

# ***Cx3cl1 Cas9-CKO Strategy***

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# Project Overview

**Project Name**

***Cx3cl1***

**Project type**

**Cas9-CKO**

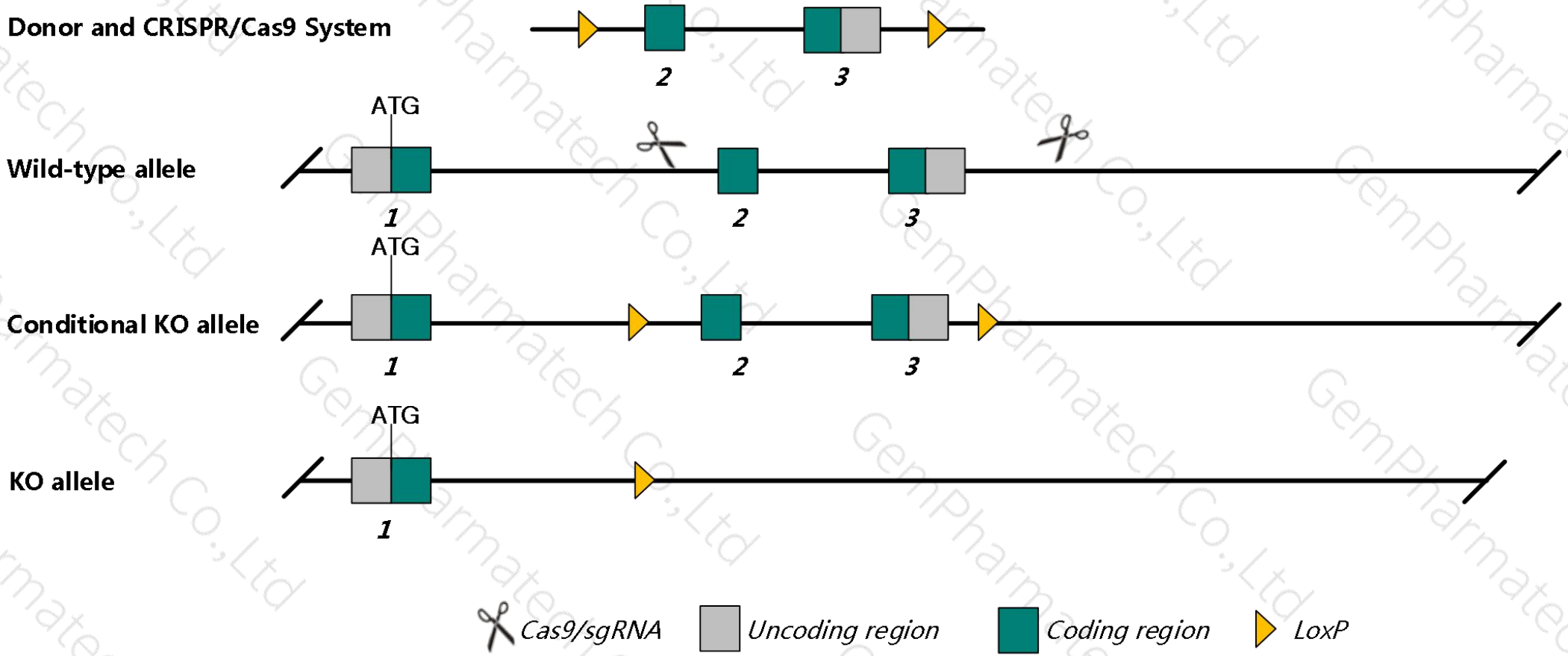
**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cx3c11* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System



- The *Cx3cll* gene has 6 transcripts. According to the structure of *Cx3cll* gene, exon2-3 of *Cx3cll*-201 (ENSMUST00000034230.6) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cx3cll* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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 or cell types.

