

Maged1 Cas9-KO Strategy

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Design Date:

2019-12-18

Project Overview

Project Name

Maged1

Project type

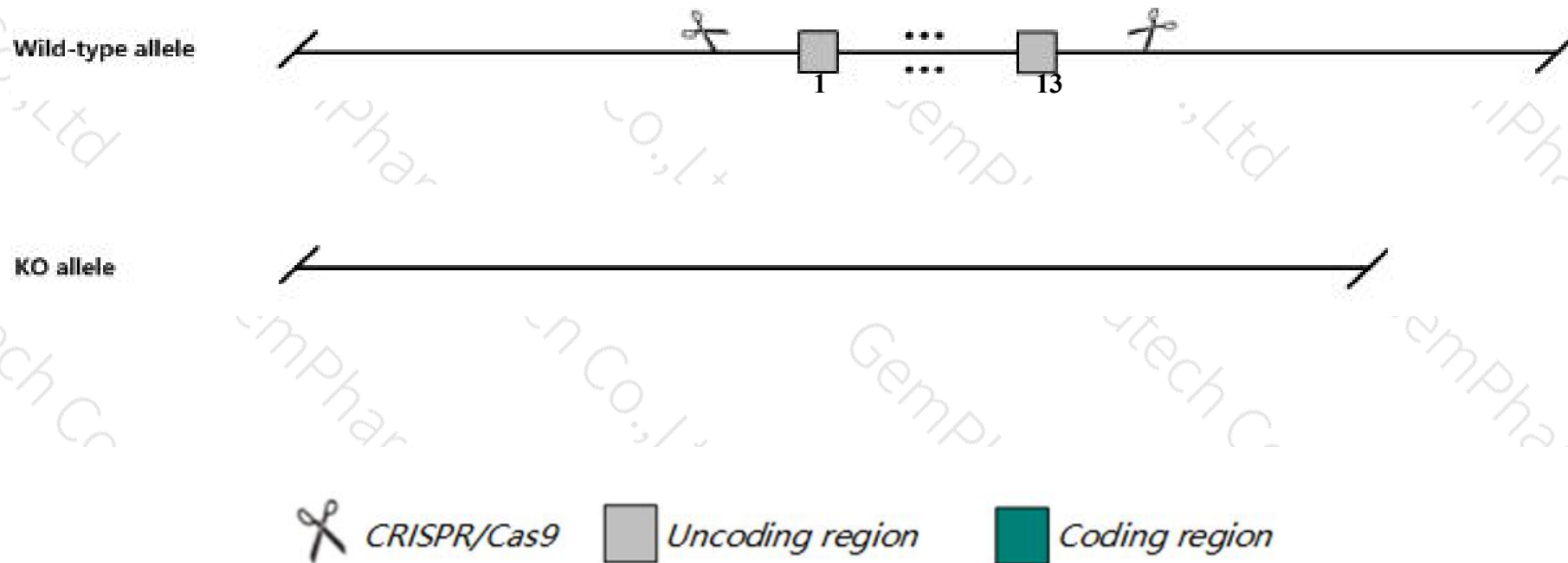
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Maged1* gene. The schematic diagram is as follows:



- The *Maged1* gene has 7 transcripts. According to the structure of *Maged1* gene, exon1-exon13 of *Maged1-201* (ENSMUST00000026142.7) transcript is recommended as the knockout region. The region contains all 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 *Maged1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display defects in apoptotic signaling affecting hair cycling and neuronal physiology. Mice homozygous for a different knock-out allele exhibit hypoactivity, decreased exploration, social withdrawal, anhedonia, behavioral despair and altered serotonin levels.
- The *Maged1* gene is located on the ChrX. 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.

