

## **Rraga** Cas9-KO Strategy

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Project Name	Rraga				
Project type	Cas9-KO				
Strain background	C57BL/6JGpt				

#### **Knockout strategy**



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



The *Rraga* gene has 1 transcript. According to the structure of *Rraga* gene, exon1 of *Rraga-201* (ENSMUST00000091064.7) transcript is recommended as the knockout region. The region contains all of coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify Rraga gene. The brief process is as follows: CRISPR/Cas9 system



According to the existing MGI data, Mice homozygous for null mutations display embryonic lethality during organogenesis, impaired growth and open neural tubes. Mice homozygous for a constitutively active knock-in allele exhibit neonatal lethality associated with impaired hepatic gluconeogenesis and impaired autophagy.

The *Rraga* gene is located on the Chr4. 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

#### Rraga Ras-related GTP binding A [ Mus musculus (house mouse) ]

Gene ID: 68441, updated on 27-Feb-2020

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Official Symbol	Rraga provided by MGI
Official Full Name	Ras-related GTP binding A provided by MGI
Primary source	MGI:MGI:1915691
See related	Ensembl:ENSMUSG0000070934
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; Mus; Mus; Mus
Also known as	RAGA; FIP-1; AI255374; 1300010C19Rik
Orthologs	human all

#### Genomic context

Location:	4; 4 C4
1920	101 102

Exon count: 1

See Rraga in Genome Data Viewer





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### **Transcript information Ensembl**

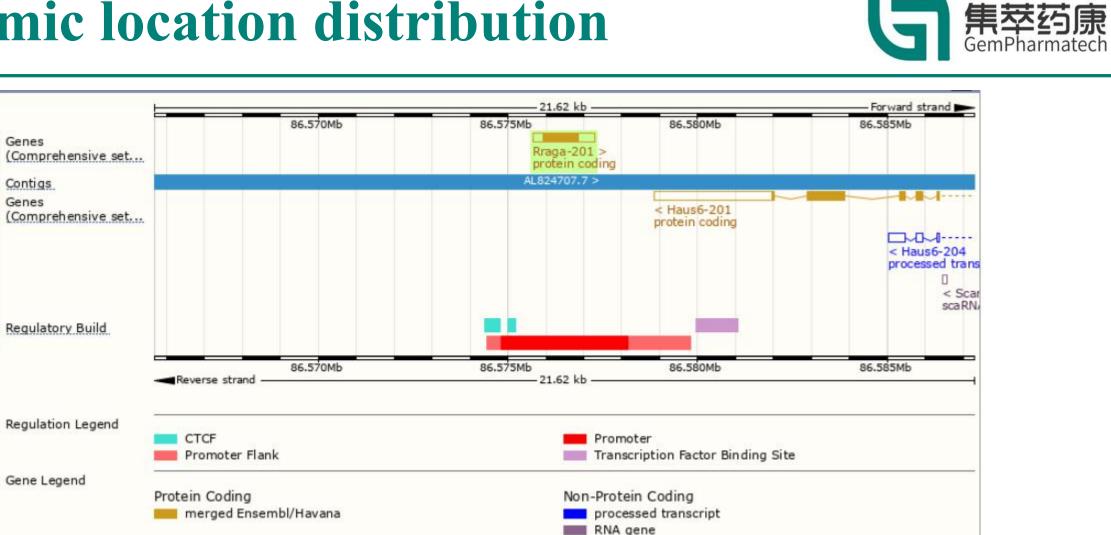


The gene has 1 transcript, and the transcript is shown below:

Name 🍦	Transcript ID	bp 🖕	Protein 💧	Biotype 💧	CCDS	UniProt		Flags	\$
Rraga-201	ENSMUST0000091064.7	1618	<u>313aa</u>	Protein coding	<u>CCDS18306</u> &	<u>Q80X95</u> @	TSL:NA	GENCODE basic	APPRIS P1

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

### **Genomic location distribution**



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### **Protein domain**

1.1	ENSMUSP00000088 Superfamily	P-loop co	ntaining nucleosid	le triphosphate hyd	rolase		i.		
1.1.1	<u>Pfam</u>	Gtr1/Rag	A G protein					_	
2	PANTHER.	PTHR11259:	SF7						
2		Gtr1/RagA G	protein						
1100	Gene3D	3.40.50.300	0				3.30.450.190		
110	CDD.	RagA/B							
1111	All sequence SNPs/i	Sequence v	variants (dbSNP	and all other sour	rces)		6		
	Variant Legend	synon	ymous variant						
	Scale bar	6	40	80	120	160	200	240	313

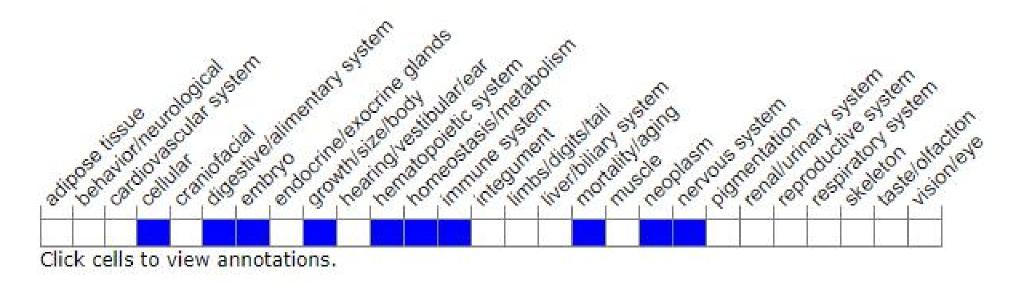
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### Mouse phenotype description(MGI)



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, Mice homozygous for null mutations display embryonic lethality during organogenesis, impaired growth and open neural tubes. Mice homozygous for a constitutively active knock-in allele exhibit neonatal lethality associated with impaired hepatic gluconeogenesis and impaired autophagy.



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





