

Plekha1 Cas9-CKO Strategy

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Project Overview

Project Name

Plekha1

Project type

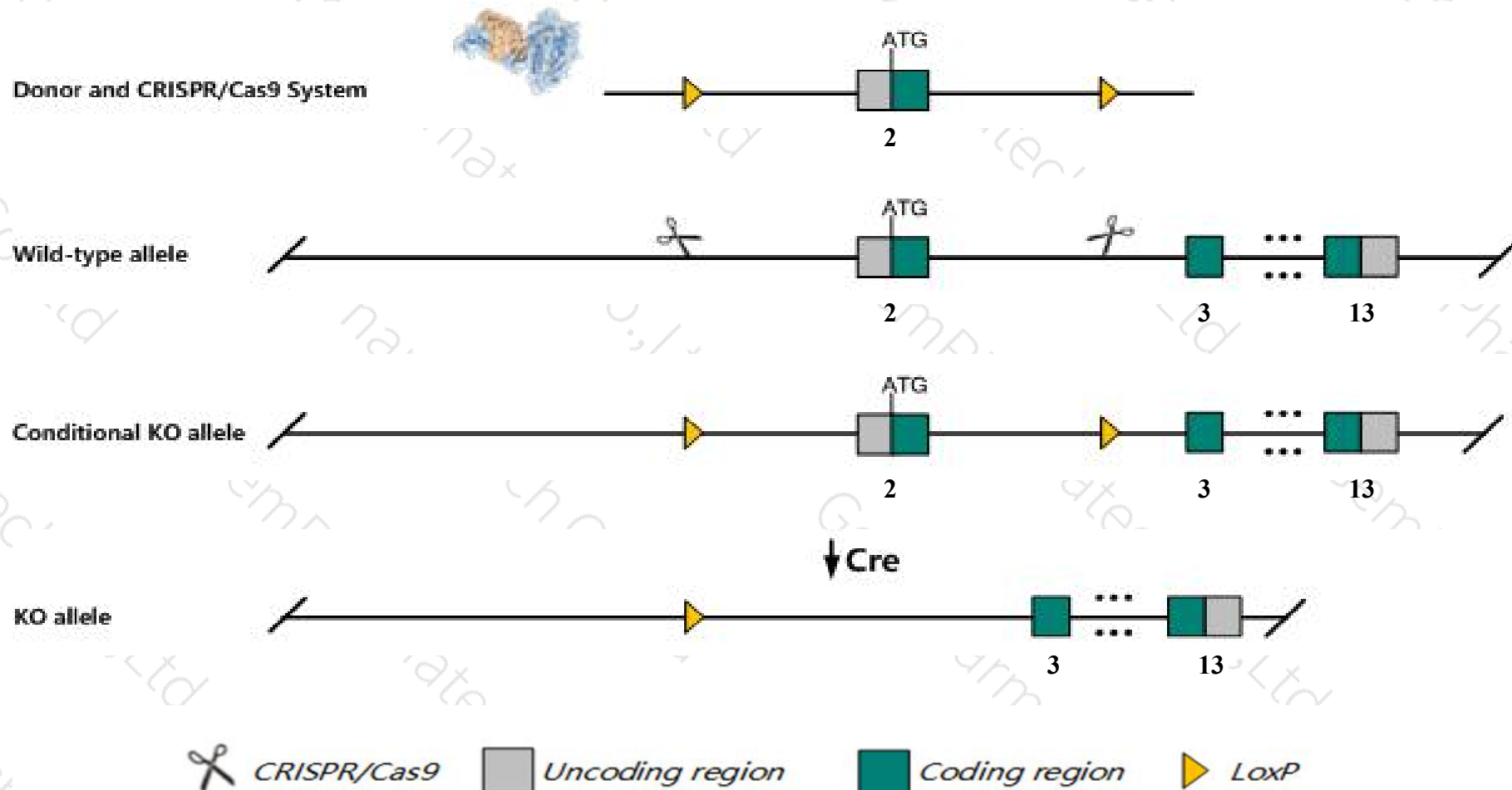
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plekha1* gene. The schematic diagram is as follows:



Technical routes

- The *Plekha1* gene has 12 transcripts. According to the structure of *Plekha1* gene, exon2 of *Plekha1*-202(ENSMUST00000075181.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plekha1* 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.

