

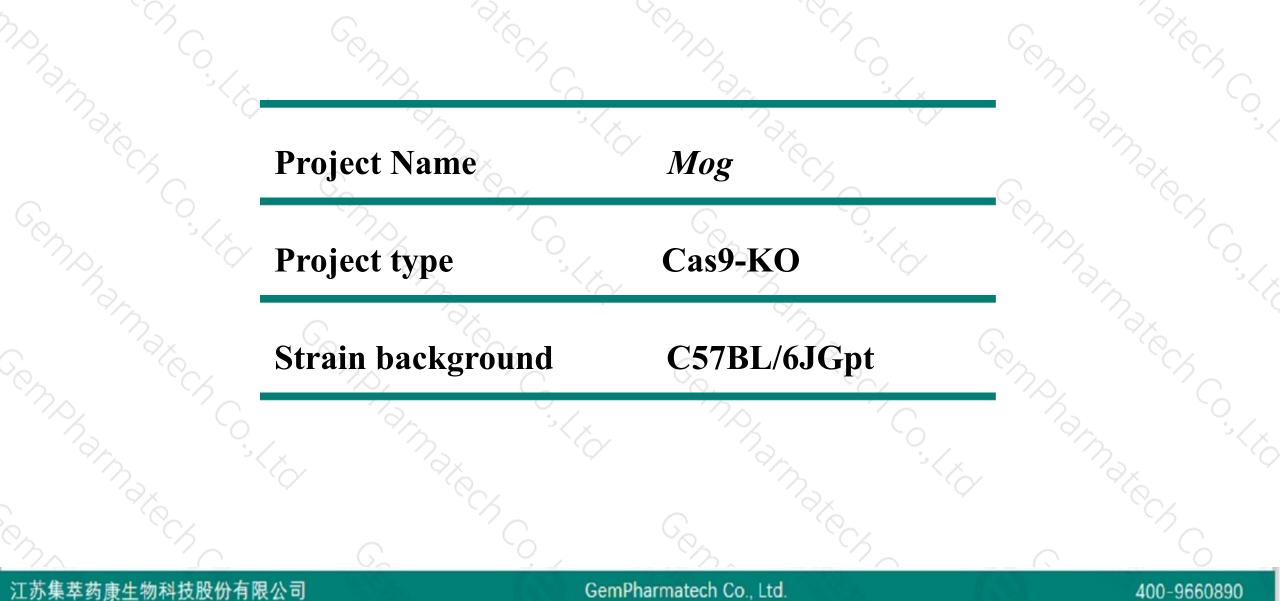
# Mog Cas9-KO Strategy

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# **Project Overview**

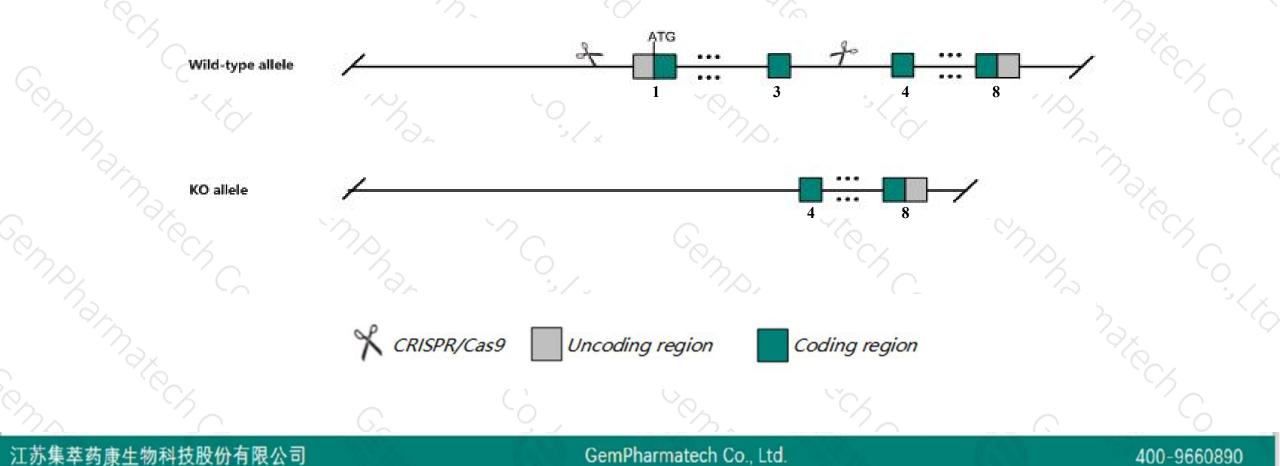




# **Knockout** strategy



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





- The Mog gene has 2 transcripts. According to the structure of Mog gene, exon1-exon3 of Mog-201 (ENSMUST00000102665.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Mog gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, While one line of homozygous mutant mice showed resistance to experimental autoimmune encephalomyelitis (EAE), another showed increased susceptibility.
- The Mog 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)**



## Mog myelin oligodendrocyte glycoprotein [ Mus musculus (house mouse) ]

Gene ID: 17441, updated on 4-Dec-2019

### Summary

Official Symbol Mog provided by MGI Official Full Name myelin oligodendrocyte glycoprotein provided by MGI MGI:MGI:97435 Primary source Ensembl:ENSMUSG00000076439 See related Gene type protein coding RefSeg status VALIDATED Organism Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Lineage Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus Also known as B230317G11Rik Expression Biased expression in cerebellum adult (RPKM 31.3), cortex adult (RPKM 21.2) and 4 other tissues See more Orthologs human all

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# **Transcript information (Ensembl)**



# The gene has 2 transcripts, all transcripts are shown below:

| Name    | Transcript ID         | bp   | Protein      | Biotype        | CCDS           | UniProt       | Flags                           |
|---------|-----------------------|------|--------------|----------------|----------------|---------------|---------------------------------|
| Mog-201 | ENSMUST00000102665.10 | 1704 | <u>247aa</u> | Protein coding | CCDS28734      | Q3UY21        | TSL:1 GENCODE basic APPRIS P2   |
| Mog-202 | ENSMUST00000167275.2  | 627  | <u>208aa</u> | Protein coding | 8 <del>.</del> | <u>Q29ZQ5</u> | TSL:1 GENCODE basic APPRIS ALT2 |

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

#### < Mog-201 protein coding

Reverse strand

- 12.66 kb -

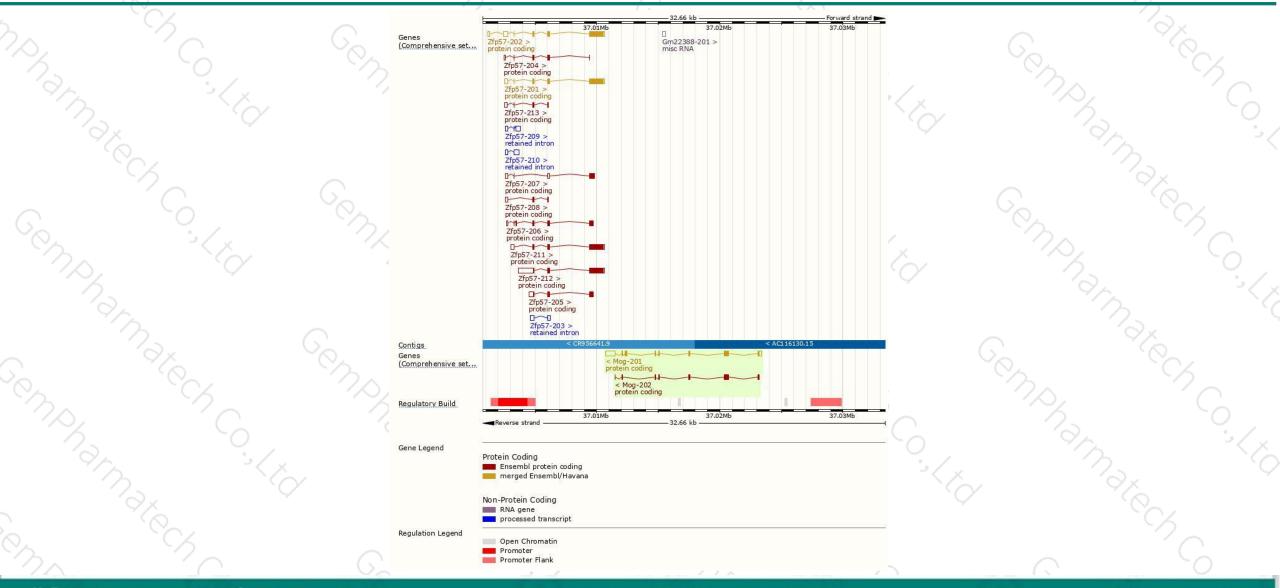
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# **Genomic location distribution**





