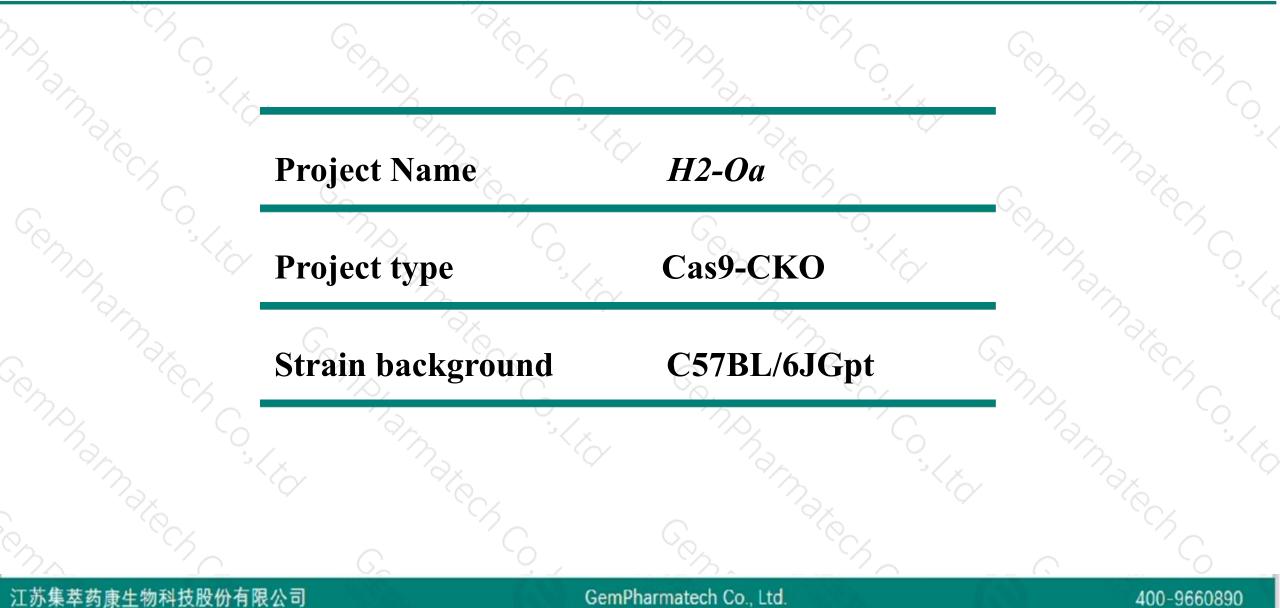


# H2-Oa Cas9-CKO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-3-13

# **Project Overview**



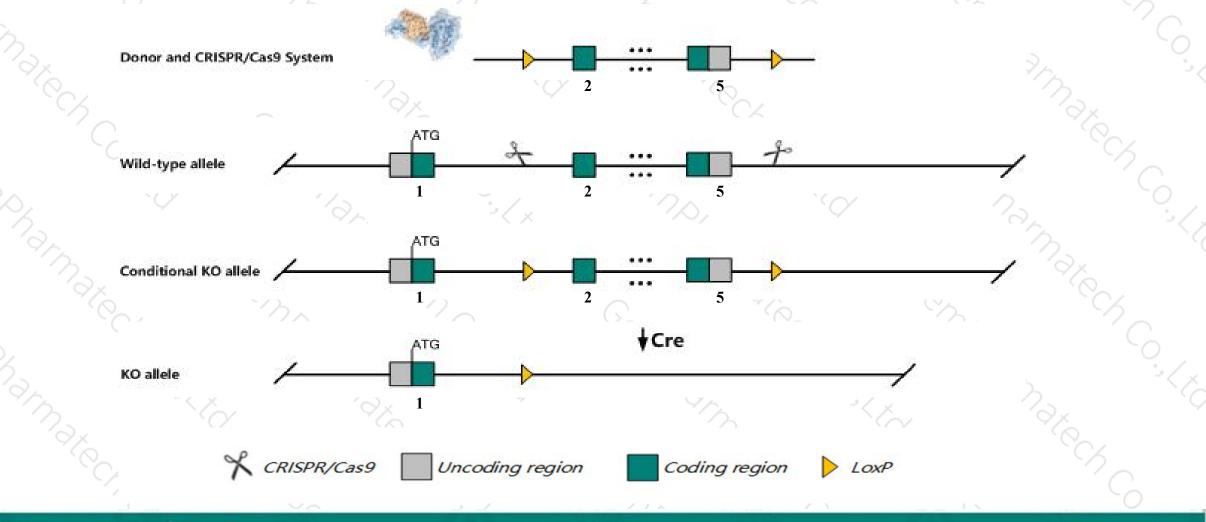


# **Conditional Knockout strategy**



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This model will use CRISPR/Cas9 technology to edit the H2-Oa gene. The schematic diagram is as follows:



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The H2-Oa gene has 7 transcripts. According to the structure of H2-Oa gene, exon2-exon5 of H2-Oa-201 (ENSMUST00000025192.7) 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 H2-Oa gene. The brief process is as follows:CRISPR/Cas9 system 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 and cell types.

# Notice



> According to the existing MGI data, Homozygous inactivation of this gene results in abnormal antigen presentation via MHC class II. Mice homozygous for a knock-out allele show enhanced selection of CD4+ single positive thymocytes. Mice homozygous for a different knock-out allele show increased serum IgG1 levels.

> The flox region overlap with part of the BC051537 gene, which may affect the regulation of this gene.

