



Models to
Accelerate Innovation



***H11-Cd8a-iCre* KI Mouse Model Strategy -Gene Editing Technology**

Designer

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Reviewer

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Date

2026-03-25



Project Overview

Project Name **H11-Cd8a-iCre**

Project Type **KI (H11)**

Background **C57BL/6JGpt**

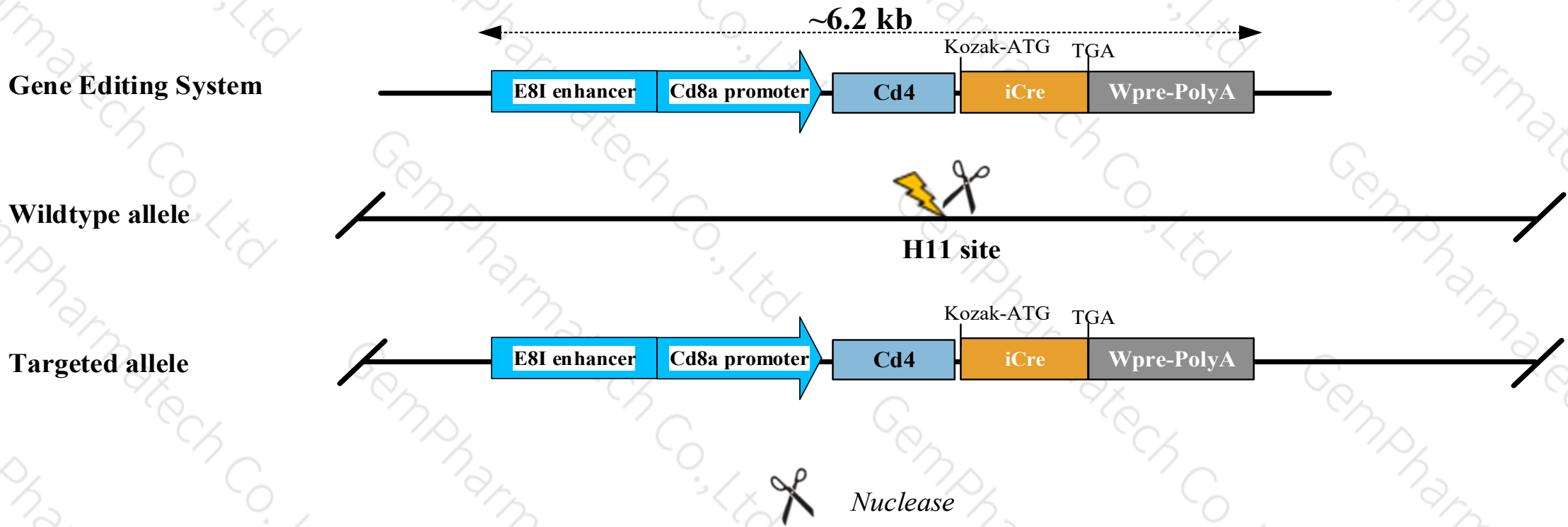
Timeline **5-8 Months**

Deliverable **3~5 F1 Heterozygous Mice**



Strategy

The schematic diagram is as follows:





Technical Description

- *H11*, located on mouse chromosome 11, is a safe site for foreign gene insertion. The foreign gene integrated into this site can be expressed stably and efficiently without destroying the function of endogenous gene.
- The targeting sequence fragment will be inserted into the H11 locus. Expression of *iCre* will be driven by the *Cd8a* enhancer (E8I) and promoter.
- In this project, the *Cd8a-iCre-WPRE-PolyA* fragment will be inserted into H11 site of the mouse genome by gene editing technology. Briefly, the donor vector and nuclease system will be constructed in vitro. Vector and nuclease system will be microinjected into fertilized eggs of C57BL/6JGpt mice to obtain positive F0 generation mice. The F0 positive mice will be bred with C57BL/6JGpt mice to obtain positive F1 mice. Pups from both F0 and F1 generations will be genotyped by PCR, followed by on-target sequencing analysis.

