

# *Gzmm* Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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# Project Overview

**Project Name**

***Gzmm***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**



# Knockout strategy

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





- The *Gzmm* gene has 2 transcripts. According to the structure of *Gzmm* gene, exon2 of *Gzmm-201* (ENSMUST00000020549.3) transcript is recommended as the knockout region. The region contains 160bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gzmm* gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for a knock-in allele display normal immune homeostasis, normal NK cell cytotoxicity and a normal response to ectromelia virus infection, but show a transient but significant increase in susceptibility to infection with the murine cytomegalovirus.
- Transcript *Gzmm*-202 may not be affected.
- The *Gzmm* gene is located on the Chr10. 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)

## Gzmm granzyme M (lymphocyte met-ase 1) [ *Mus musculus* (house mouse) ]

Gene ID: 16904, updated on 12-Aug-2019

### Summary

- Official Symbol** Gzmm provided by [MGI](#)
- Official Full Name** granzyme M (lymphocyte met-ase 1) provided by [MGI](#)
- Primary source** [MGI:MGI:99549](#)
- See related** [Ensembl:ENSMUSG00000054206](#)
- 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** Lmet1; MMET-1
- Summary** The protein encoded by this gene is a member of a family of cytotoxic lymphocyte serine proteases called granzymes, which are expressed by cytotoxic T lymphocytes and natural killer cells. This protein belongs to a subfamily of granzymes that cleave after methionine residues. Natural killer cell development, homeostasis and cytotoxicity are normal in mice deficient for this gene, but they demonstrate increased susceptibility to murine cytomegalovirus. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]
- Expression** Ubiquitous expression in heart adult (RPKM 1.8), placenta adult (RPKM 0.9) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 10 C1; 10 39.72 cM See Gzmm in [Genome Data Viewer](#)

**Exon count:** 7

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	10	NC_000076.6 (79689020..79695261)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	10	NC_000076.5 (79151765..79158005)

