

Atad1 Cas9-KO Strategy

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Reviewer: Huimin Su

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Project Overview



Project Name Atad1

Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Atad1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Atad1* gene has 10 transcripts. According to the structure of *Atad1* gene, exon4-exon5 of *Atad1-201* (ENSMUST0000070210.5) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Atad1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased body size, seizure, absent LTD, enhanced LTP, enhanced AMPA-mediated currents, and premature death.
- The *Atad1* gene is located on the Chr19. 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)



Atad1 ATPase family, AAA domain containing 1 [Mus musculus (house mouse)]

Gene ID: 67979, updated on 19-Mar-2019

Summary

↑ ?

Official Symbol Atad1 provided by MGI

Official Full Name ATPase family, AAA domain containing 1 provided by MGI

Primary source MGI:MGI:1915229

See related Ensembl: ENSMUSG00000013662

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 4921525H23Rik, AW107648, Thorase

Expression Broad expression in CNS E18 (RPKM 23.5), CNS E14 (RPKM 20.1) and 24 other tissuesSee more

Orthologs <u>human all</u>

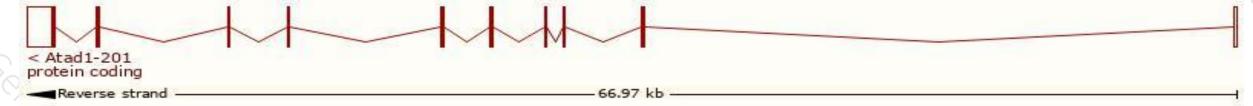
Transcript information (Ensembl)



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

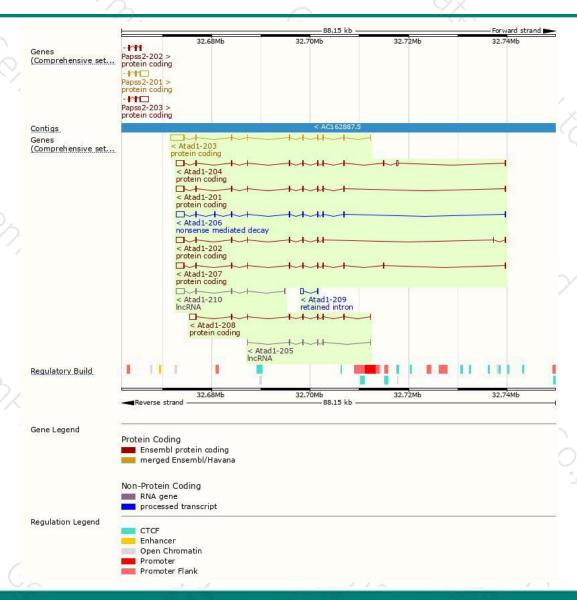
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Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000235412.1	3771	<u>361aa</u>	Protein coding	CCDS29752	15	GENCODE basic APPRIS P1
ENSMUST00000236011.1	2943	<u>361aa</u>	Protein coding	CCDS29752		GENCODE basic APPRIS P1
ENSMUST00000236985.1	2722	<u>361aa</u>	Protein coding	CCDS29752	(2)	GENCODE basic APPRIS P1
ENSMUST00000070210.5	2666	<u>361aa</u>	Protein coding	CCDS29752	Q9D5T0	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000235142.1	2535	<u>276aa</u>	Protein coding	-		GENCODE basic
ENSMUST00000237752.1	2269	322aa	Protein coding	*		GENCODE basic
ENSMUST00000236701.1	2736	303aa	Nonsense mediated decay	24	12	
ENSMUST00000237933.1	611	No protein	Retained intron	20	1525	
ENSMUST00000238016.1	1905	No protein	IncRNA	-	-	
ENSMUST00000236546.1	624	No protein	IncRNA	-		
	ENSMUST00000236011.1 ENSMUST00000236985.1 ENSMUST00000070210.5 ENSMUST00000235142.1 ENSMUST00000237752.1 ENSMUST00000236701.1 ENSMUST00000237933.1 ENSMUST00000238016.1	ENSMUST00000235412.1 3771 ENSMUST00000236011.1 2943 ENSMUST00000236985.1 2722 ENSMUST00000070210.5 2666 ENSMUST00000235142.1 2535 ENSMUST00000237752.1 2269 ENSMUST00000236701.1 2736 ENSMUST00000237933.1 611 ENSMUST00000238016.1 1905	ENSMUST00000235412.1 3771 361aa ENSMUST00000236011.1 2943 361aa ENSMUST00000236985.1 2722 361aa ENSMUST00000070210.5 2666 361aa ENSMUST00000235142.1 2535 276aa ENSMUST00000237752.1 2269 322aa ENSMUST00000236701.1 2736 303aa ENSMUST00000237933.1 611 No protein ENSMUST00000238016.1 1905 No protein	ENSMUST00000235412.1 3771 361aa Protein coding ENSMUST00000236011.1 2943 361aa Protein coding ENSMUST00000236985.1 2722 361aa Protein coding ENSMUST00000070210.5 2666 361aa Protein coding ENSMUST00000235142.1 2535 276aa Protein coding ENSMUST00000237752.1 2269 322aa Protein coding ENSMUST00000236701.1 2736 303aa Nonsense mediated decay ENSMUST00000237933.1 611 No protein Retained intron ENSMUST00000238016.1 1905 No protein IncRNA	ENSMUST00000235412.1 3771 361aa Protein coding CCDS29752 ENSMUST00000236011.1 2943 361aa Protein coding CCDS29752 ENSMUST00000236985.1 2722 361aa Protein coding CCDS29752 ENSMUST00000070210.5 2666 361aa Protein coding CCDS29752 ENSMUST00000235142.1 2535 276aa Protein coding - ENSMUST00000237752.1 2269 322aa Protein coding - ENSMUST00000236701.1 2736 303aa Nonsense mediated decay - ENSMUST00000237933.1 611 No protein Retained intron - ENSMUST00000238016.1 1905 No protein IncRNA -	ENSMUST00000235412.1 3771 361aa Protein coding CCDS29752 - ENSMUST00000236011.1 2943 361aa Protein coding CCDS29752 - ENSMUST00000236985.1 2722 361aa Protein coding CCDS29752 - ENSMUST00000070210.5 2666 361aa Protein coding CCDS29752 Q9D5T0 ENSMUST00000235142.1 2535 276aa Protein coding - - ENSMUST00000237752.1 2269 322aa Protein coding - - ENSMUST00000236701.1 2736 303aa Nonsense mediated decay - - ENSMUST00000237933.1 611 No protein Retained intron - - ENSMUST00000238016.1 1905 No protein IncRNA - -

