

***Galnt14* Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Galnt14

Project type

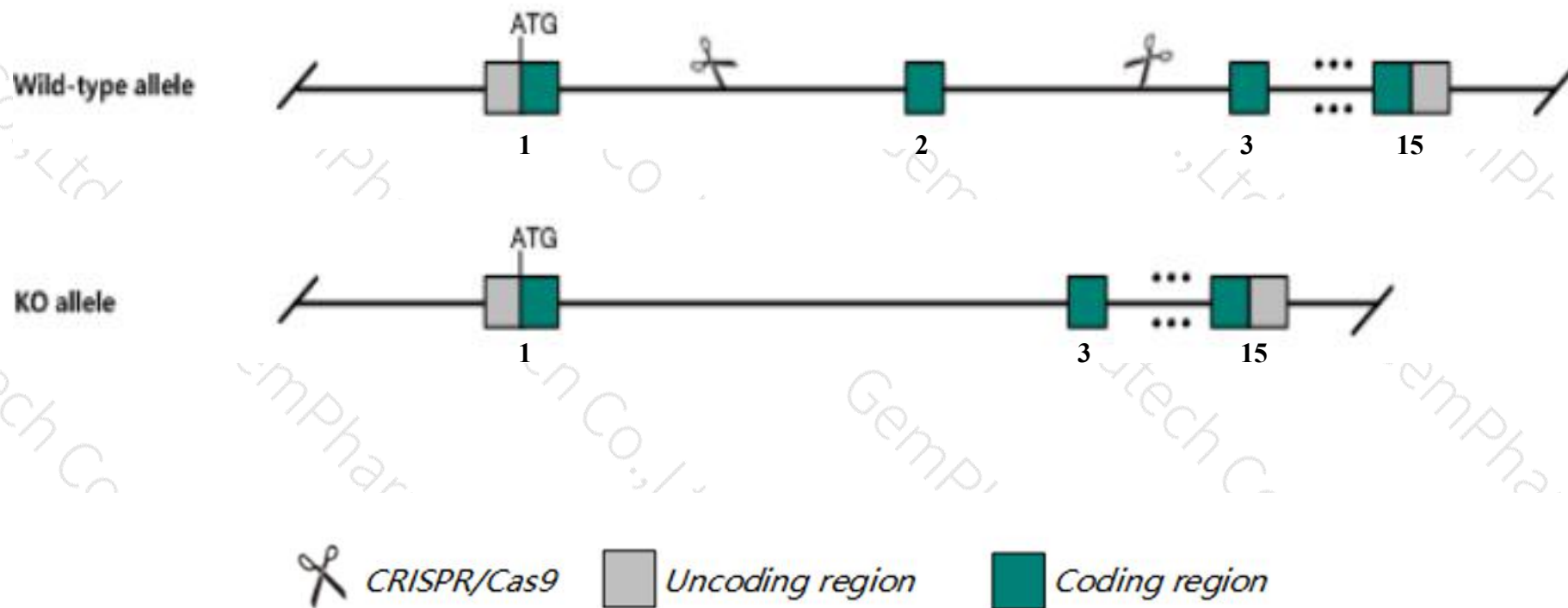
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Galnt14* gene. The schematic diagram is as follows:



- The *Galnt14* gene has 5 transcripts. According to the structure of *Galnt14* gene, exon2 of *Galnt14-201* (ENSMUST00000024858.11) transcript is recommended as the knockout region. The region contains 170bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Galnt14* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous mutant mice exhibit enhanced motor coordination during inverted screen testing when compared with controls.
- Transcript *Galnt14*-204 may not be affected.
- The *Galnt14* gene is located on the Chr17. 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)

Galnt14 polypeptide N-acetylgalactosaminyltransferase 14 [Mus musculus (house mouse)]

