

# *Traf3* Cas9-KO Strategy

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**Design Date:** 2020-5-6

# Project Overview

**Project Name**

***Traf3***

**Project type**

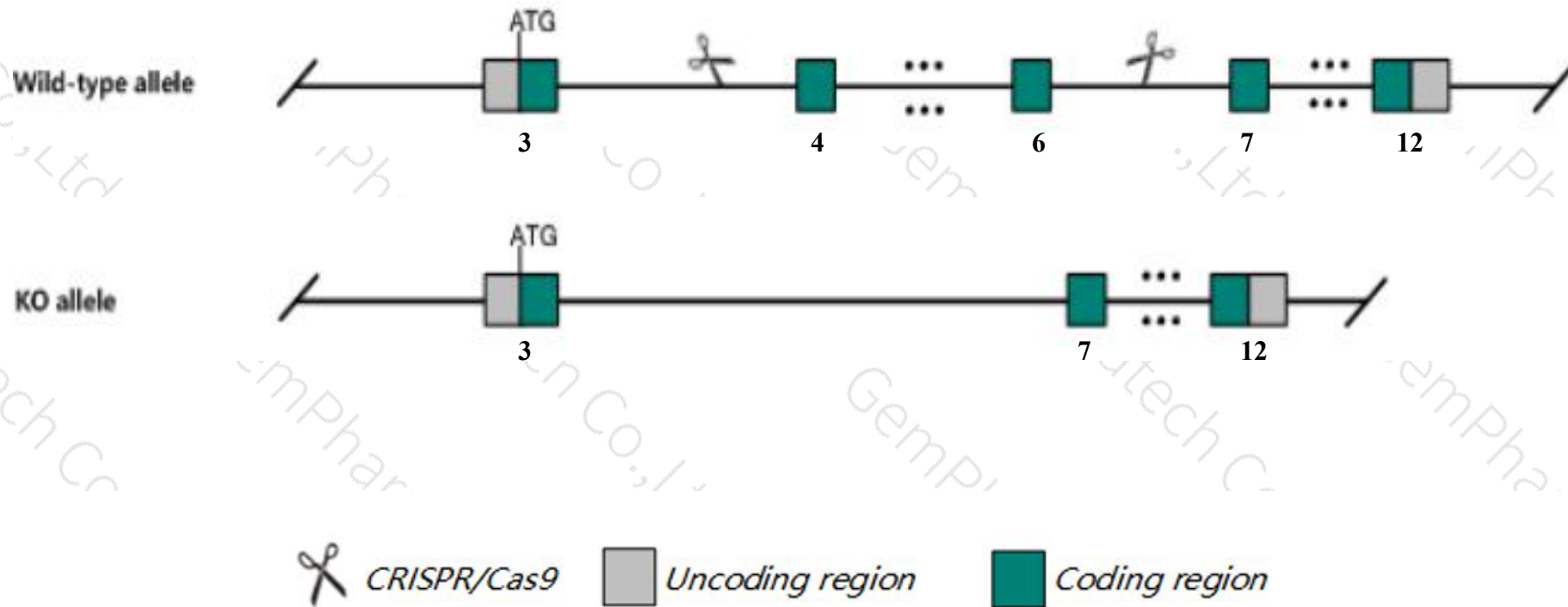
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Traf3* gene. The schematic diagram is as follows:



- The *Traf3* gene has 5 transcripts. According to the structure of *Traf3* gene, exon4-exon6 of *Traf3-201* (ENSMUST00000021706.10) transcript is recommended as the knockout region. The region contains 325bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Traf3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous mutation of this gene results in progressive runting, hypoglycemia, and depletion of peripheral white blood cells, leading to death by 10 days of age. immune responses to t-dependent antigen are impaired in lethally irradiated mice reconstituted with mutant cells.
- The *Traf3* gene is located on the Chr12. 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)