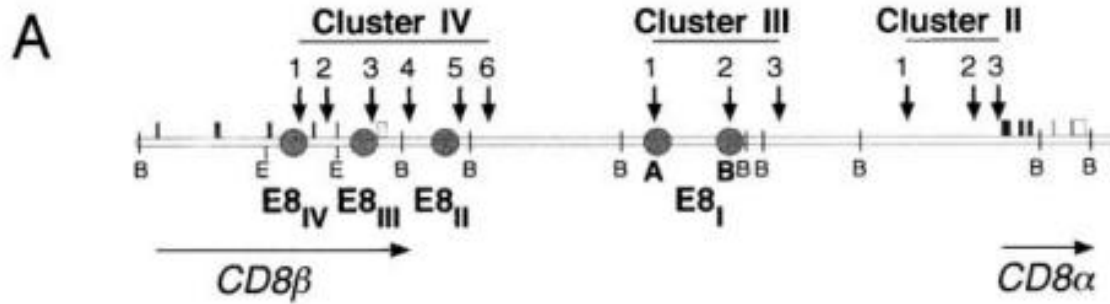


Note

- H11 is located on Chr11. Please take the loci in consideration when breeding the Knock-in mice with other gene modified (e.g., iCre) strains, if the other gene is also on Chr11, it may be extremely hard to get double gene positive homozygotes.
- This strategy is designed based on the currently available information in the existing databases. Due to the complexity of gene expression regulation, the effect of this strategy on gene expression cannot be completely predicted at the present technology level.



Reference



METHODS

Mice and cell culture. Female B6 and BALB/c mice 6–8 weeks of age were from Japan SLC. *Notch2^{ff}* mice have been described⁴¹. For the generation of E8I-Cre-transgenic mice, the 1.6-kilobase core of E8I enhancer fragment was inserted in front of the *Cd8a* promoter, and cDNA encoding Cre and an internal ribosomal entry site–GFP–poly(A) cassette were inserted after the *Cd8a* promoter to generate the E8I-Cre transgene (I.T., data not shown). The

PMID: 12049715
PMID: 18724371



Target Gene

| | |
|----------------------------|---|
| Gene name | mouse <i>Cd8a</i> |
| Gene ID (NCBI) | 12525 |
| Gene link (NCBI) | https://www.ncbi.nlm.nih.gov/gene/12525 |
| Gene link (Ensembl) | http://asia.ensembl.org/Mus_musculus/Gene/Summary?g=ENSMUSG00000053977;r=6:71350411-71356157 |
| Chromosome location | Chr 6 |



Gene Information (NCBI)



Cd8a CD8 subunit alpha [*Mus musculus* (house mouse)]

Gene ID: 12525, updated on 3-Mar-2026

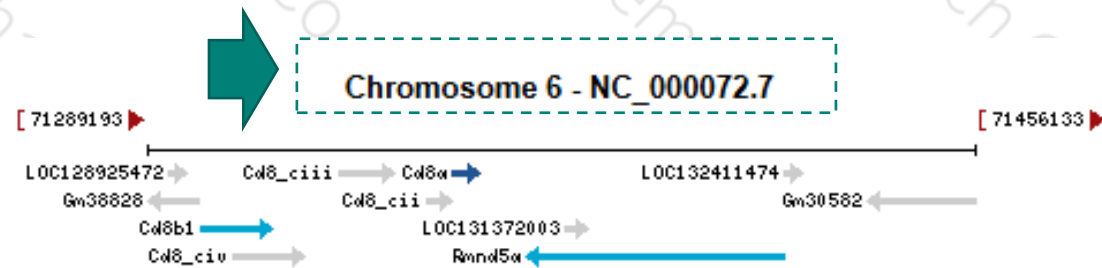
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Summary

Official Symbol Cd8a provided by [MGI](#)
Official Full Name CD8 subunit alpha provided by [MGI](#)
Primary source [MGI:MGI:88346](#)
See related [Ensembl:ENSMUSG00000053977](#) [AllianceGenome:MGI:88346](#)
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 Ly-2; Ly-B; Ly-35; Lyt-2
Summary Enables identical protein binding activity. Acts upstream of or within several processes, including cytotoxic T cell differentiation; defense response to virus; and positive regulation of calcium-mediated signaling. Located in external side of plasma membrane. Part of receptor complex. Is expressed in several structures, including endocrine gland; exocrine gland; genitourinary system; gut; and immune system. Human ortholog(s) of this gene implicated in immunodeficiency 116. Orthologous to human CD8A (CD8 subunit alpha). [provided by Alliance of Genome Resources, Jul 2025]
Expression Restricted expression toward thymus adult (RPKM 213.1) [See more](#)
Orthologs [all](#)

