Ptpn9 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

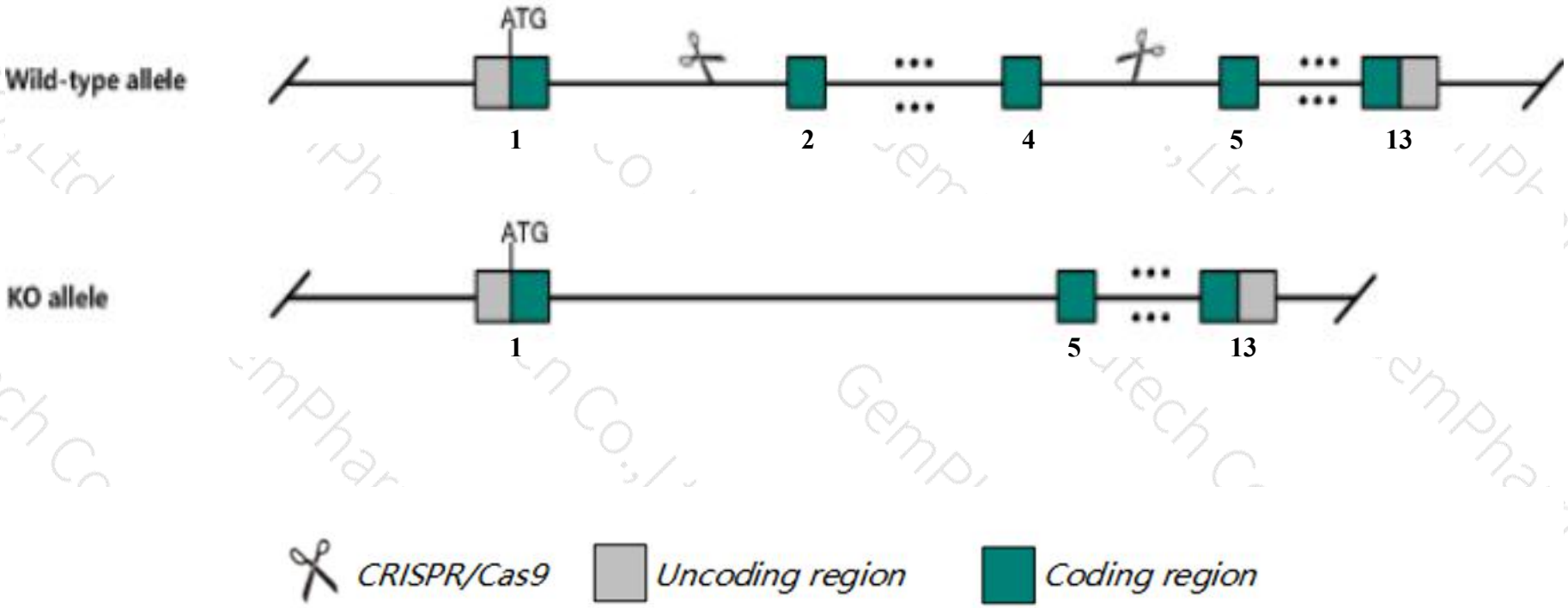
Design Date: 2020-5-6

Project Overview

Project Name	***Ptpn9***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptpn9* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ptpn9* gene has 4 transcripts. According to the structure of *Ptpn9* gene, exon2-exon4 of *Ptpn9-201* (ENSMUST00000034832.7) transcript is recommended as the knockout region.The region contains 359bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ptpn9* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a null allele display hemorrhages, craniofacial anomalies, neural tube defects such as exencephaly and meningomyeloceles, cerebral infarctions, abnormal bone development, and >90% late embryonic lethality in addition to severe defectsin t lymphocyte and platelet activation.
- Transcript *Ptpn9-202, 203* may not be affected.
- The *Ptpn9* gene is located on the Chr9. 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）

集萃药康 GemPharmatech

Ptpn9 protein tyrosine phosphatase, non-receptor type 9 [Mus musculus (house mouse)]

