# *Pcmt1* Cas9-KO Strategy


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**Reviewer:** Xiaojing Li


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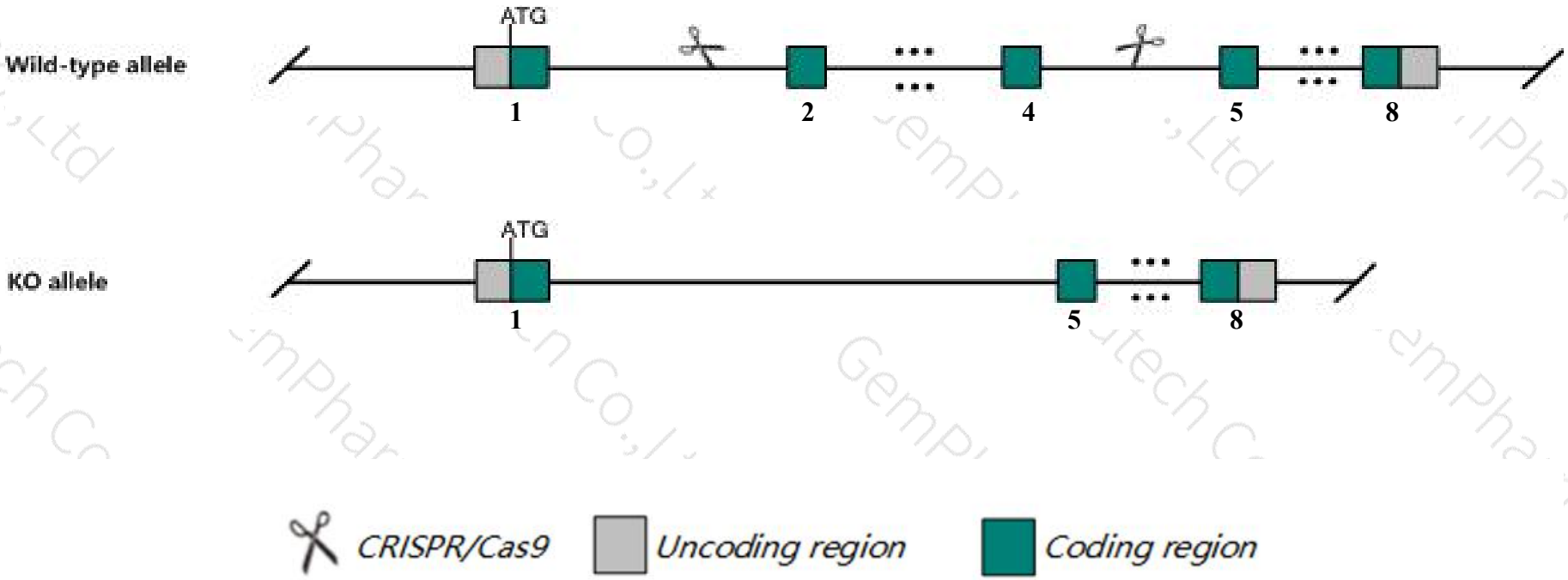
# Project Overview

| | |
|---|---|
| **Project Name** | ***Pcmt1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pcmt1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Pcmt1* gene has 10 transcripts. According to the structure of *Pcmt1* gene, exon2-exon4 of *Pcmt1-208* (ENSMUST00000162606.7) transcript is recommended as the knockout region.The region contains 242bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pcmt1* gene. The brief process is as follows: CRISPR/Cas9 system v

# Notice

- According to the existing MGI data,Homozygous disruption of this gene causes accumulation of modified proteins, growth retardation and fatal epileptic seizures. Homozygotes for one null allele also show a small spleen, altered lipid, hormone, mineral and enzyme profiles, kyphosis, enlarged brain and abnormal dendritic arborizations.

- The *Pcmt1* 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.

