

# *Aatk* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Aatk*

**Project type**

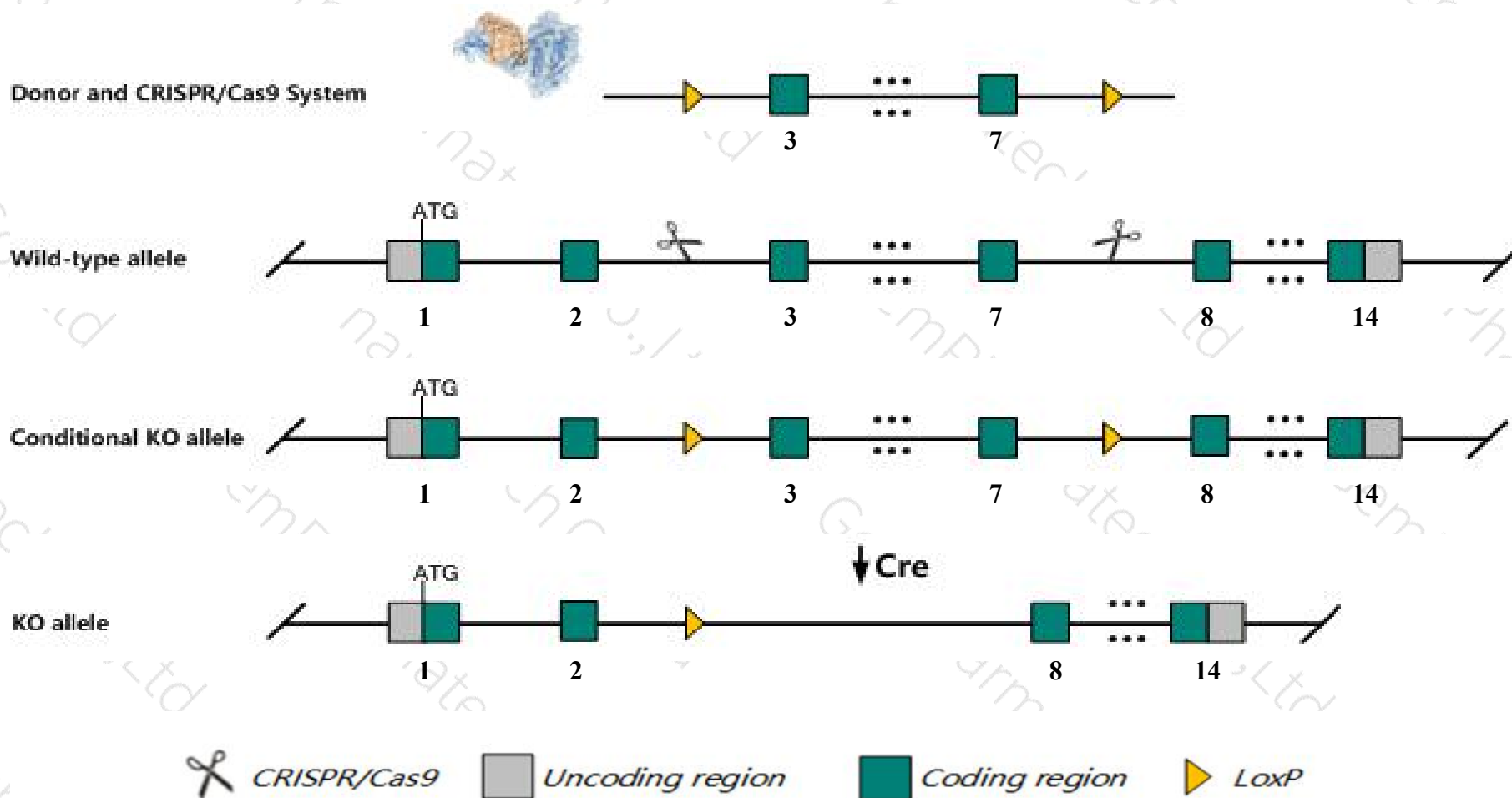
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- The *Aatk* gene has 9 transcripts. According to the structure of *Aatk* gene, exon3-exon7 of *Aatk-201*(ENSMUST00000064307.9) transcript is recommended as the knockout region. The region contains 569bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Aatk* 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 knock-out allele exhibit decreased brain size, longer axons and fewer neurites.
- The flox region is about 300bp away from the 5th end of the Mir338 gene, which may affect the regulation of this gene or delete it directly.
- The flox region is about 300bp away from the 3th end of the Mir3065 gene, which may affect the regulation of this gene or delete it directly.
- The *Aatk* gene is located on the Chr11. 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)

