Spire1 Cas9-KO *Strategy*

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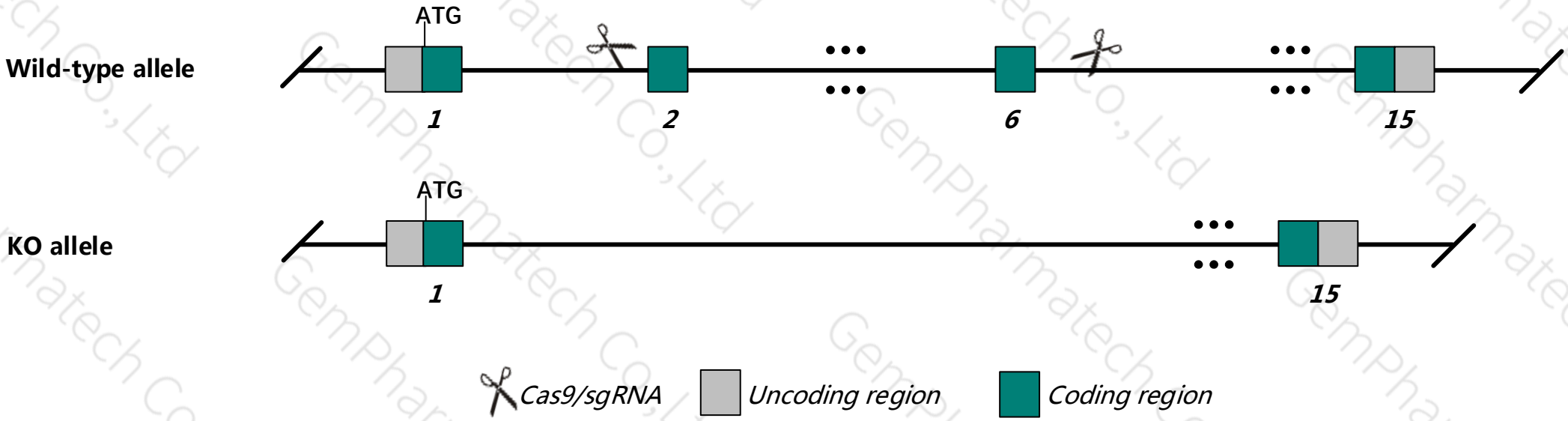
Project Overview

Project Name	***Spire1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Spire1* gene. The schematic diagram is as follows:



Technical routes

- The *Spire1* gene has 8 transcripts.According to the structure of *Spire1* gene, exon2-exon6 of *Spire1*-201 (
- ENSMUST00000045105.12) transcript is recommended as the knockout region.The region contains 586bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Spire1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9, sgRNA 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.

Notice

- According to the existing MGI data，Mice homozygous for a knock-out allele are viable and fertile with normal brain anatomy and intact visual and motor functions in both sexes, but show a male-specific increase in contextual and cued fear memory.

- The *Spire1* gene is located on the Chr18. 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）

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Spire1 spire type actin nucleation factor 1 [*Mus musculus* (house mouse)]

Gene ID: 68166, updated on 13-Mar-2020

Summary

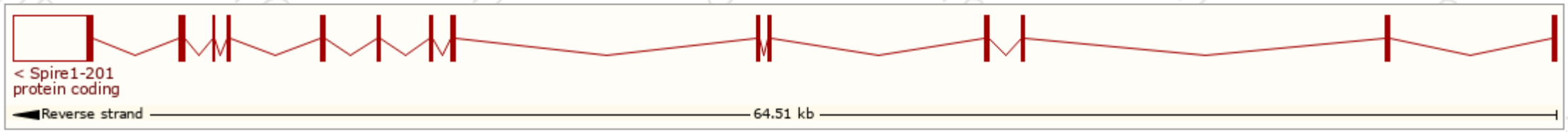
Official Symbol	Spire1 provided by MGI
Official Full Name	spire type actin nucleation factor 1 provided by MGI
Primary source	MGI:MGI:1915416
See related	Ensembl:ENSMUSG00000024533
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Spir-1; AI415299; AU022898; AW550622; 6030430B19Rik
Expression	Broad expression in cerebellum adult (RPKM 16.5), frontal lobe adult (RPKM 16.3) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

