

# *Eif3k* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Eif3k*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif3k* gene. The schematic diagram is as follows:



- The *Eif3k* gene has 6 transcripts. According to the structure of *Eif3k* gene, exon3-exon4 of *Eif3k-201* (ENSMUST00000066070.6) transcript is recommended as the knockout region. The region contains 196bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif3k* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Eif3k* 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.
- The knockout area of this strategy is about 3.5kb away from the 5-terminal of Map4k1, which may affect its 5-terminal regulation after knockout.
- 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.



# Gene information (NCBI)

## Eif3k eukaryotic translation initiation factor 3, subunit K [Mus musculus (house mouse)]

Gene ID: 73830, updated on 13-Mar-2020

### Summary



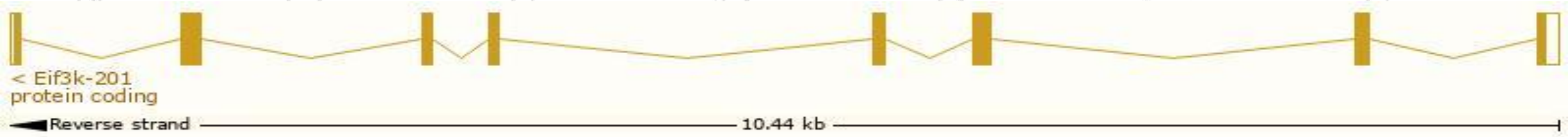
<b>Official Symbol</b>	Eif3k provided by <a href="#">MGI</a>
<b>Official Full Name</b>	eukaryotic translation initiation factor 3, subunit K provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1921080</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000053565</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	1200009C21Rik, Eif3s12
<b>Expression</b>	Ubiquitous expression in liver E14.5 (RPKM 97.7), placenta adult (RPKM 93.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

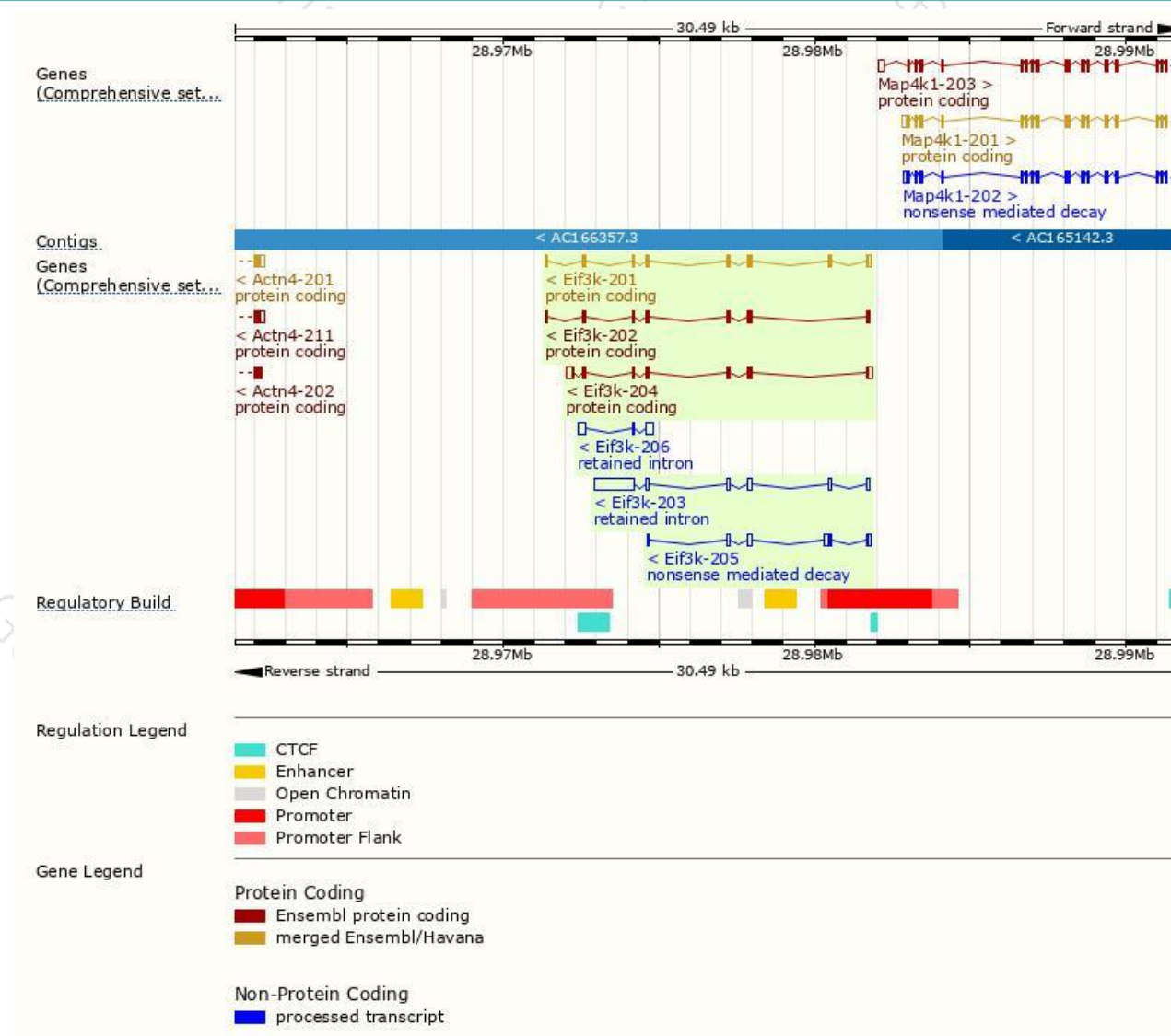
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif3k-204	<a href="#">ENSMUST00000208616.1</a>	909	<a href="#">192aa</a>	Protein coding	<a href="#">CCDS85255</a>	<a href="#">Q3TY56</a>	TSL:1 GENCODE basic
Eif3k-201	<a href="#">ENSMUST00000066070.6</a>	774	<a href="#">218aa</a>	Protein coding	<a href="#">CCDS21062</a>	<a href="#">Q9DBZ5</a>	TSL:1 GENCODE basic APPRIS P1
Eif3k-202	<a href="#">ENSMUST00000207683.1</a>	647	<a href="#">185aa</a>	Protein coding	<a href="#">CCDS85254</a>	<a href="#">Q9DBZ5</a>	TSL:1 GENCODE basic
Eif3k-205	<a href="#">ENSMUST00000208707.1</a>	578	<a href="#">53aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LJ59</a>	TSL:5
Eif3k-203	<a href="#">ENSMUST00000207762.1</a>	1782	No protein	Retained intron	-	-	TSL:1
Eif3k-206	<a href="#">ENSMUST00000208810.1</a>	537	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Eif3k-201* transcript,the transcription is shown below:

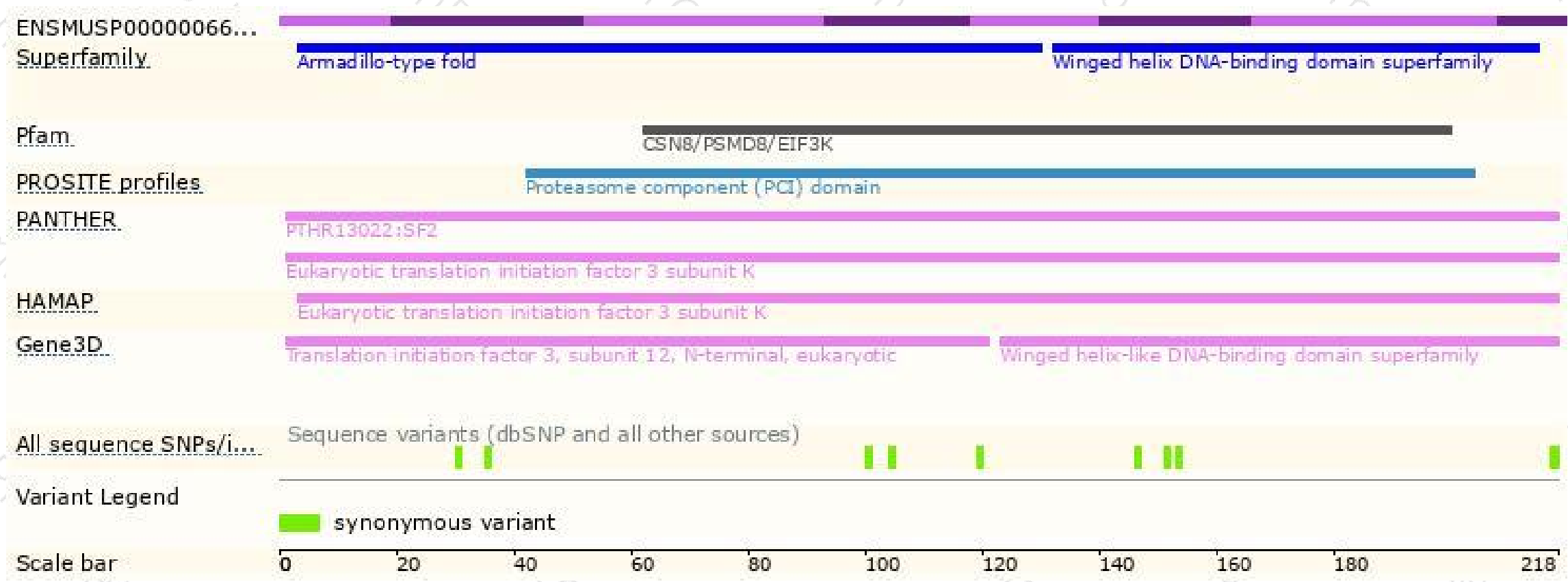


# Genomic location distribution





# Protein domain



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

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