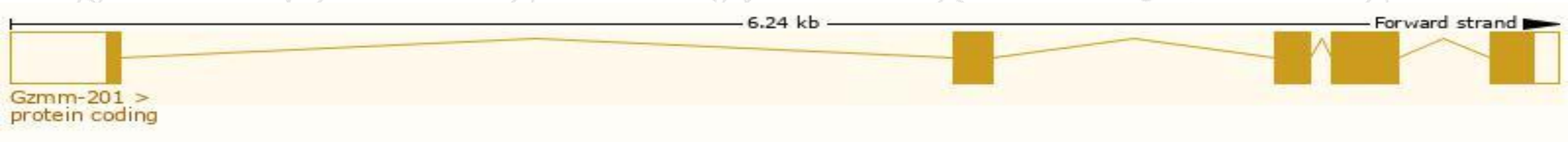


# Transcript information (Ensembl)

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

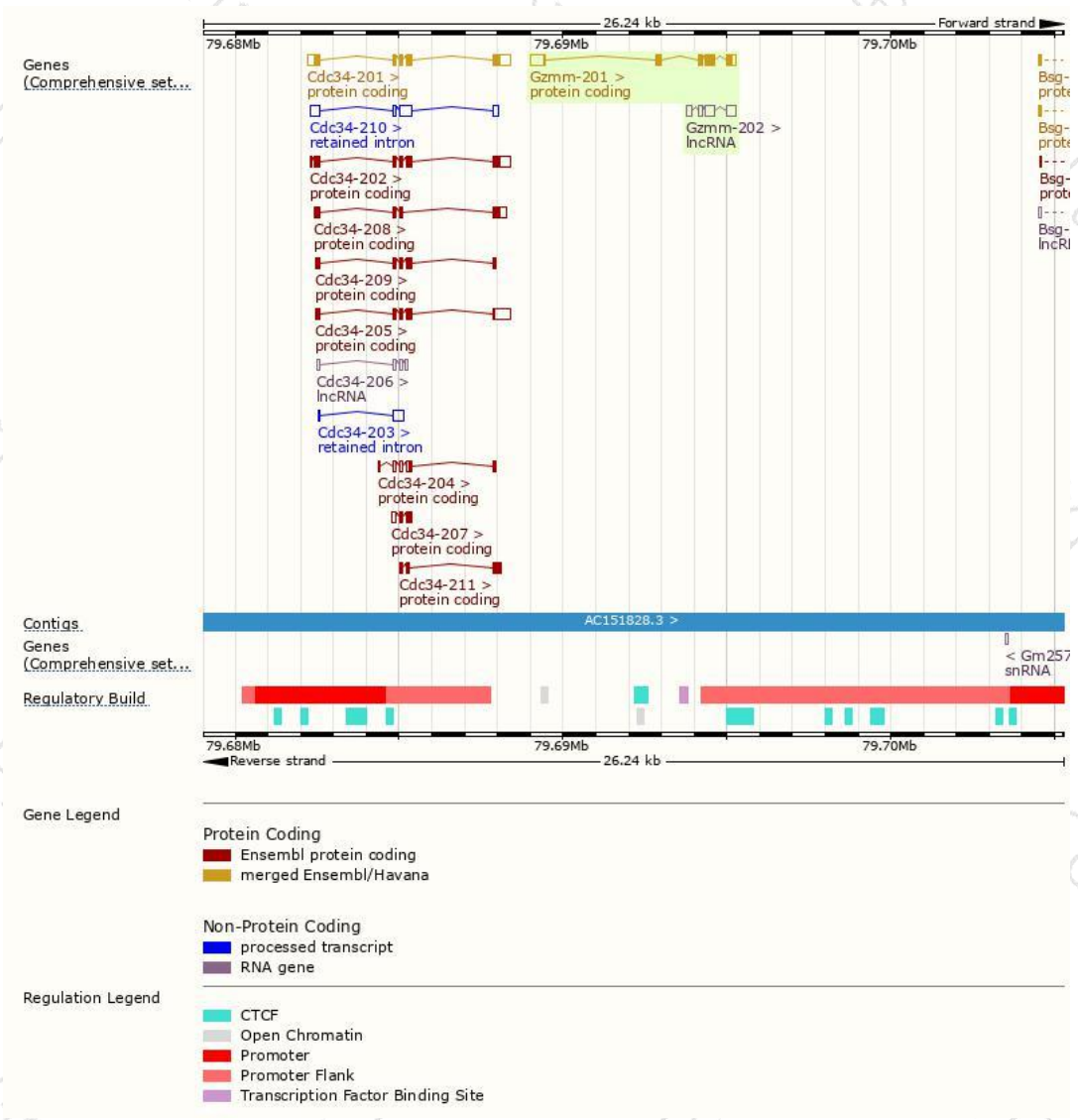
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gzmm-201	<a href="#">ENSMUST00000020549.3</a>	1287	<a href="#">264aa</a>	Protein coding	<a href="#">CCDS23984</a>	<a href="#">Q08643</a>	TSL:1 GENCODE basic APPRIS P1
Gzmm-202	<a href="#">ENSMUST00000151213.1</a>	865	No protein	lncRNA	-	-	TSL:1