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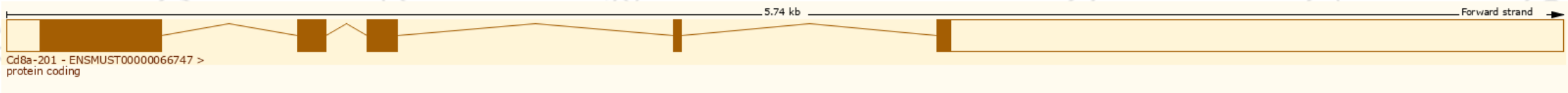


Transcript Information (Ensembl)

The gene has 3 transcripts, as shown below:

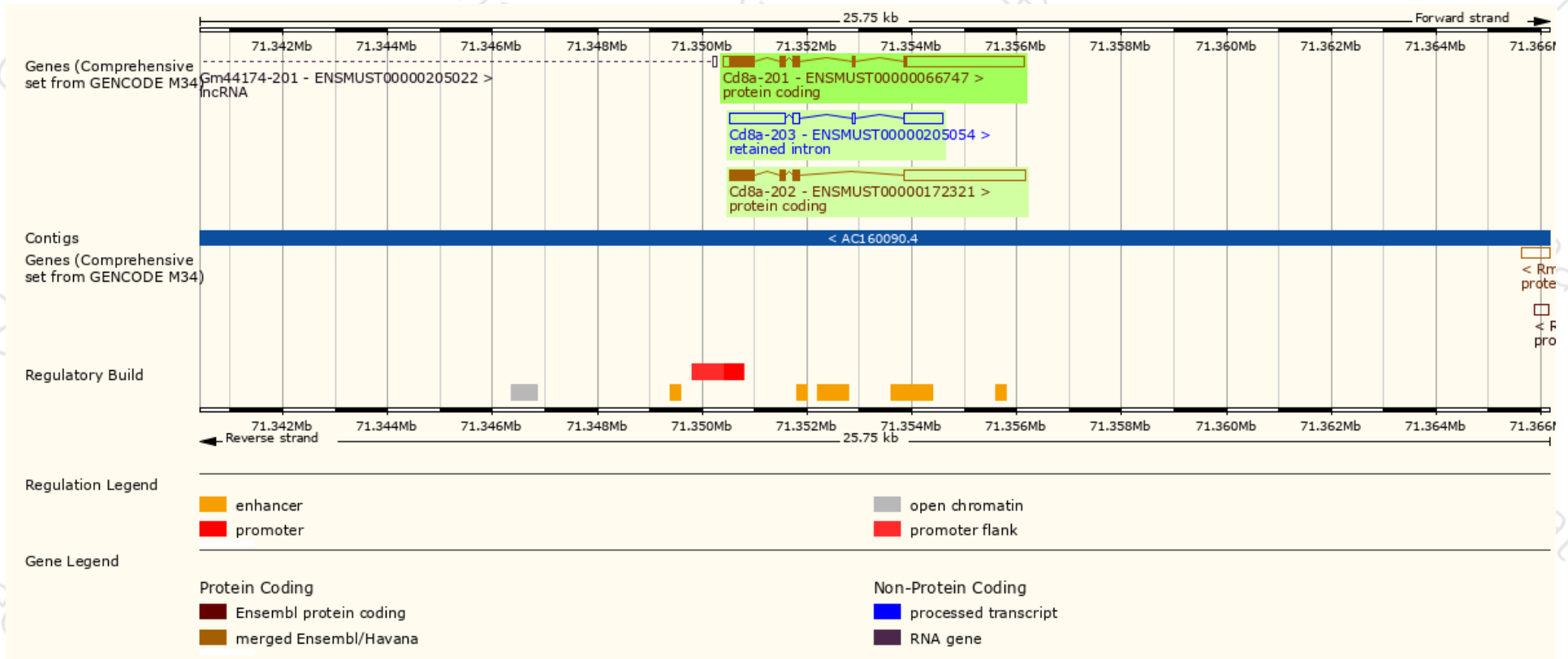
| Show/hide columns (1 hidden) | | Filter | | | | | |
|---------------------------------------|----------|--------|-----------------------|-----------------|---------------------------|--------------------------|---|
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
| ENSMUST00000066747.14 | Cd8a-201 | 3128 | 247aa | Protein coding | CCDS39507 | P01731-1 | Ensembl Canonical Gencode basic APPRIS P2 TSL:1 |
| ENSMUST00000172321.3 | Cd8a-202 | 2975 | 222aa | Protein coding | CCDS51806 | Q8CAX3 | Gencode basic APPRIS ALT2 TSL:1 |
| ENSMUST00000205054.2 | Cd8a-203 | 1950 | No protein | Retained intron | | - | TSL:1 |

