

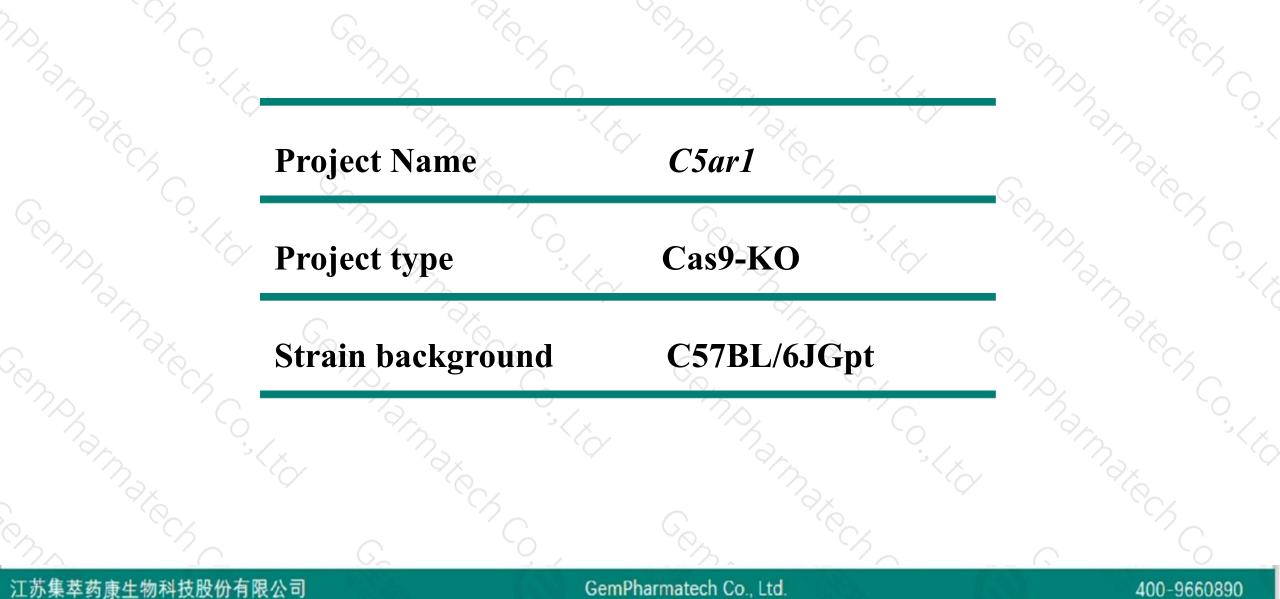
# C5ar1 Cas9-KO Strategy Andraker Contra

Cemphalmater Co. Designer: Yanhua Shen Design Date: 2019-08-06

CMPHarmarect

# **Project Overview**

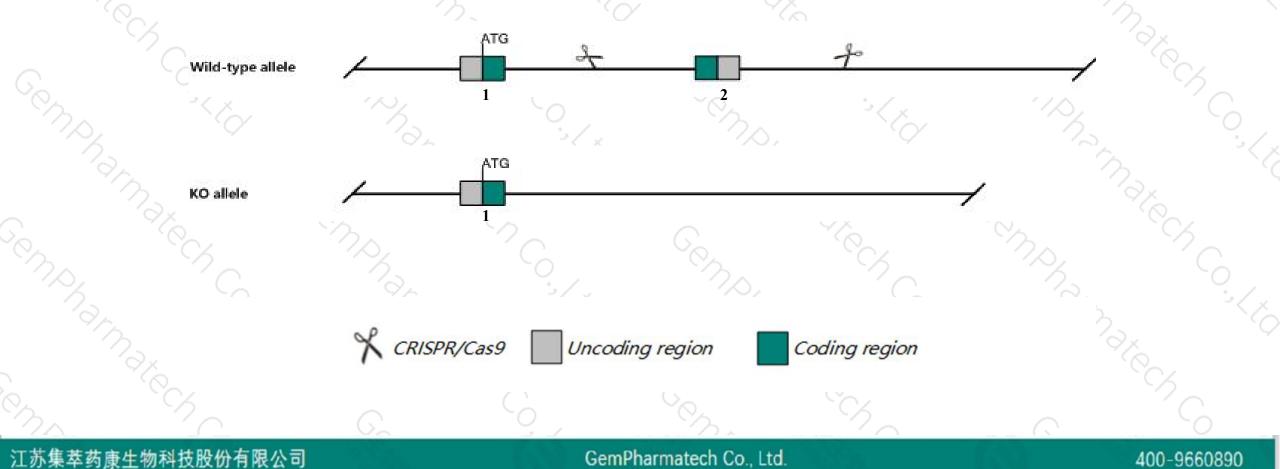




# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the C5ar1 gene. The schematic diagram is as follows:





- The C5ar1 gene has 3 transcripts. According to the structure of C5ar1 gene, exon2 of C5ar1-202 (ENSMUST00000168818.1) 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 C5ar1 gene. The brief process is as follows: CRISPR/Cas9 system

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- According to the existing MGI data, Homozygous targeted mutants have impaired C5 responses that can show increased or decreased acute inflammation under different circumstances, and thus affect severity of disease or infection.
- The knockout region is about 2.6 kb away from the 5th end of the C5ar2 gene, may affect the regulation of the 5th end of the C5ar2 gene.
- The C5ar1 gene is located on the Chr7. 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.

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# **Gene information (NCBI)**



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## C5ar1 complement component 5a receptor 1 [Mus musculus (house mouse)]

Gene ID: 12273, updated on 19-Mar-2019

### Summary

Official Symbol	C5ar1 provided by MGI
Official Full Name	complement component 5a receptor 1 provided by MGI
<b>Primary source</b>	MGI:MGI:88232
See related	Ensembl:ENSMUSG00000049130
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	C5aR, C5r1, Cd88, D7Msu1
Expression	Broad expression in lung adult (RPKM 10.0), mammary gland adult (RPKM 8.9) and 20 other tissues See more
Orthologs	human all

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# **Transcript information (Ensembl)**



## The gene has 3 transcripts, all transcripts are shown below:

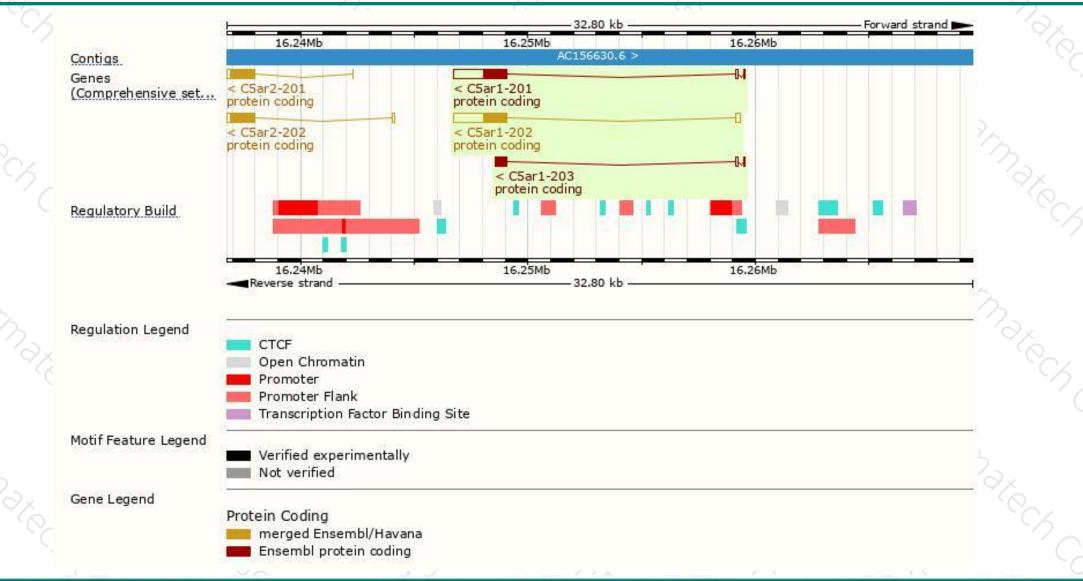
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C5ar1-202	ENSMUST00000168818.1	2540	<u>351aa</u>	Protein coding	CCDS20846	P30993	TSL:1 GENCODE basic APPRIS P1
C5ar1-201	ENSMUST0000050770.5	2481	<u>351aa</u>	Protein coding	CCDS20846	P30993	TSL:3 GENCODE basic APPRIS P1
C5ar1-203	ENSMUST00000209442.1	674	<u>181aa</u>	Protein coding	-	A0A1B0GT01	CDS 3' incomplete TSL:3

