



U2af1 Cas9-CKO Strategy

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Project Overview

Project Name

U2af1

Project type

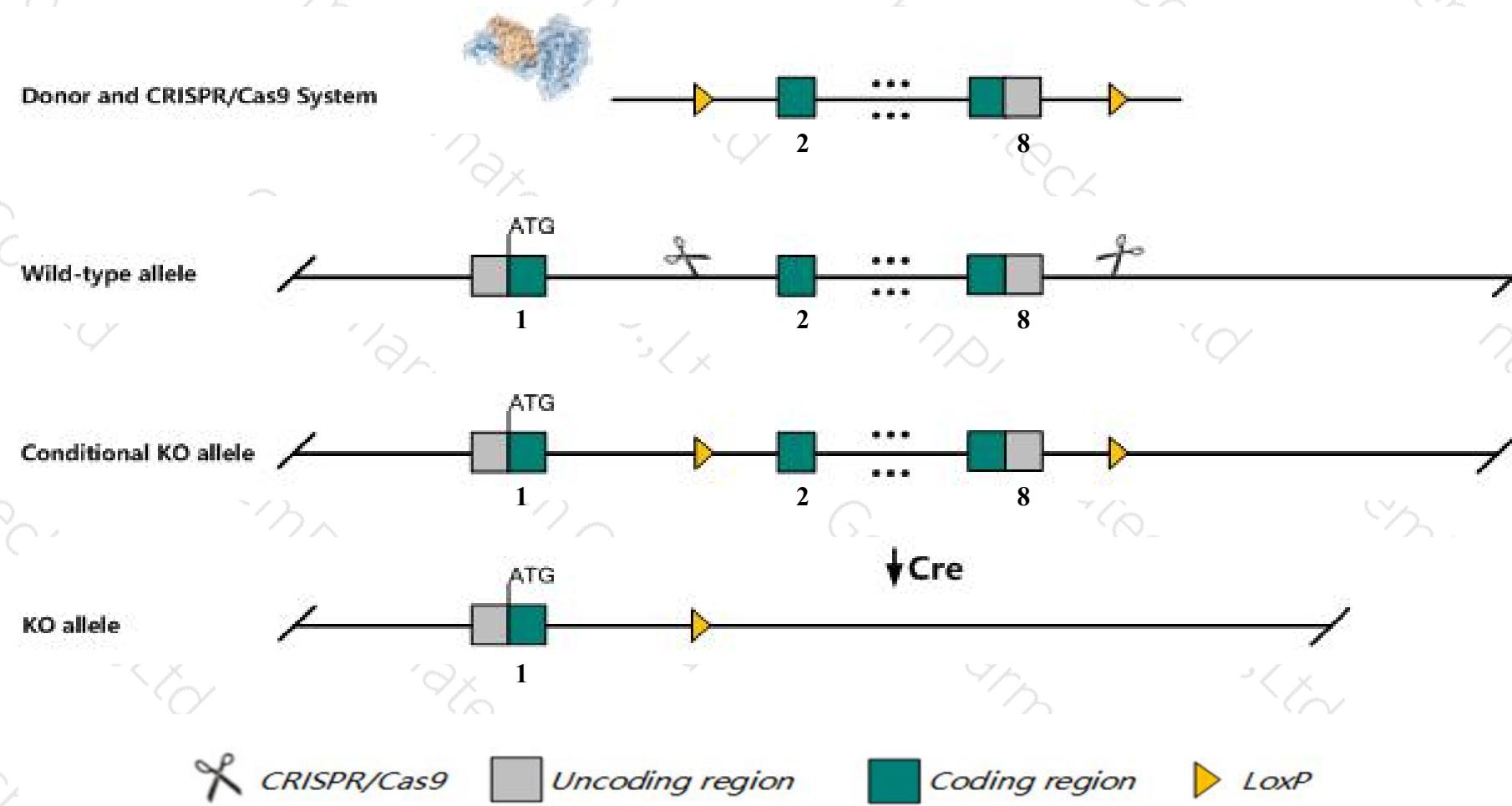
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *U2af1* gene. The schematic diagram is as follows:



Technical routes

- The *U2af1* gene has 9 transcripts. According to the structure of *U2af1* gene, exon2-exon8 of *U2af1-201* (ENSMUST00000014684.5) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *U2af1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



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Notice

- The floxed region is near to the N-terminal of *Rps2-ps8* gene, this strategy may influence the regulatory function of the N-terminal of *Rps2-ps8* gene.
- The effect on transcript *U2af1-207* is unknown.
- The *U2af1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