The strategy is based on the design of Atad1-201 transcript, The transcription is shown below



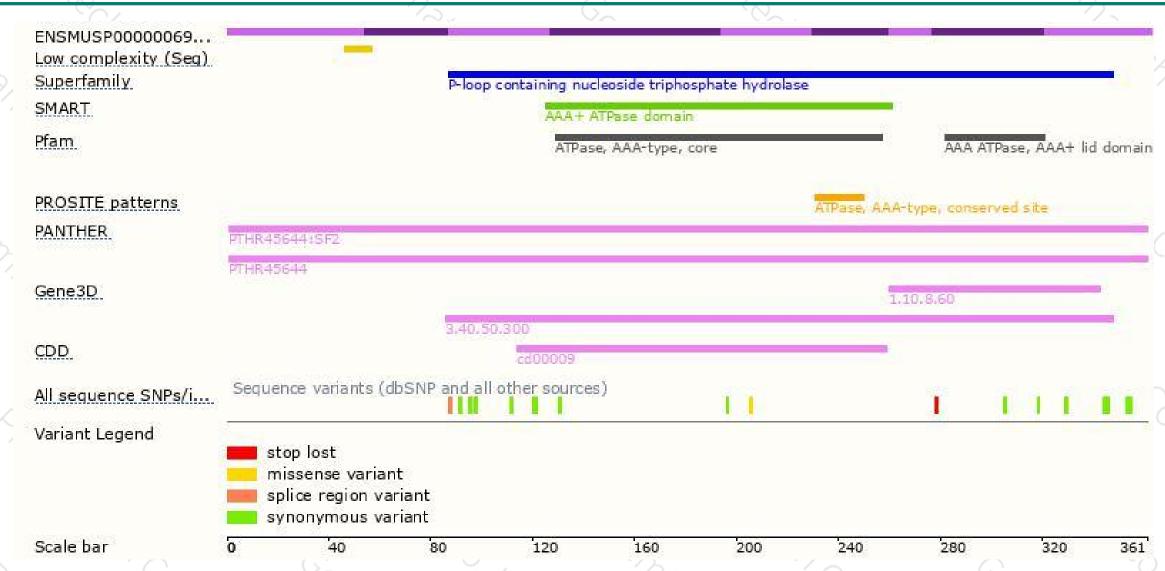
Genomic location distribution





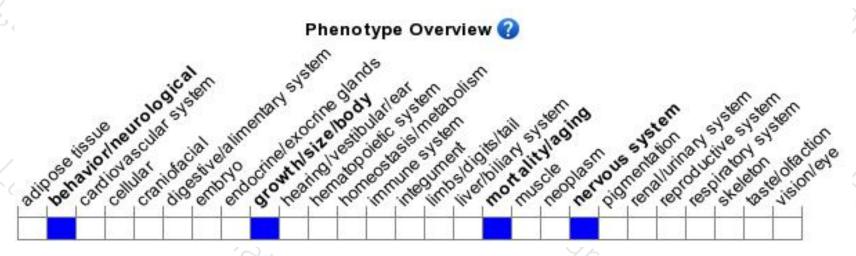
Protein domain





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 decreased body size, seizure, absent LTD, enhanced LTP, enhanced AMPA-mediated currents, and premature death.



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





