

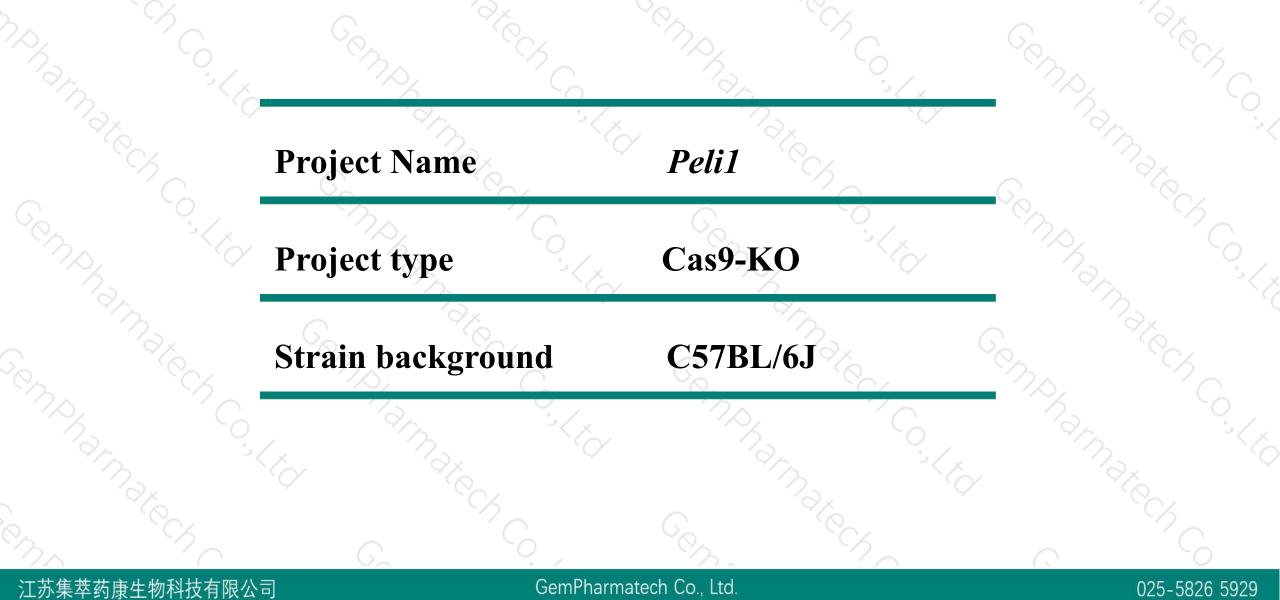
Peli1 Cas9-KO Strategy

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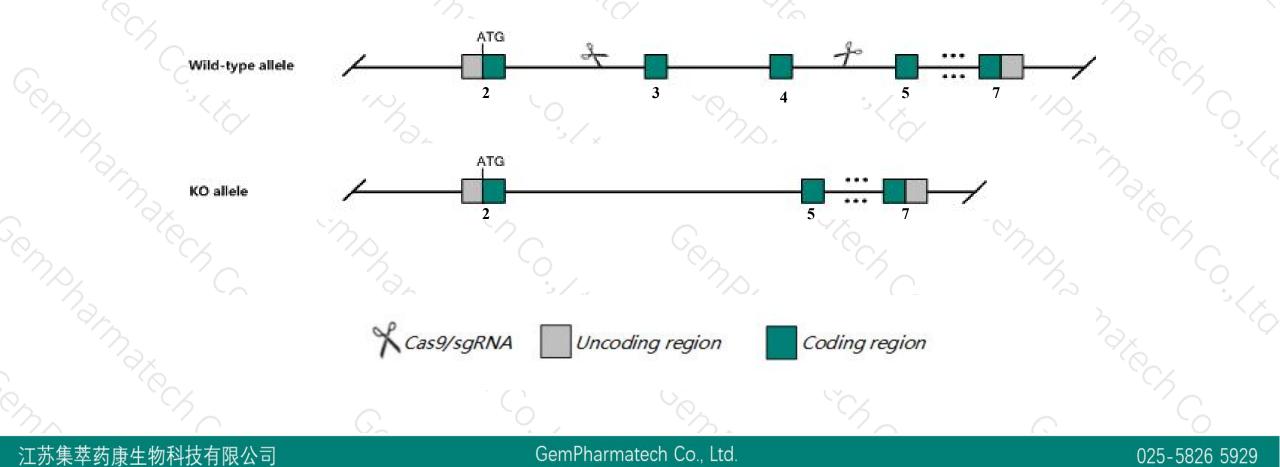
Project Overview







This model will use CRISPR/Cas9 technology to edit the *Peli1* gene. The schematic diagram is as follows:





- The Pelil gene has 4 transcripts. According to the structure of Pelil gene, exon3-exon4 of Pelil-201 (ENSMUST00000093290.11) transcript is recommended as the knockout region. The region contains 232bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Peli1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

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- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit reduced proinflammatory cytokine production, B cell proliferation, and mortality following treatment with LPS or pIpC.
- The *Peli1* gene is located on the Chr11. 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)



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Peli1 pellino 1 [Mus musculus (house mouse)]

Gene ID: 67245, updated on 19-Mar-2019

Summary

Official Symbol	Peli1 provided by MGI
Official Full Name	pellino 1 provided byMGI
Primary source	MGI:MGI:1914495
See related	Ensembl:ENSMUSG0000020134
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	2810468L03Rik, A930031K15Rik, AA409794, AI586297, D11Ertd676e
Expression	Ubiquitous expression in CNS E14 (RPKM 20.6), whole brain E14.5 (RPKM 20.6) and 28 other tissues See more
Orthologs	human all

