

# ***Ctnnd1* Cas9-CKO Strategy**

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# Project Overview

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**Project Name**

***Ctnnd1***

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**Project type**

**Cas9-CKO**

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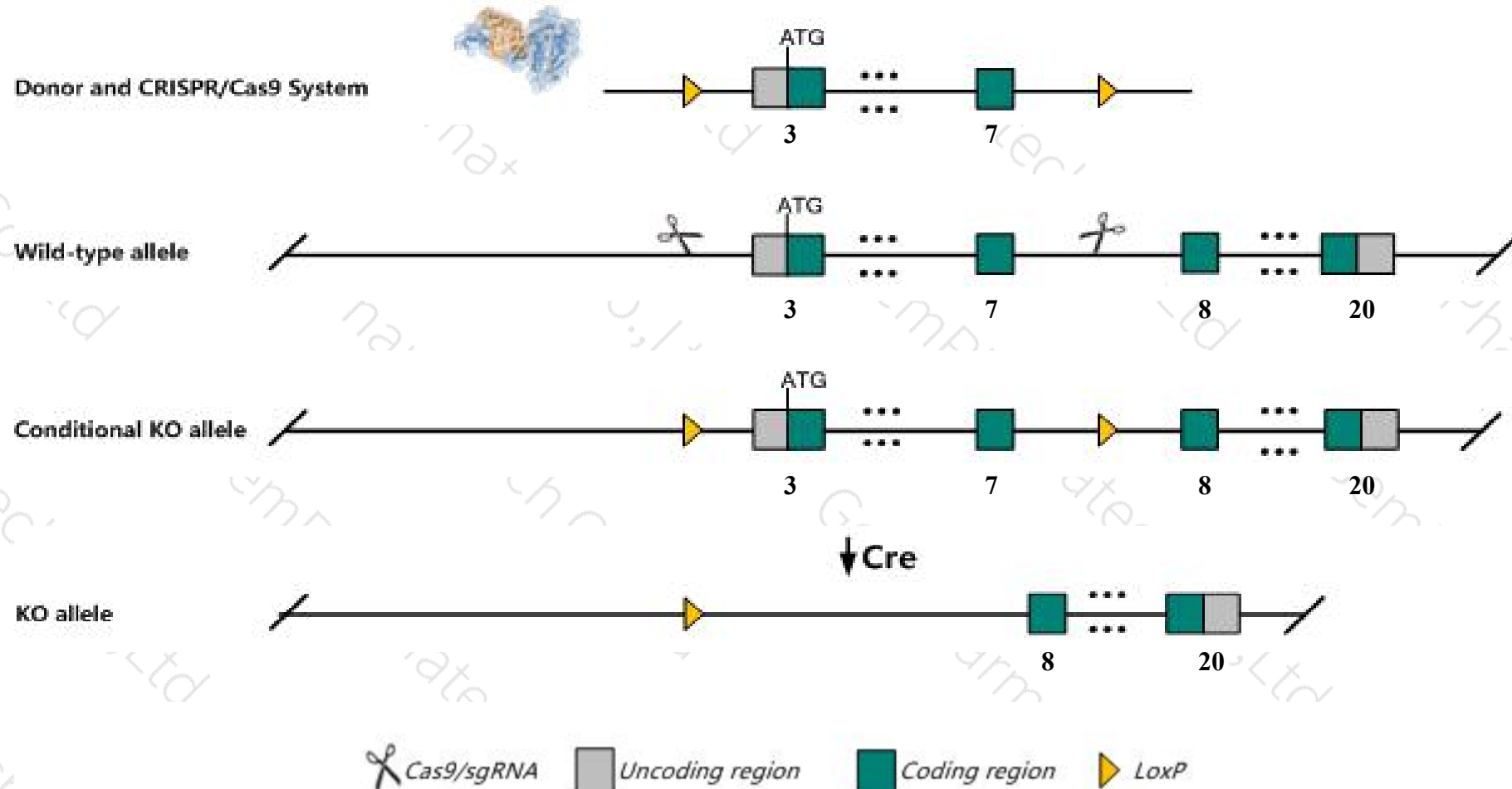
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ctnnd1* gene. The schematic diagram is as follows:



- The *Ctnnd1* gene has 30 transcripts. According to the structure of *Ctnnd1* gene, exon3-exon7 of *Ctnnd1*-203(ENSMUST00000067232.9) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ctnnd1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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.