The H2-Oa gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

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# Gene information (NCBI)



### H2-Oa histocompatibility 2, O region alpha locus [ Mus musculus (house mouse) ]

Gene ID: 15001, updated on 5-Nov-2019

Summary

| ?

Official Symbol	H2-Oa provided by MGI
Official Full Name	histocompatibility 2, O region alpha locus provided by MGI
Primary source	MGI:MGI:95924
See related	Ensembl:ENSMUSG0000024334
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	H-2Oa
Expression	Biased expression in spleen adult (RPKM 116.7), thymus adult (RPKM 40.6) and 3 other tissues See more
Orthologs	human all

# **Transcript information (Ensembl)**



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

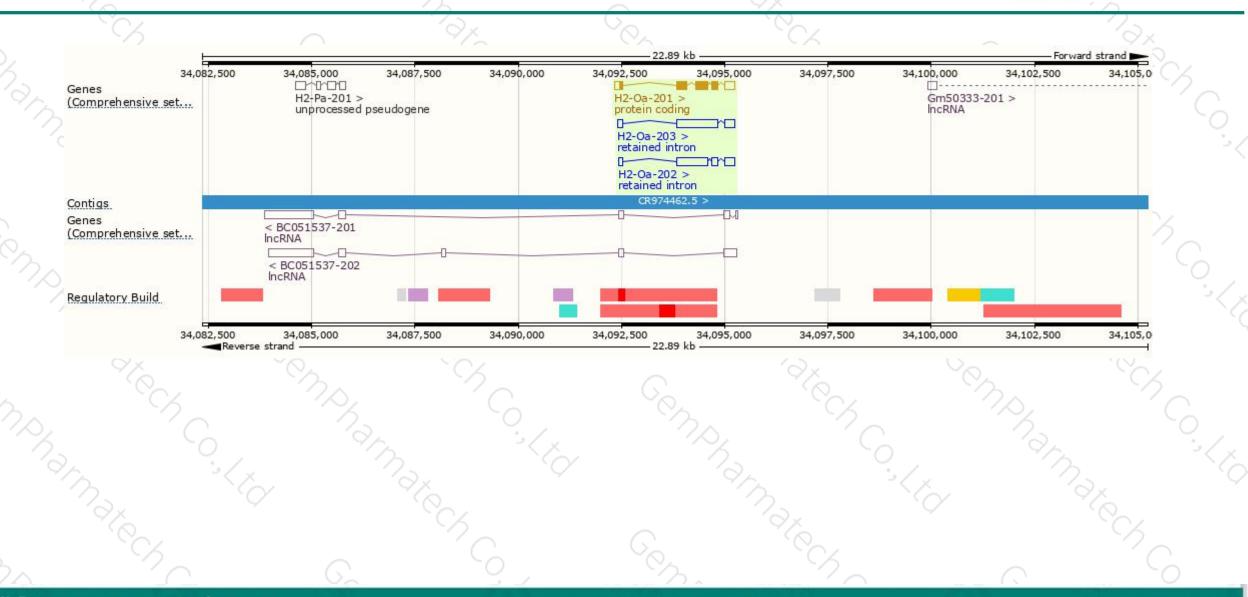
Name 🖕	Transcript ID	bp 🖕	Protein 🖕	Biotype 🖕	CCDS 🖕	UniProt	Flags		
H2-Oa-201	ENSMUST0000025192.7	1088	<u>250aa</u>	Protein coding	<u>CCDS37577</u> &	<u>Q9QWV1</u> ₽	TSL:1	GENCODE basic	APPRIS P1
H2-Oa-203	ENSMUST00000236684.1	1340	No protein	Retained intron	170	55	-		
H2-Oa-202	ENSMUST00000174670.1	1231	No protein	Retained intron	57.5	5	TSL:1		