## Traf3 TNF receptor-associated factor 3 [Mus musculus (house mouse)]

Gene ID: 22031, updated on 13-Mar-2020

### Summary



<b>Official Symbol</b>	Traf3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	TNF receptor-associated factor 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:108041</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000021277</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AI528849, CAP-1, CD40bp, CRAF1, LAP1, T-BAM, TRAFAMN, amn
<b>Expression</b>	Ubiquitous expression in spleen adult (RPKM 14.4), thymus adult (RPKM 12.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

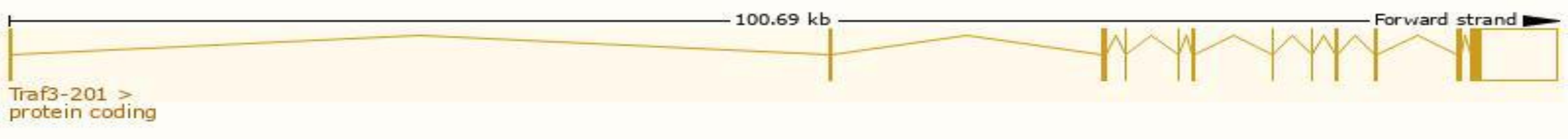
# Transcript information（Ensembl）



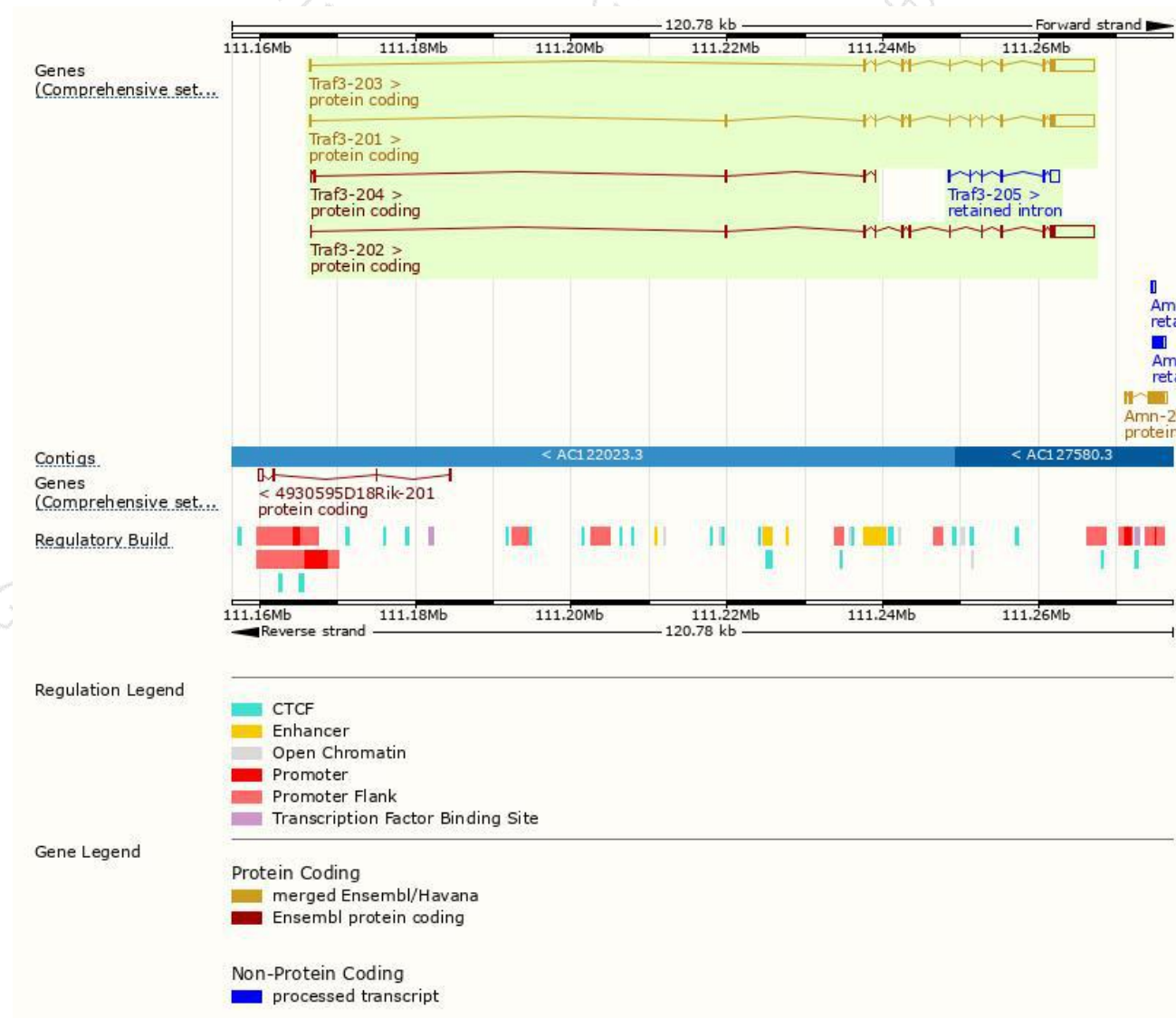
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Traf3-201	<a href="#">ENSMUST00000021706.10</a>	7060	<a href="#">567aa</a>	Protein coding	<a href="#">CCDS26175</a>	<a href="#">Q60803</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Traf3-203	<a href="#">ENSMUST00000117269.7</a>	6972	<a href="#">542aa</a>	Protein coding	<a href="#">CCDS36563</a>	<a href="#">Q3UHV1</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Traf3-202	<a href="#">ENSMUST00000060274.6</a>	6896	<a href="#">542aa</a>	Protein coding	<a href="#">CCDS36563</a>	<a href="#">Q3UHV1</a>	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Traf3-204	<a href="#">ENSMUST00000139162.7</a>	645	<a href="#">97aa</a>	Protein coding	-	<a href="#">D3Z343</a>	CDS 3' incomplete TSL:3
Traf3-205	<a href="#">ENSMUST00000143395.1</a>	1720	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Traf3-201* transcript,the transcription is shown below

