

Sash1 Cas9-CKO Strategy

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Project Overview

Project Name

Sash1

Project type

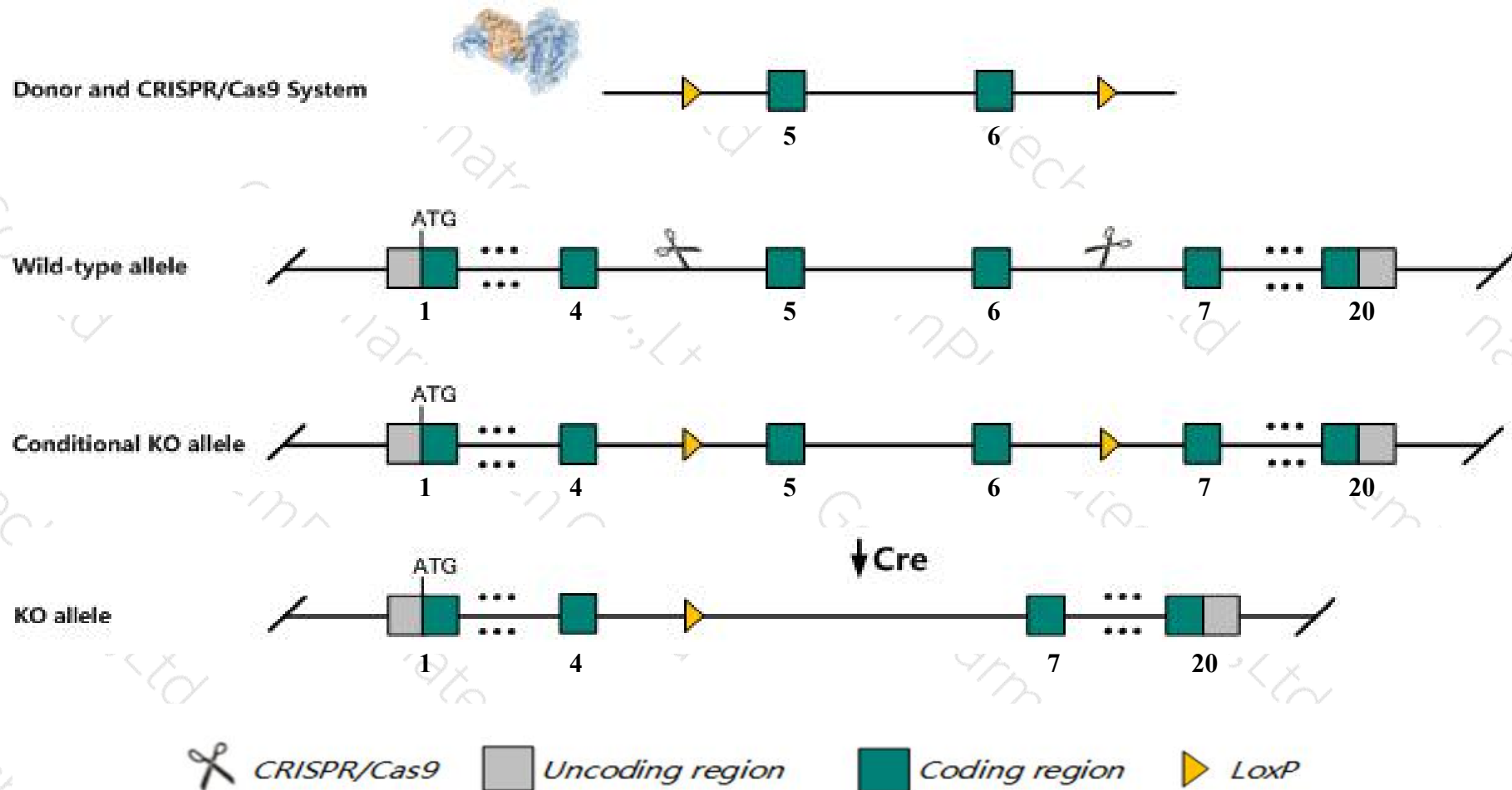
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sash1* gene. The schematic diagram is as follows:



Technical routes

- The *Sash1* gene has 4 transcripts. According to the structure of *Sash1* gene, exon5-exon6 of *Sash1*-201 (ENSMUST00000015449.5) transcript is recommended as the knockout region. The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sash1* 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.

