## Casp6 Cas9-KO Strategy

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## Project Overview

## Project Name

## Project type

Strain background

## Casp6

Cas9－KO

## Knockout strategy

This model will use CRISPR／Cas9 technology to edit the Casp6 gene．The schematic diagram is as follows：

Wild－type allele


KO allele


## Technical routes

＞The Casp6 gene has 4 transcripts．According to the structure of Casp6 gene，exon3－exon5 of Casp6－201
（ENSMUST00000029626．8）transcript is recommended as the knockout region．The region contains 403bp coding sequence． Knock out the region will result in disruption of protein function．
－In this project we use CRISPR／Cas9 technology to modify Casp6 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，
＞According to the existing MGI data，Mice homozygous for a knock－out allele exhibit failure to induce increased lysis of fluorogenic substrate VEID－AMC in staurosporine treated of lenses．Mice homozygous for a different knock－out allele exhibit resistance to excitotoxicity and axonal degeneration．
＞The Casp6 gene is located on the Chr3．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）

## Casp6 caspase 6 ［Mus musculus（house mouse）］

Gene ID：12368，updated on 19－Mar－2019

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Summary
    Official Symbol Casp6 provided by MGI
Official Full Name caspase 6 provided byMG|
    Primary source MGl:MGI:1312921
        See related Ensembl:ENSMUSG00000027997
        Gene type protein coding
    RefSeq status REVIEWED
        Organism Mus musculus
            Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
                Muroidea; Muridae; Murinae; Mus; Mus
    Also known as CASP-6, Mch2
            Summary This gene encodes a member of the cysteine proteases that plays important roles in regulating apoptosis and neurodegeneration. The encoded protein is involved in the transmission of pain and axonal degeneration．Genetic deletion of this gene in mice results in the delay of axon pruning and protects from axon degeneration．［provided by RefSeq，Apr 2015］
Expression Ubiquitous expression in duodenum adult（RPKM 36．2），small intestine adult（RPKM 29．7）and 27 other tissuesSee more Orthologs human all
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## Transcript information（Ensembl）

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GemPharmatech

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

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Casp6－201 | ENSMUST00000029626．8 | 1456 | $\underline{276 a a}$ | Protein coding | CCDS17838 | O08738 Q3TPJ9 | TSL：1 GENCODE basic APPRIS P1 |
| Casp6－202 | ENSMUST00000137314．1 | 477 | No protein | Processed transcript | - | - |  |
| Casp6－204 | ENSMUST00000197175．1 | 3914 | No protein | Retained intron | - | TSL：2 |  |
| Casp6－203 | ENSMUST00000152622．1 | 664 | No protein | Retained intron | - | TSL：NA |  |

The strategy is based on the design of Casp6－201 transcript，The transcription is shown below


Casp6－201＞
protein coding

## Genomic location distribution

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## Protein domain

ENSMUSP00000029．． Conserved Domains． hmmpanther．

Superfamily domains SMART domains．

Prints domain
Pfam domain
PROSTE profiles

PROSTTE patterns

Gene3D
All sequence $S N P s / i . .$.
Variant Legend

Scale bar


## Caspase－like domain superfamily

Peptidase C14A，caspase catalytic domain
Peptidase C14A，caspase catalytic domain
PF00656
Peptidase C14，p20 domain Peptidase C14，caspase non－catalytic subunit p1

Peptidase family C14A，His active site
Peptidase family C14A，cysteine active site

### 3.40 .50 .1460

$\square$missense variant
synonymous variant

## 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 failure to induce increased lysis of fluorogenic substrate VEID－AMC in staurosporine treated of lenses．Mice homozygous for a different knock－out allele exhibit resistance to excitotoxicity and axonal degeneration．

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


