

# Senp6 Cas9-KO Strategy

Designer: Design Date:

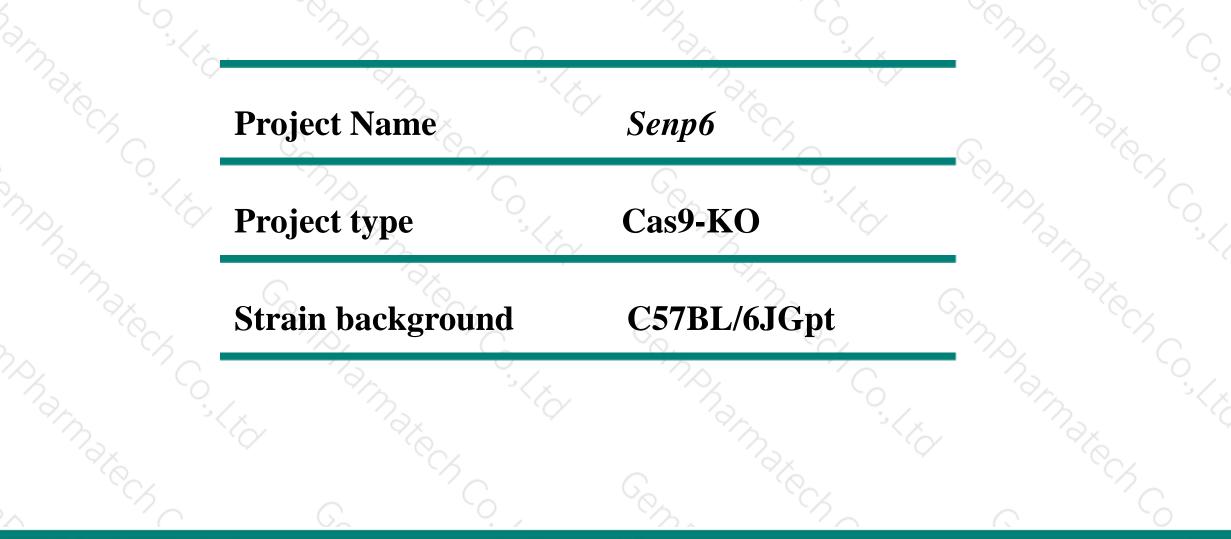
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Qiong Zhou 2018/6/4

### **Project Overview**

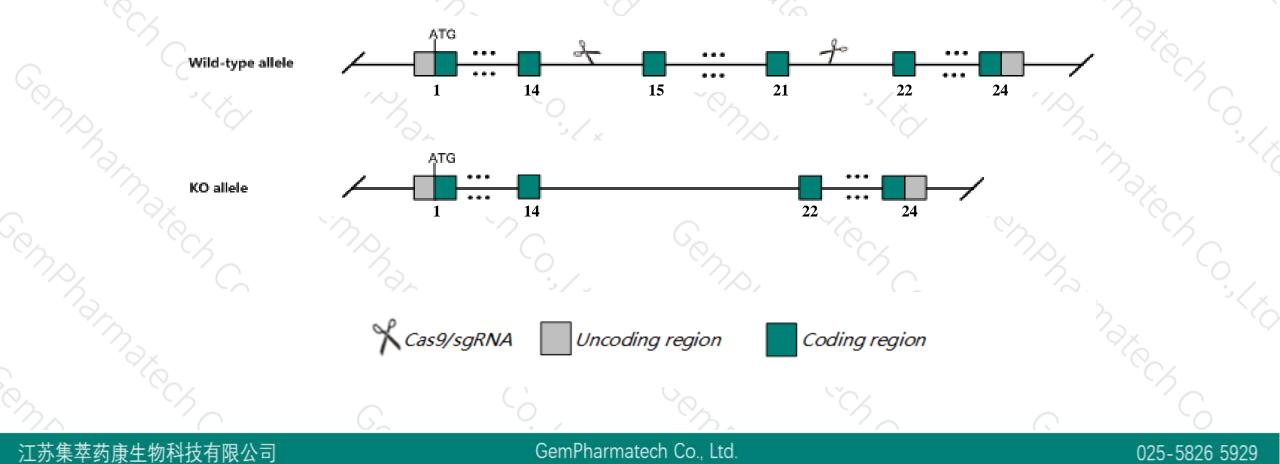


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This model will use CRISPR/Cas9 technology to edit the Senp6 gene. The schematic diagram is as follows:





The Senp6 gene has 15 transcripts. According to the structure of Senp6 gene, exon14-exon20 of Senp6-203 (ENSMUST00000165607.8) transcript is recommended as the knockout region. The region contains 1058bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Senp6* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.





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- > According to the existing MGI data, Mice homozygous for a gene trap insertion exhibit prenatal lethality.
- ➤ Both transcripts *Senp6-213* and *Senp6-214* are incomplete, so the effect on them are unknown.
- The Senp6 gene is located on the Chr9. 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)**



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Senp6 SUMO/sentrin specific peptidase 6 [ Mus musculus (house mouse) ]

Gene ID: 215351, updated on 12-Aug-2019

Summary

Official Symbol	Senp6 provided by MGI
Official Full Name	SUMO/sentrin specific peptidase 6 provided by MGI
Primary source	MGI:MGI:1922075
See related	Ensembl:ENSMUSG00000034252
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	Susp1; mKIAA0797; 2810017C20Rik; E130319N12Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 16.8), CNS E14 (RPKM 11.2) and 27 other tissues See more
Orthologs	human all

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# **Transcript information (Ensembl)**



Name 💧	Transcript ID 💧	bp 🖕	Protein 💧	Biotype	CCDS 💧	UniProt 🖕	Flags	
Senp6-201	ENSMUST0000037484.14	5111	<u>1132aa</u>	Protein coding	CCDS40705@	<u>Q6P7W0</u> 교	TSL:1 GENCODE basic APPRIS P3	
Senp6-203	ENSMUST00000165607.8	3495	<u>1139aa</u>	Protein coding	<u>CCDS81040</u> &	<u>F6Z9A1</u> ₽	TSL:1 GENCODE basic APPRIS ALT2	
Senp6-202	ENSMUST00000164859.7	3853	<u>966aa</u>	Protein coding	-	<u>Q6P7W0</u> ₽	TSL:1 GENCODE basic APPRIS ALT2	
Senp6-213	ENSMUST00000176640.7	1150	<u>131aa</u>	Protein coding	-	<u>H3BKR4</u> ₽	CDS 3' incomplete TSL:5	
Senp6-209	ENSMUST00000176360.7	855	<u>285aa</u>	Protein coding	-	<u>H3BJS8</u> 龄	CDS 5' and 3' incomplete TSL:5	
Senp6-210	ENSMUST00000176527.1	612	<u>204aa</u>	Protein coding	-	<u>H3BLA9</u> &	CDS 5' and 3' incomplete TSL:2	
Senp6-214	ENSMUST00000176648.1	596	<u>179aa</u>	Protein coding	-	<u>H3BK20</u> &	CDS 5' incomplete TSL:2	
Senp6-208	ENSMUST00000175999.7	4706	<u>48aa</u>	Nonsense mediated decay	-	<u>H3BKI2</u> @	TSL:1	
Senp6-204	ENSMUST00000175673.1	1916	No protein	Retained intron	-	-	TSL:1	
Senp6-206	ENSMUST00000175758.7	1445	No protein	Retained intron	-	-	TSL:1	
Senp6-211	ENSMUST00000176563.1	614	No protein	Retained intron	-	-	TSL:2	
Senp6-205	ENSMUST00000175722.7	492	No protein	Retained intron	-	-	TSL:2	
Senp6-212	ENSMUST00000176607.7	3319	No protein	IncRNA	-	-	TSL:1	
Senp6-207	ENSMUST00000175910.1	662	No protein	IncRNA	-	-	TSL:3	
Senp6-215	ENSMUST00000177544.1	341	No protein	IncRNA		TSL:3		