- According to the existing MGI data , Mice homozygous for a knock-out allele show a specific reduction in Gr1(low) monocyte levels, and increased neuronal cell loss in a neurotoxin (MPTP)-induced model of Parkinson disease. Mice homozygous for a different knock-out allele are less susceptible to cerebral ischemia-reperfusion injury.
- The *Cx3cl1* gene is located on the Chr8. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information ( NCBI )

## Cx3cl1 chemokine (C-X3-C motif) ligand 1 [ *Mus musculus* (house mouse) ]

Gene ID: 20312, updated on 13-Mar-2020

### Summary

Official Symbol	Cx3cl1 provided by MGI
Official Full Name	chemokine (C-X3-C motif) ligand 1 provided by MGI
Primary source	<a href="#">MGI:MGI:1097153</a>
See related	<a href="#">Ensembl:ENSMUSG000000031778</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CX3C; Cxc3; Scyd1; ABCD-3; AB030188; AI848747; D8Bwg0439e
Expression	Biased expression in cortex adult (RPKM 170.7), frontal lobe adult (RPKM 132.2) and 14 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information ( Ensembl )

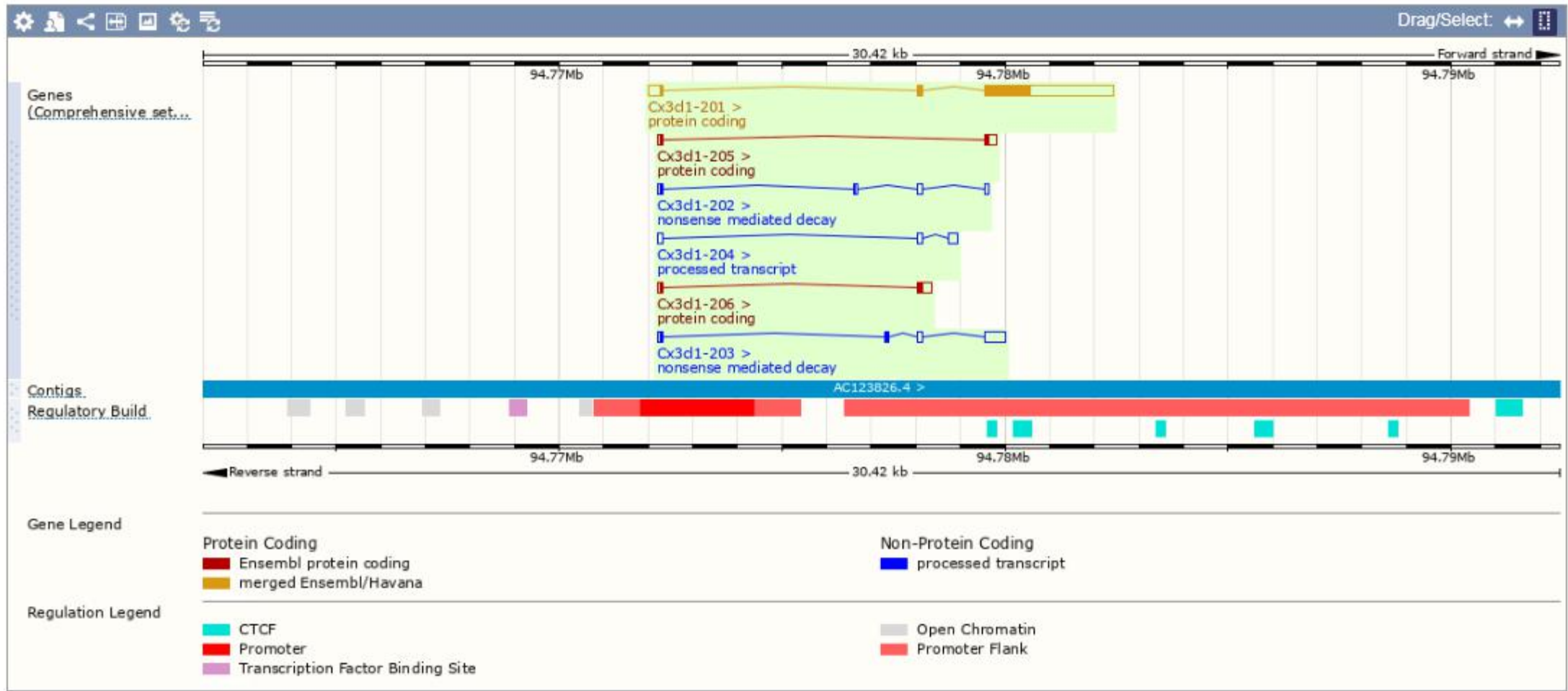
The gene has 6 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Cx3cl1-201	<a href="#">ENSMUST00000034230.6</a>	3315	<a href="#">395aa</a>	Protein coding	<a href="#">CCDS22548</a>	<a href="#">Q35188</a>	TSL:1	GENCODE basic APPRIS P1
Cx3cl1-206	<a href="#">ENSMUST00000211956.1</a>	470	<a href="#">64aa</a>	Protein coding	-	<a href="#">A0A1D5RMK8</a>	TSL:2	GENCODE basic
Cx3cl1-205	<a href="#">ENSMUST00000211947.1</a>	377	<a href="#">45aa</a>	Protein coding	-	<a href="#">A0A1D5RLW9</a>	TSL:5	GENCODE basic
Cx3cl1-203	<a href="#">ENSMUST00000150307.1</a>	780	<a href="#">57aa</a>	Nonsense mediated decay	-	<a href="#">D6RCV0</a>	TSL:3	
Cx3cl1-202	<a href="#">ENSMUST00000135970.1</a>	432	<a href="#">37aa</a>	Nonsense mediated decay	-	<a href="#">E0CXC3</a>	TSL:3	
Cx3cl1-204	<a href="#">ENSMUST00000151783.8</a>	462	No protein	Processed transcript	-	-	TSL:3	

