

# Pde7a Cas9-KO Strategy

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## **Project Overview**



**Project Name** 

Pde7a

**Project type** 

Cas9-KO

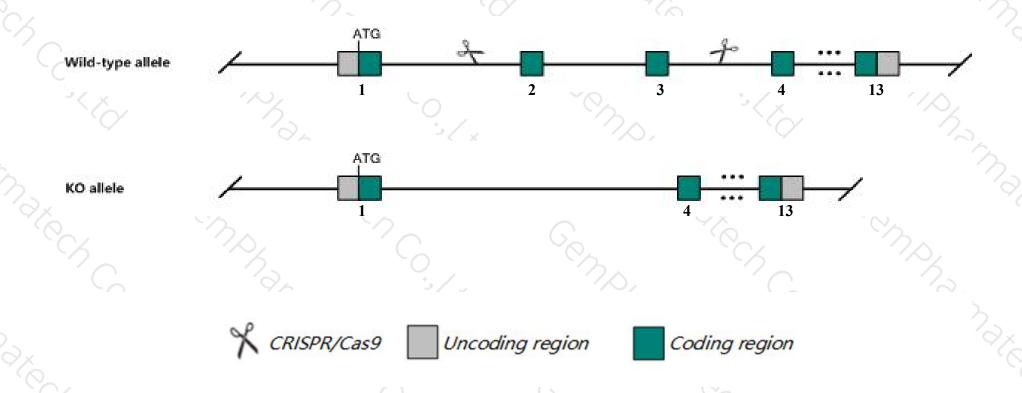
Strain background

C57BL/6JGpt

## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Pde7a* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Pde7a* gene has 10 transcripts. According to the structure of *Pde7a* gene, exon2-exon3 of *Pde7a-202*(ENSMUST00000099195.9) transcript is recommended as the knockout region. The region contains 145bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Pde7a* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > According to the existing MGI data, Homozygous inactivation of this locus does not impair T cell function but affects the humoral immune response.
- > The *Pde7a* gene is located on the Chr3. 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)



#### Pde7a phosphodiesterase 7A [Mus musculus (house mouse)]

Gene ID: 18583, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Pde7a provided by MGI

Official Full Name phosphodiesterase 7A provided by MGI

Primary source MGI:MGI:1202402

See related Ensembl:ENSMUSG00000069094

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 AU015378, AW047537

Expression Broad expression in CNS E11.5 (RPKM 11.8), whole brain E14.5 (RPKM 10.9) and 24 other tissuesSee more

Orthologs <u>human</u> all

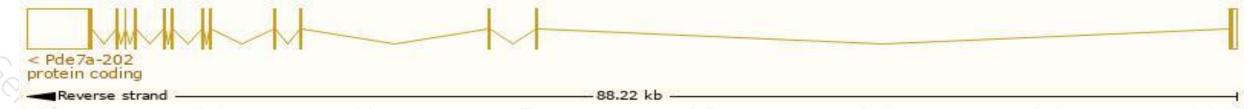
## Transcript information (Ensembl)



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

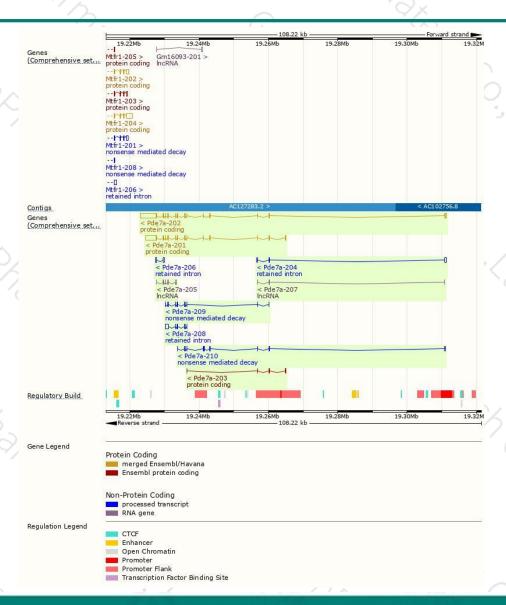
Name	Transcript ID	bp	Protein	Biotype	ccds	UniProt	Flags
Pde7a-202	ENSMUST00000099195.9	6298	482aa	Protein coding	CCDS50871	P70453 Q3U3Y7	TSL:1 GENCODE basic APPRIS ALT1
Pde7a-201	ENSMUST00000091314.10	4454	<u>456aa</u>	Protein coding	CCDS38398	P70453	TSL:1 GENCODE basic APPRIS P3
Pde7a-203	ENSMUST00000121951.1	382	<u>68aa</u>	Protein coding	ų.	D3Z6W6	TSL:3 GENCODE basic
Pde7a-210	ENSMUST00000156652.7	927	<u>176aa</u>	Nonsense mediated decay		D6RIM5	TSL:5
Pde7a-209	ENSMUST00000149081.7	724	<u>31aa</u>	Nonsense mediated decay	a	F6VJY9	CDS 5' incomplete TSL:5
Pde7a-208	ENSMUST00000148590.7	1120	No protein	Retained intron	-	+8	TSL:5
Pde7a-206	ENSMUST00000141621.1	798	No protein	Retained intron	ų.	20	TSL:2
Pde7a-204	ENSMUST00000129060.7	670	No protein	Retained intron	2	20	TSL:3
Pde7a-205	ENSMUST00000139426.7	605	No protein	IncRNA	a	-	TSL:3
Pde7a-207	ENSMUST00000143120.1	245	No protein	IncRNA	-		TSL:5

