

# *Bgn* Cas9-KO Strategy

Designer: Lixin Lv

# Project Overview

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**Project Name**

*Bgn*

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**Project type**

**Cas9-KO**

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**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Bgn* gene has 8 transcripts. According to the structure of *Bgn* gene, exon2-exon8 of *Bgn-201* (ENSMUST00000033741.14) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bgn* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mutants display reduced growth and develop age-dependent osteopenia. Age-related osteoporosis is associated with defects in bone marrow stromal cells, including increased apoptosis, reduced numbers of colony-forming units-fibroblastic (CFU-F), and decreased collagen production.
- The *Bgn* gene is located on the ChrX. 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)

## Bgn biglycan [Mus musculus (house mouse)]

Gene ID: 12111, updated on 3-Feb-2019

### Summary



**Official Symbol** Bgn provided by [MGI](#)

**Official Full Name** biglycan provided by [MGI](#)

**Primary source** [MGI:MGI:88158](#)

**See related** [Ensembl:ENSMUSG00000031375](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** BG, DSPG1, PG-S1, PGI, SLRR1A

**Summary** This gene encodes a small, leucine-rich repeat proteoglycan that plays important roles in bone mineralization and connective tissue metabolism. The encoded preproprotein undergoes post-translational processing during which chondroitin sulfate or dermatan sulfate chains are attached before incorporation into the extracellular matrix. Mice lacking the encoded protein exhibit reduced growth rate and acquire diminished bone mass progressively with age. [provided by RefSeq, Oct 2015]

**Expression** Broad expression in bladder adult (RPKM 238.1), lung adult (RPKM 231.1) and 22 other tissues [See more](#)

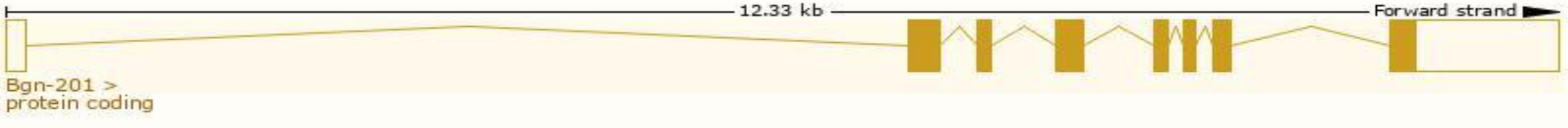
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

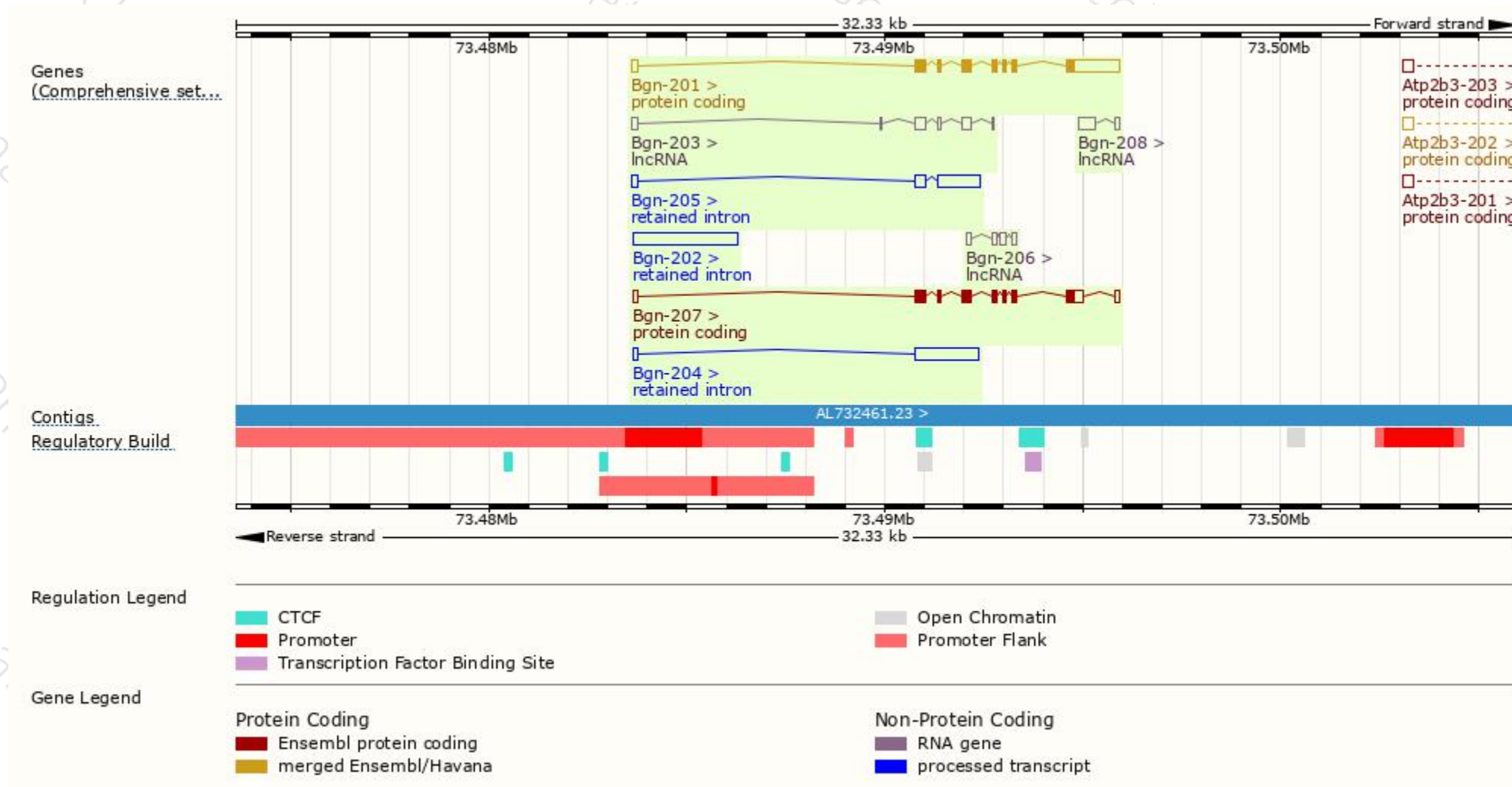
The gene has 8 transcripts,all transcripts are shown below:

| Name    | Transcript ID                         | bp   | Protein               | Biotype              | CCDS                      | UniProt                       | Flags                         |
|---------|---------------------------------------|------|-----------------------|----------------------|---------------------------|-------------------------------|-------------------------------|
| Bgn-201 | <a href="#">ENSMUST00000033741.14</a> | 2419 | <a href="#">369aa</a> | Protein coding       | <a href="#">CCDS30204</a> | <a href="#">P28653 Q3TNY9</a> | TSL:1 GENCODE basic APPRIS P1 |
| Bgn-207 | <a href="#">ENSMUST00000169489.1</a>  | 1574 | <a href="#">369aa</a> | Protein coding       | <a href="#">CCDS30204</a> | <a href="#">P28653 Q3TNY9</a> | TSL:2 GENCODE basic APPRIS P1 |
| Bgn-203 | <a href="#">ENSMUST00000133394.7</a>  | 828  | No protein            | Processed transcript | -                         | -                             | TSL:3                         |
| Bgn-208 | <a href="#">ENSMUST00000183174.1</a>  | 548  | No protein            | Processed transcript | -                         | -                             | TSL:3                         |
| Bgn-206 | <a href="#">ENSMUST00000155231.1</a>  | 460  | No protein            | Processed transcript | -                         | -                             | TSL:3                         |
| Bgn-202 | <a href="#">ENSMUST00000130873.2</a>  | 2666 | No protein            | Retained intron      | -                         | -                             | TSL:NA                        |
| Bgn-204 | <a href="#">ENSMUST00000140803.1</a>  | 1728 | No protein            | Retained intron      | -                         | -                             | TSL:2                         |
| Bgn-205 | <a href="#">ENSMUST00000141945.1</a>  | 1473 | No protein            | Retained intron      | -                         | -                             | TSL:2                         |