## Aatk apoptosis-associated tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 11302, updated on 20-Mar-2020

### Summary



**Official Symbol** Aatk provided by [MGI](#)

**Official Full Name** apoptosis-associated tyrosine kinase provided by [MGI](#)

**Primary source** [MGI:MGI:1197518](#)

**See related** [Ensembl:ENSMUSG00000025375](#)

**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** AATYK, aatyk1, mKIAA0641

**Expression** Broad expression in cerebellum adult (RPKM 51.8), cortex adult (RPKM 38.4) and 15 other tissues [See more](#)

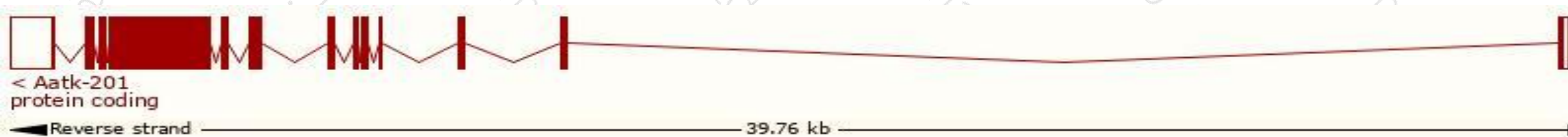
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

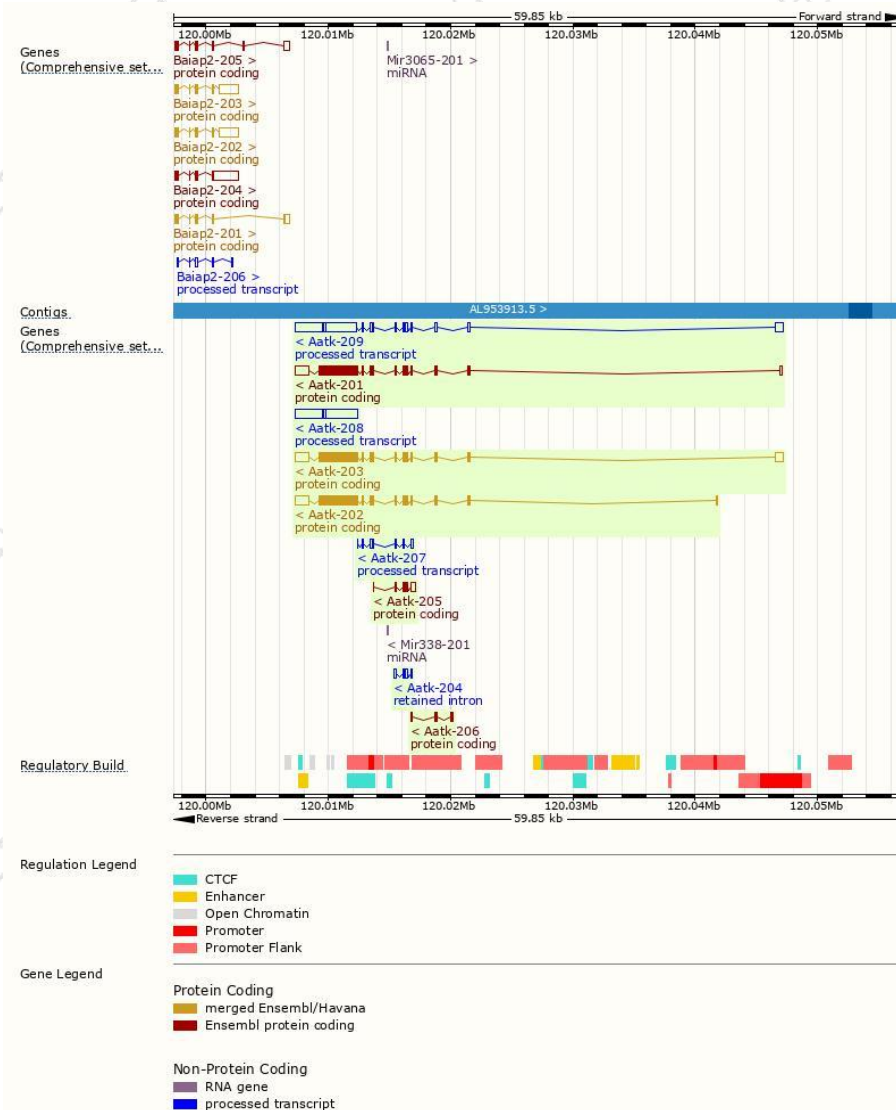
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aatk-203	<a href="#">ENSMUST00000103020.7</a>	5687	<a href="#">1317aa</a>	Protein coding	<a href="#">CCDS25725</a>	<a href="#">B1AZF9</a>	TSL:1 GENCODE basic APPRIS P3
Aatk-201	<a href="#">ENSMUST00000064307.9</a>	5336	<a href="#">1374aa</a>	Protein coding	<a href="#">CCDS56826</a>	<a href="#">B1AZF3</a>	TSL:1 GENCODE basic APPRIS ALT2
Aatk-202	<a href="#">ENSMUST00000103019.1</a>	5177	<a href="#">1317aa</a>	Protein coding	<a href="#">CCDS25725</a>	<a href="#">B1AZF9</a>	TSL:1 GENCODE basic APPRIS P3
Aatk-205	<a href="#">ENSMUST00000132575.7</a>	815	<a href="#">99aa</a>	Protein coding	-	-	CDS 3' incomplete TSL:3
Aatk-206	<a href="#">ENSMUST00000134319.1</a>	365	<a href="#">95aa</a>	Protein coding	-	-	CDS 3' incomplete TSL:3
Aatk-209	<a href="#">ENSMUST00000150730.7</a>	6455	No protein	Processed transcript	-	-	TSL:1
Aatk-208	<a href="#">ENSMUST00000142959.1</a>	4886	No protein	Processed transcript	-	-	TSL:2
Aatk-207	<a href="#">ENSMUST00000136386.7</a>	781	No protein	Processed transcript	-	-	TSL:3
Aatk-204	<a href="#">ENSMUST00000128836.1</a>	553	No protein	Retained intron	-	-	TSL:3

