

# *Cxadr* Cas9-KO Strategy

**Designer:**

**JiaYu**

**Reviewer:**

**Xiaojing Li**

**Design Date:**

**2019-8-22**

# Project Overview

**Project Name**

***Cxadr***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Cxadr* gene has 6 transcripts. According to the structure of *Cxadr* gene, exon2 of *Cxadr-201* (ENSMUST00000023572.14) transcript is recommended as the knockout region. The region contains 167bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cxadr* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display embryonic lethality with focal cardiomyocyte apoptosis and extensive thoracic hemorrhaging.
- The *Cxadr* gene is located on the Chr16. 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)

## Cxadr coxsackie virus and adenovirus receptor [Mus musculus (house mouse)]

Gene ID: 13052, updated on 19-Feb-2019

### Summary



<b>Official Symbol</b>	Cxadr provided by <a href="#">MGI</a>
<b>Official Full Name</b>	coxsackie virus and adenovirus receptor provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1201679</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022865</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<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>	2610206D03Rik, AU016810, AW553441, CAR, MCAR, MCVADR
<b>Summary</b>	This gene encodes a protein that is part of the Cortical Thymocyte marker in Xenopus (CTX) subfamily within the immunoglobulin superfamily. Members of this subfamily, predominantly expressed on the surface of endothelial and epithelial cells, help establish cell polarity and provide a barrier function, regulating migration of immune cells. This protein, first identified as the receptor for adenovirus subgroup C and coxsackieviruses group B, is developmentally regulated and plays an important role in cardiac development. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Jan 2013]
<b>Expression</b>	Broad expression in CNS E18 (RPKM 24.6), whole brain E14.5 (RPKM 17.4) and 23 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

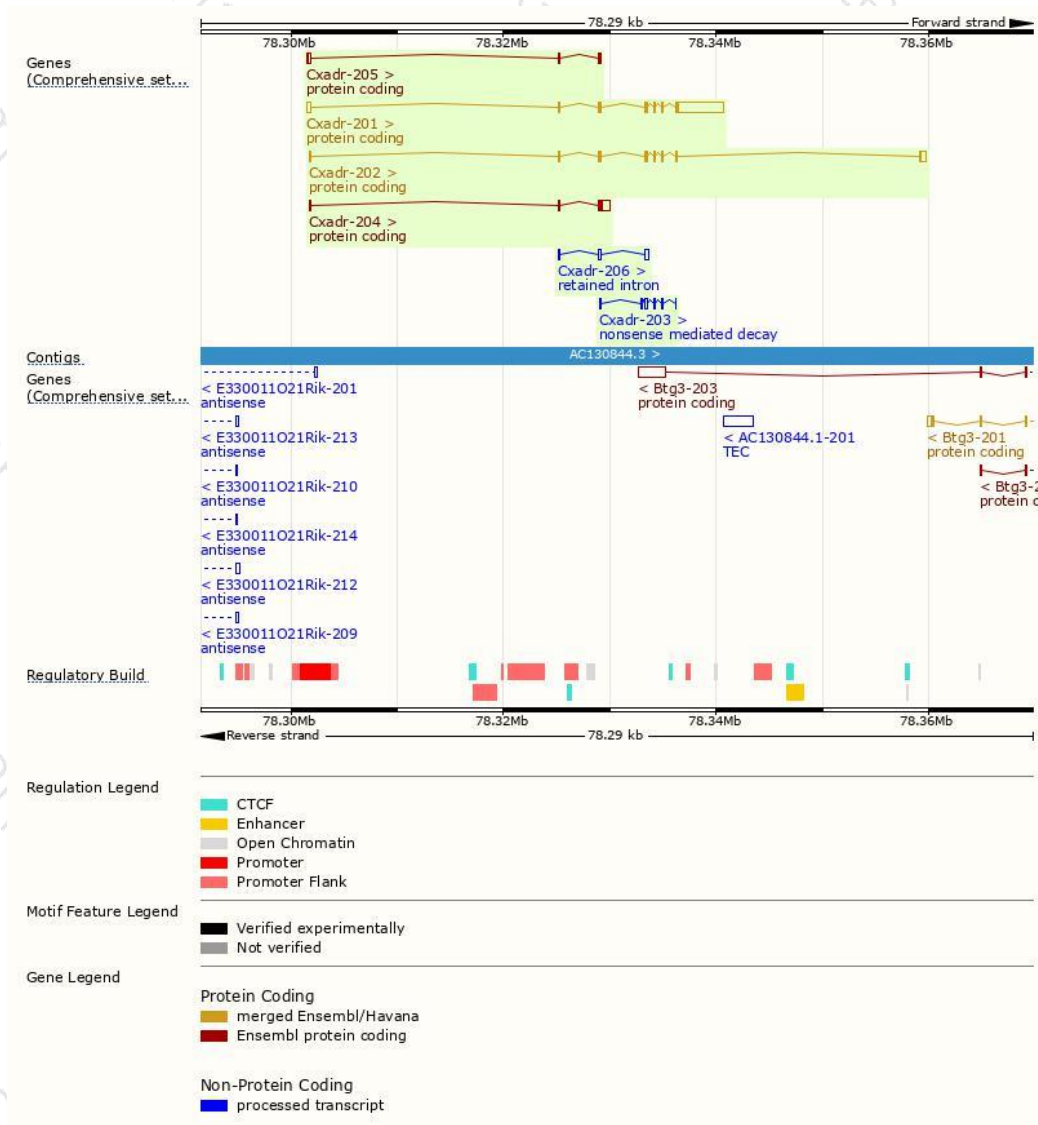
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cxadr-201	<a href="#">ENSMUST00000023572.14</a>	5742	<a href="#">365aa</a>	Protein coding	<a href="#">CCDS28276</a>	<a href="#">P97792</a>	TSL:1 GENCODE basic APPRIS P3
Cxadr-202	<a href="#">ENSMUST00000114229.3</a>	1657	<a href="#">352aa</a>	Protein coding	<a href="#">CCDS37379</a>	<a href="#">P97792</a>	TSL:1 GENCODE basic APPRIS ALT2
Cxadr-204	<a href="#">ENSMUST00000231356.1</a>	1298	<a href="#">164aa</a>	Protein coding	-	<a href="#">P97792</a>	GENCODE basic
Cxadr-205	<a href="#">ENSMUST00000232148.1</a>	650	<a href="#">136aa</a>	Protein coding	-	<a href="#">A0A338P6N1</a>	CDS 3' incomplete
Cxadr-203	<a href="#">ENSMUST00000231251.1</a>	688	<a href="#">52aa</a>	Nonsense mediated decay	-	<a href="#">A0A338P6U1</a>	CDS 5' incomplete
Cxadr-206	<a href="#">ENSMUST00000232189.1</a>	678	No protein	Retained intron	-	-	