Gene ID: 71685, updated on 13-Mar-2020

Summary



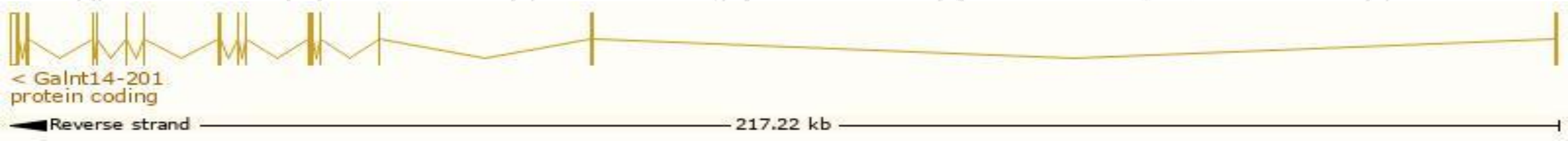
Official Symbol	Galnt14 provided by MGI
Official Full Name	polypeptide N-acetylgalactosaminyltransferase 14 provided by MGI
Primary source	MGI:MGI:1918935
See related	Ensembl:ENSMUSG00000024064
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610033M06Rik
Expression	Biased expression in kidney adult (RPKM 4.0), CNS E18 (RPKM 1.7) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

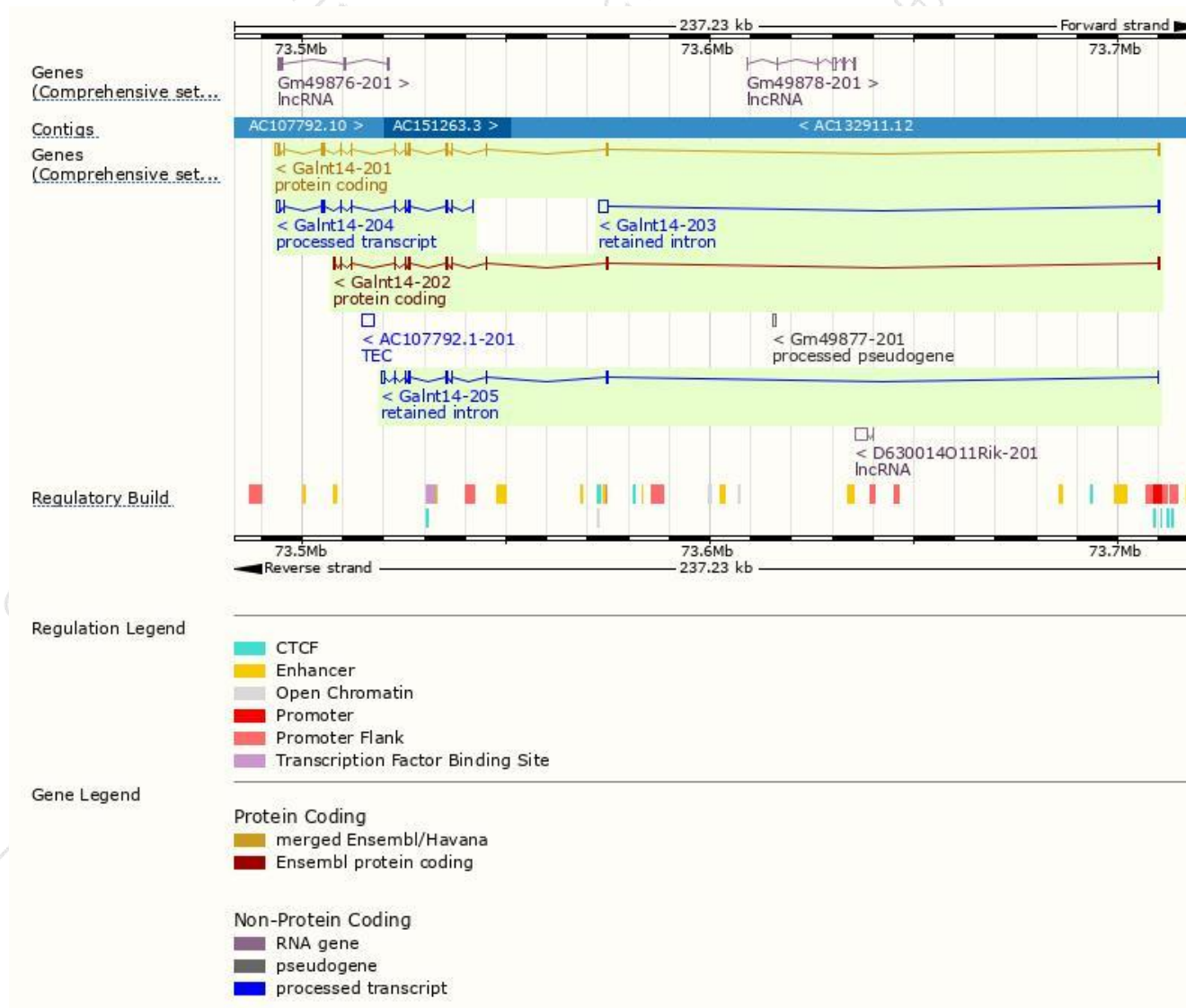
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Galnt14-201	ENSMUST00000024858.1	2990	550aa	Protein coding	CCDS28965	Q08EC9	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Galnt14-202	ENSMUST00000112591.2	1843	429aa	Protein coding	-	Q8BVG5	TSL:1 GENCODE basic
Galnt14-204	ENSMUST00000232785.1	1840	No protein	Processed transcript	-	-	
Galnt14-203	ENSMUST00000146565.1	2713	No protein	Retained intron	-	-	TSL:1
Galnt14-205	ENSMUST00000233326.1	1321	No protein	Retained intron	-	-	

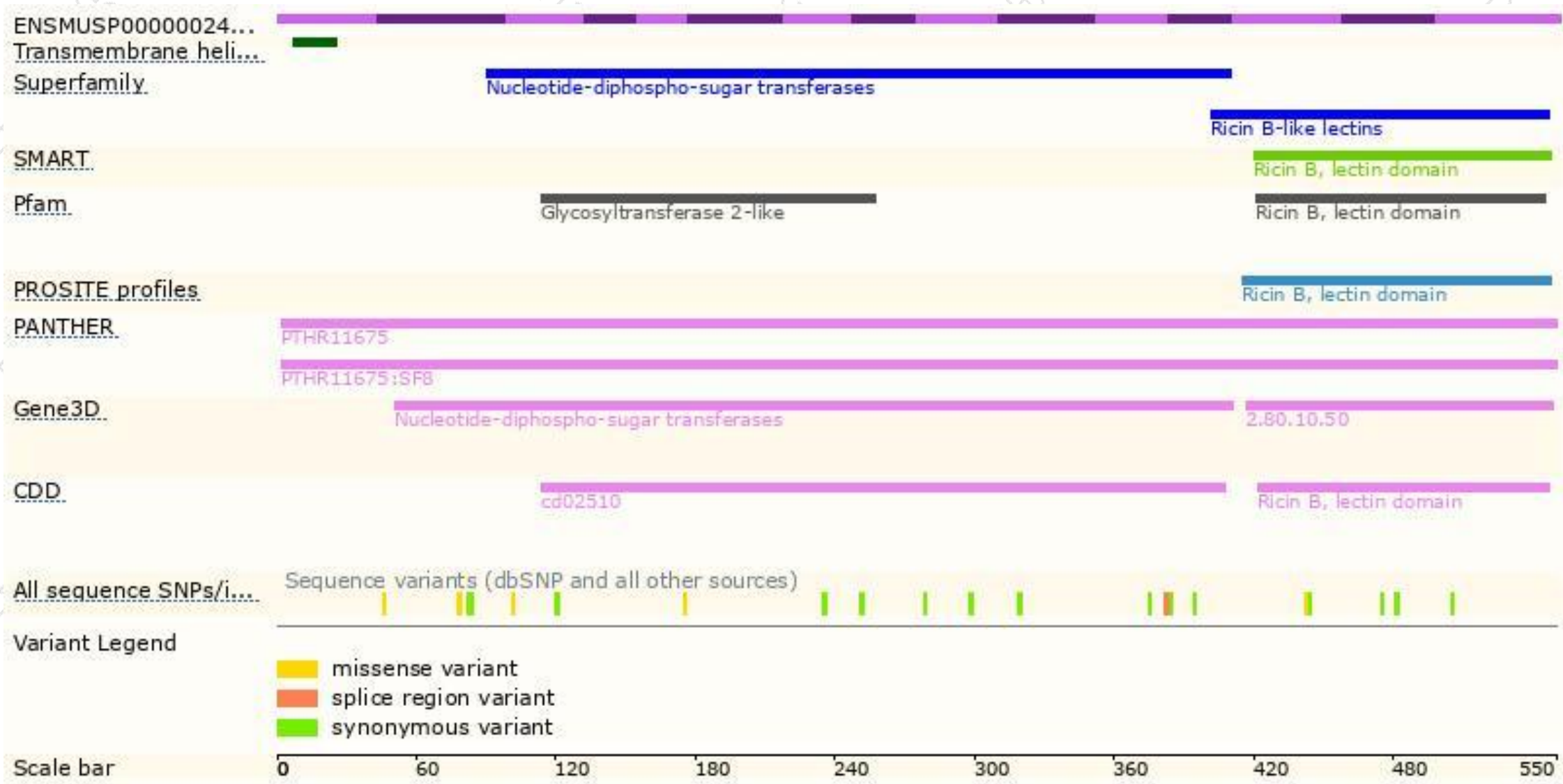
The strategy is based on the design of *Galnt14-201* transcript,The transcription is shown below



