

# *Atp2b3* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Atp2b3*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp2b3* gene. The schematic diagram is as follows:



- The *Atp2b3* gene has 3 transcripts. According to the structure of *Atp2b3* gene, exon3-exon11 of *Atp2b3-202* (ENSMUST00000088429.7) transcript is recommended as the knockout region. The region contains 1615bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp2b3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Atp2b3* gene is located on the ChrX. 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)

## Atp2b3 ATPase, Ca++ transporting, plasma membrane 3 [ *Mus musculus* (house mouse) ]

Gene ID: 320707, updated on 9-Feb-2020

### Summary

- Official Symbol** Atp2b3 provided by [MGI](#)
- Official Full Name** ATPase, Ca++ transporting, plasma membrane 3 provided by [MGI](#)
- Primary source** [MGI:MGI:1347353](#)
- See related** [Ensembl:ENSMUSG00000031376](#)
- 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** Pmca3; 6430519O13Rik
- Expression** Biased expression in cerebellum adult (RPKM 35.0), genital fat pad adult (RPKM 15.6) and 6 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** X; X A7.3 See Atp2b3 in [Genome Data Viewer](#)

**Exon count:** 26

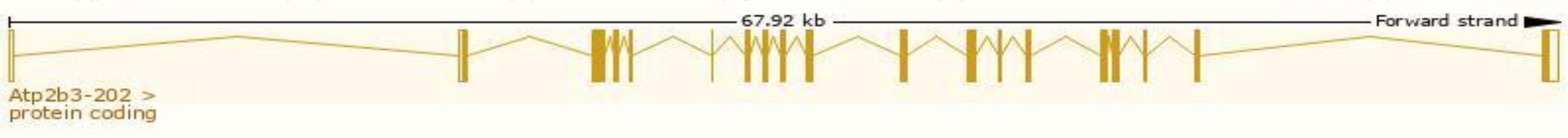
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	X	NC_000086.7 (73502749..73573275)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	X	NC_000086.6 (70748425..70816344)

# Transcript information (Ensembl)

The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp2b3-202	<a href="#">ENSMUST00000088429.7</a>	4483	<a href="#">1220aa</a>	Protein coding	<a href="#">CCDS30205</a>	<a href="#">Q0VF55</a>	TSL:1 GENCODE basic APPRIS P2
Atp2b3-201	<a href="#">ENSMUST00000033744.11</a>	3894	<a href="#">1144aa</a>	Protein coding	<a href="#">CCDS85778</a>	<a href="#">Q8C048</a>	TSL:1 GENCODE basic
Atp2b3-203	<a href="#">ENSMUST00000114479.1</a>	4637	<a href="#">1173aa</a>	Protein coding	-	<a href="#">A2ALL9</a>	TSL:5 GENCODE basic APPRIS ALT 1

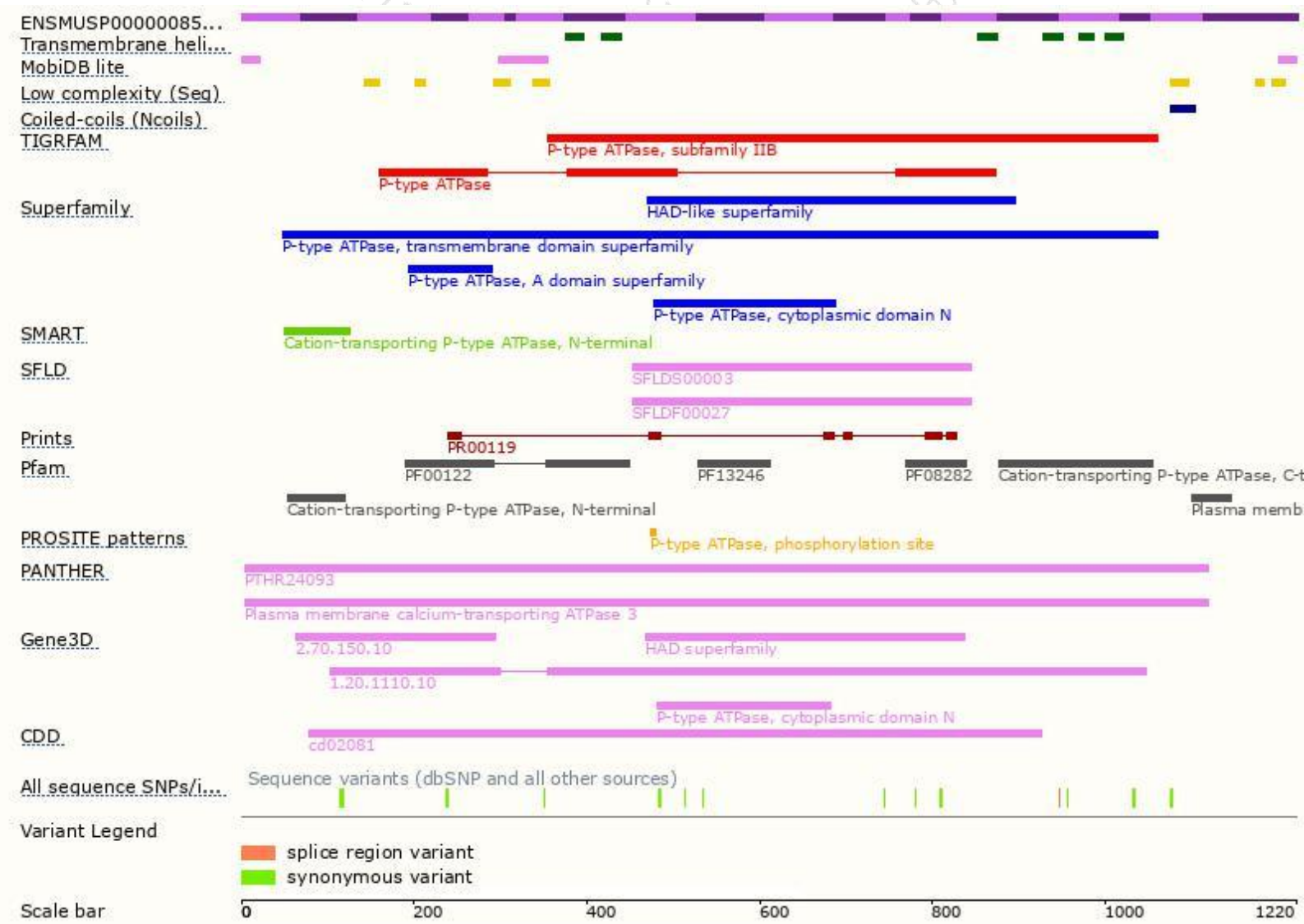
The strategy is based on the design of *Atp2b3-202* transcript,The transcription is shown below



# Genomic location distribution



# Protein domain



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

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