

# Donal Day College Il15 Cas9-KO Strategy Rohalmakech Co.

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# **Project Overview**



**Project Name** 

Project type Cas9-KO

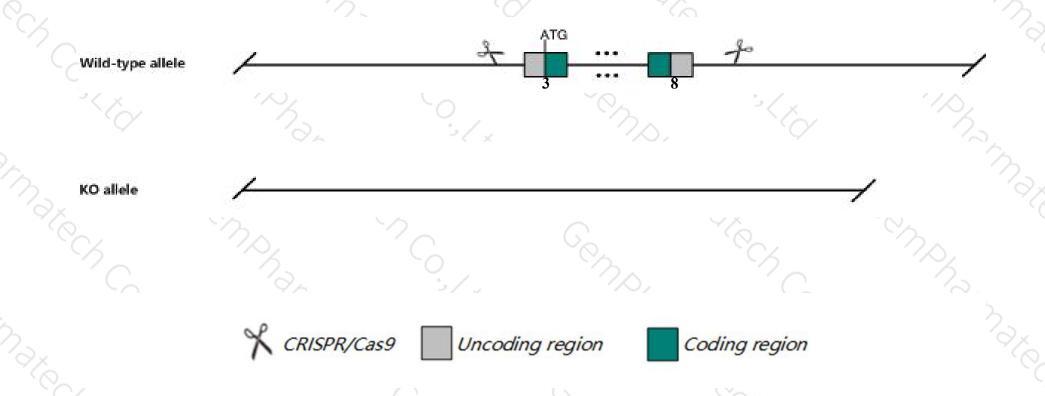
Strain background C57BL/6JGpt

*Il15* 

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Il15* gene. The schematic diagram is as follows:



## **Technical routes**



- ➤ The *Il15* gene has 10 transcripts. According to the structure of *Il15* gene, exon3-exon8 of *Il15-201* (ENSMUST00000034148.6) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Il15* gene. The brief process is as follows: CRISPR/Cas9 system w

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for disruptions of this gene have normal life spans but display a variety of immune system abnormalities and maternal placental defects.
- The *Il15* gene is located on the Chr8. 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)



#### II15 interleukin 15 [Mus musculus (house mouse)]

Gene ID: 16168, updated on 19-Mar-2019

#### Summary

☆ ?

Official Symbol II15 provided by MGI

Official Full Name interleukin 15 provided by MGI

Primary source MGI:MGI:103014

See related Ensembl:ENSMUSG00000031712

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 Al503618, IL-15

Summary This gene encodes a a pleiotropic cytokine of the interleukin family of proteins that plays important roles in the innate and adaptive cell

homeostasis, as well as peripheral immune function. The encoded protein undergoes proteolytic processing to generate a mature cytokine that stimulates the proliferation of natural killer cells. The transgenic mice overexpressing the encoded protein exhibit an increase in the number of memory CD8+ T cells in a naive state and enhanced protection against bacterial infections. Mice lacking the encoded protein

exhibit impaired protection against a strain of attenuated Mycobacterium. [provided by RefSeq, Aug 2016]

Expression Broad expression in heart adult (RPKM 5.2), duodenum adult (RPKM 3.3) and 24 other tissuesSee more

Orthologs <u>human</u> all

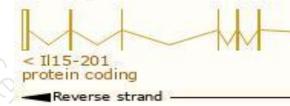
# Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

Transcript ID  ENSMUST00000034148.6	<b>bp</b> 1908	Protein	Biotype	CCDS	UniProt	Flags
	1908	400				90
		162aa	Protein coding	CCDS40401	P48346 Q3U1Z6	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000209363.1	1251	<u>162aa</u>	Protein coding	CCDS40401	P48346 Q3U1Z6	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000209573.2	1164	<u>162aa</u>	Protein coding	CCDS40401	P48346 Q3U1Z6	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000210094.1	430	<u>48aa</u>	Protein coding	(4	A0A1B0GQZ2	CDS 3' incomplete TSL:3
ENSMUST00000211565.1	766	<u>61aa</u>	Nonsense mediated decay	15	A0A1B0GQZ8	TSL:3
ENSMUST00000210472.1	618	No protein	Processed transcript	19 <del>5</del>		TSL:3
ENSMUST00000211722.1	433	No protein	Processed transcript	<u> </u>	· ·	TSL:1
ENSMUST00000209687.1	430	No protein	Processed transcript	(4	_	TSL:1
ENSMUST00000211282.1	258	No protein	Processed transcript	15		TSL:5
ENSMUST00000210885.1	234	No protein	Processed transcript	-		TSL:5
	ENSMUST00000209573.2 ENSMUST00000210094.1 ENSMUST00000211565.1 ENSMUST00000210472.1 ENSMUST00000211722.1 ENSMUST00000209687.1 ENSMUST00000211282.1	ENSMUST00000210094.1 430 ENSMUST00000211565.1 766 ENSMUST00000210472.1 618 ENSMUST00000211722.1 433 ENSMUST00000209687.1 430 ENSMUST00000211282.1 258	ENSMUST00000210094.1 430 48aa ENSMUST00000211565.1 766 61aa ENSMUST00000210472.1 618 No protein ENSMUST00000211722.1 433 No protein ENSMUST00000209687.1 430 No protein ENSMUST00000211282.1 258 No protein	ENSMUST00000209573.2         1164         162aa         Protein coding           ENSMUST00000210094.1         430         48aa         Protein coding           ENSMUST00000211565.1         766         61aa         Nonsense mediated decay           ENSMUST00000210472.1         618         No protein         Processed transcript           ENSMUST00000211722.1         433         No protein         Processed transcript           ENSMUST00000209687.1         430         No protein         Processed transcript           ENSMUST00000211282.1         258         No protein         Processed transcript	NSMUST00000210094.1   430   48aa   Protein coding	NSMUST00000210094.1   430   48aa   Protein coding   -   A0A1B0GQZ2