- According to the existing MGI data, mice homozygous for a gene trapped allele exhibit postnatal lethality and increased body weight.
- The flox region is in the intron of the *Fgfr2* gene, which may affect the regulation of this gene.
- Transcript 204 CDS 5' incomplete the influences is unknown.
- The *Plekha1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Plekha1 pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 [Mus musculus (house mouse)]

Gene ID: 101476, updated on 13-Mar-2020

Summary



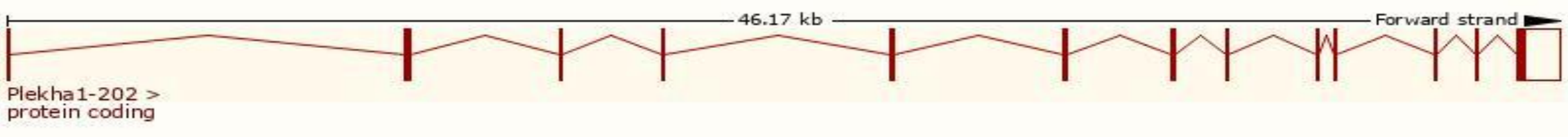
Official Symbol	Plekha1 provided by MGI
Official Full Name	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 provided by MGI
Primary source	MGI:MGI:2442213
See related	Ensembl:ENSMUSG00000040268
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA960558, C920009D07Rik, TAPP1
Expression	Broad expression in CNS E18 (RPKM 32.7), whole brain E14.5 (RPKM 25.8) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