The strategy is based on the design of H2-Oa-201 transcript, The transcription is shown below

	~003P*	7.1	2.90 kb			Forward strand	
H2-Oa-201 > protein coding							
2				00			
24	10	<u> </u>		<u> </u>	10		

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# **Genomic location distribution**



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# **Protein domain**



	ENSMUSP00000025						
	Transmembrane heli Low complexity (Seg)						
	Cleavage site (Sign						
	Superfamily	MHC classes I/II-I	ike antigen recognition protein	Immunoglobulin-like do	main superfamily		
$\square$							
	SMART	MHC class II, alp	ha chain, N-terminal	Immunog	obulin C1-set		•
	Pfam.	MHC class II, alph	a chain, N-terminal	Immunoglobulin C1-	set		
	PROSITE profiles			Immunoglobulin-like	domain		
	PROSITE patterns					Immunoglobulin/major histocon	npatibility complex
	PANTHER	PTHR19944					
		PTHR19944:SF44					
	Gene3D	MHC class II, alpha	a/beta chain, N-terminal	Immunoglobulin-like fold			
	CDD			cd05767			
	All sequence SNPs/i	Sequence variants (dbSNP and all o	ther sources)	00000		<b>1</b> 1	n ar 115
		<b>I</b> I					
S.							<u>`</u> O
		1					3/
	>						×
	Variant Legend	frameshift variant		infran	ne deletion		
		missense variant		synor	iymous variant		
	Scale bar	<b>o</b> 40	80	120	160	200	250
	0		0		$\gamma_{a}$		

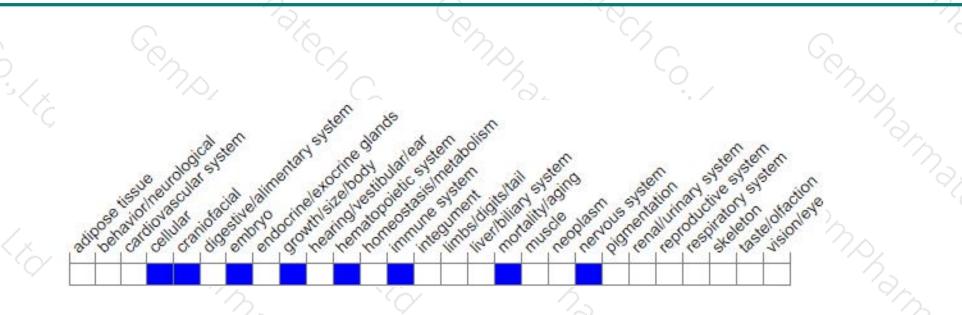
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# Mouse phenotype description(MGI)





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 inactivation of this gene results in abnormal antigen presentation via MHC class II. Mice homozygous for a knock-out allele show enhanced selection of CD4+ single positive thymocytes. Mice homozygous for a different knock-out allele show increased serum IgG1 levels.

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



