

# *Atp6v1g3* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Atp6v1g3*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v1g3* gene. The schematic diagram is as follows:



- The *Atp6v1g3* gene has 1 transcript. According to the structure of *Atp6v1g3* gene, exon1-exon3 of *Atp6v1g3-201* (ENSMUST00000027643.5) transcript is recommended as the knockout region. The region contains all 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 *Atp6v1g3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Atp6v1g3* gene is located on the Chr1. 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)

## Atp6v1g3 ATPase, H<sup>+</sup> transporting, lysosomal V1 subunit G3 [Mus musculus (house mouse)]

Gene ID: 338375, updated on 19-Mar-2019

### Summary



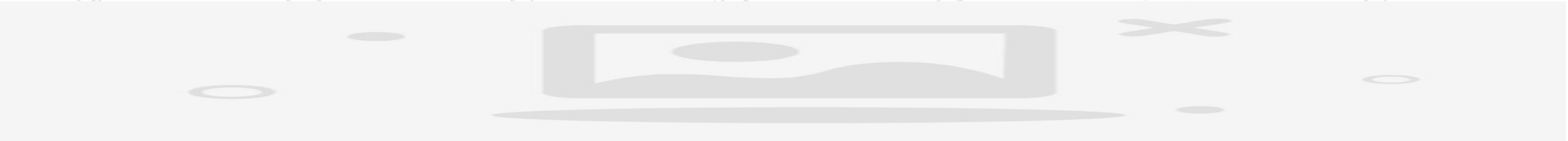
<b>Official Symbol</b>	Atp6v1g3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ATPase, H <sup>+</sup> transporting, lysosomal V1 subunit G3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2450548</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000026394</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Expression</b>	Biased expression in kidney adult (RPKM 3.8) and genital fat pad adult (RPKM 1.2) <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

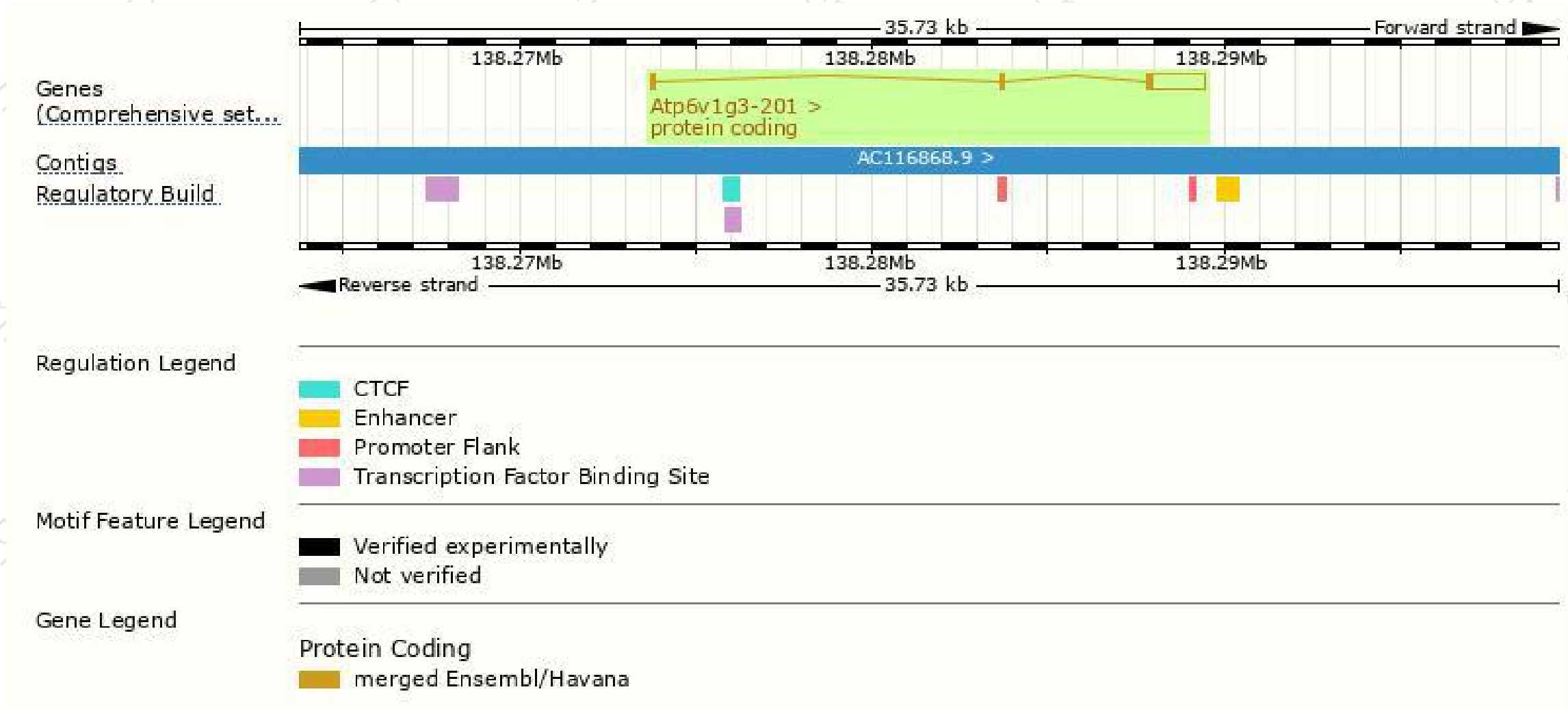
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v1g3-201	<a href="#">ENSMUST00000027643.5</a>	1887	<a href="#">118aa</a>	Protein coding	<a href="#">CCDS15331</a>	<a href="#">Q8BMC1</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Atp6v1g3-201* 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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