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# **Protein domain**

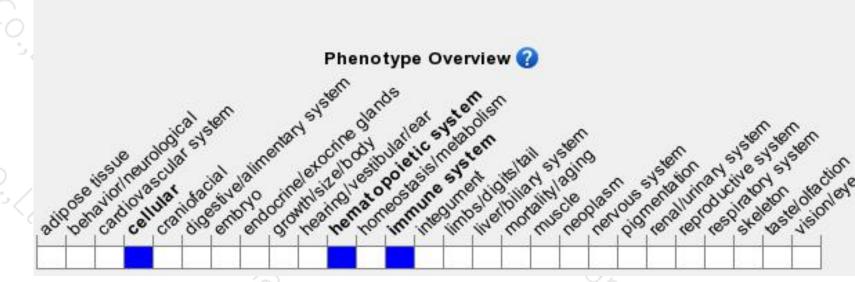
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|---|---------------------------------------|--|-------------------------------|------------------------|----------------|-------|-----|-------------|--|--|
|   | Scale bar                             | 0                                      | 40                            | 80                     | 120            | 160   | 200 | 247         |  |  |
|   | Variant Legend                        |  | nse variant<br>/mous variant  |                        |                |       |     |             |  |  |
| 9 | All sequence SNPs/i                   | Sequence v                             | variants (dbSNP ar            | nd all other sources)  | ( <b>1</b>     | ECE   | 10  | -0.<br>-< x |  |  |
|   | CDD                                   |  | cd05713                       | Í.                     |                |       |     | <u> </u>    |  |  |
|   | Gene3D                                | PTHR2410                               | 10 :SF71<br>Immunoglobulin-li | ke fold                |                |       |     |             |  |  |
|   | PANTHER                               | PTHR24100                              |                               |                        |                |       |     |             |  |  |
| 2 | PIRSF                                 | Myelin-oligod                          | endrocyte glycopro            | tein                   |                |       |     | 0           |  |  |
|   | PROSITE profiles                      |  |                               |                        |                |       |     |             |  |  |
|   | Pfam.                                 |  | Immunogle                     | obulin V-set domain    |                |       |     |             |  |  |
|   |                                       |  | Immun                         | oglobulin V-set domair | 1              |       |     |             |  |  |
|   | SMART                                 |  | Immunoglob                    | oulin subtype          |                |       |     | ÷.          |  |  |
| 2 | Cleavage site (Sign<br>Superfamily    | Immunoglobulin-like domain superfamily |                               |                        |                |       |     |             |  |  |
|   | Low complexity (Seg)                  | _                                      |                               |                        |                |       |     | 3           |  |  |
|   | ENSMUSP00000099<br>Transmembrane heli |  |                               |                        |                |       |     |             |  |  |

# 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, While one line of homozygous mutant mice showed resistance to experimental autoimmune encephalomyelitis (EAE), another showed increased susceptibility.



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