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

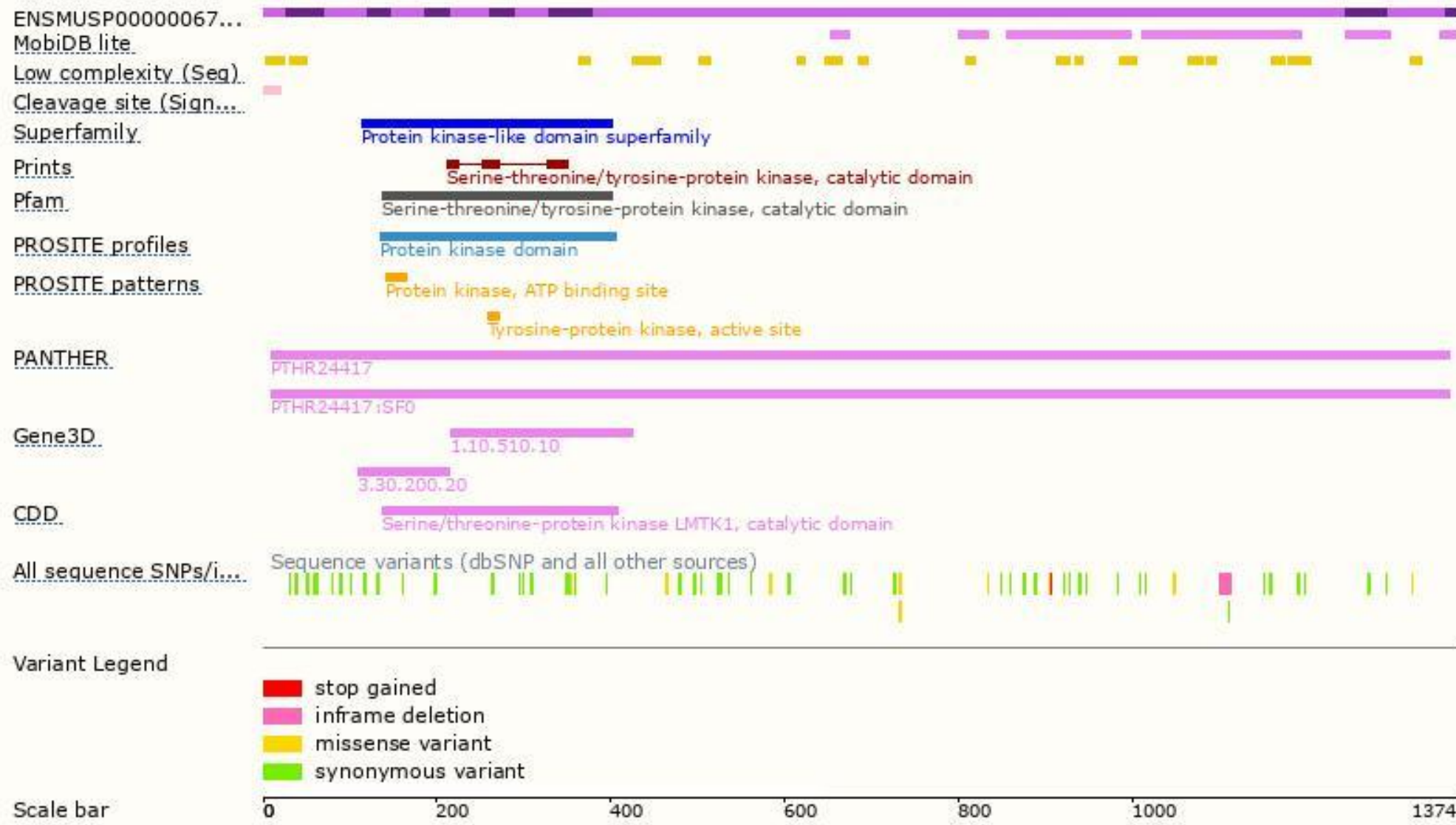


# Genomic location distribution

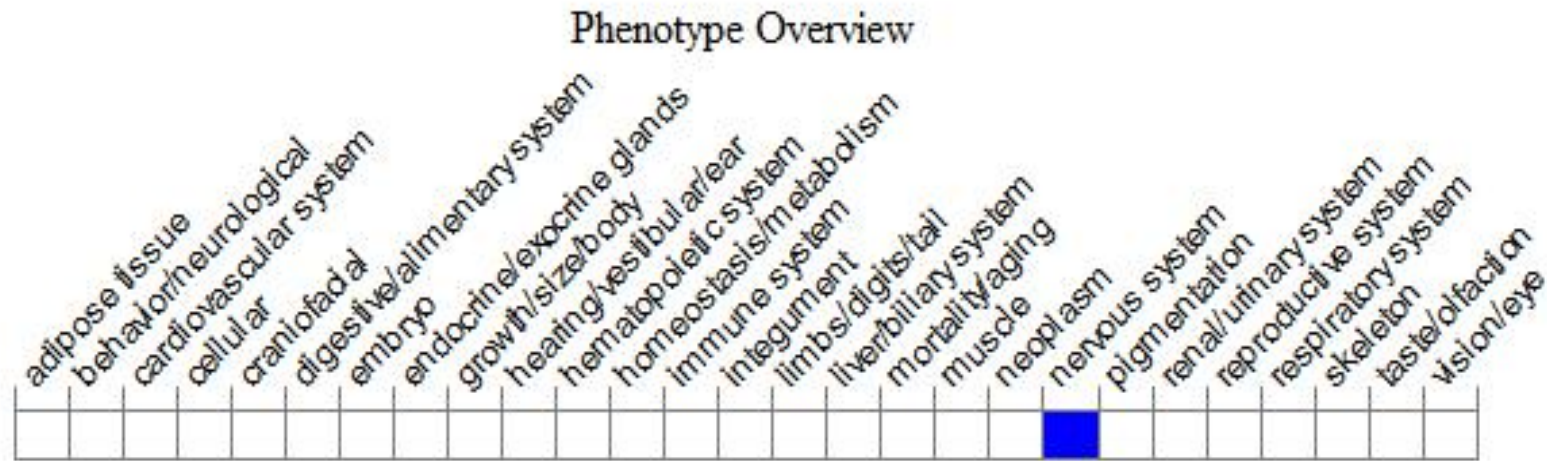




# Protein domain



# 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, mice homozygous for a knock-out allele exhibit decreased brain size, longer axons and fewer neurites.

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

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