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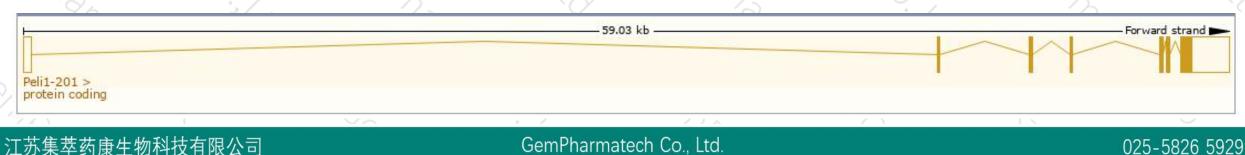
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Peli1-202	ENSMUST00000101477.1	3703	<u>418aa</u>	Protein coding	CCDS24462	Q5SRW7 Q8C669	TSL:1 GENCODE basic APPRIS P1
Peli1-201	ENSMUST0000093290.11	3514	<u>418aa</u>	Protein coding	CCDS24462	Q5SRW7 Q8C669	TSL:1 GENCODE basic APPRIS P1
Peli1-203	ENSMUST00000149675.1	3529	No protein	Retained intron	84	3 4	TSL:1
Peli1-204	ENSMUST00000156122.7	1108	No protein	Retained intron	62	<u>64</u>	TSL:1

The strategy is based on the design of *Peli1-201* transcript, The transcription is shown below

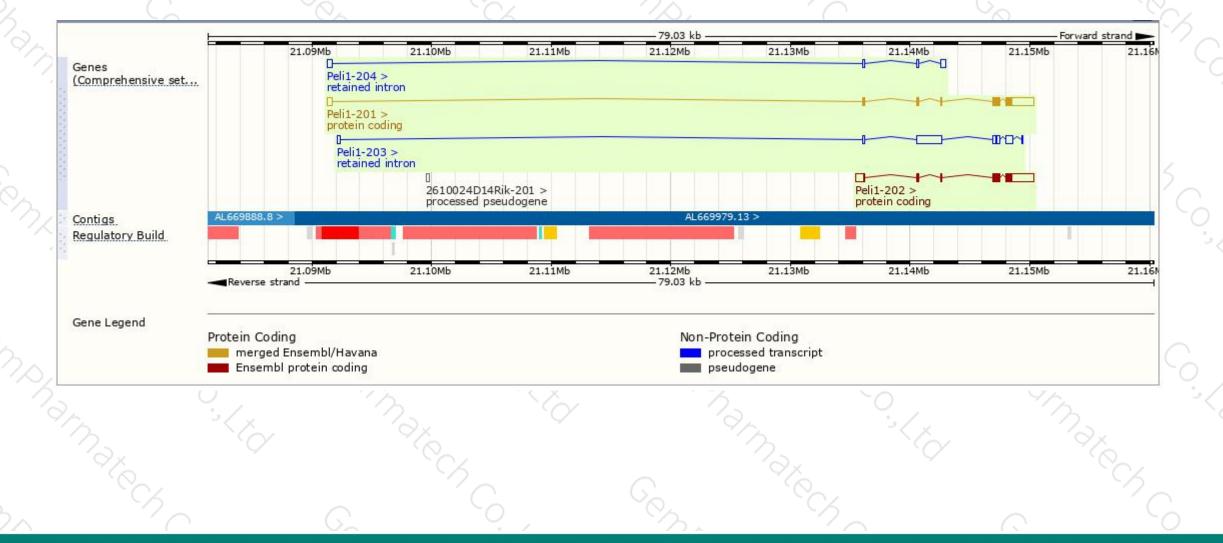


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Genomic location distribution



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Protein domain



ENSMUSP00000090. https://www.anther.	Pellino family PTHR12098:S										
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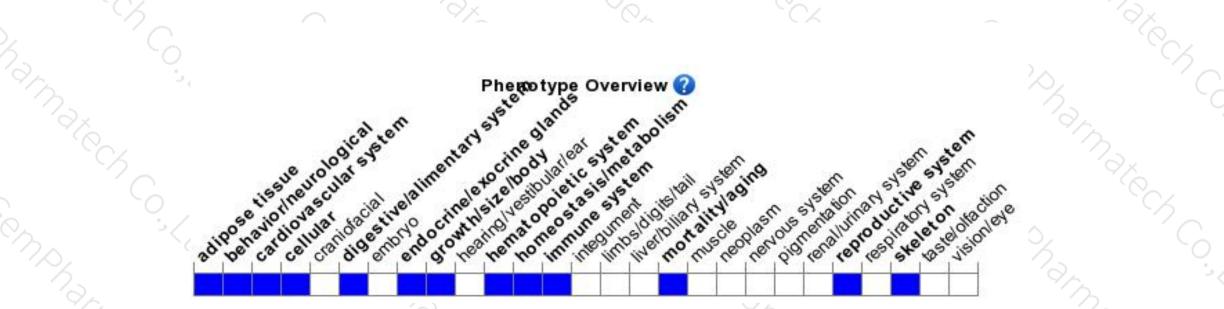
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Mouse phenotype description(MGI)



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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 reduced proinflammatory cytokine production, B cell proliferation, and mortality following treatment with LPS or pIpC.



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