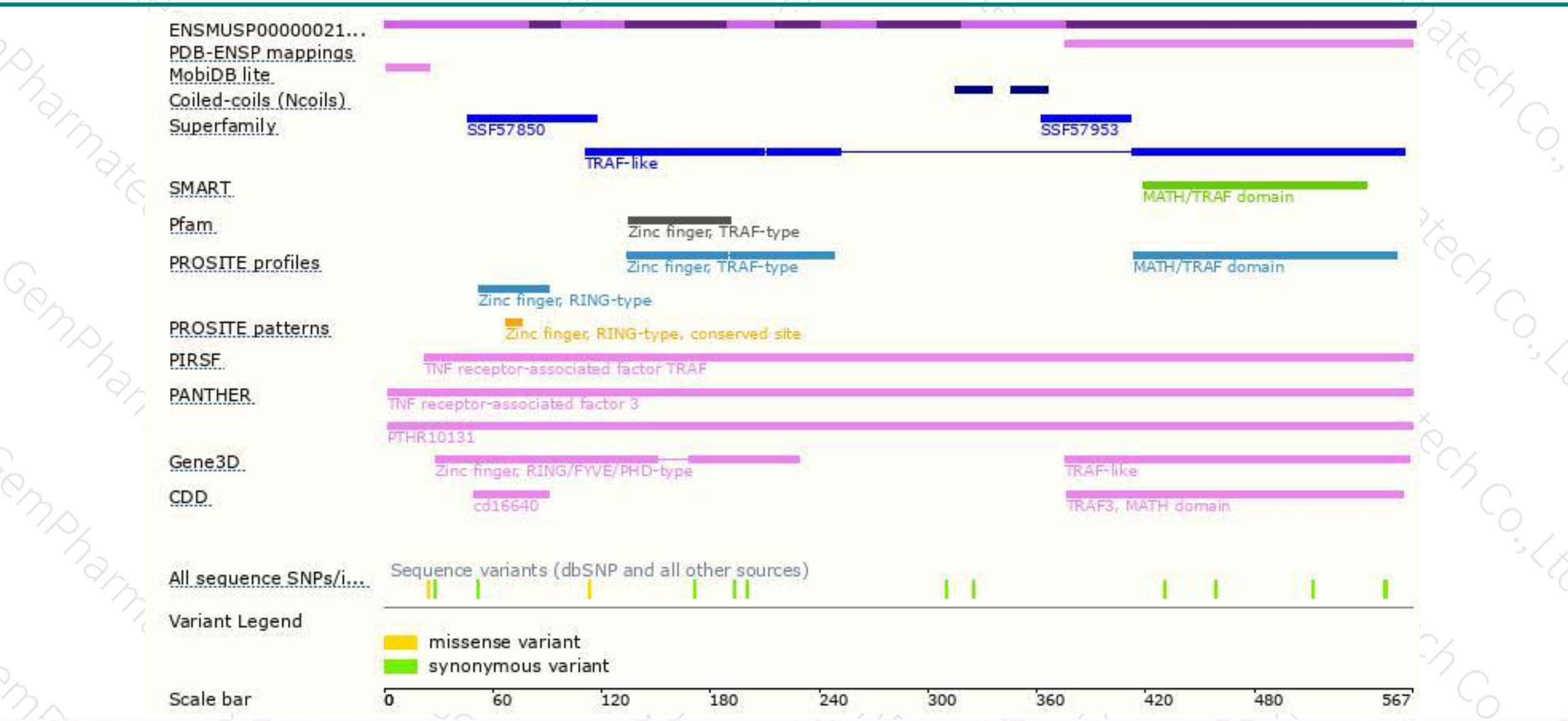


# Genomic location distribution

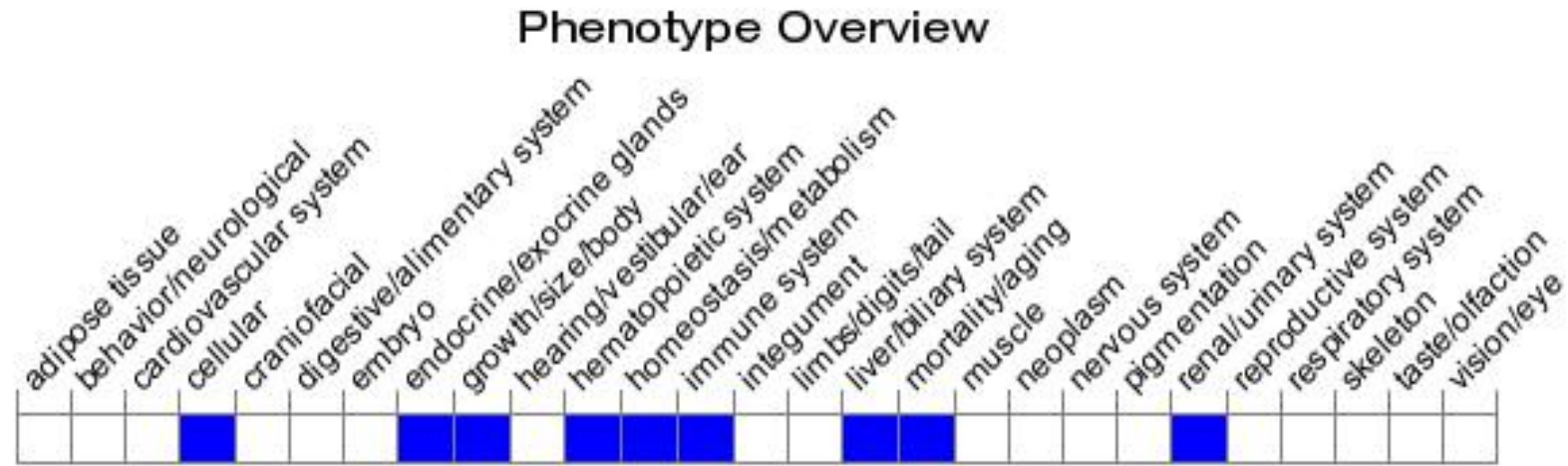




# Protein domain



# 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, homozygous mutation of this gene results in progressive runting, hypoglycemia, and depletion of peripheral white blood cells, leading to death by 10 days of age. Immune responses to T-dependent antigen are impaired in lethally irradiated mice reconstituted with mutant cells.

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

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