen adult (RPKM 91.4), heart adult (RPKM 60.2) and 26 other tissues [See more](#)

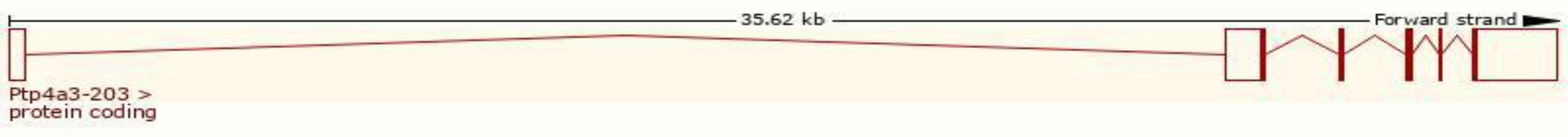
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

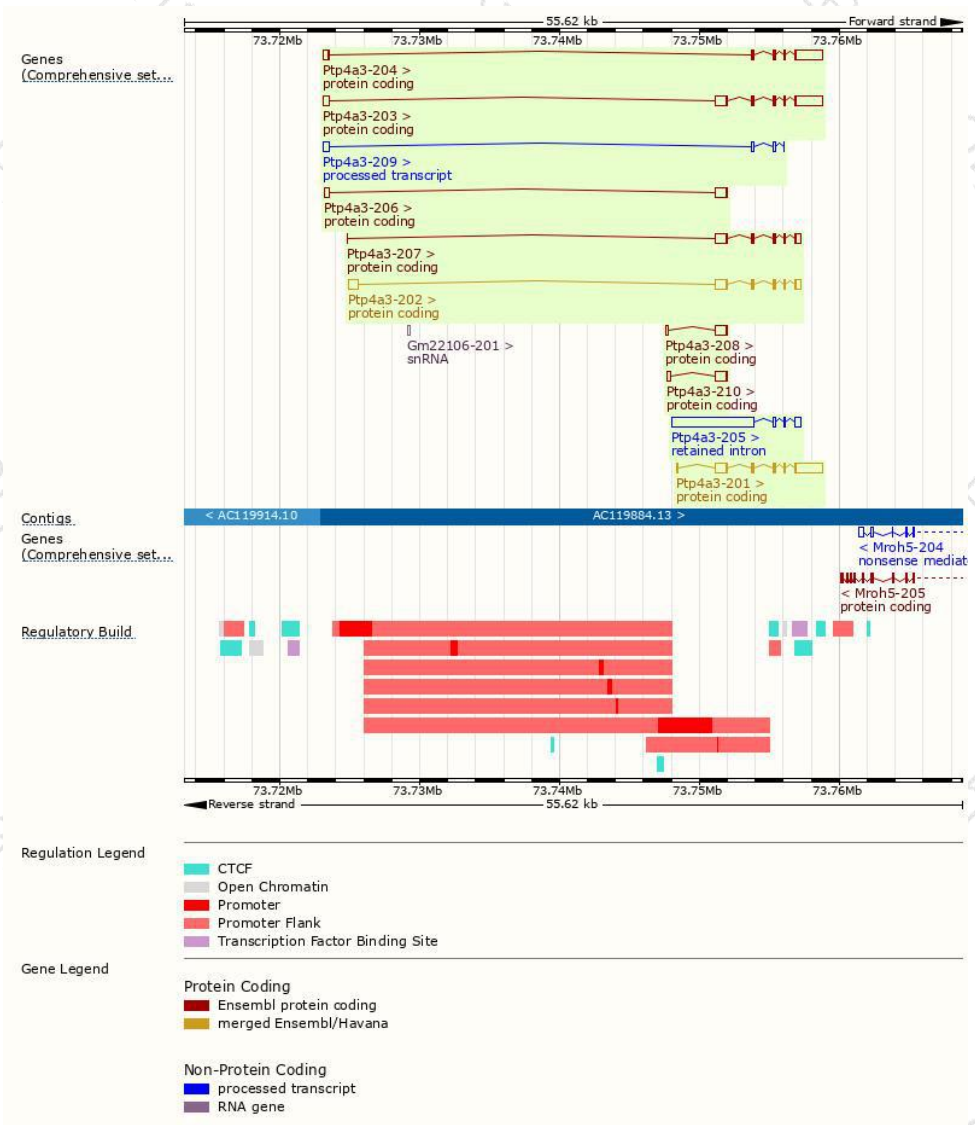
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptp4a3-203	<a href="#">ENSMUST00000165541.7</a>	3539	<a href="#">173aa</a>	<a href="#">Protein coding</a>	<a href="#">CCDS27519</a>	<a href="#">Q9D658</a>	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
Ptp4a3-201	<a href="#">ENSMUST00000053232.7</a>	3260	<a href="#">173aa</a>	<a href="#">Protein coding</a>	<a href="#">CCDS27519</a>	<a href="#">Q9D658</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 P1
Ptp4a3-202	<a href="#">ENSMUST00000163582.8</a>	2270	<a href="#">173aa</a>	<a href="#">Protein coding</a>	<a href="#">CCDS27519</a>	<a href="#">Q9D658</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 P1
Ptp4a3-207	<a href="#">ENSMUST00000230177.1</a>	1680	<a href="#">173aa</a>	<a href="#">Protein coding</a>	<a href="#">CCDS27519</a>	<a href="#">Q9D658</a>	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
Ptp4a3-204	<a href="#">ENSMUST00000167582.7</a>	2640	<a href="#">154aa</a>	<a href="#">Protein coding</a>	-	<a href="#">E9PXS4</a>	TSL:5 GENCODE basic
Ptp4a3-206	<a href="#">ENSMUST00000230044.1</a>	1245	<a href="#">35aa</a>	<a href="#">Protein coding</a>	-	<a href="#">A0A2R8VHQ8</a>	CDS 3' incomplete
Ptp4a3-210	<a href="#">ENSMUST00000231209.1</a>	1105	<a href="#">35aa</a>	<a href="#">Protein coding</a>	-	<a href="#">A0A2R8VHQ8</a>	CDS 3' incomplete
Ptp4a3-208	<a href="#">ENSMUST00000230307.1</a>	1037	<a href="#">35aa</a>	<a href="#">Protein coding</a>	-	<a href="#">A0A2R8VHQ8</a>	CDS 3' incomplete
Ptp4a3-209	<a href="#">ENSMUST00000230864.1</a>	639	No protein	<a href="#">Processed transcript</a>	-	-	
Ptp4a3-205	<a href="#">ENSMUST00000229339.1</a>	6459	No protein	<a href="#">Retained intron</a>	-	-	