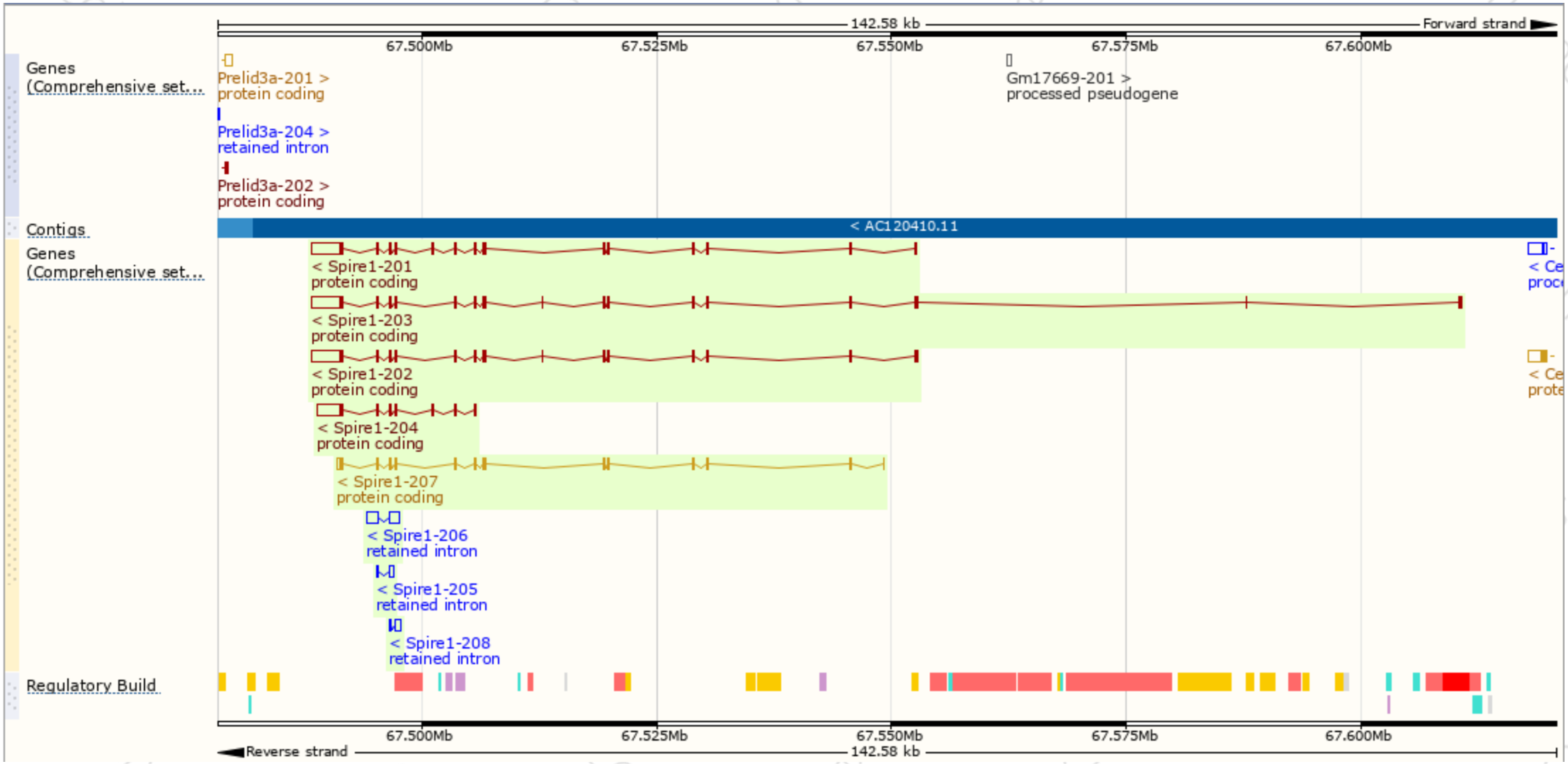
The gene has 8 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spire1-201	ENSMUST00000045105.12	5033	643aa	Protein coding	CCDS29323	D3YTL8	TSL:5 GENCODE basic
Spire1-207	ENSMUST00000224799.1	2059	515aa	Protein coding	CCDS37849	A0A286YDN9	GENCODE basic
Spire1-203	ENSMUST00000115050.9	5405	743aa	Protein coding	-	Q52KF3	TSL:1 GENCODE basic APPRIS P1
Spire1-202	ENSMUST00000082243.6	4950	598aa	Protein coding	-	Q52KF3	TSL:1 GENCODE basic
Spire1-204	ENSMUST00000224122.1	3551	344aa	Protein coding	-	A0A286YE32	CDS 5' incomplete
Spire1-206	ENSMUST00000224659.1	2251	No protein	Retained intron	-	-	-
Spire1-205	ENSMUST00000224189.1	616	No protein	Retained intron	-	-	-
Spire1-208	ENSMUST00000226000.1	612	No protein	Retained intron	-	-	-