Gene information (NCBI)

U2af1 U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1 [*Mus musculus* (house mouse)]

Gene ID: 108121, updated on 12-Aug-2019

Summary

Official Symbol	U2af1 provided by MGI
Official Full Name	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1 provided by MGI
Primary source	MGI:MG1:98884
See related	Ensembl:ENSMUSG00000061613
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	2010107D16Rik
Expression	Broad expression in CNS E11.5 (RPKM 119.0), placenta adult (RPKM 69.8) and 23 other tissues See more
Orthologs	human all

Genomic context

Location: 17; 17 B1

[See U2af1 in Genome Data Viewer](#)

Exon count: 10

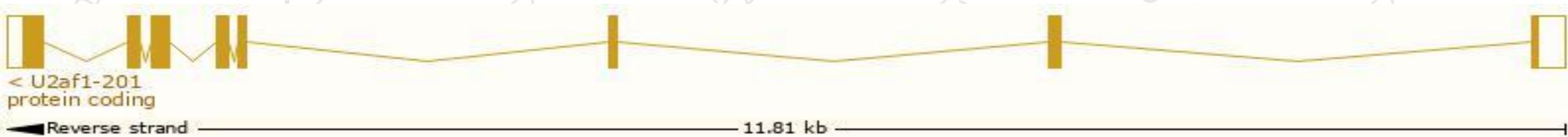
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (31647081..31659148, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (31784027..31795699, complement)

Transcript information (Ensembl)

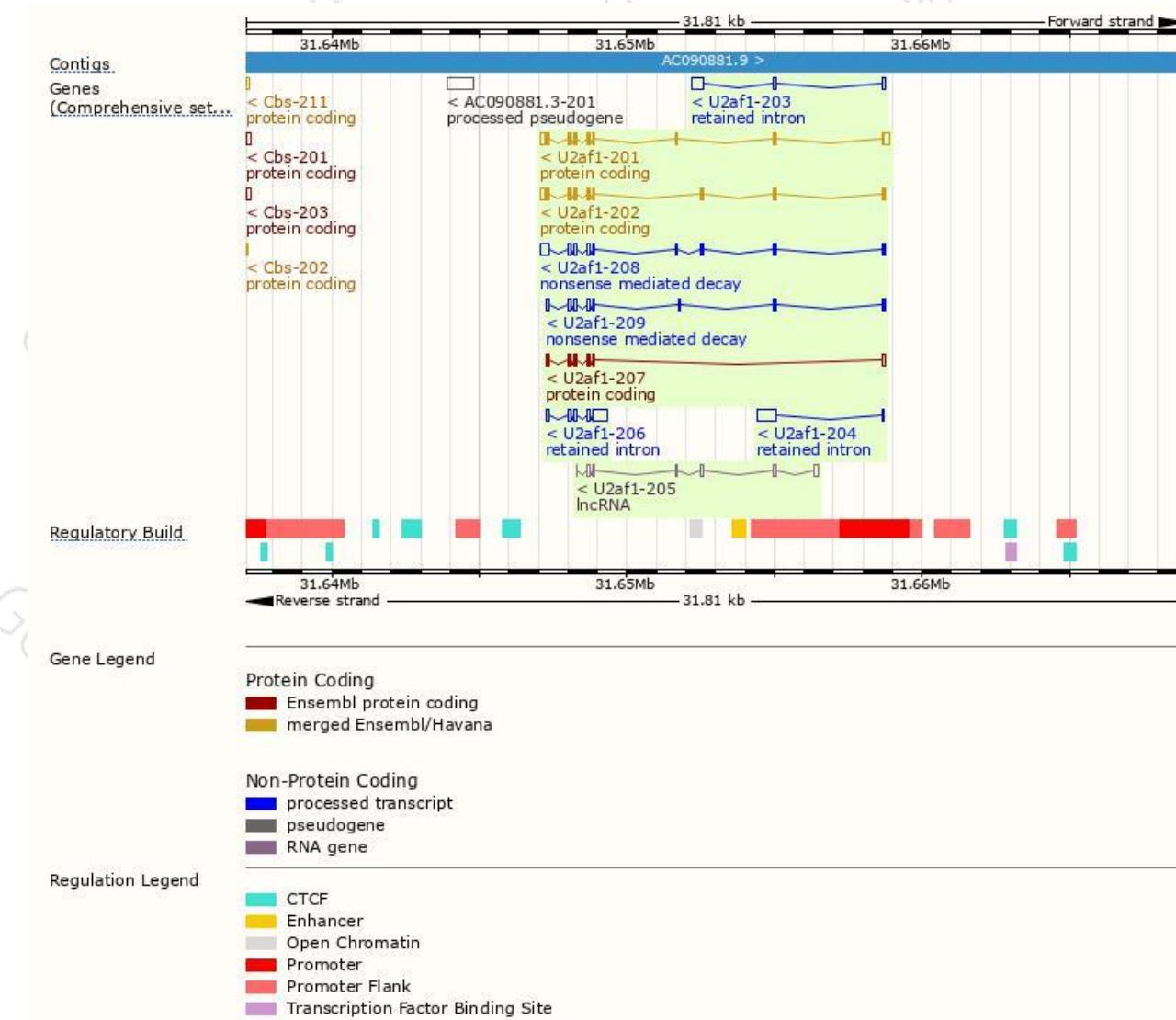
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
U2af1-201	ENSMUST0000014684.5	1046	239aa	Protein coding	CCDS28611	Q14C24 Q9D883	TSL:1 GENCODE basic APPRIS P3
U2af1-202	ENSMUST00000166526.8	923	239aa	Protein coding	CCDS50055	G3UW94	TSL:2 GENCODE basic APPRIS ALT2
U2af1-207	ENSMUST00000236475.1	532	126aa	Protein coding	-	-	CDS 3' incomplete
U2af1-208	ENSMUST00000237323.1	975	75aa	Nonsense mediated decay	-	-	
U2af1-209	ENSMUST00000238046.1	722	45aa	Nonsense mediated decay	-	-	
U2af1-206	ENSMUST00000236293.1	861	No protein	Retained intron	-	-	
U2af1-204	ENSMUST00000235969.1	703	No protein	Retained intron	-	-	
U2af1-203	ENSMUST00000235600.1	541	No protein	Retained intron	-	-	
U2af1-205	ENSMUST00000236260.1	539	No protein	lncRNA	-	-	