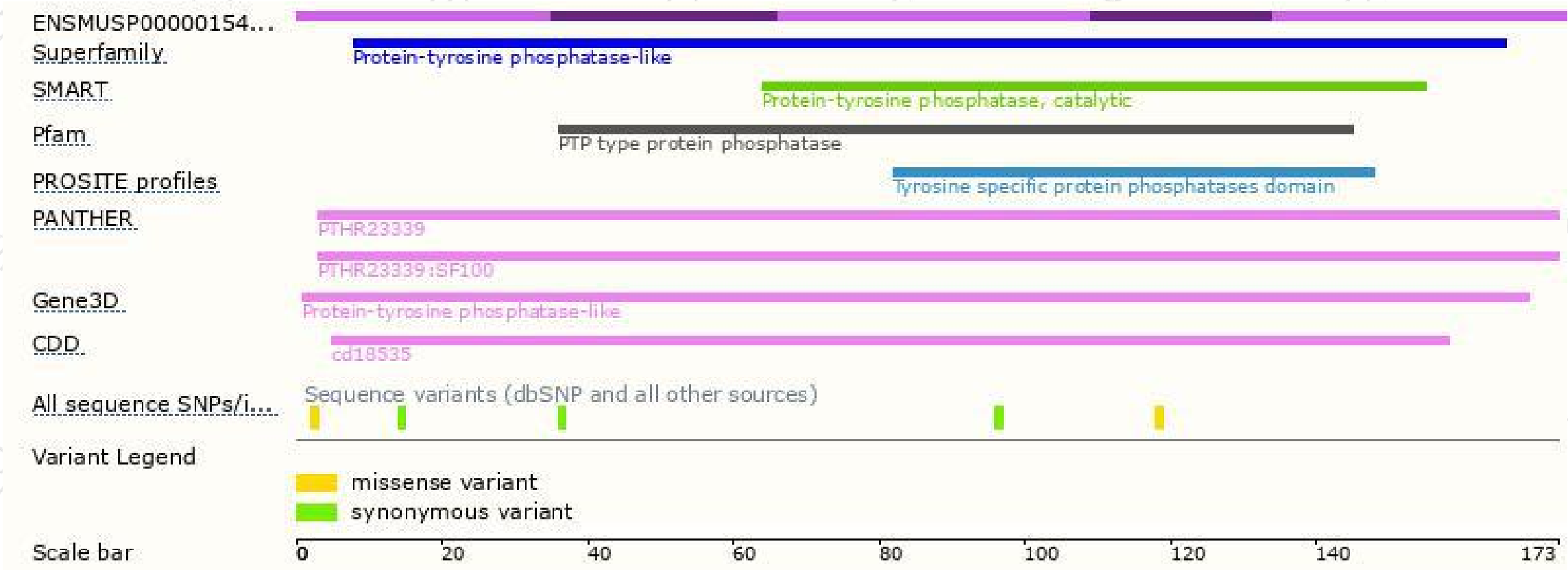
The strategy is based on the design of *Ptp4a3-203* transcript,the transcription is shown below:



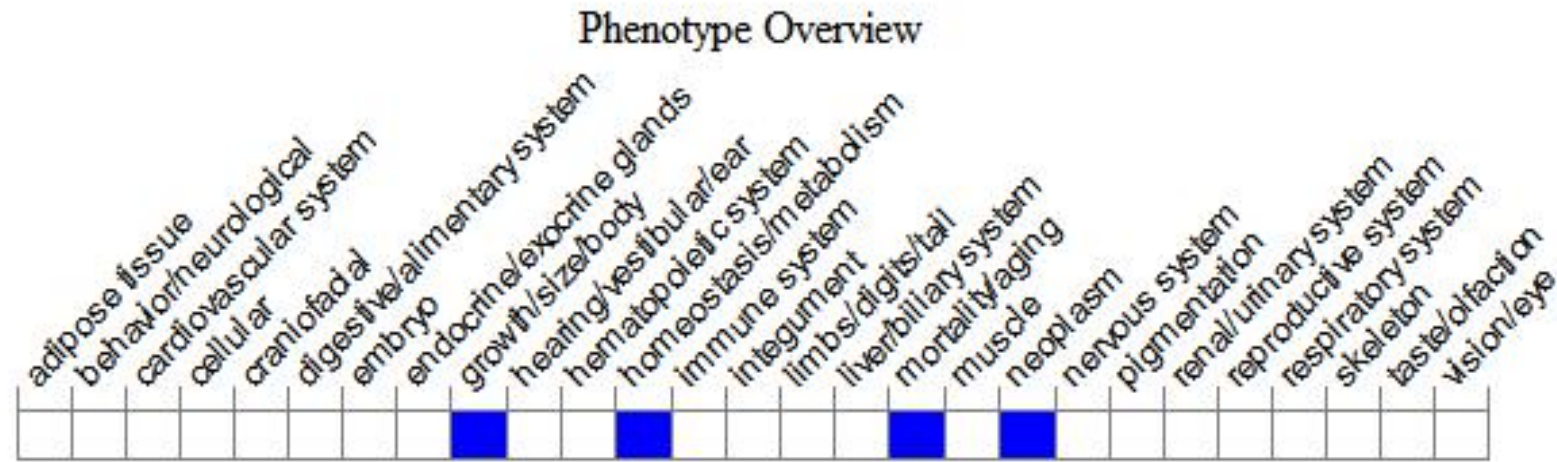
# Genomic location distribution



# 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 knock-out allele exhibit partial preweaning lethality and decreased incidence of AOM-DDS induced tumors. Mice homozygous for a different targeted allele exhibit decreased circulating glucose levels in an intraperitoneal glucose tolerance test.

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

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