

# *Atf2* Cas9-KO Strategy

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<b>Design Date:</b>	<b>2019-11-16</b>

# Project Overview

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**Project Name**

*Atf2*

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**Project type**

**Cas9-KO**

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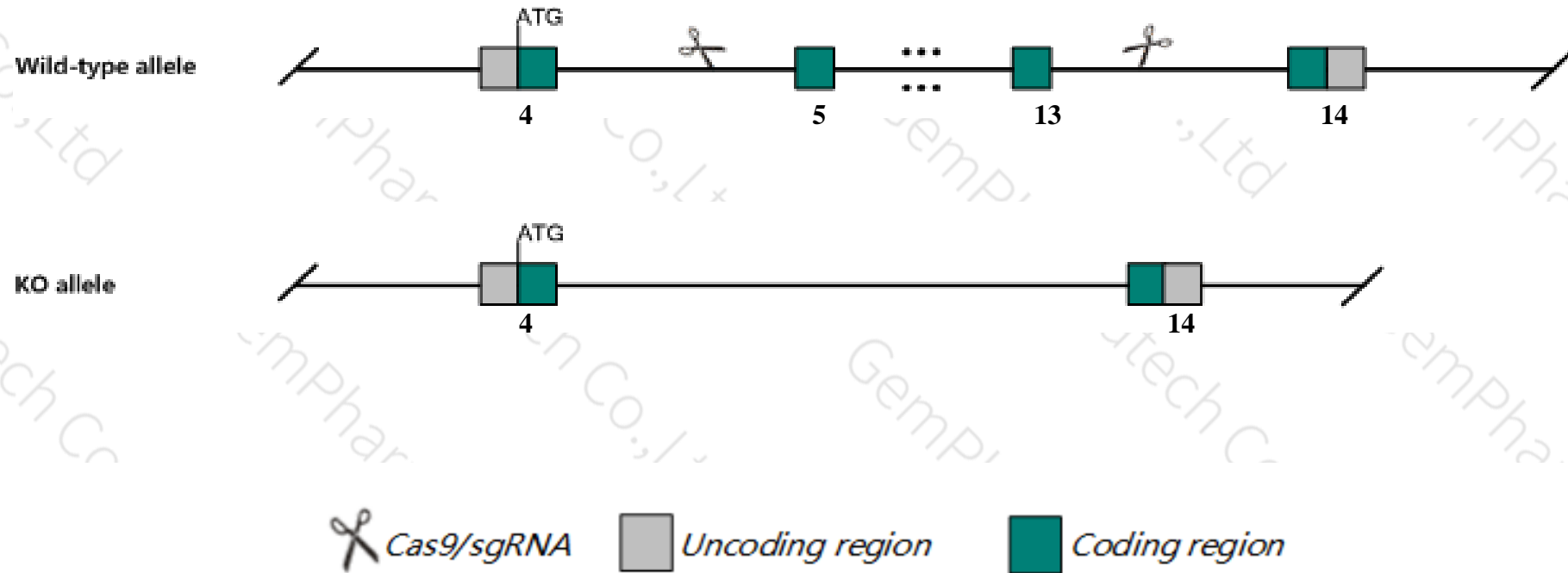
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atf2* gene. The schematic diagram is as follows:



- The *Atf2* gene has 19 transcripts. According to the structure of *Atf2* gene, exon5-exon13 of *Atf2-201* (ENSMUST00000055833.11) transcript is recommended as the knockout region. The region contains 1189bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atf2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Homozygous mutation of this gene results in increased postnatal lethality, skeletal development defects, runting, decreased hearing, inner ear and brain abnormalities, hyperactivity, and ataxia.
- Transcript *Atf2-209/213/217* may not be affected. The KO region overlaps with *Gm27421* gene. Knockout the region may affect the function of *Gm27421* gene.
- The *Atf2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