The strategy is based on the design of Senp6-203transcript, The transcription is shown below

76.41 kb

Senp6-203 > protein coding

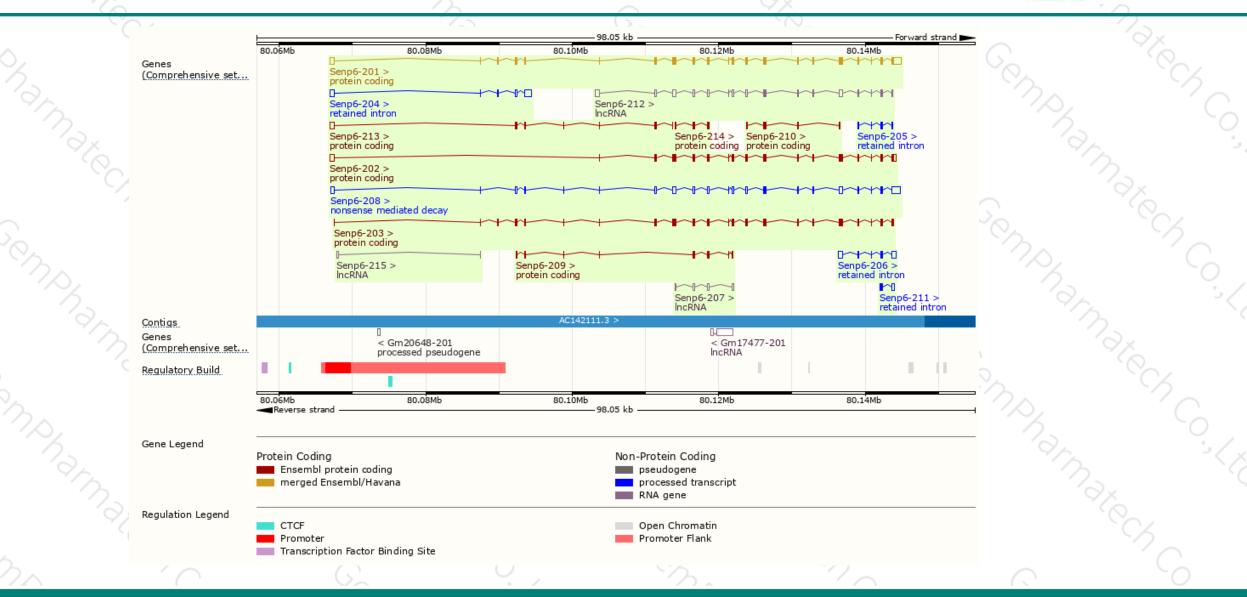
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Forward strand 📂

### **Genomic location distribution**



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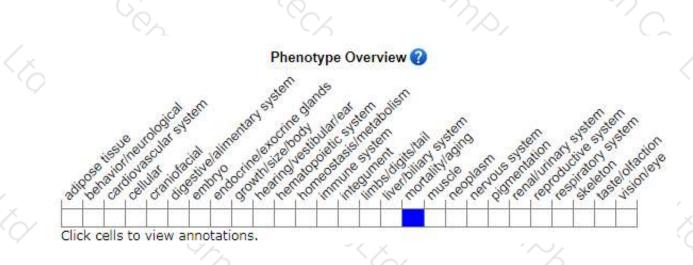
### **Protein domain**



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	ENSMUSP00000126 MobiDB lite Low complexity (Seg)				_	_	_
	Coiled-coils (Ncoils) Superfamily				Papain-like cysteine peptidase	superfamily	<b>-</b> , <sup>1</sup>
	Pfam PROSITE profiles				Ulp1 protease family, C-t	erminal catalytic domain	
	PANTHER	PTHR46896			Ulp1 protease family, C-ter	minal catalytic domain	
	Gene3D	PTHR46896:SF1			1.10.418.20		- 6
	All sequence SNPs/i	Sequence variants (dbSN	P and all other sources)		3.30.310.130		°< >∝
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## 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 gene trap insertion exhibit prenatal lethality.





If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



