

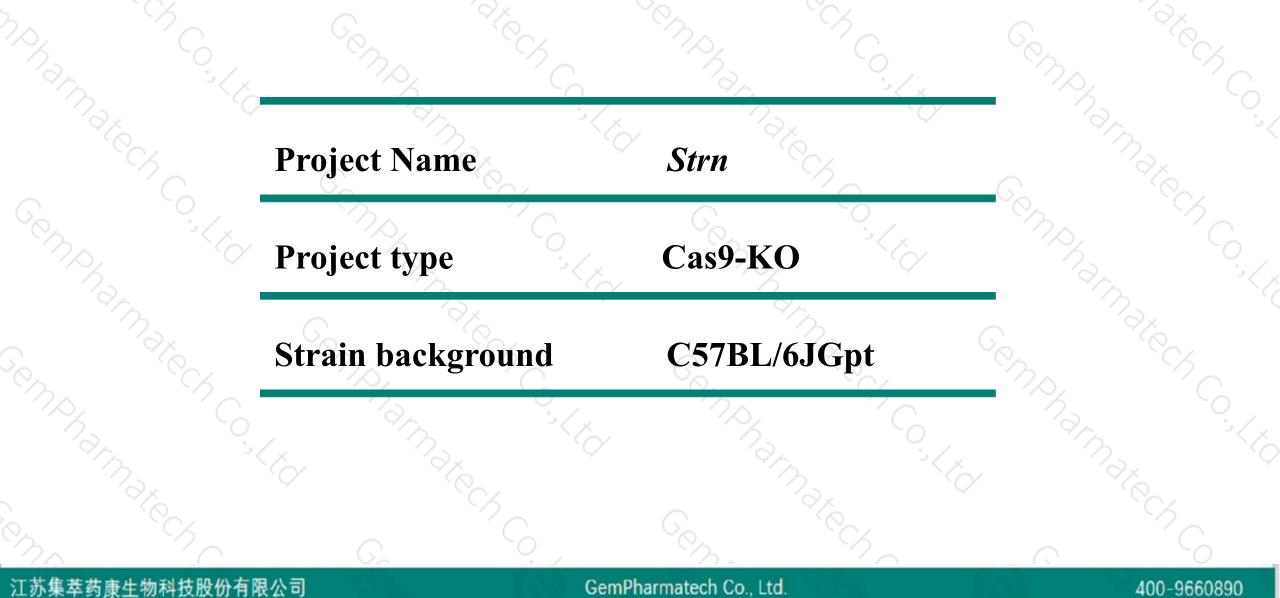
Strn Cas9-KO Strategy

Designer: Reviewer: Design Date:

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Project Overview

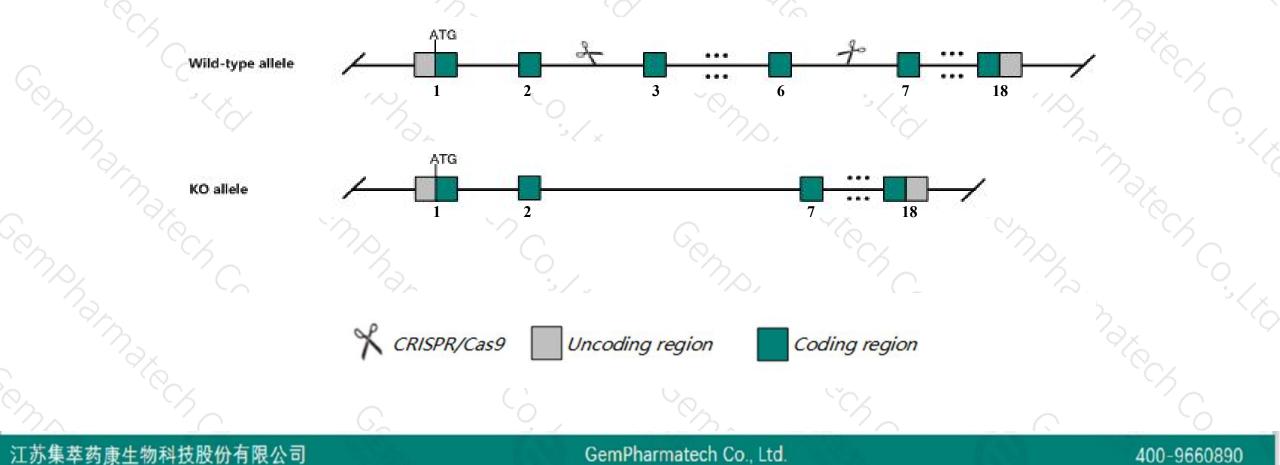




Knockout strategy



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





- The Strn gene has 3 transcripts. According to the structure of Strn gene, exon3-exon6 of Strn-203 (ENSMUST00000145910.8) transcript is recommended as the knockout region. The region contains 457bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Strn gene. The brief process is as follows: CRISPR/Cas9 system w