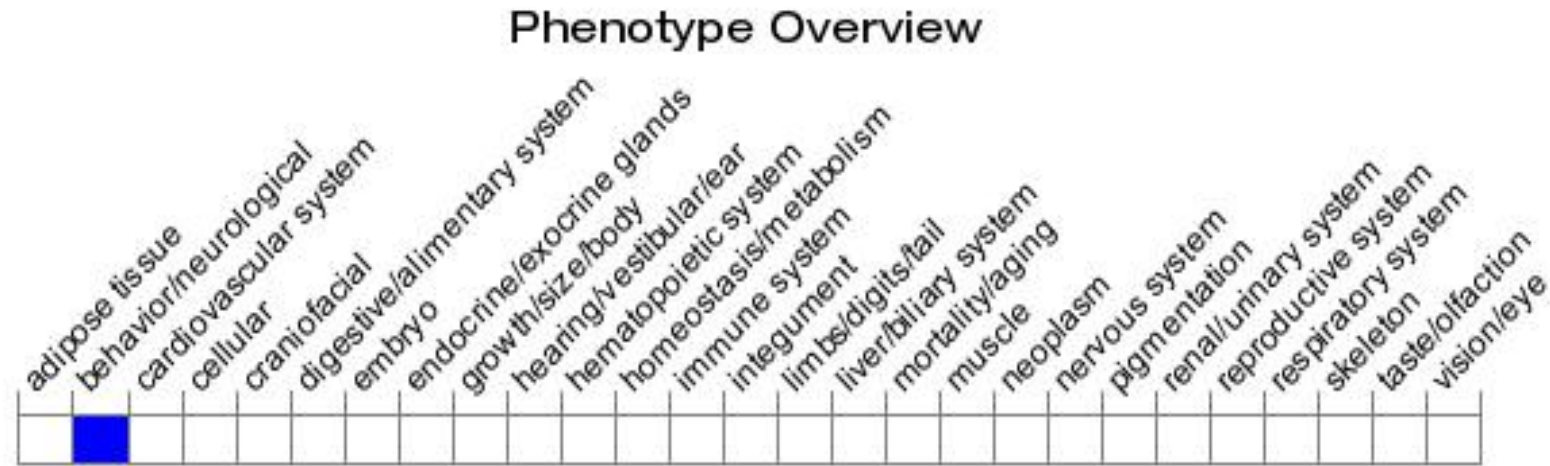
Genomic location distribution



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 mutant mice exhibit enhanced motor coordination during inverted screen testing when compared with controls.

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

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