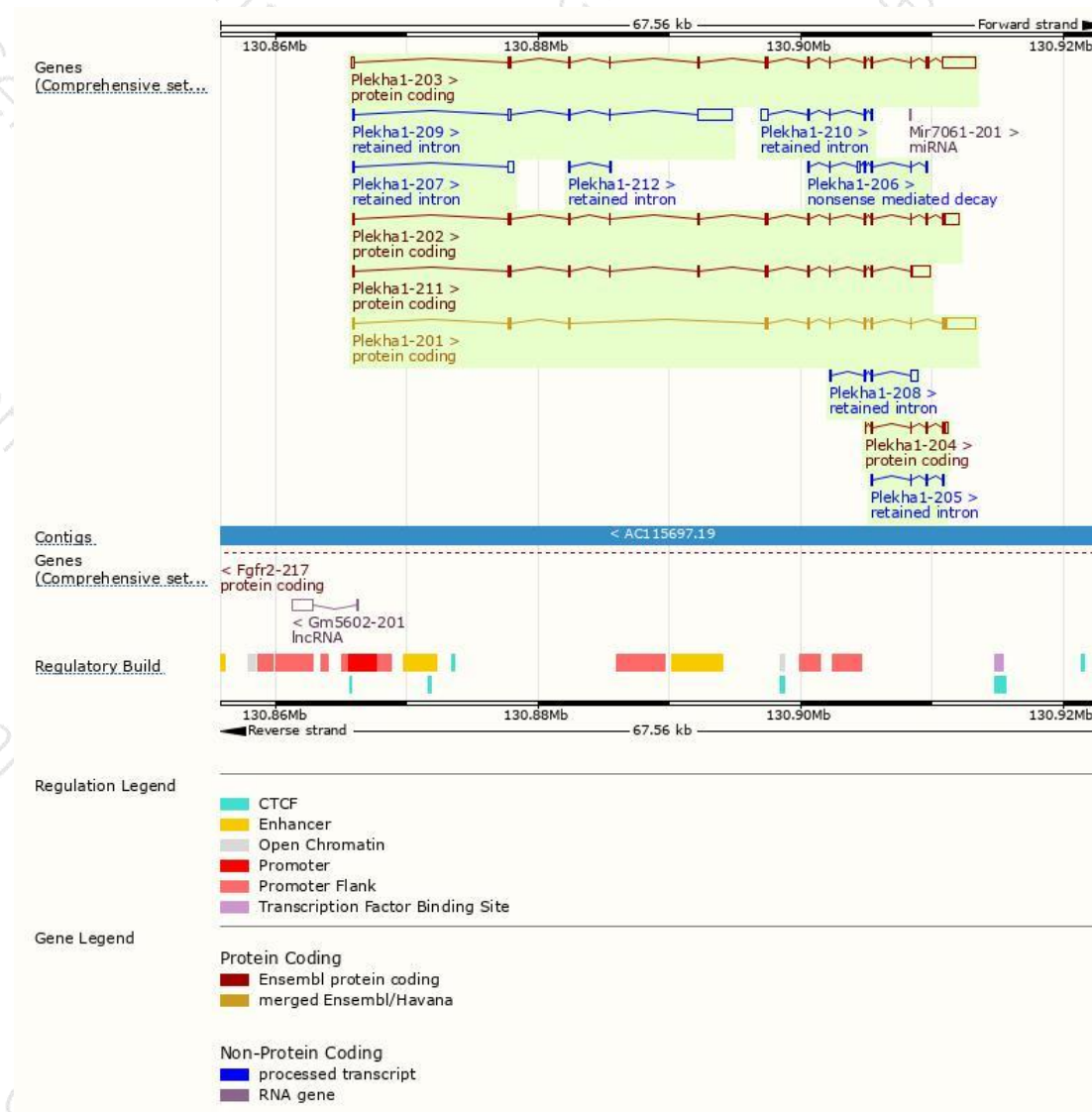
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plekha1-201	ENSMUST00000048180.11	3321	356aa	Protein coding	CCDS21907	Q8BUL6	TSL:1 GENCODE basic
Plekha1-202	ENSMUST00000075181.10	2301	383aa	Protein coding	CCDS85434	Q8BUL6	TSL:1 GENCODE basic APPRIS P1
Plekha1-203	ENSMUST00000120441.7	3777	334aa	Protein coding	-	D3YU01	TSL:5 GENCODE basic
Plekha1-211	ENSMUST00000151119.8	2397	316aa	Protein coding	-	D6RCU3	TSL:1 GENCODE basic
Plekha1-204	ENSMUST00000126355.1	588	155aa	Protein coding	-	F6YLP9	CDS 5' incomplete TSL:3
Plekha1-206	ENSMUST00000136963.7	743	71aa	Nonsense mediated decay	-	A0A140LIT3	CDS 5' incomplete TSL:3
Plekha1-209	ENSMUST00000148513.1	2941	No protein	Retained intron	-	-	TSL:1
Plekha1-210	ENSMUST00000149029.7	774	No protein	Retained intron	-	-	TSL:3
Plekha1-208	ENSMUST00000146111.1	726	No protein	Retained intron	-	-	TSL:3
Plekha1-207	ENSMUST00000140153.1	517	No protein	Retained intron	-	-	TSL:2
Plekha1-205	ENSMUST00000135359.1	352	No protein	Retained intron	-	-	TSL:3
Plekha1-212	ENSMUST00000154282.1	153	No protein	Retained intron	-	-	TSL:3