The strategy is based on the design of C5ar1-202 transcript, The transcription is shown below

< C5ar1-202 protein coding					[]``C
Reverse strand		12		f	
TA SI	Va.		1 / A	(<`	$\sim$ $\sim$
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## **Genomic location distribution**





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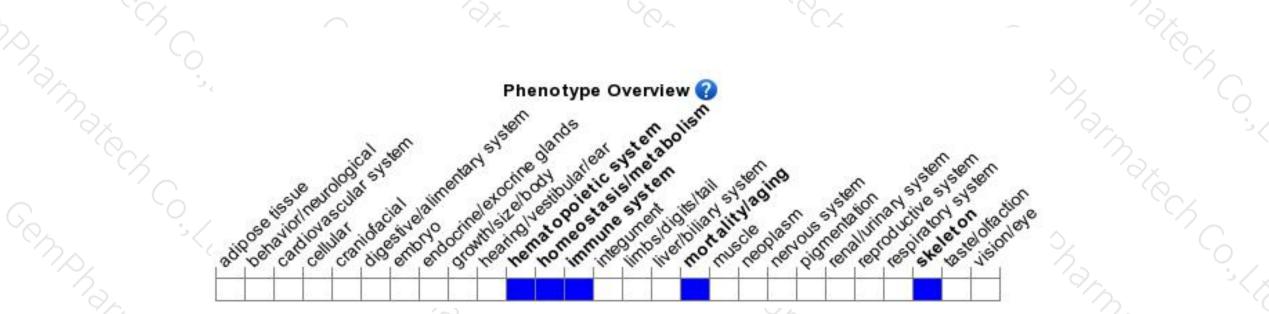
# **Protein domain**



ENSMUSP00000129 Transmembrane heli MubDB lite.  Formyl peptide receptor related    Sweerfamily. domains.  PHR2422515F2/3    Sweerfamily. domains.  SF81321    Prints. domain.  SF81321    Brints. domain.  SF81321    PROS.ITE.profiles.  G protein-coupled receptor rhodopsin-like    PROS.ITE.profiles.  G protein-coupled receptor rhodopsin-like    PROS.ITE.profiles.  G protein-coupled receptor rhodopsin-like    G protein-coupled receptor rhodopsin-like  G protein-coupled receptor rhodopsin-like    Variant Legend  I.20.1070.10    Variant Legend  missense variant    Scale bar  0  40  80  120  160  200  240  280  351											
Superfamily domains  SSF81321    Prints domain  G protein-coupled receptor, rhodopsin-like    CS1/CS32 anaphylatoxin chemotactic receptor    Anaphylatoxin chemotactic receptor    Pfam. domain.  G protein-coupled receptor, rhodopsin-like    PROSITE profiles  G protein-coupled receptor, rhodopsin-like    PROSITE patterns:  G protein-coupled receptor, rhodopsin-like    Gene3D.  1.20.1070.10    All sequence SNPs/Lime  Sequence variants (dbSNP and all other sources)    Variant Legend  missense variant    Scale bar  0  40  80  120  160  200  240  280  351		Transmembrane heli MobiDB lite Low complexity (Seg)		ie receptor-rela	ited						50
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Pfam. domain.  G protein-coupled receptor, rhodopsin-like    PROSITE profiles.  GPCR, rhodopsin-like, 7TM    PROSITE patterns.  G protein-coupled receptor, rhodopsin-like    Gene3D.  1.20.1070.10    All sequence SNPs/i  Sequence variants (db SNP and all other sources)    Variant Legend  missense variant    Scale bar  0  40  80  120  160  200  240  280  351		Prints domain						_			
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missense variant    synonymous variant    Scale bar  0  40  120  160  200  240  280  351		All sequence SNPs/i	Sequence variants (	dbSNP and all	l other sources)	0.00	ti di		100		
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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/).

According to the existing MGI data, Homozygous targeted mutants have impaired C5 responses that can show increased or decreased acute inflammation under different circumstances, and thus affect severity of disease or infection.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



