

# Odad1 Cas9-KO Strategy

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### Overview

#### Target Gene Name

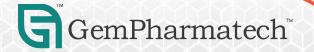
• Odad1

### Project Type

• Cas9-KO

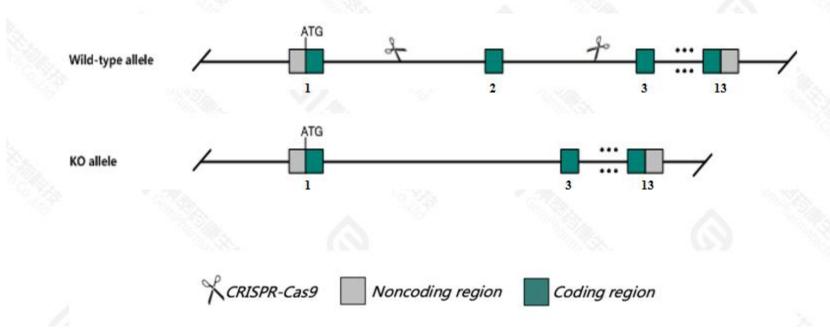
#### Genetic Background

• C57BL/6JGpt



## Strain Strategy

This model will use CRISPR-Cas9 technology to edit the Odad1 gene. The schematic diagram is as follows:

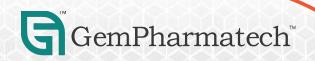


Schematic representation of CRISPR-Cas9 engineering used to edit the Odad1 gene.



### Technical Information

- The *Odad1* gene has 7 transcripts. According to the structure of *Odad1* gene, exon2 of *Odad1-201*(ENSMUST00000038720.8) transcript is recommended as the knockout region. The region contains 190bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Odad1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



#### Gene Information

#### Odad1 outer dynein arm docking complex subunit 1 [Mus musculus (house mouse)]

Gene ID: 211535, updated on 28-Apr-2022

#### Summary

☆ ?

Official Symbol Odad1 provided by MGI

Official Full Name outer dynein arm docking complex subunit 1 provided by MGI

Primary source MGI:MGI:2446120

See related Ensembl: ENSMUSG00000040189

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 Ccdc114

Expression Broad expression in testis adult (RPKM 7.8), adrenal adult (RPKM 6.5) and 24 other tissuesSee more

Orthologs human all

Source: https://www.ncbi.nlm.nih.gov/

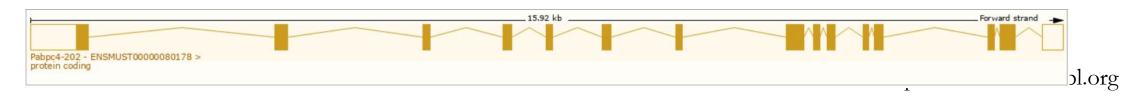


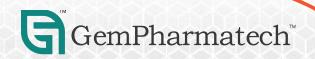
## Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

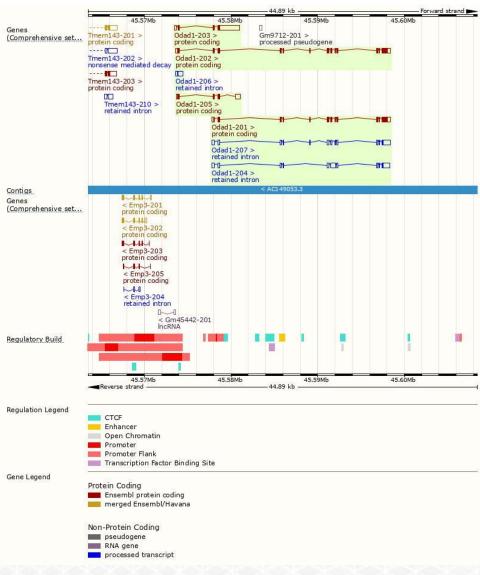
| Name      | Transcript ID        | bp   | Protein      | Biotype         | CCDS         | UniProt | Flags                                 |
|-----------|----------------------|------|--------------|-----------------|--------------|---------|---------------------------------------|
| Odad1-201 | ENSMUST00000038720.8 | 2453 | 658aa        | Protein coding  | CCDS21271    |         | TSL:1 , GENCODE basic , APPRIS P2 ,   |
| Odad1-203 | ENSMUST00000210602.2 | 2928 | 136aa        | Protein coding  | 1-1          |         | TSL:1 , GENCODE basic , APPRIS ALT2 , |
| Odad1-202 | ENSMUST00000210039.3 | 2598 | <u>697aa</u> | Protein coding  | -            |         | TSL:5 , GENCODE basic , APPRIS ALT2 , |
| Odad1-205 | ENSMUST00000211367.2 | 1078 | <u>134aa</u> | Protein coding  | 0.00         |         | TSL:1, GENCODE basic, APPRIS ALT2,    |
| Odad1-204 | ENSMUST00000210867.2 | 2677 | No protein   | Retained intron | 848          |         | TSL:1,                                |
| Odad1-207 | ENSMUST00000236631.2 | 2460 | No protein   | Retained intron | 4 <u>=</u> 3 |         |                                       |
| Odad1-206 | ENSMUST00000211628.2 | 741  | No protein   | Retained intron | 1-1          |         | TSL:1,                                |

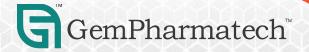
The strategy is based on the design of *Odad1-201* transcript, the transcription is shown below:





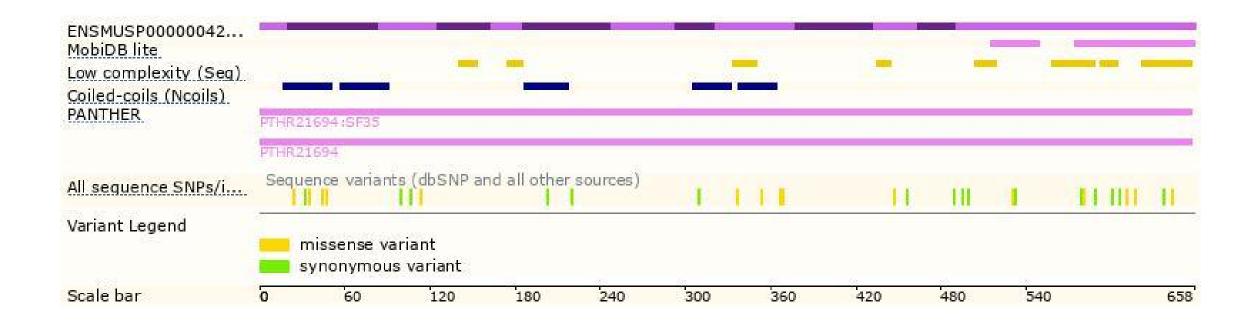
### Genomic Information





Source: : https://www.ensembl.org

#### Protein Information





Source: : https://www.ensembl.org

### Important Information

- Odad1 is located on Chr7. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