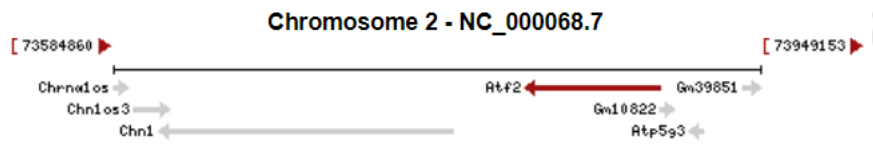
# Gene information (NCBI)

## Atf2 activating transcription factor 2 [ *Mus musculus* (house mouse) ]

Gene ID: 11909, updated on 27-Aug-2019

### Summary

Official Symbol	Atf2 provided by MGI
Official Full Name	activating transcription factor 2 provided by MGI
Primary source	MGI:MGI:109349
See related	Ensembl:ENSMUSG00000027104
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	mXBP; Atf-2; Creb2; CRE-BP; D18875; D130078H02Rik; Tg(Gzma-Klra1)7Wum
Expression	Ubiquitous expression in CNS E14 (RPKM 7.9), frontal lobe adult (RPKM 7.8) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>



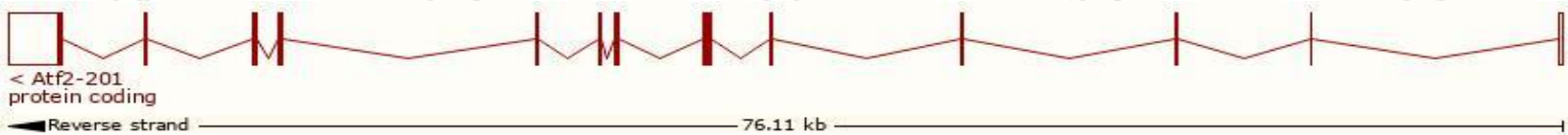


# Transcript information (Ensembl)

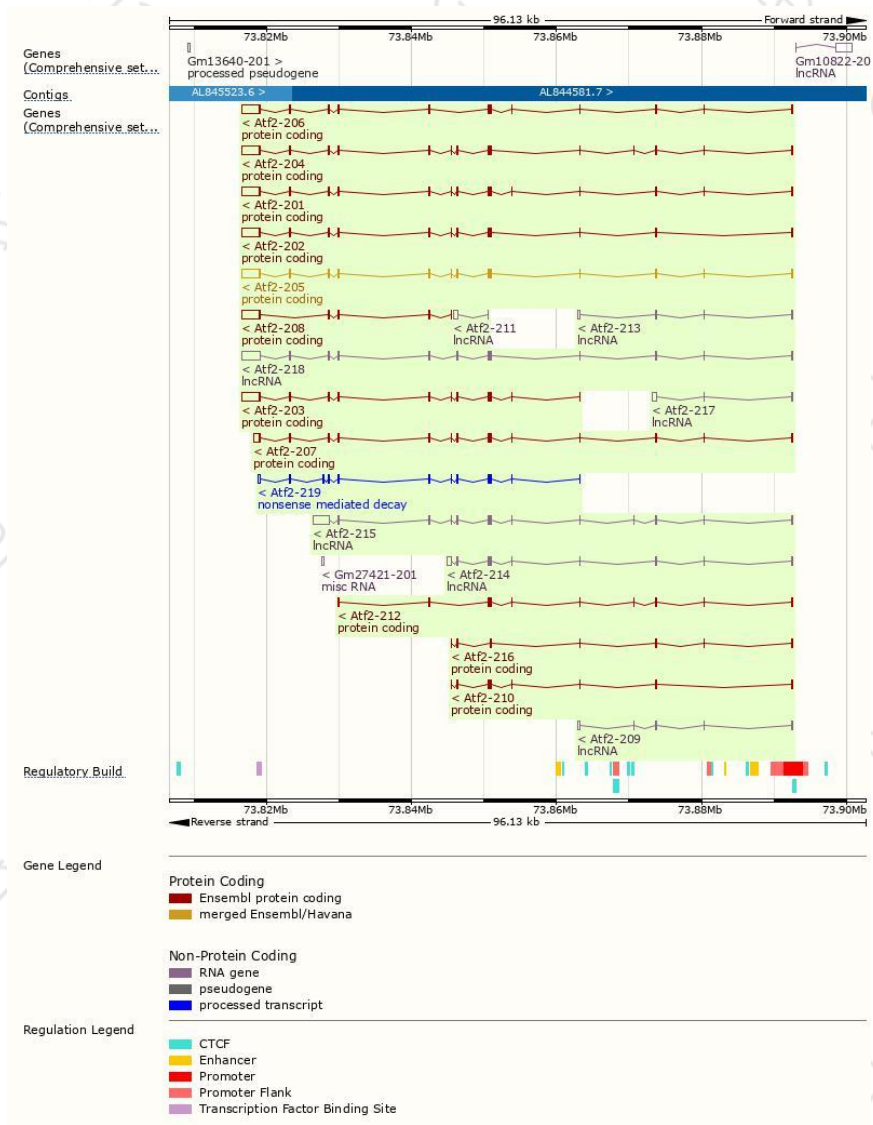
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Atf2-201	<a href="#">ENSMUST00000055833.11</a>	4210	487aa	<a href="#">ENSMUSP00000058521.5</a>	Protein coding	<a href="#">CCDS16134</a>	<a href="#">P16951</a>	TSL:5 GENCODE basic APPRIS P3
Atf2-204	<a href="#">ENSMUST00000112007.7</a>	4195	447aa	<a href="#">ENSMUSP00000107638.1</a>	Protein coding	<a href="#">CCDS16135</a>	<a href="#">P16951</a> <a href="#">Q543G2</a>	TSL:1 GENCODE basic
Atf2-205	<a href="#">ENSMUST00000112010.8</a>	4037	447aa	<a href="#">ENSMUSP00000107641.2</a>	Protein coding	<a href="#">CCDS16135</a>	<a href="#">P16951</a> <a href="#">Q543G2</a>	TSL:1 GENCODE basic
Atf2-202	<a href="#">ENSMUST00000090802.10</a>	4016	447aa	<a href="#">ENSMUSP00000088311.4</a>	Protein coding	<a href="#">CCDS16135</a>	<a href="#">P16951</a> <a href="#">Q543G2</a>	TSL:5 GENCODE basic
Atf2-206	<a href="#">ENSMUST00000112016.8</a>	3943	389aa	<a href="#">ENSMUSP00000107647.2</a>	Protein coding	<a href="#">CCDS71076</a>	<a href="#">P16951</a> <a href="#">Q640L6</a>	TSL:1 GENCODE basic APPRIS ALT2