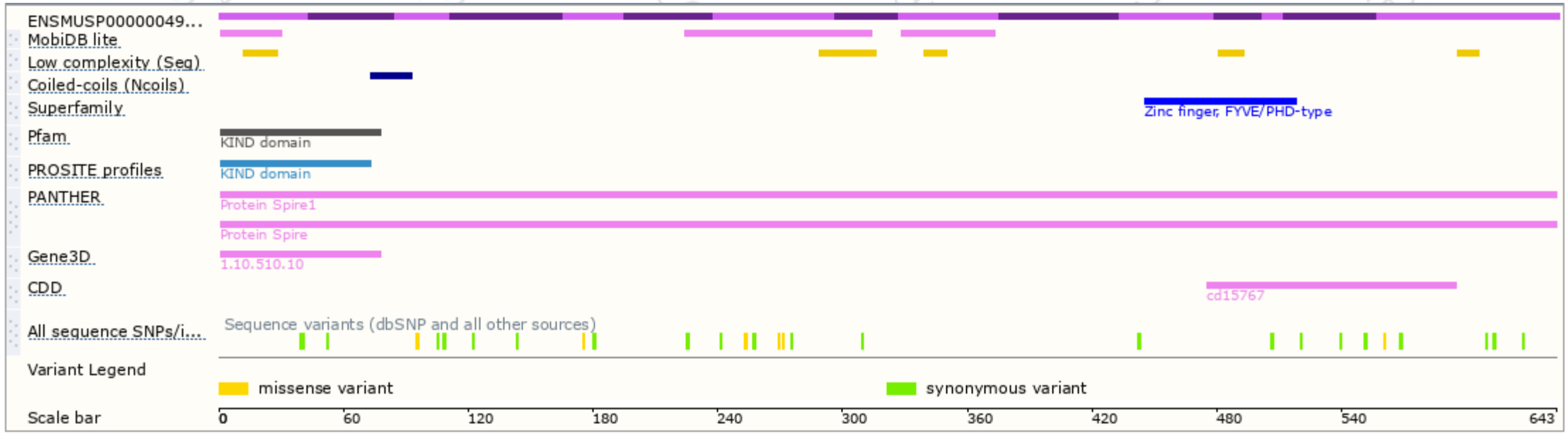
The strategy is based on the design of *Spire1*-201 transcript,The transcription is shown below



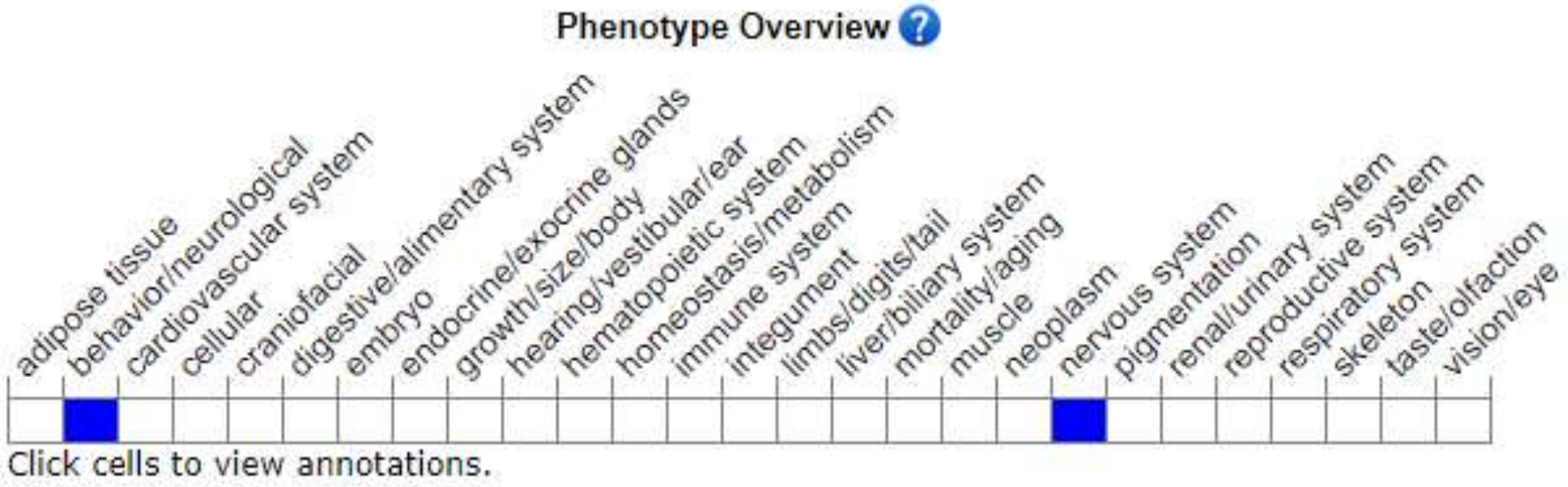
Genomic location distribution



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 are viable and fertile with normal brain anatomy and intact visual and motor functions in both sexes, but show a male-specific increase in contextual and cued fear memory.

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

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