- According to the existing MGI data, mice homozygous for disruptions of this gene die shortly after birth and have morphological abnormalities of the salivary glands and lacrimal gland.
- The KO region contains the *Gm28635* gene. Knockout the region may affect the function of *Gm28635* gene.
- The *Ctnnd1* gene is located on the Chr2. 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)

## Ctnnd1 catenin (cadherin associated protein), delta 1 [Mus musculus (house mouse)]

Gene ID: 12388, updated on 13-Mar-2020

### Summary



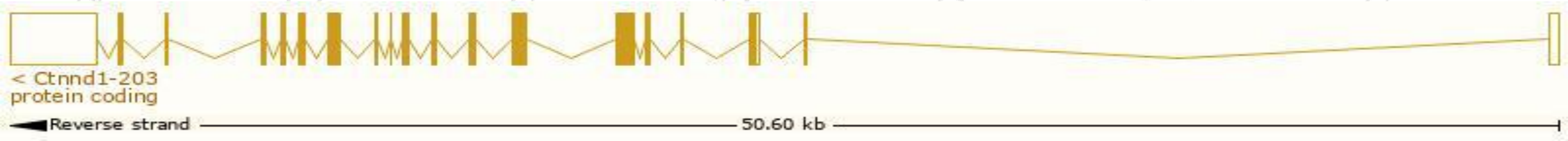
<b>Official Symbol</b>	Ctnnd1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	catenin (cadherin associated protein), delta 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:105100</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000034101</a>
<b>Gene type</b>	protein 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>	AA409437, AU019353, Ca, Catns, Ctn, Ctnnd, P12, P120, mKIAA0384
<b>Expression</b>	Ubiquitous expression in lung adult (RPKM 34.1), large intestine adult (RPKM 31.9) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