The strategy is based on *Cd8a-201* transcript, which contains 5 exons, is 3128 bps long, and encodes 247 amino acids.



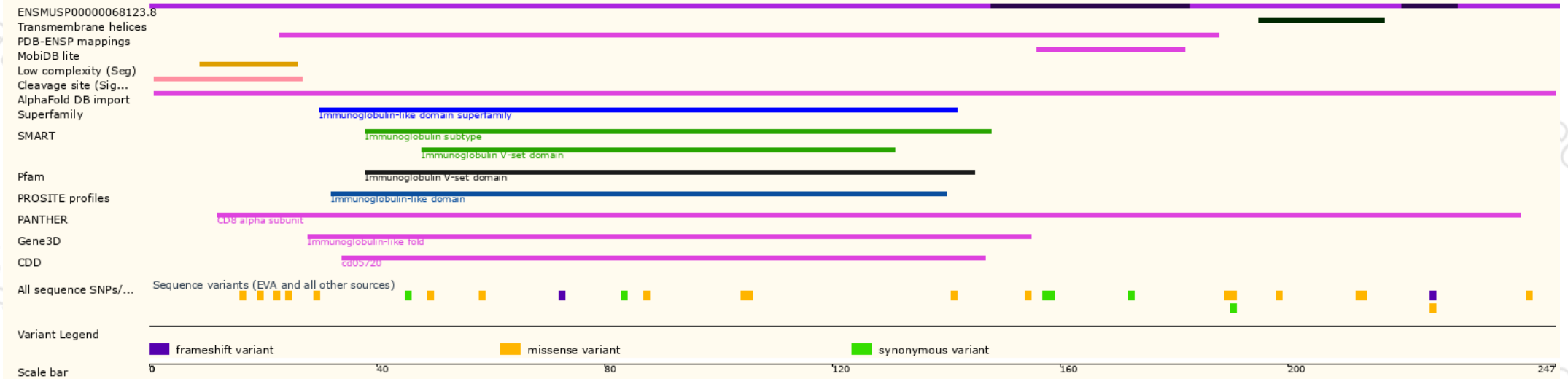


Genomic Information



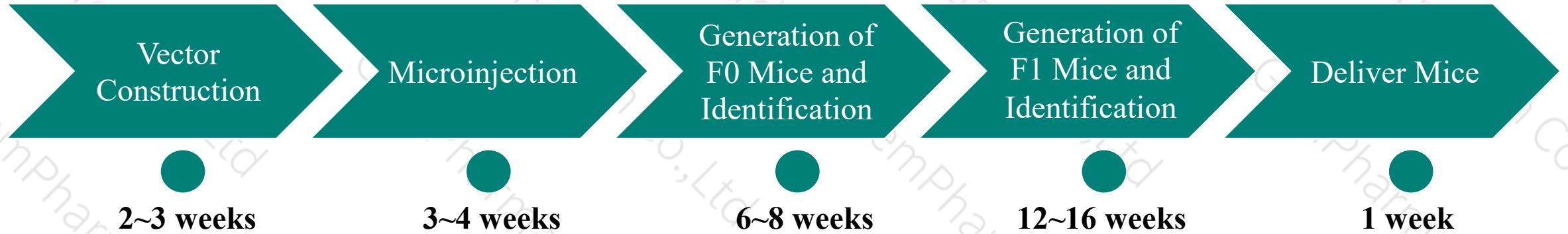


Protein Information





Work Flow





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