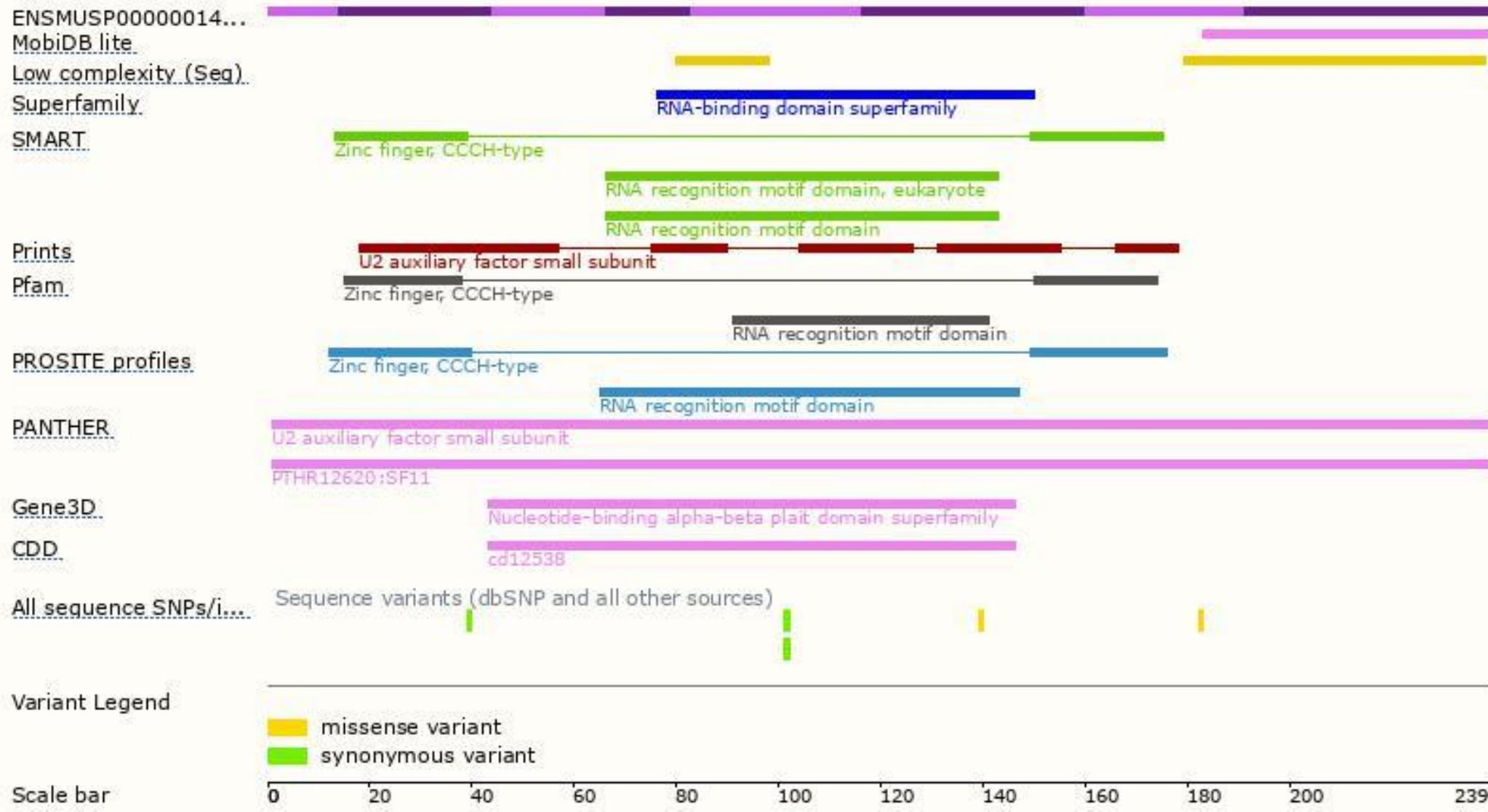
The strategy is based on the design of *U2af1-201* transcript, The transcription is shown below