The strategy is based on the design of Pde7a-202 transcript, The transcription is shown below



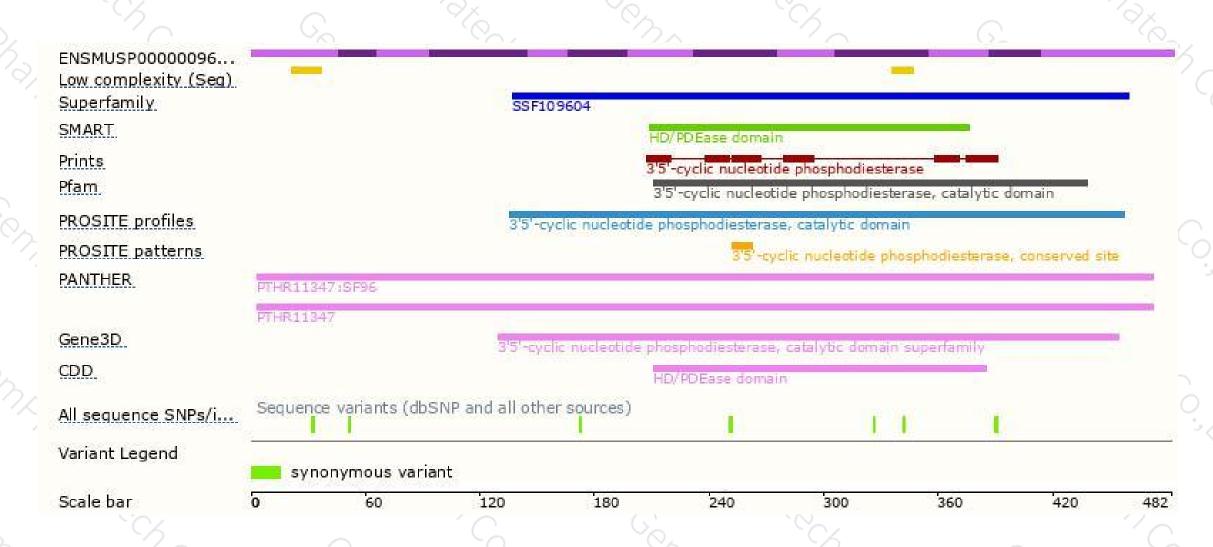
### Genomic location distribution





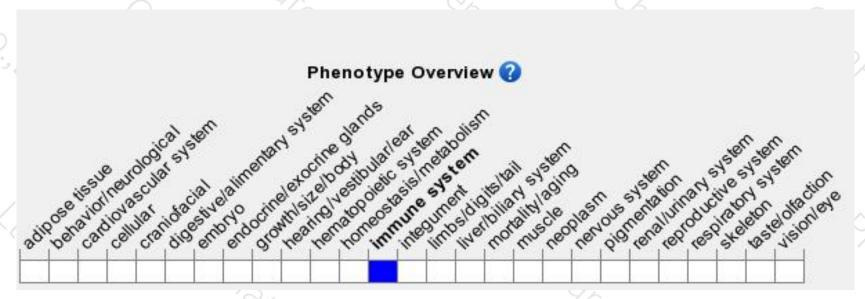
### Protein domain





## 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 inactivation of this locus does not impair T cell function but affects the humoral immune response.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