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- According to the existing MGI data, mice heterozygous for a knock-out allele exhibit increased blood pressure and circulating aldosterone when fed a liberal salt diet. No mice could be generated that were homozygous for the allele.
- > The *Strn* gene is located on the Chr17. 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.

Notice

Gene information (NCBI)



| ?

Strn striatin, calmodulin binding protein [Mus musculus (house mouse)]

Gene ID: 268980, updated on 21-Aug-2019

Summary

Official Symbol	Strn provided by MGI
Official Full Name	striatin, calmodulin binding protein provided by MGI
Primary source	MGI:MGI:1333757
See related	Ensembl:ENSMUSG0000024077
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	AU022939; D130055P19
Expression	Ubiquitous expression in cerebellum adult (RPKM 6.6), cortex adult (RPKM 6.5) and 28 other tissues See more
Orthologs	human all
	$\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$ $\mathcal{A}_{\mathbf{X}}$

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Transcript information (Ensembl)



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

Name 🍦	Transcript ID	bp 🖕	Protein 🛔	Biotype 🍦	CCDS 🖕	UniProt 🖕	Flags
Strn-203	ENSMUST00000145910.8	8629	<u>780aa</u>	Protein coding	CCDS28978	<u>055106</u> &	TSL:1 GENCODE basic APPRIS P1
Strn-201	ENSMUST0000024881.13	2967	<u>627aa</u>	Protein coding	-	F8WH41	TSL:1 GENCODE basic
Strn-202	ENSMUST00000145480.1	800	<u>267aa</u>	Protein coding	1070	F6Z700	CDS 5' and 3' incomplete TSL:3

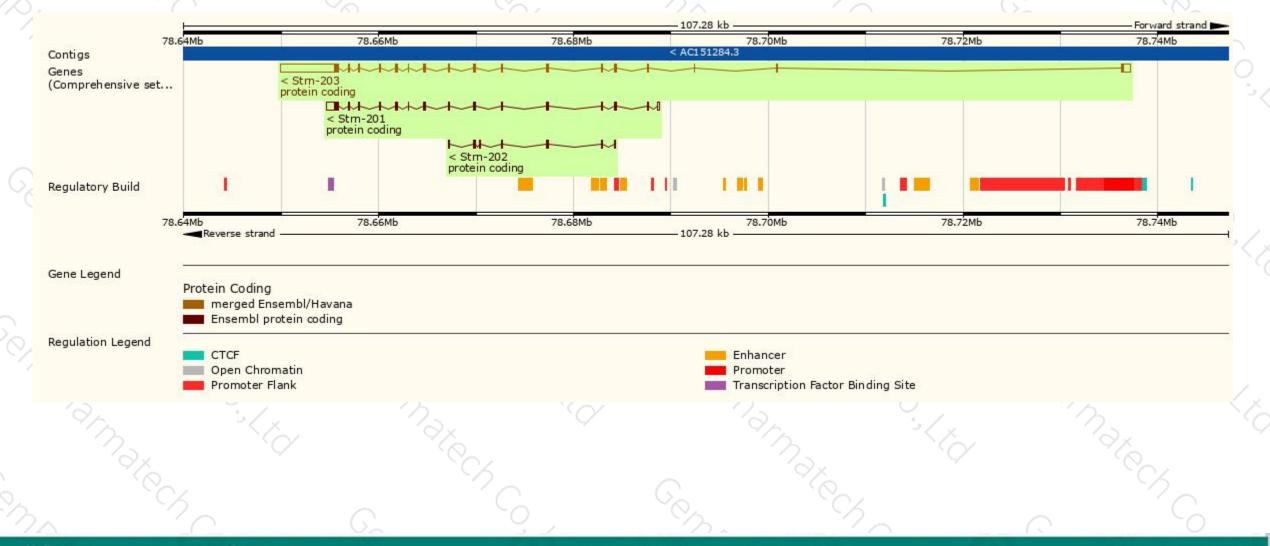
The strategy is based on the design of *Strn-203* transcript, the transcription is shown below:

< Stm-203 protein coding

Reverse strand

Genomic location distribution





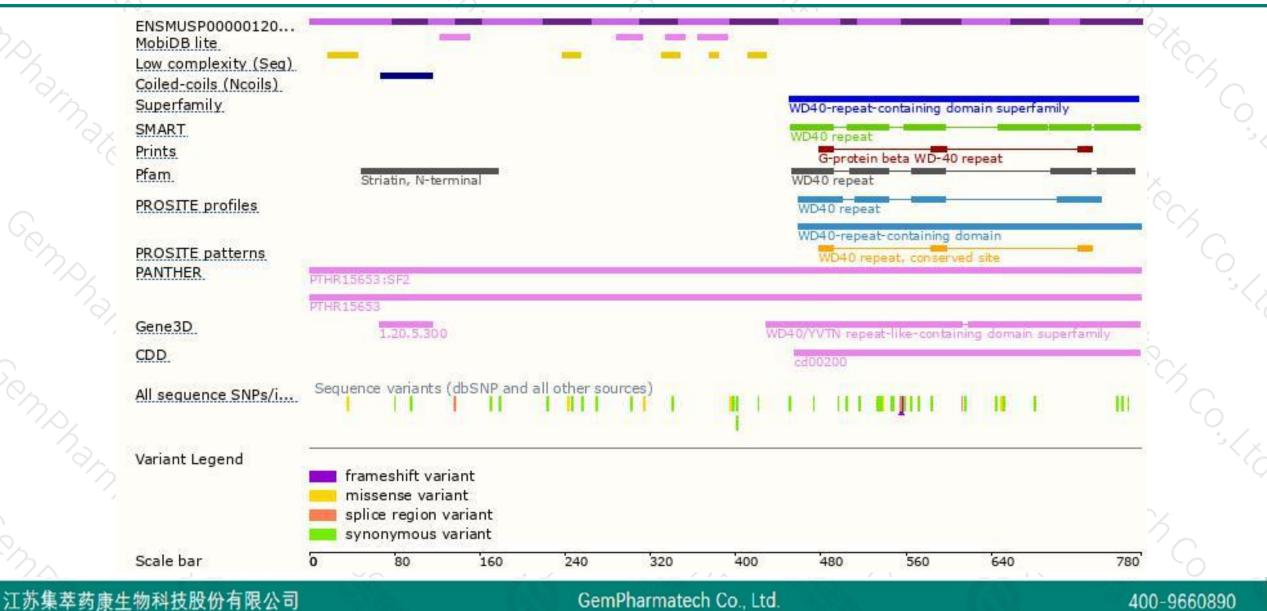
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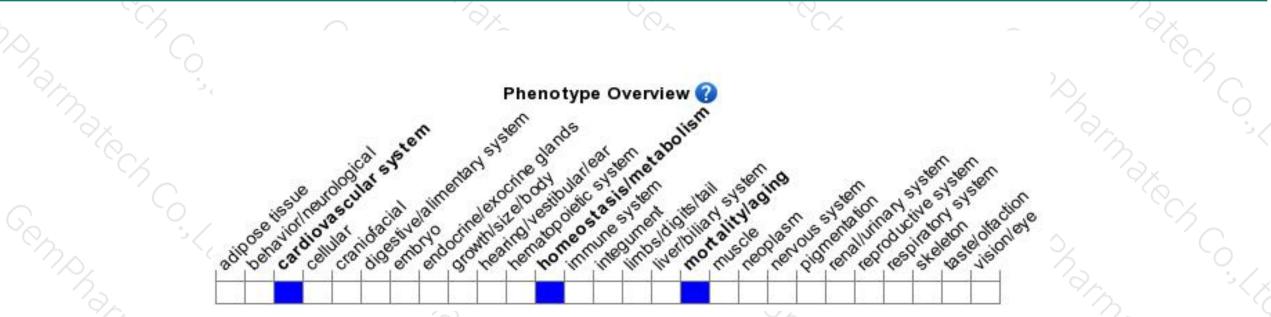
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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