Genomic location distribution



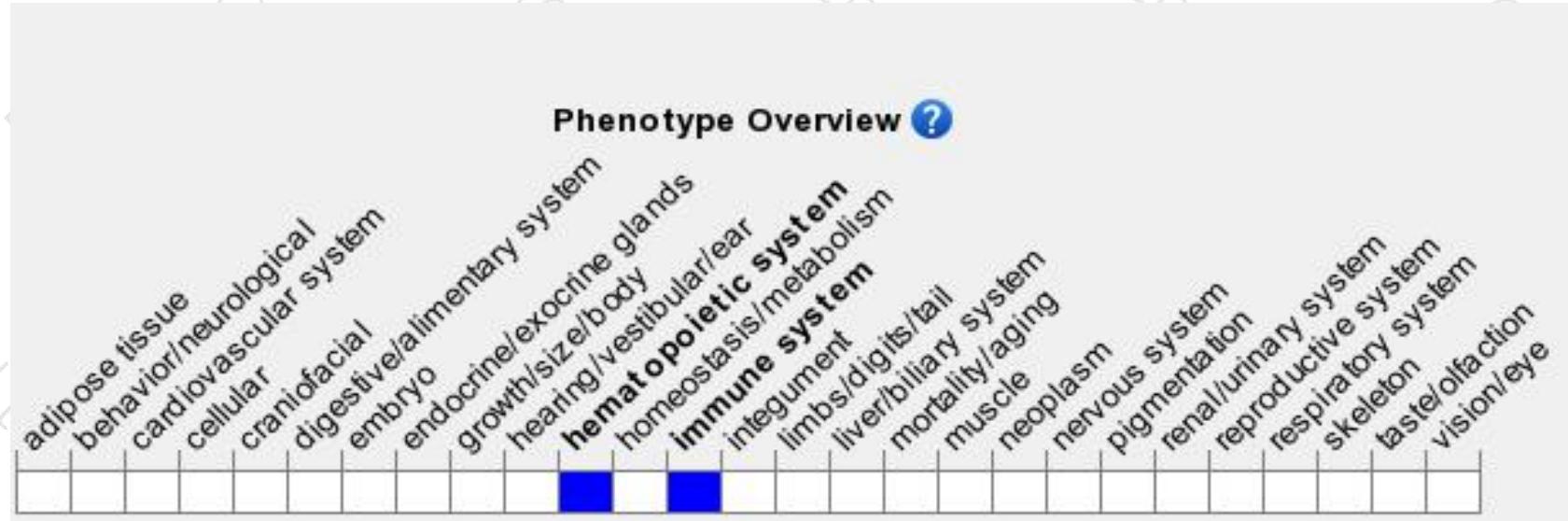
Protein domain





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Mouse phenotype description(MGI)



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



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

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