- 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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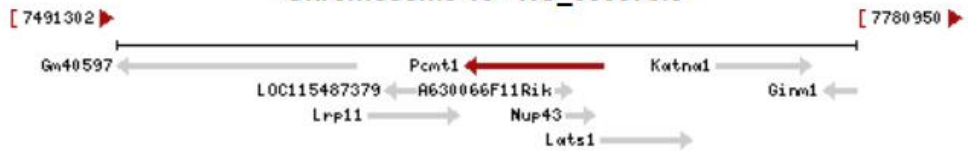
## Pcmt1 protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 18537, updated on 12-Aug-2019

### Summary

| | |
|---|---|
| **Official Symbol** | Pcmt1 provided by MGI |
| **Official Full Name** | protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 provided by MGI |
| **Primary source** | MGI:MGI:97502 |
| **See related** | Ensembl:ENSMUSG00000019795 |
| **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** | PIMT; C79501 |
| **Expression** | Ubiquitous expression in testis adult (RPKM 29.8), cerebellum adult (RPKM 17.1) and 27 other tissues See more |
| **Orthologs** | human all |

**Chromosome 10 - NC_000076.6**

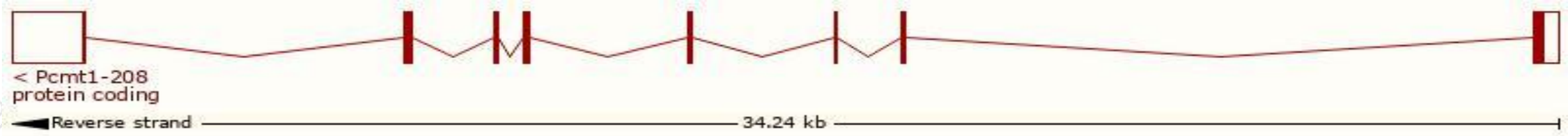


# Transcript information（Ensembl）

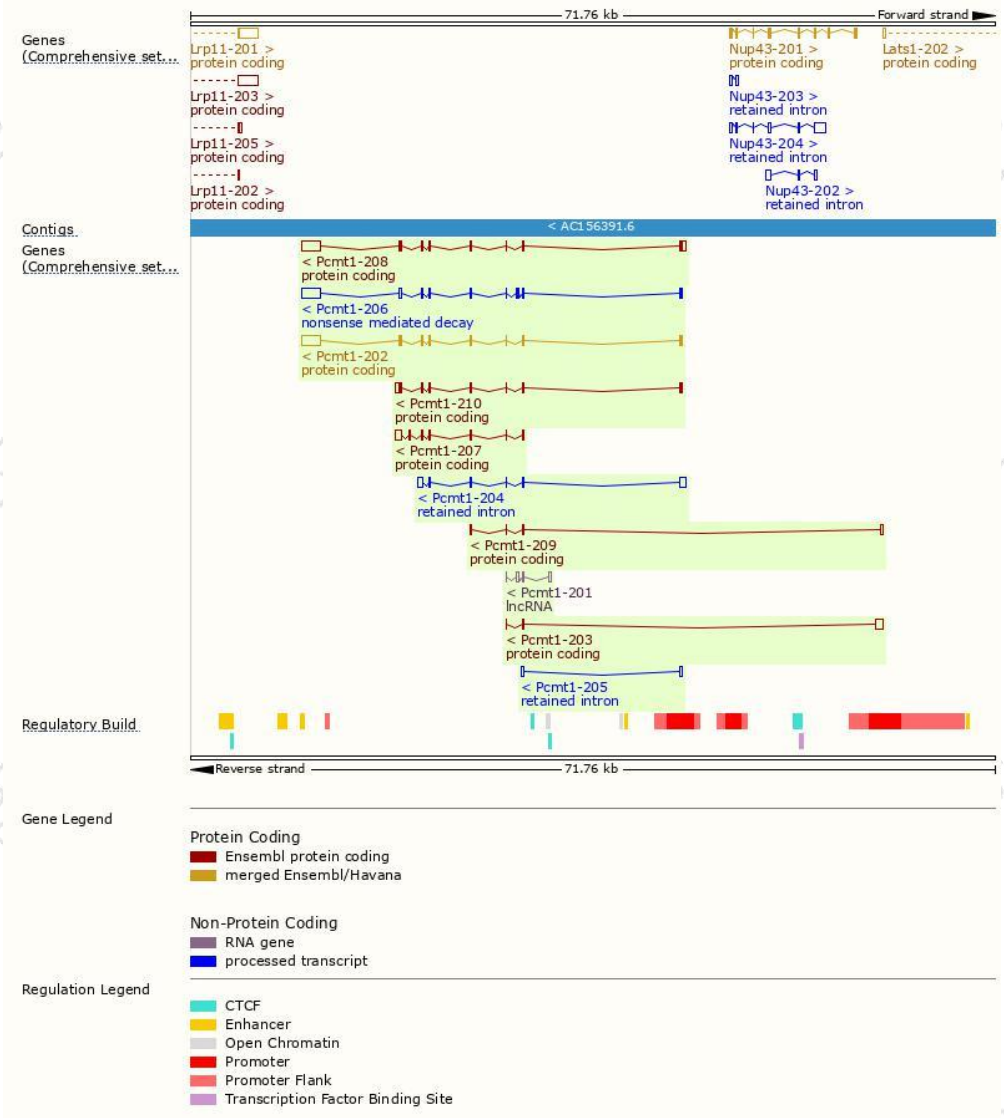
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Pcmt1-208 | ENSMUST00000162606.7 | 2757 | 286aa | Protein coding | CCDS83677 | E0CYV0 | TSL:1 GENCODE basic APPRIS ALT2 |
| Pcmt1-202 | ENSMUST00000159917.7 | 2491 | 285aa | Protein coding | CCDS23687 | E9PWE0 | TSL:1 GENCODE basic APPRIS P3 |
| Pcmt1-210 | ENSMUST00000163085.7 | 1132 | 271aa | Protein coding | - | F7D432 | CDS 5' incomplete TSL:1 |
| Pcmt1-207 | ENSMUST00000161428.7 | 1073 | 177aa | Protein coding | - | F6V9F1 | CDS 5' incomplete TSL:1 |
| Pcmt1-203 | ENSMUST00000159977.1 | 756 | 23aa | Protein coding | - | E0CYJ5 | CDS 3' incomplete TSL:5 |
| Pcmt1-209 | ENSMUST00000162682.7 | 465 | 65aa | Protein coding | - | E0CYF2 | CDS 3' incomplete TSL:3 |
| Pcmt1-206 | ENSMUST00000161123.7 | 2607 | 111aa | Nonsense mediated decay | - | F6TXE3 | CDS 5' incomplete TSL:5 |
| Pcmt1-204 | ENSMUST00000160250.1 | 1369 | No protein | Retained intron | - | - | TSL:1 |
| Pcmt1-205 | ENSMUST00000160517.1 | 381 | No protein | Retained intron | - | - | TSL:2 |
| Pcmt1-201 | ENSMUST00000159835.7 | 514 | No protein | lncRNA | - | - | TSL:3 |

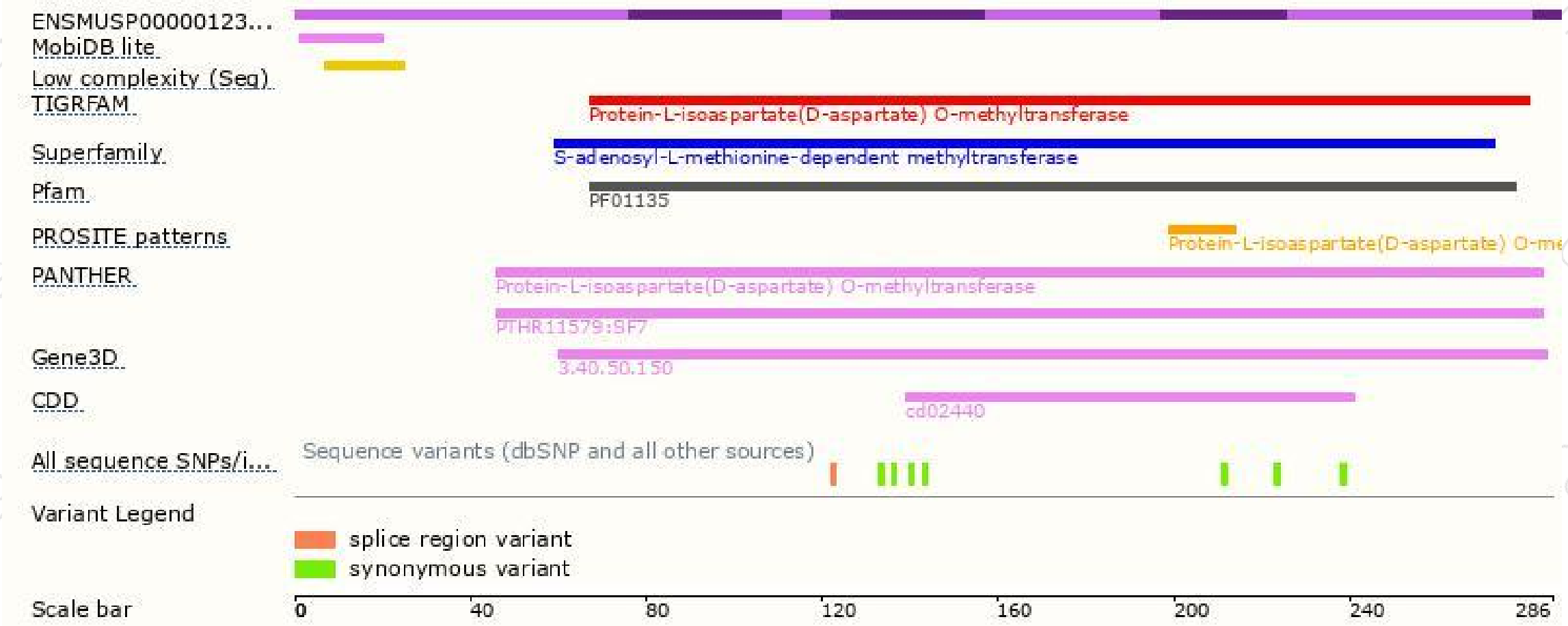
The strategy is based on the design of *Pcmt1-208* transcript,The transcription is shown below



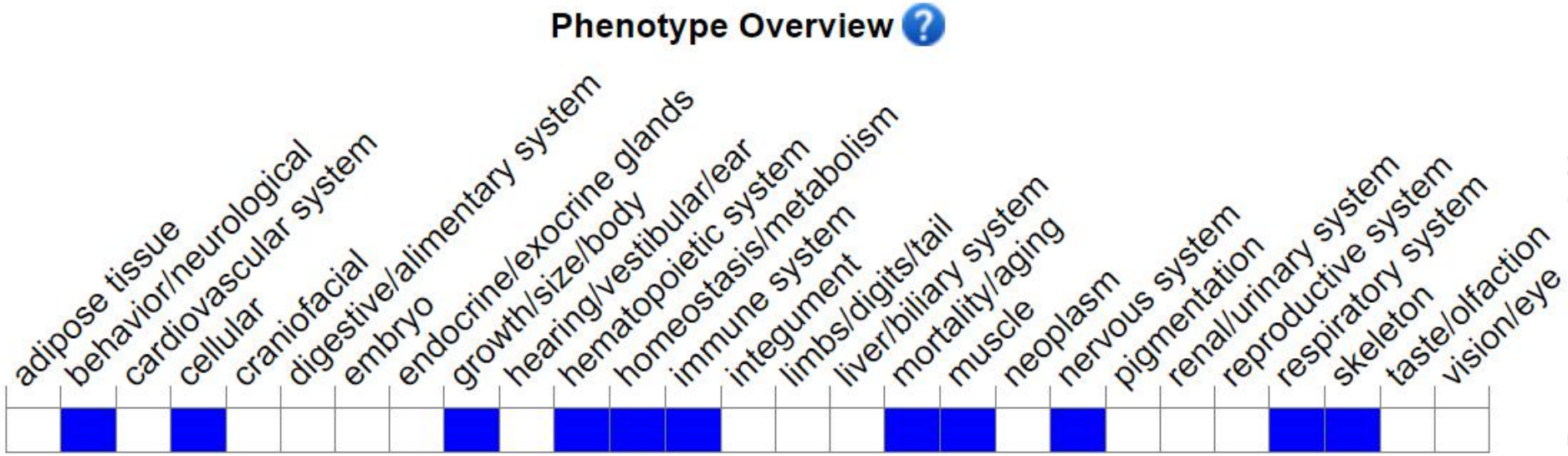
# Genomic location distribution



# 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/).*

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

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