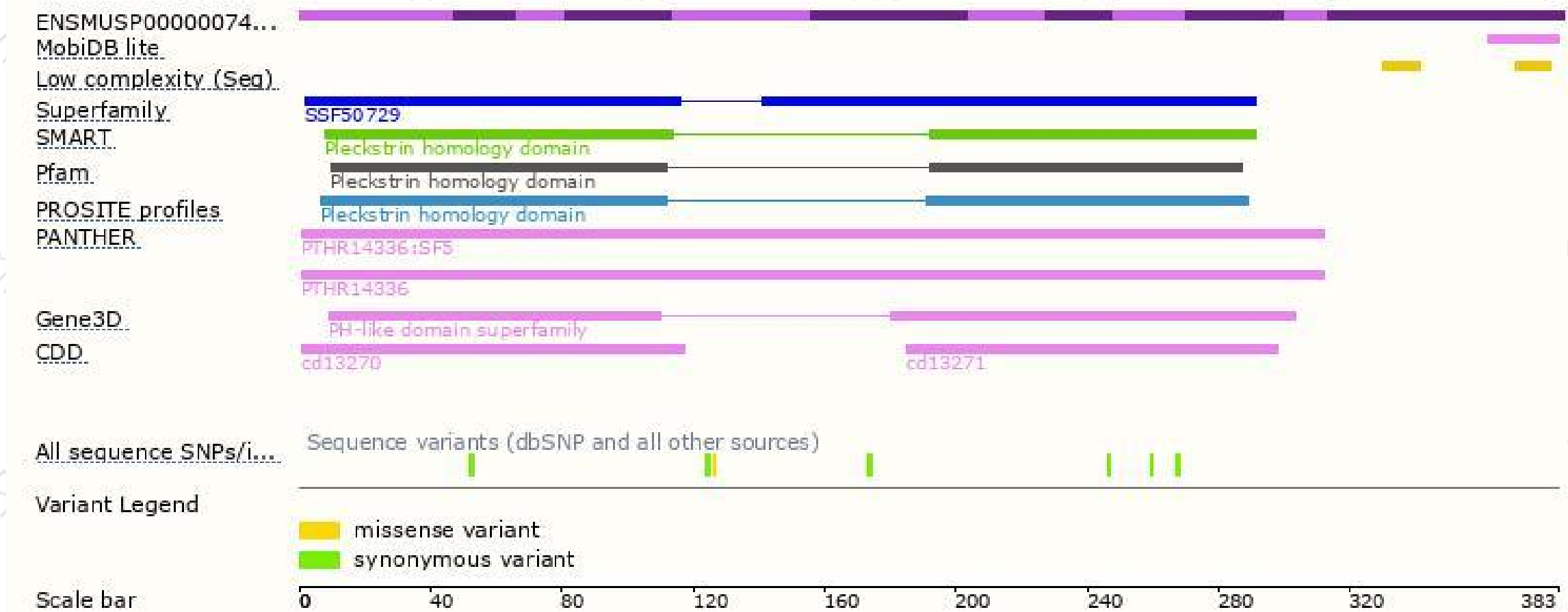
The strategy is based on the design of *Plekha1-202* transcript,the transcription is shown below:



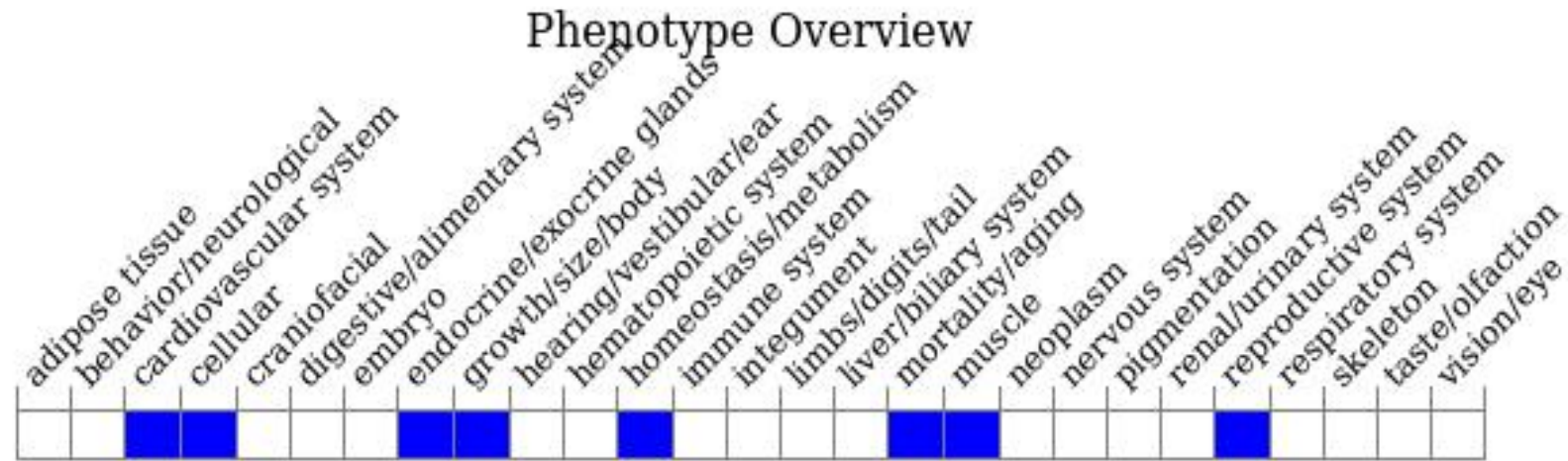
Genomic location distribution



Protein domain



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, *mcie* homozygous for a gene trapped allele exhibit postnatal lethality and increased body weight.

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

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