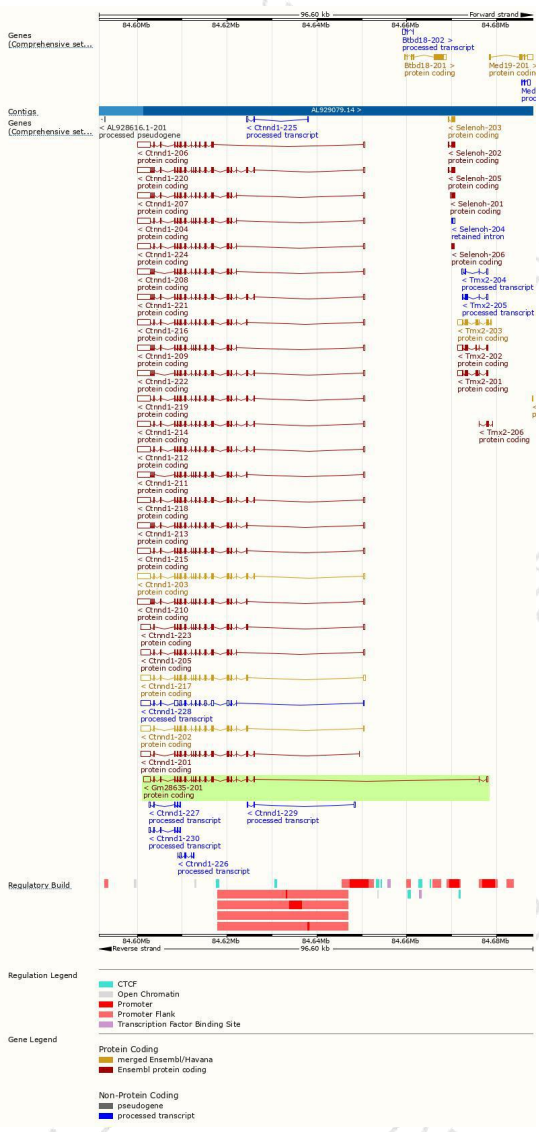
The gene has 30 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ctnnd1-203	ENSMUST00000067232.2	6119	938aa	Protein coding	CCDS16186	P30999	TSL1 GENCODE basic APPRIS P2
Ctnnd1-217	ENSMUST00000111691.1	5380	938aa	Protein coding	CCDS16186	P30999	TSL1 GENCODE basic APPRIS P2
Ctnnd1-223	ENSMUST00000111697.8	5294	917aa	Protein coding	CCDS50623	P30999	TSL5 GENCODE basic
Ctnnd1-201	ENSMUST00000036811.12	5126	917aa	Protein coding	CCDS50623	P30999	TSL1 GENCODE basic
Ctnnd1-205	ENSMUST00000111670.8	5047	930aa	Protein coding	CCDS50621	E9Q986	TSL1 GENCODE basic
Ctnnd1-202	ENSMUST00000066177.9	5044	911aa	Protein coding	CCDS50622	P30999	TSL1 GENCODE basic
Ctnnd1-220	ENSMUST00000111694.7	6362	967aa	Protein coding	-	E9Q8Z8	TSL5 GENCODE basic APPRIS ALT1
Ctnnd1-221	ENSMUST00000111695.7	6344	961aa	Protein coding	-	E9Q8Z8	TSL5 GENCODE basic APPRIS ALT1
Ctnnd1-222	ENSMUST00000111696.7	6281	940aa	Protein coding	-	E9Q8Z5	TSL5 GENCODE basic
Ctnnd1-219	ENSMUST00000111693.7	6255	932aa	Protein coding	-	G3X9V2	TSL5 GENCODE basic
Ctnnd1-218	ENSMUST00000111692.7	6170	932aa	Protein coding	-	G3X9V2	TSL5 GENCODE basic
Ctnnd1-214	ENSMUST00000111688.7	6146	978aa	Protein coding	-	E9Q8Z9	TSL5 GENCODE basic
Ctnnd1-212	ENSMUST00000111686.7	6061	978aa	Protein coding	-	E9Q8Z9	TSL5 GENCODE basic
Ctnnd1-213	ENSMUST00000111687.7	6030	907aa	Protein coding	-	E9Q901	TSL5 GENCODE basic
Ctnnd1-210	ENSMUST00000111684.7	6021	913aa	Protein coding	-	E9Q904	TSL5 GENCODE basic
Ctnnd1-211	ENSMUST00000111685.7	5985	892aa	Protein coding	-	E9Q903	TSL5 GENCODE basic
Ctnnd1-215	ENSMUST00000111689.7	5961	884aa	Protein coding	-	D3Z2H2	TSL5 GENCODE basic
Ctnnd1-216	ENSMUST00000111690.7	5945	878aa	Protein coding	-	E9Q8Z9	TSL5 GENCODE basic
Ctnnd1-209	ENSMUST00000111678.7	5870	866aa	Protein coding	-	E9Q805	TSL5 GENCODE basic APPRIS ALT1
Ctnnd1-207	ENSMUST00000111676.7	5852	860aa	Protein coding	-	E9Q907	TSL5 GENCODE basic
Ctnnd1-224	ENSMUST00000111698.7	5850	868aa	Protein coding	-	E9Q8Z4	TSL5 GENCODE basic
Ctnnd1-208	ENSMUST00000111677.7	5789	839aa	Protein coding	-	E9Q906	TSL5 GENCODE basic
Ctnnd1-204	ENSMUST00000099941.8	5783	837aa	Protein coding	-	D3Z7H8	TSL5 GENCODE basic
Ctnnd1-206	ENSMUST00000111675.7	5089	609aa	Protein coding	-	D3Z2H7	TSL5 GENCODE basic
Ctnnd1-228	ENSMUST00000145312.7	5391	No protein	Processed transcript	-	-	TSL2
Ctnnd1-227	ENSMUST00000141161.7	823	No protein	Processed transcript	-	-	TSL2
Ctnnd1-230	ENSMUST00000150940.1	810	No protein	Processed transcript	-	-	TSL3
Ctnnd1-226	ENSMUST00000131926.1	676	No protein	Processed transcript	-	-	TSL3
Ctnnd1-229	ENSMUST00000149317.1	467	No protein	Processed transcript	-	-	TSL3
Ctnnd1-225	ENSMUST00000126092.7	406	No protein	Processed transcript	-	-	TSL3

The strategy is based on the design of *Ctnnd1-203* transcript,the transcription is shown below:

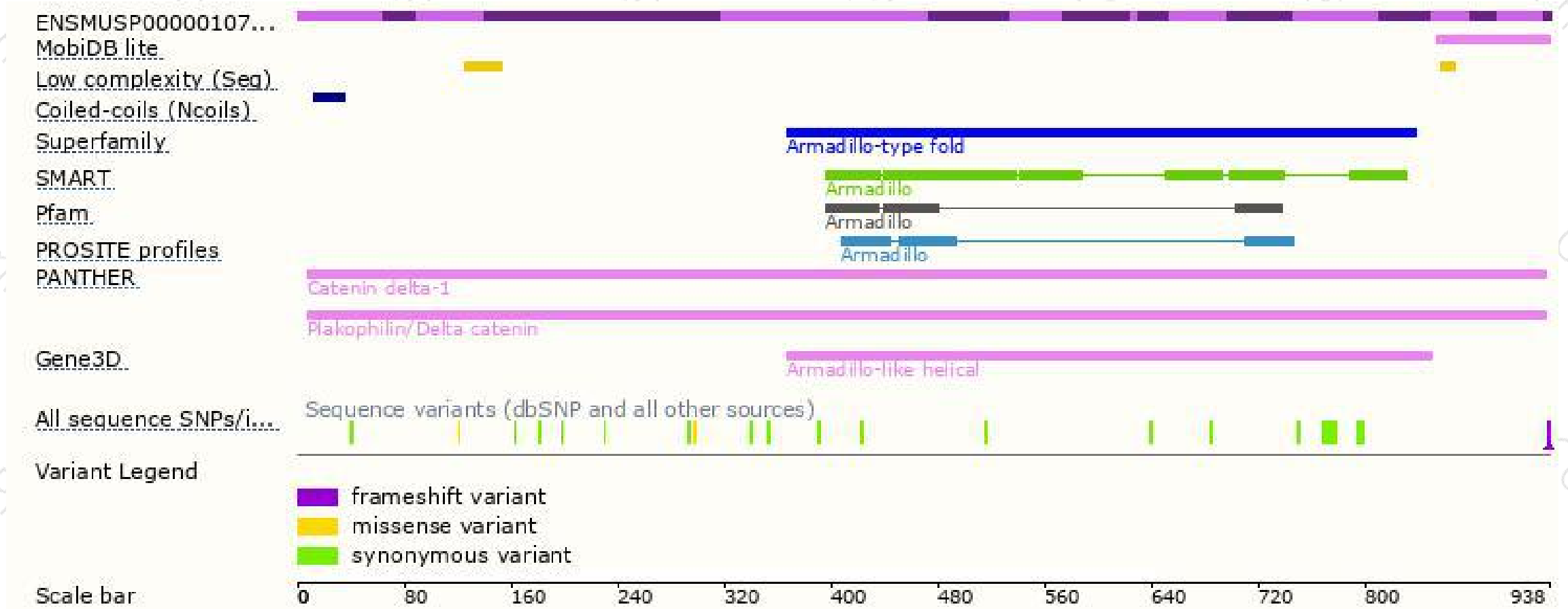


# Genomic location distribution

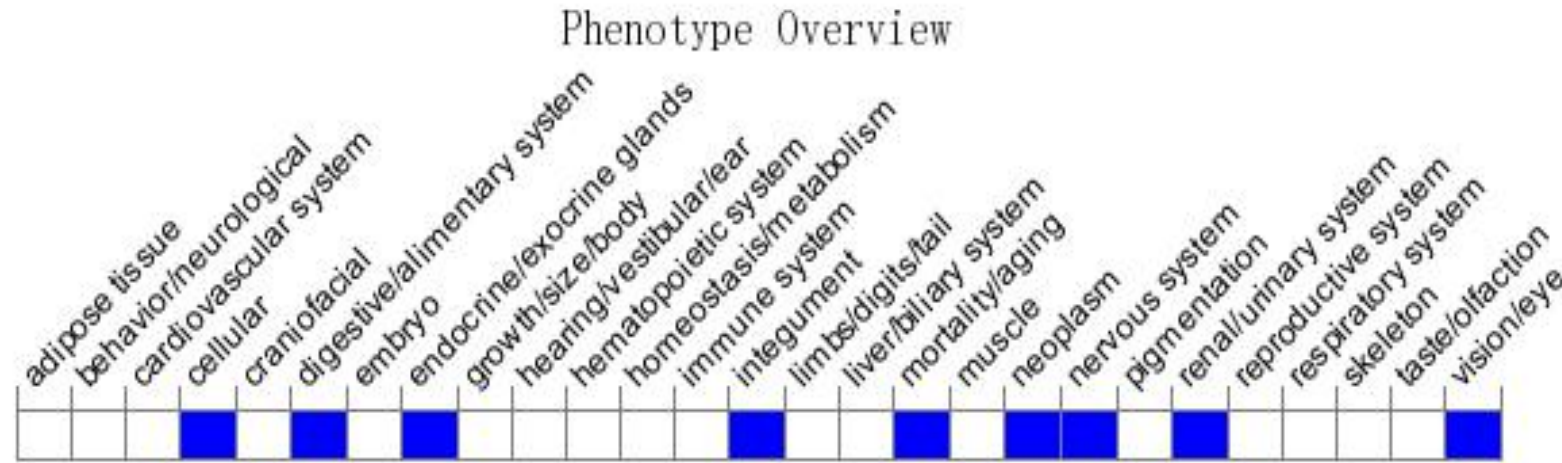




# Protein domain



# 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 disruptions of this gene die shortly after birth and have morphological abnormalities of the salivary glands and lacrimal gland.

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

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