- The *Sash1* gene is located on the Chr10. 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 N-terminal of *Sash1* gene will remain 102aa, it may remain the partial function of *Sash1* gene.
- Transcript *Sash1*-204 may not be affected. And the effect on transcript *Sash1*-202&203 is unknown.
- 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)

Sash1 SAM and SH3 domain containing 1 [Mus musculus (house mouse)]

Gene ID: 70097, updated on 19-Mar-2019

Summary



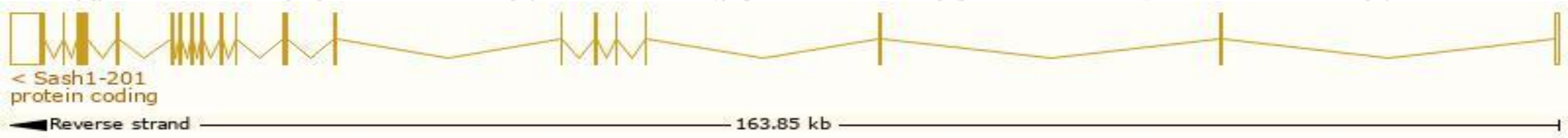
Official Symbol	Sash1 provided by MGI
Official Full Name	SAM and SH3 domain containing 1 provided by MGI
Primary source	MGI:MGI:1917347
See related	Ensembl:ENSMUSG00000015305
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1100001C18Rik, 2500002E12Rik, A330076K04Rik, mKIAA0790
Expression	Ubiquitous expression in lung adult (RPKM 10.4), subcutaneous fat pad adult (RPKM 8.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

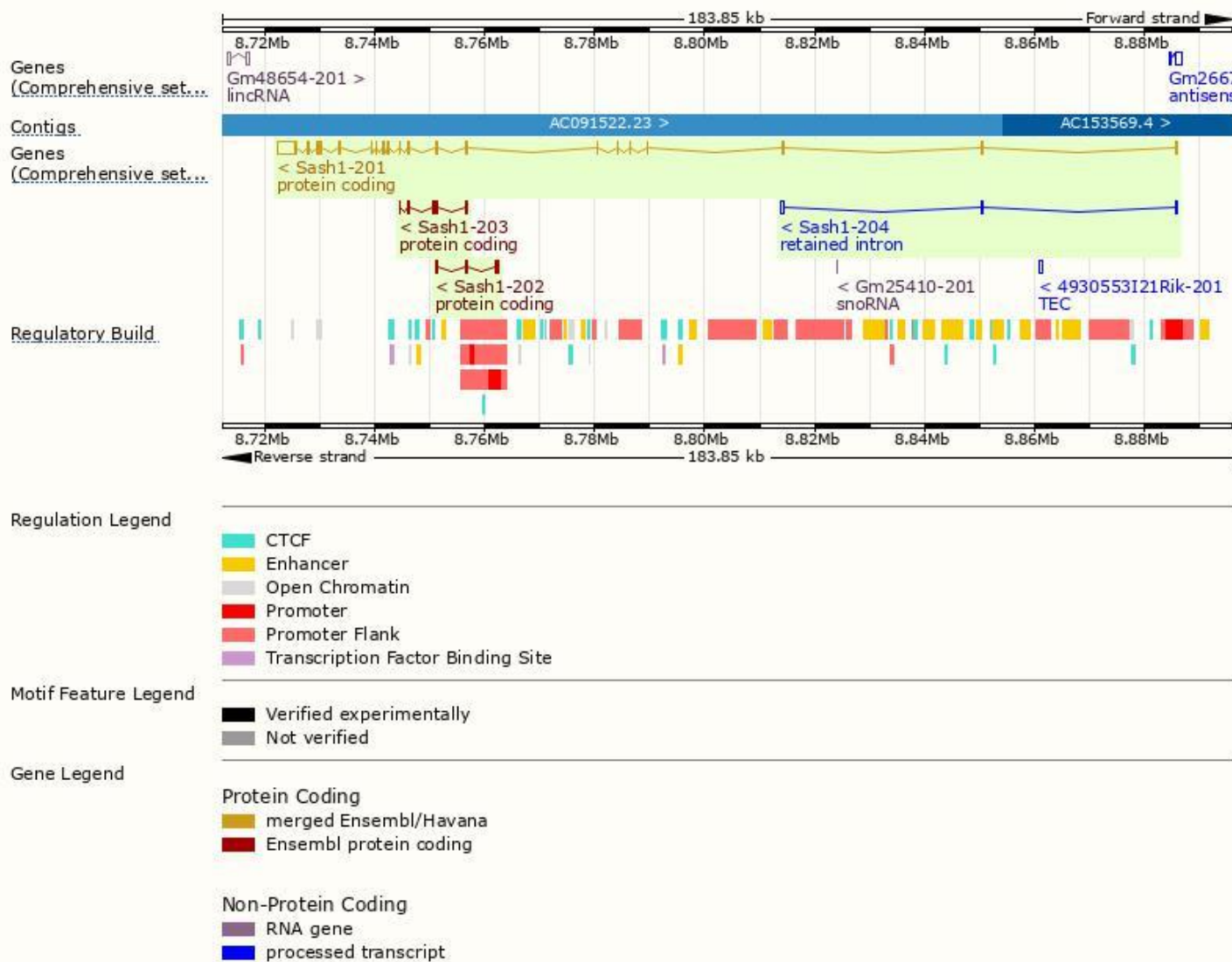
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sash1-201	ENSMUST00000015449.5	7183	1230aa	Protein coding	CCDS23692	F8VQK5	TSL:1 GENCODE basic APPRIS P1
Sash1-203	ENSMUST000000212869.1	1074	358aa	Protein coding	-	A0A1D5RMH4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sash1-202	ENSMUST000000212553.1	840	157aa	Protein coding	-	A0A1D5RM71	CDS 3' incomplete TSL:2
Sash1-204	ENSMUST000000213032.1	1078	No protein	Retained intron	-	-	TSL:1