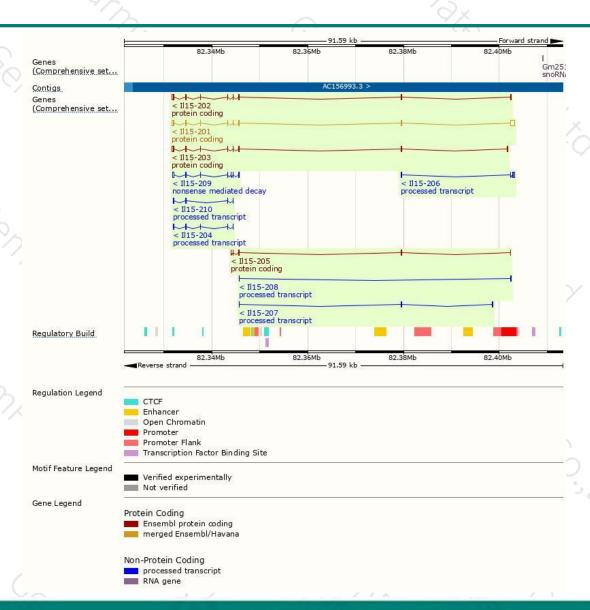
The strategy is based on the design of *Il15-201* transcript, The transcription is shown below



71.59 kb

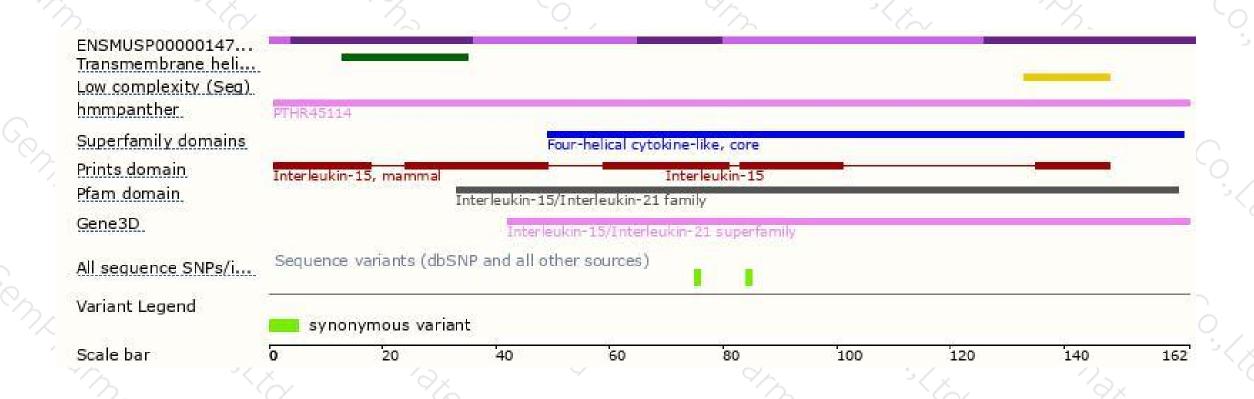
## Genomic location distribution





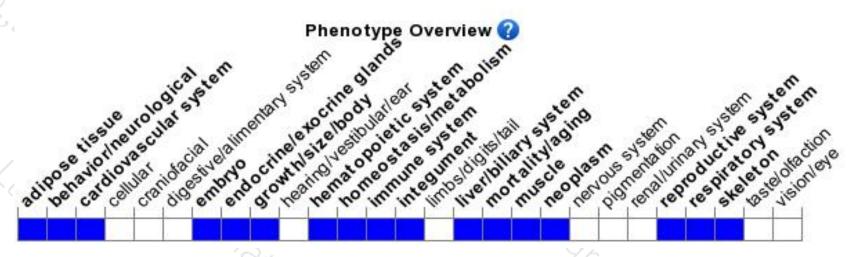
## Protein domain





## Mouse phenotype description(MGI)





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

According to the existing MGI data, Mice homozygous for disruptions of this gene have normal life spans but display a variety of immune system abnormalities and maternal placental defects.



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