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



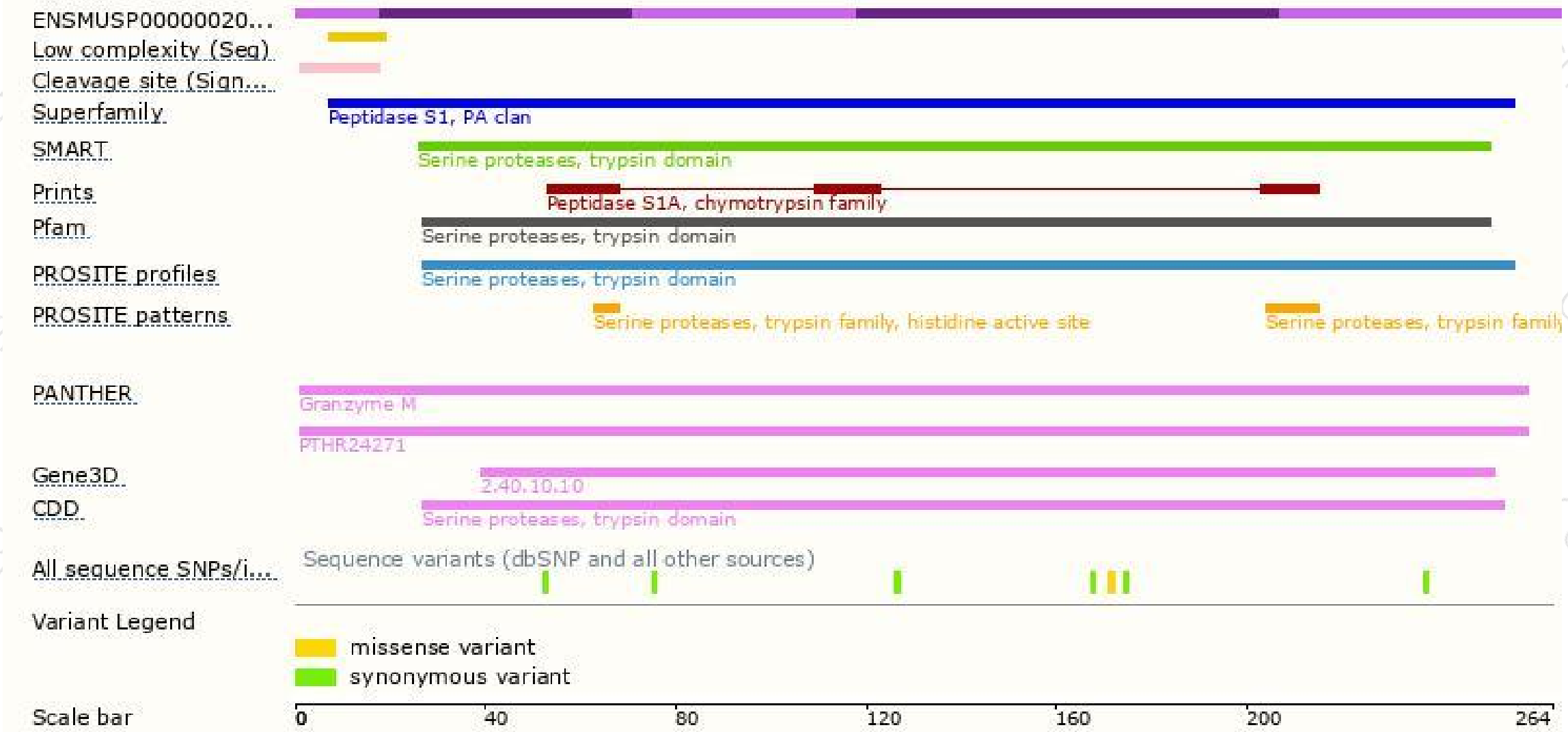


# Genomic location distribution



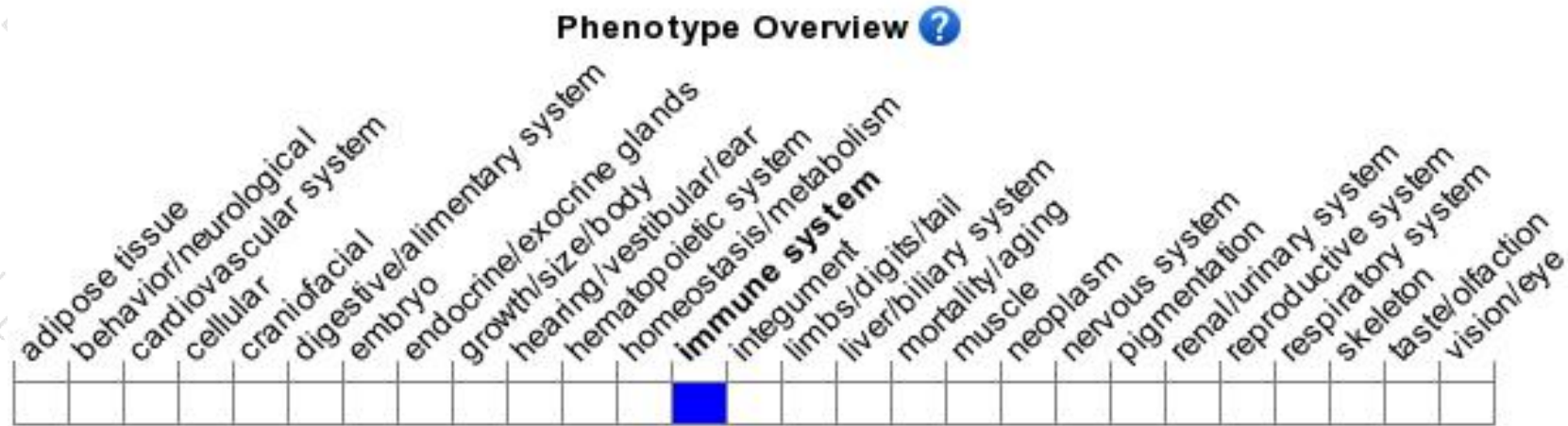


# Protein domain





# 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 a knock-in allele display normal immune homeostasis, normal NK cell cytotoxicity and a normal response to ectromelia virus infection, but show a transient but significant increase in susceptibility to infection with the murine cytomegalovirus.



If you have any questions, you are welcome to inquire.

Tel: 400-9660890