Atf2-203	<a href="#">ENSMUST00000100009.10</a>	3936	487aa	<a href="#">ENSMUSP00000097588.4</a>	Protein coding	<a href="#">CCDS16134</a>	<a href="#">P16951</a>	TSL:1 GENCODE basic APPRIS P3
Atf2-207	<a href="#">ENSMUST00000112017.7</a>	2396	487aa	<a href="#">ENSMUSP00000107648.1</a>	Protein coding	<a href="#">CCDS16134</a>	<a href="#">P16951</a>	TSL:5 GENCODE basic APPRIS P3
Atf2-208	<a href="#">ENSMUST00000124737.7</a>	3151	212aa	<a href="#">ENSMUSP00000114828.1</a>	Protein coding	-	<a href="#">F6Z2B2</a>	CDS 5' incomplete TSL:3
Atf2-212	<a href="#">ENSMUST00000136958.7</a>	935	207aa	<a href="#">ENSMUSP00000118357.1</a>	Protein coding	-	<a href="#">A2AQE9</a>	CDS 3' incomplete TSL:3
Atf2-210	<a href="#">ENSMUST00000128531.7</a>	863	228aa	<a href="#">ENSMUSP00000118560.1</a>	Protein coding	-	<a href="#">A2AQF0</a>	CDS 3' incomplete TSL:3
Atf2-216	<a href="#">ENSMUST00000154456.7</a>	775	146aa	<a href="#">ENSMUSP00000118719.1</a>	Protein coding	-	<a href="#">A2AQF1</a>	CDS 3' incomplete TSL:5
Atf2-219	<a href="#">ENSMUST00000173010.7</a>	1658	377aa	<a href="#">ENSMUSP00000133632.1</a>	Nonsense mediated decay	-	<a href="#">G3UXC3</a>	TSL:5
Atf2-218	<a href="#">ENSMUST00000156455.7</a>	4003	No protein	-	lncRNA	-	-	TSL:1
Atf2-215	<a href="#">ENSMUST00000143714.7</a>	3641	No protein	-	lncRNA	-	-	TSL:1
Atf2-214	<a href="#">ENSMUST00000141050.7</a>	1604	No protein	-	lncRNA	-	-	TSL:1
Atf2-209	<a href="#">ENSMUST00000125159.7</a>	660	No protein	-	lncRNA	-	-	TSL:2
Atf2-211	<a href="#">ENSMUST00000129555.1</a>	658	No protein	-	lncRNA	-	-	TSL:5
Atf2-213	<a href="#">ENSMUST00000138098.7</a>	656	No protein	-	lncRNA	-	-	TSL:2
Atf2-217	<a href="#">ENSMUST00000154965.1</a>	645	No protein	-	lncRNA	-	-	TSL:2

The strategy is based on the design of *Atf2-201* transcript,The transcription is shown below



# Genomic location distribution

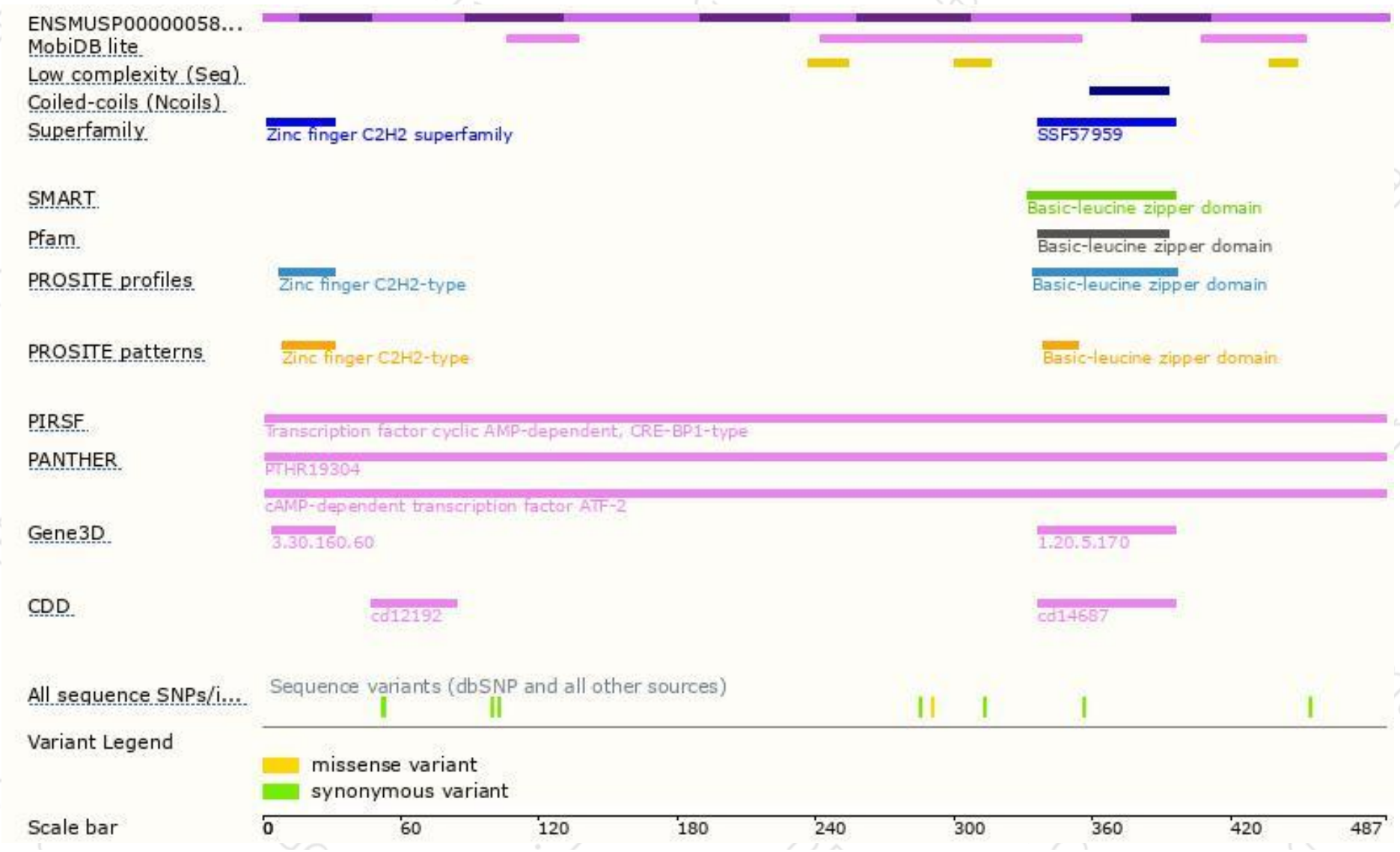




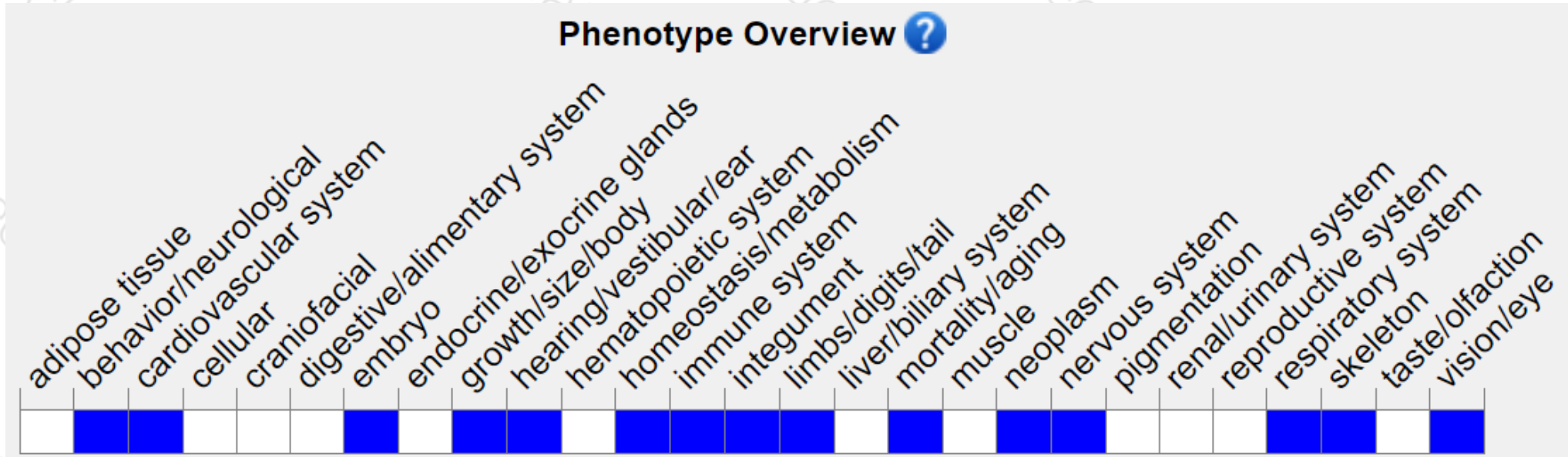
# Protein domain



集萃药康  
GemPharmatech



# 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 increased postnatal lethality, skeletal development defects, runting, decreased hearing, inner ear and brain abnormalities, hyperactivity, and ataxia.

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

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