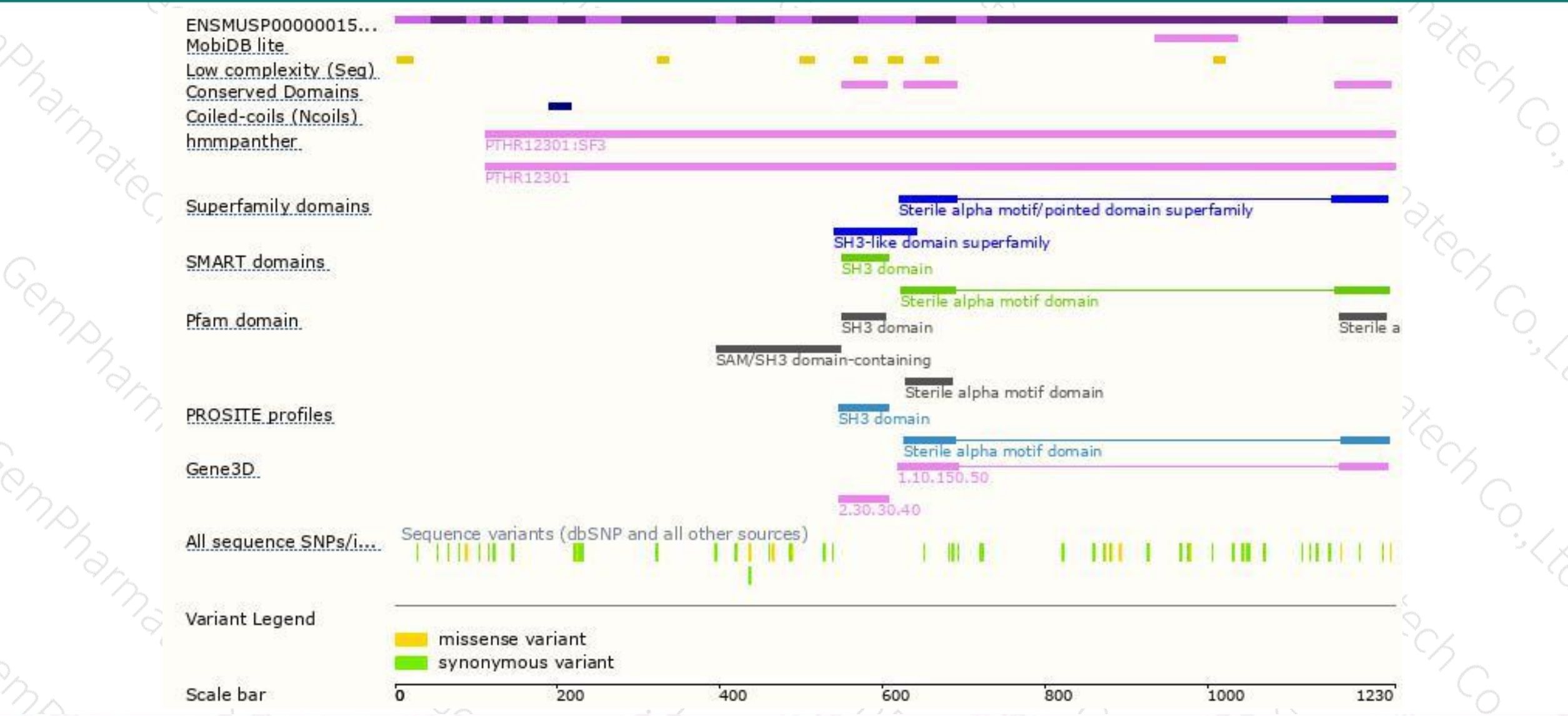
The strategy is based on the design of *Sash1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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