Gene information (NCBI)

Maged1 melanoma antigen, family D, 1 [Mus musculus (house mouse)]

Gene ID: 94275, updated on 7-Apr-2019

Summary



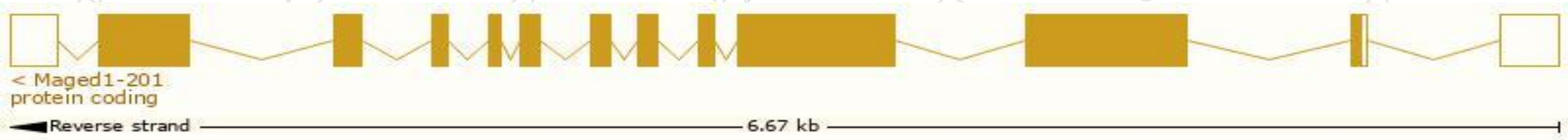
Official Symbol	Maged1 provided by MGI
Official Full Name	melanoma antigen, family D, 1 provided by MGI
Primary source	MGI:MGI:1930187
See related	Ensembl:ENSMUSG00000025151
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810433C11Rik, 5430405L04Rik, DXBwg1492e, Dlixin, Dlixin-1, Dlixin1, MAGE-D1, NRAGE
Expression	Ubiquitous expression in limb E14.5 (RPKM 316.2), CNS E14 (RPKM 313.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

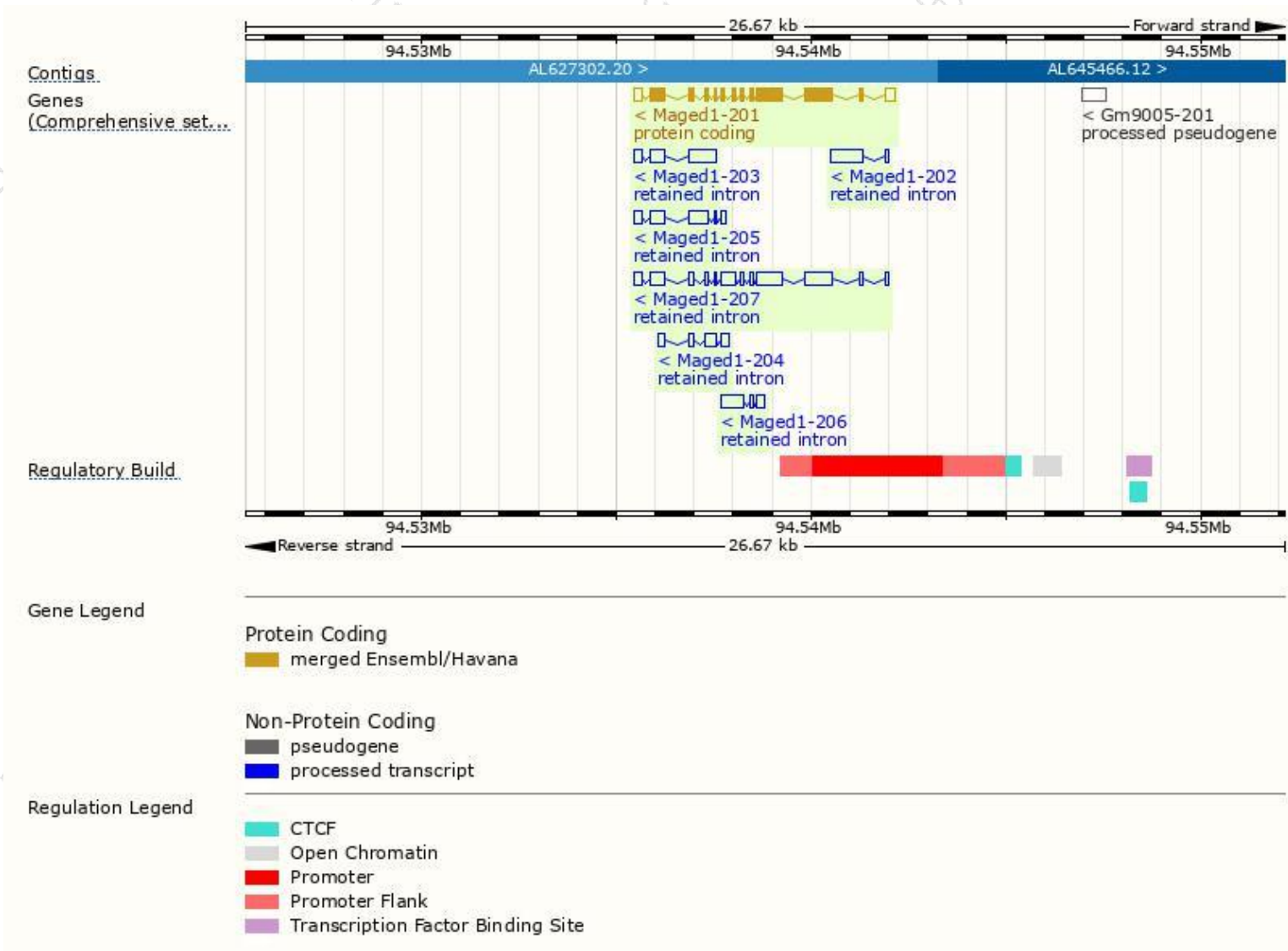
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Maged1-201	ENSMUST00000026142.7	2821	775aa	Protein coding	CCDS30280	Q9QYH6	TSL:1 GENCODE basic APPRIS P1
Maged1-207	ENSMUST00000153386.7	2884	No protein	Retained intron	-	-	TSL:1
Maged1-203	ENSMUST00000138146.1	1278	No protein	Retained intron	-	-	TSL:5
Maged1-205	ENSMUST00000139375.7	1274	No protein	Retained intron	-	-	TSL:1
Maged1-202	ENSMUST00000133982.1	943	No protein	Retained intron	-	-	TSL:2
Maged1-206	ENSMUST00000141702.1	873	No protein	Retained intron	-	-	TSL:2
Maged1-204	ENSMUST00000138731.1	779	No protein	Retained intron	-	-	TSL:3

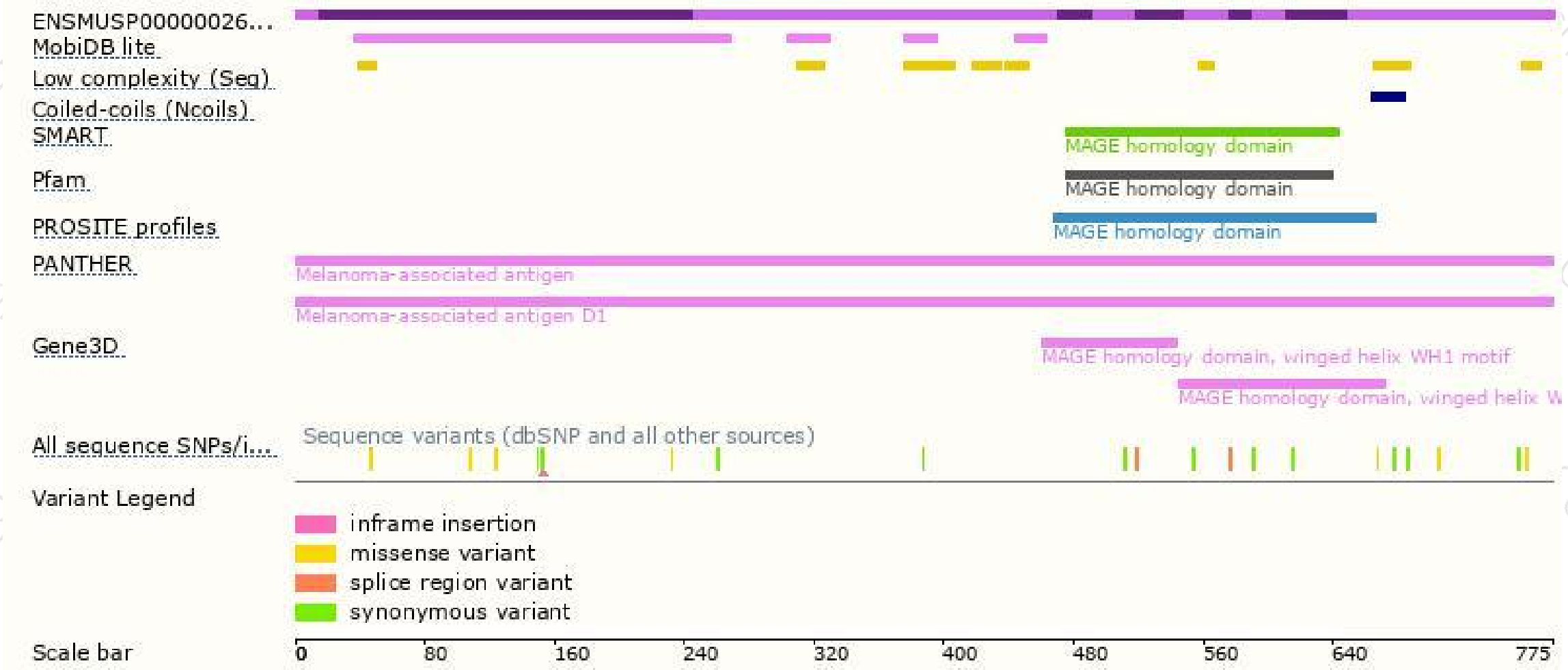
The strategy is based on the design of *Maged1-201* transcript,The transcription is shown below



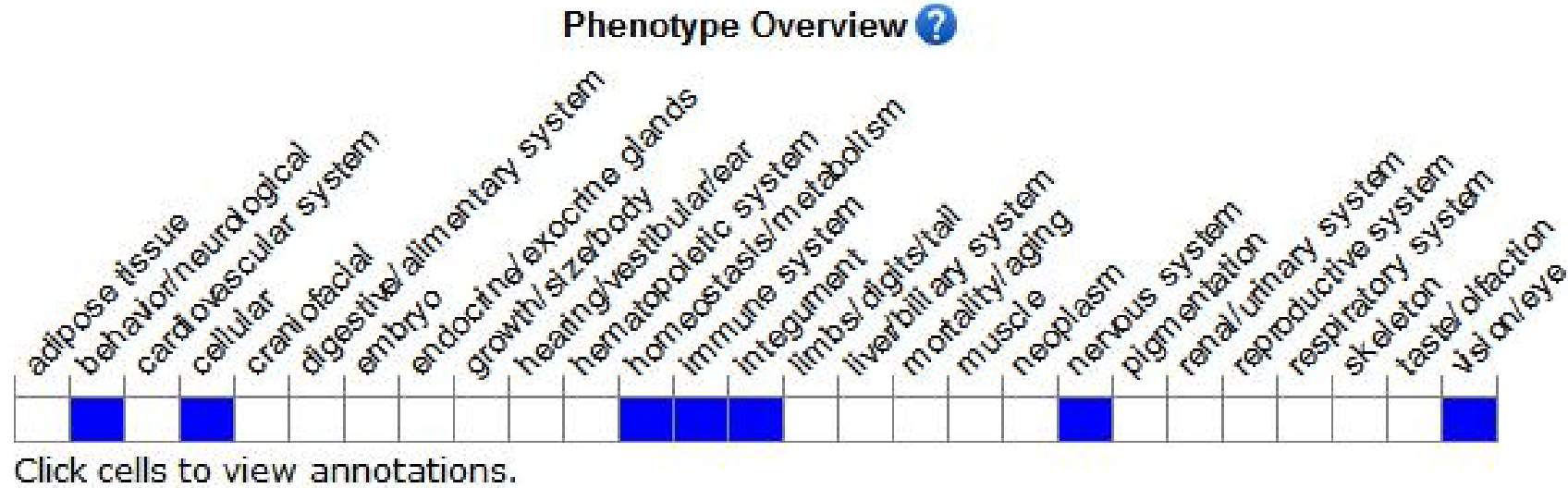
Genomic location distribution



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, Homozygous null mice display defects in apoptotic signaling affecting hair cycling and neuronal physiology. Mice homozygous for a different knock-out allele exhibit hypoactivity, decreased exploration, social withdrawal, anhedonia, behavioral despair and altered serotonin levels.

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

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