The strategy is based on the design of Cx3cl1-201 transcript, The transcription is shown below



# Genomic location distribution

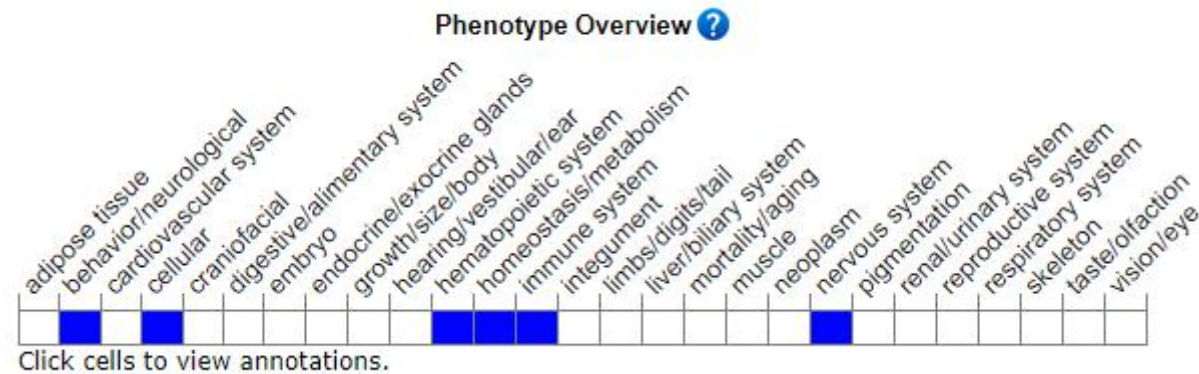




# Protein domain



# 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, Mice homozygous for a knock-out allele show a specific reduction in Gr1(low) monocyte levels, and increased neuronal cell loss in a neurotoxin (MPTP)-induced model of Parkinson disease.

Mice homozygous for a different knock-out allele are less susceptible to cerebral ischemia-reperfusion injury.

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