Gene ID: 56294, updated on 13-Mar-2020

Summary

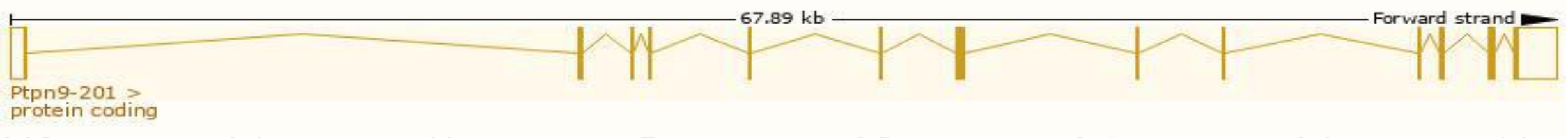
Official Symbol	Ptpn9 provided by MGI
Official Full Name	protein tyrosine phosphatase, non-receptor type 9 provided by MGI
Primary source	MGI:MGI:1928376
See related	Ensembl:ENSMUSG00000032290
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MEG2
Expression	Ubiquitous expression in adrenal adult (RPKM 23.8), limb E14.5 (RPKM 15.2) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

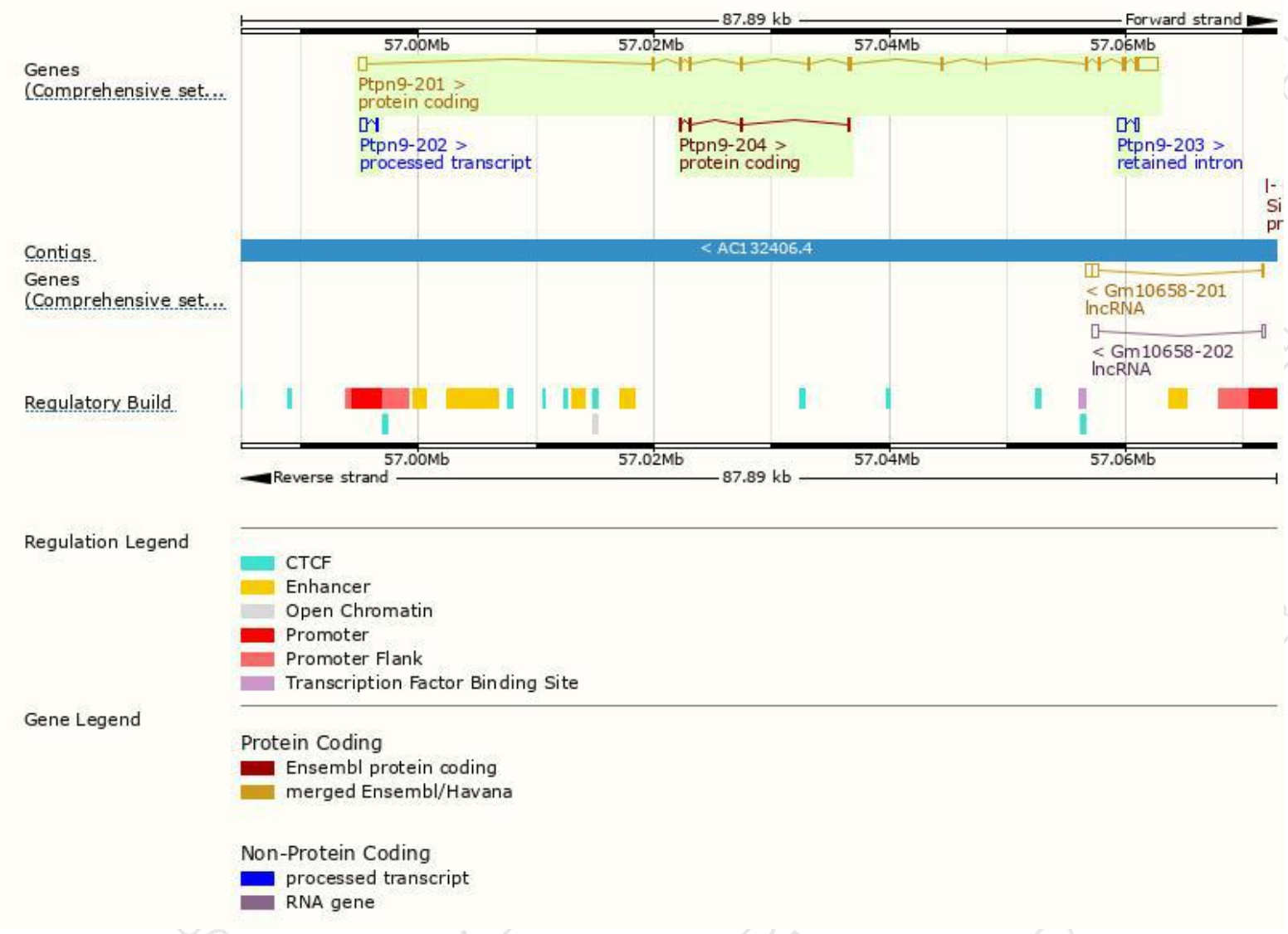
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptpn9-201	ENSMUST00000034832.7	4101	593aa	Protein coding	CCDS23215	O35239 Q2M4G8	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
Ptpn9-204	ENSMUST00000216034.1	434	144aa	Protein coding	-	A0A1L1STP0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ptpn9-202	ENSMUST00000213500.1	701	No protein	Processed transcript	-	-	TSL:3
Ptpn9-203	ENSMUST00000215707.1	886	No protein	Retained intron	-	-	TSL:1