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



# Genomic location distribution

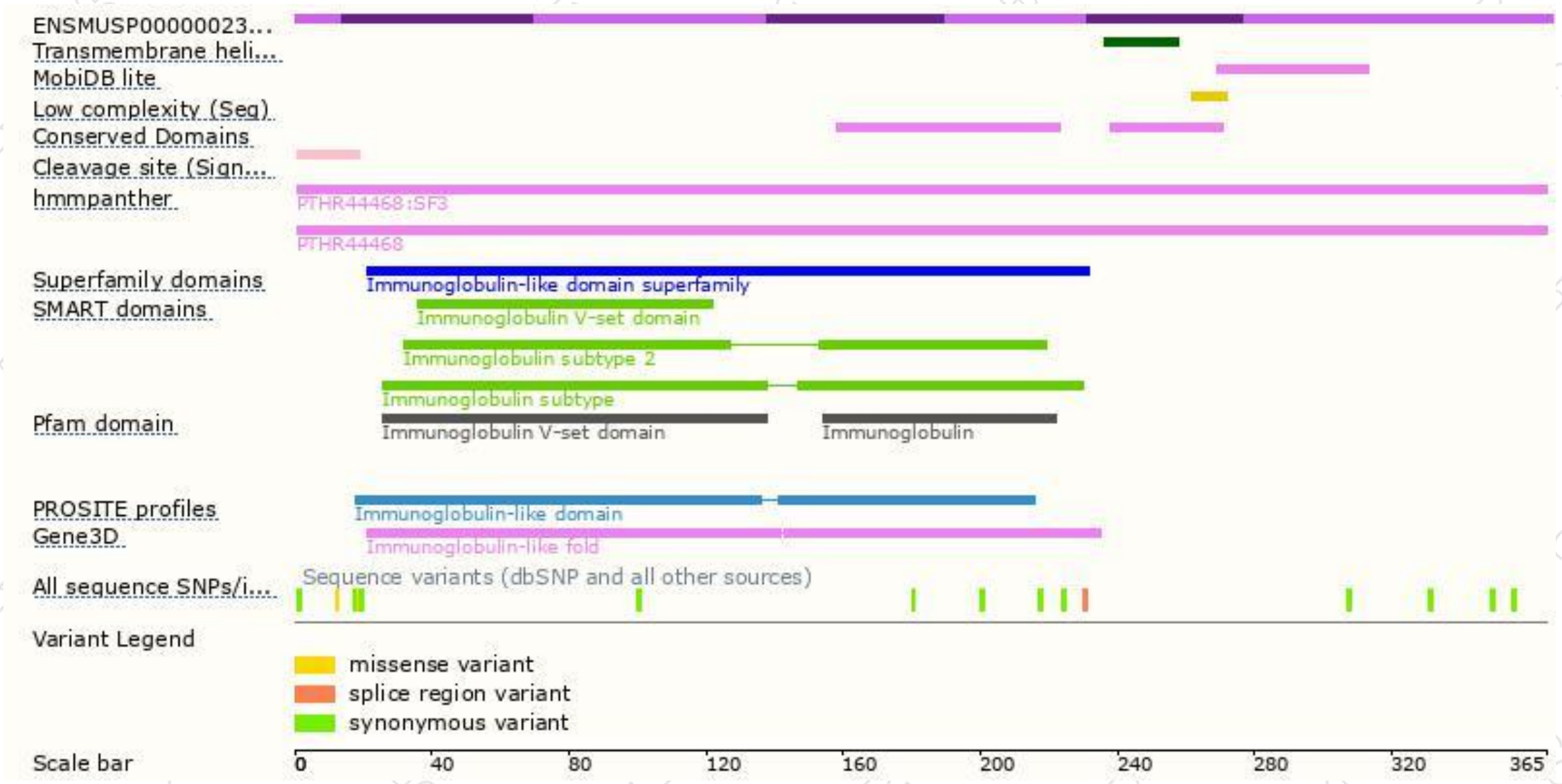




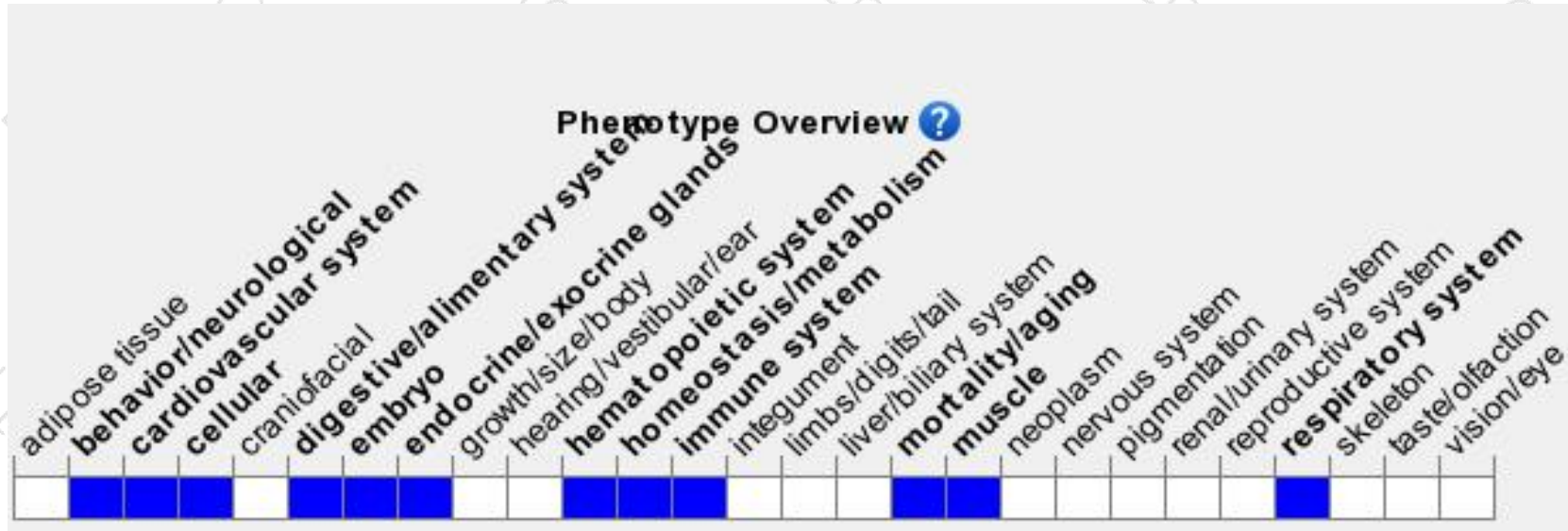
# Protein domain



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 null mice display embryonic lethality with focal cardiomyocyte apoptosis and extensive thoracic hemorrhaging.

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

Tel: 400-9660890