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

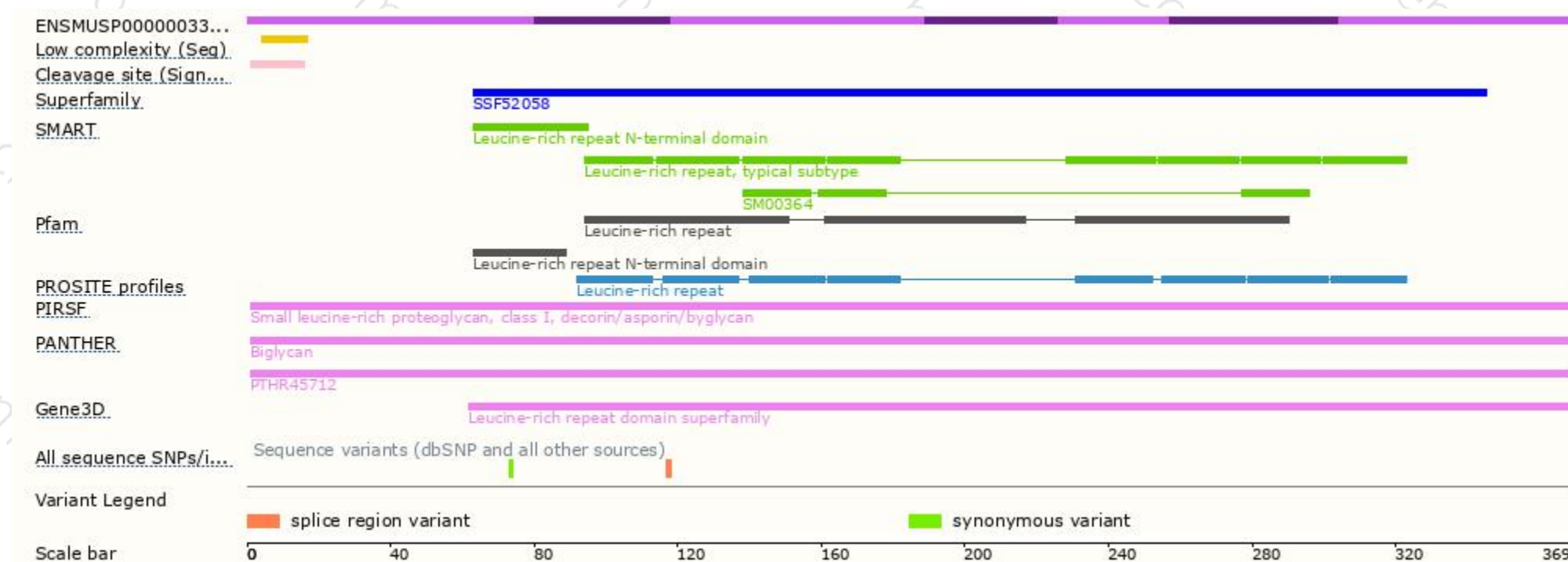


# Genomic location distribution

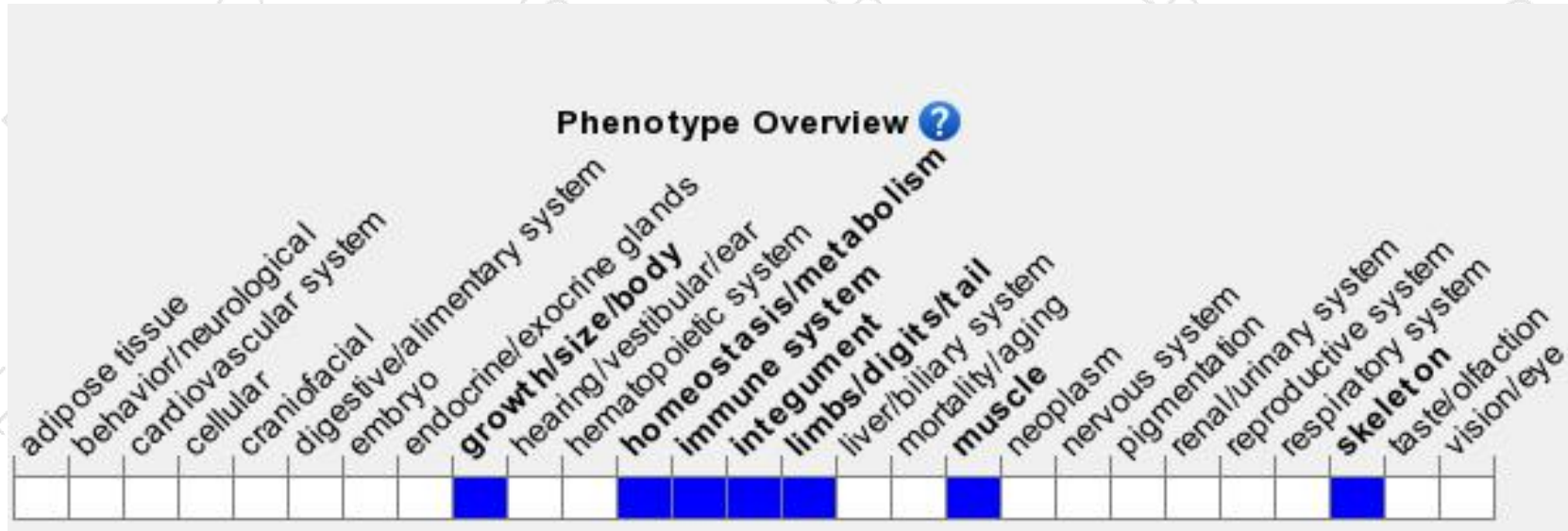




# Protein domain



# 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 null mutants display reduced growth and develop age-dependent osteopenia.

Age-related osteoporosis is associated with defects in bone marrow stromal cells, including increased apoptosis, reduced numbers of colony-forming units-fibroblastic (CFU-F), and decreased collagen production.

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

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