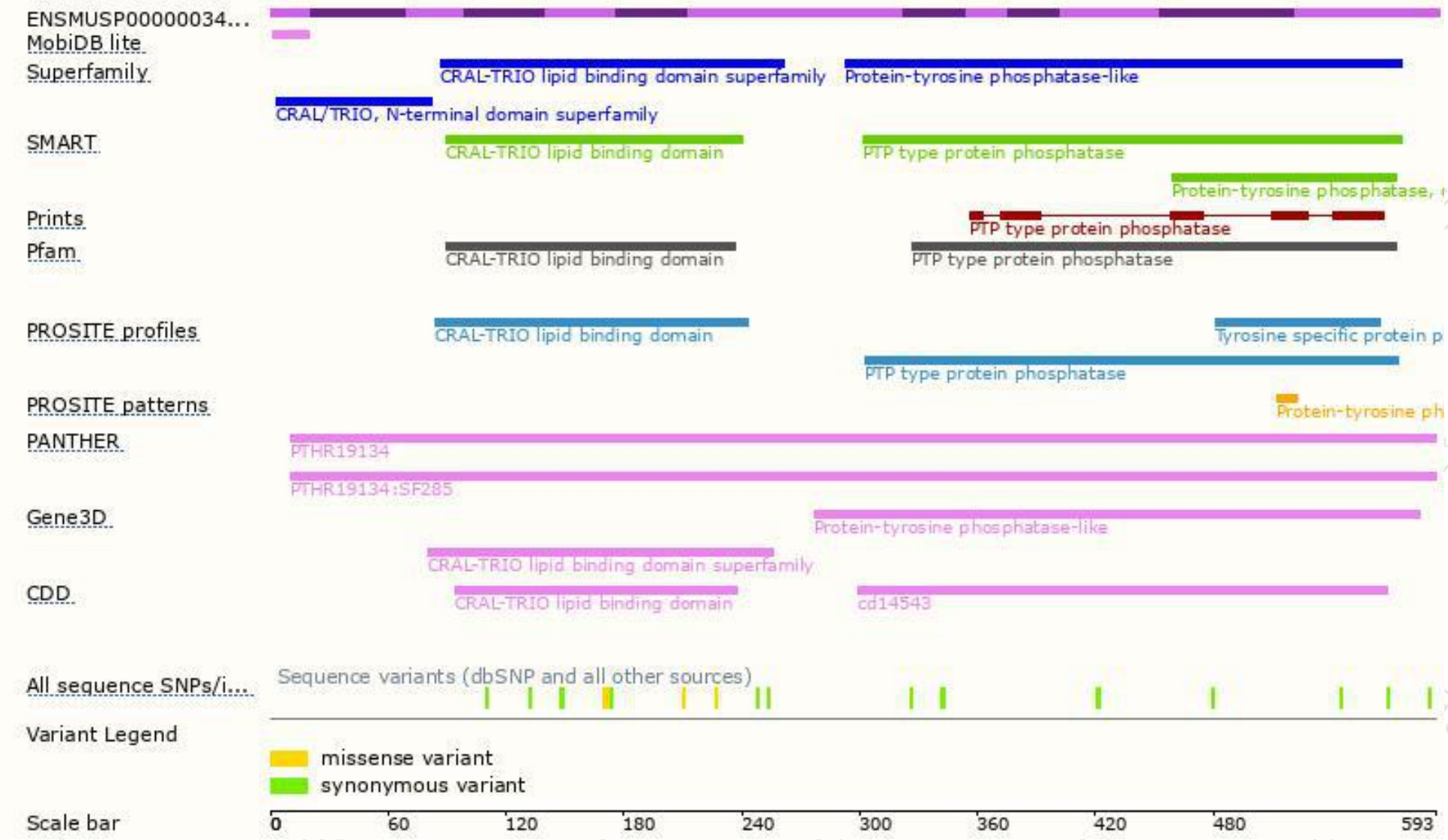
The strategy is based on the design of *Ptpn9-201* transcript,the transcription is shown below:



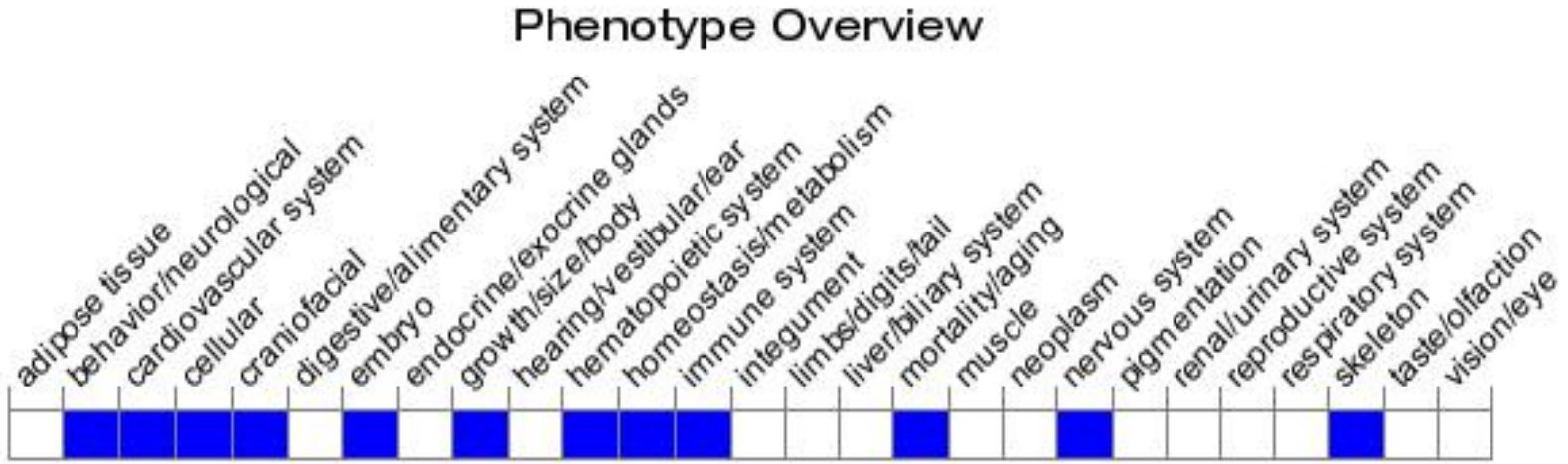
Genomic location distribution



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 null allele display hemorrhages, craniofacial anomalies, neural tube defects such as exencephaly and meningomyeloceles, cerebral infarctions, abnormal bone development, and >90% late embryonic lethality in addition to severe defectsin T lymphocyte and platelet activation.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd