

# *Scarf1* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Scarf1*

**Project type**

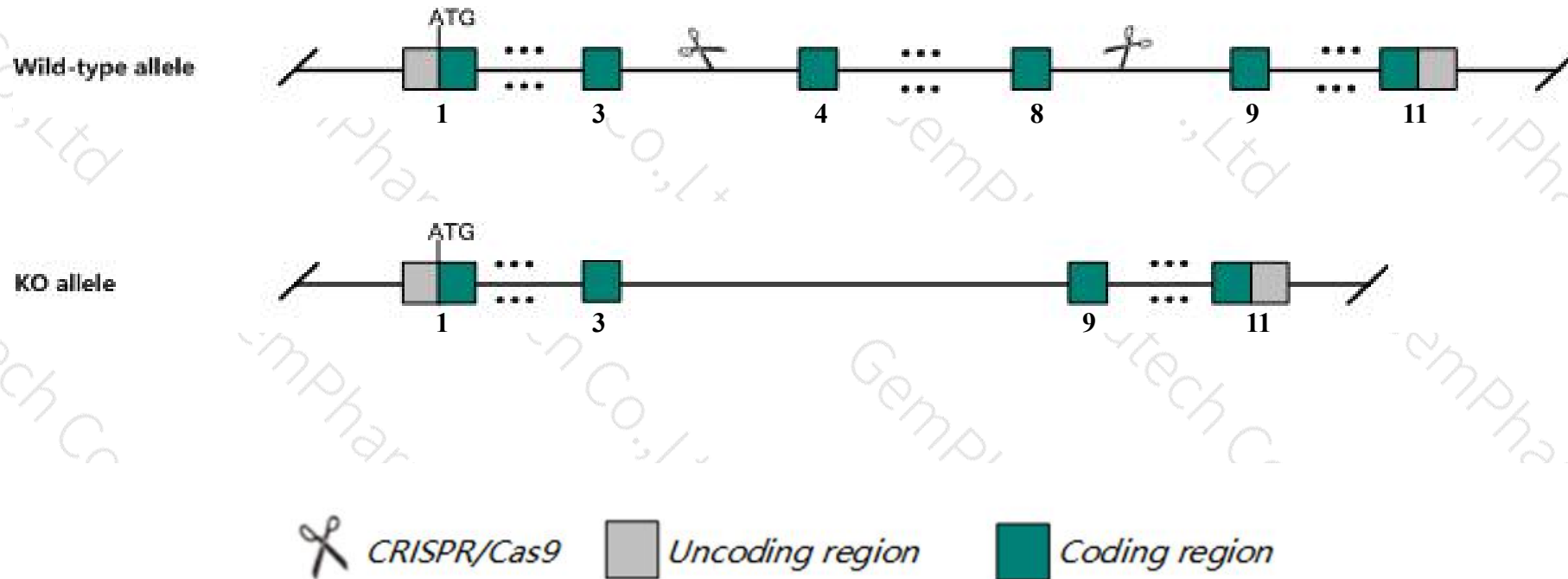
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scarf1* gene. The schematic diagram is as follows:



- The *Scarf1* gene has 3 transcripts. According to the structure of *Scarf1* gene, exon4-exon8 of *Scarf1-201* (ENSMUST00000042808.12) transcript is recommended as the knockout region. The region contains 1093bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Scarf1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice are viable and fertile with no abnormalities detected in plasma glucose, cholesterol, or triglycerides, or in the brain, lung, heart, kidney, liver, or testes. Mice homozygous for a targeted allele exhibit impaired clearance of apoptotic cells and autoimmune disease.
- The N-terminal of *Scarfl* gene will remain several amino acids, it may remain the partial function of *Scarfl* gene.
- The knockout region is near to the C-terminal of *Rilp* gene, this strategy may influence the regulatory function of the C-terminal of *Rilp* gene.
- The *Scarfl* gene is located on the Chr11. 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)

## Scarf1 scavenger receptor class F, member 1 [ *Mus musculus* (house mouse) ]

Gene ID: 380713, updated on 12-Aug-2019

### Summary

- Official Symbol** Scarf1 provided by [MGI](#)
- Official Full Name** scavenger receptor class F, member 1 provided by [MGI](#)
- Primary source** [MGI:MGI:2449455](#)
- See related** [Ensembl:ENSMUSG00000038188](#)
- 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** SREC; SREC-I; AA986099; mKIAA0149
- Expression** Broad expression in lung adult (RPKM 24.0), adrenal adult (RPKM 13.3) and 24 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

### Genomic context

**Location:** 11; 11 B5 See Scarf1 in [Genome Data Viewer](#)

**Exon count:** 10

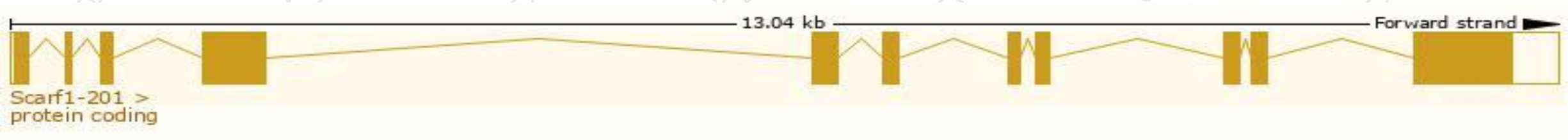
| Annotation release  | Status            | Assembly                                       | Chr | Location                         |
|---------------------|-------------------|--|-----|----------------------------------|
| <a href="#">108</a> | current           | GRCm38.p6 ( <a href="#">GCF_000001635.26</a> ) | 11  | NC_000077.6 (75513489..75526582) |
| Build 37.2          | previous assembly | MGSCv37 ( <a href="#">GCF_000001635.18</a> )   | 11  | NC_000077.5 (75327043..75340082) |

# Transcript information (Ensembl)

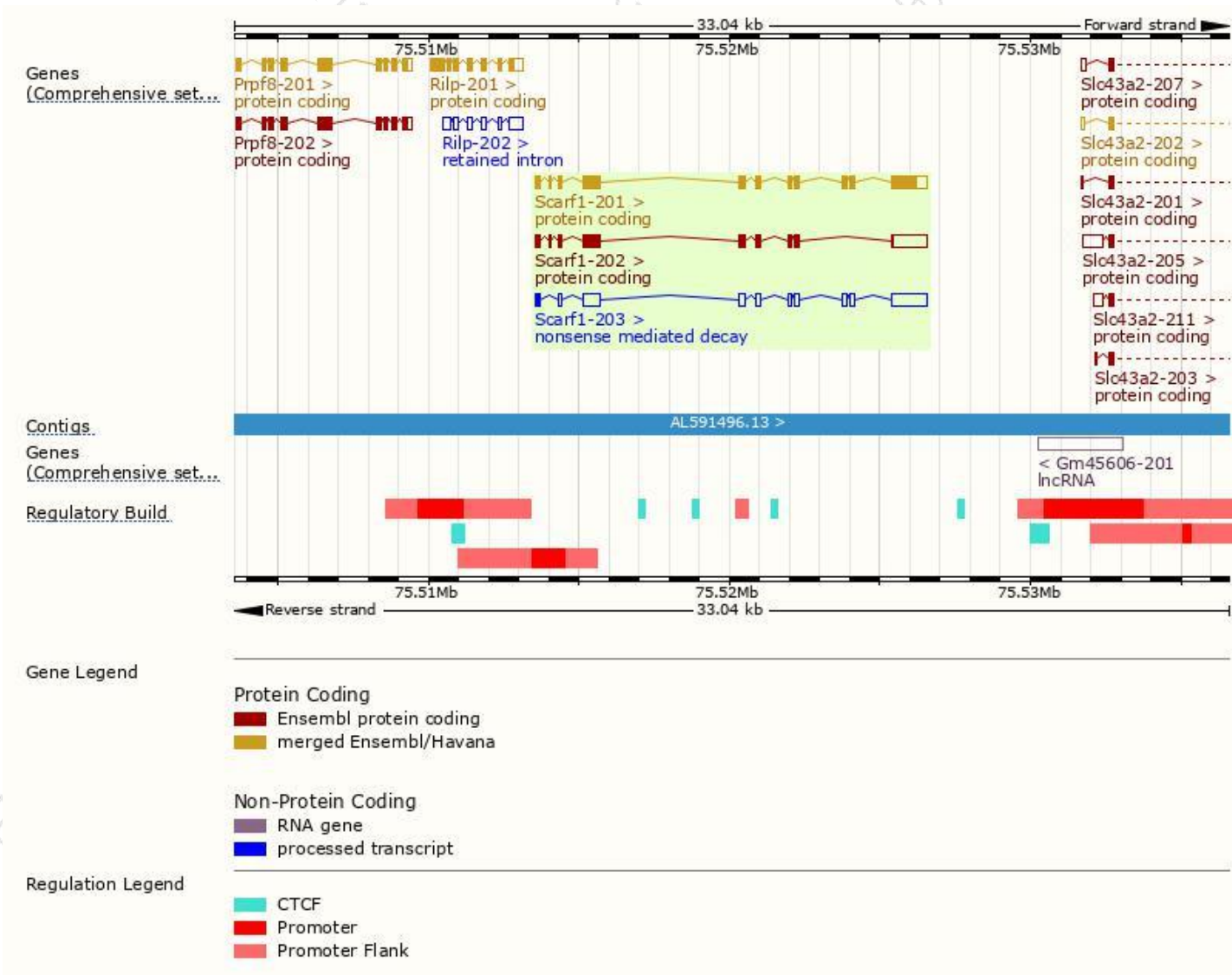
The gene has 3 transcripts,all transcripts are shown below:

| Name       | Transcript ID                         | bp   | Protein               | Biotype                 | CCDS                      | UniProt                | Flags                           |
|------------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|---------------------------------|
| Scarf1-201 | <a href="#">ENSMUST00000042808.12</a> | 2887 | <a href="#">820aa</a> | Protein coding          | <a href="#">CCDS25050</a> | <a href="#">Q5ND28</a> | TSL:1 GENCODE basic APPRIS P2   |
| Scarf1-202 | <a href="#">ENSMUST00000118243.1</a>  | 2617 | <a href="#">478aa</a> | Protein coding          | -                         | <a href="#">B7ZC28</a> | TSL:1 GENCODE basic APPRIS ALT2 |
| Scarf1-203 | <a href="#">ENSMUST00000123819.1</a>  | 2789 | <a href="#">40aa</a>  | Nonsense mediated decay | -                         | <a href="#">D6RJK6</a> | TSL:1                           |

The strategy is based on the design of *Scarf1-201* transcript,The transcription is shown below



# Genomic location distribution

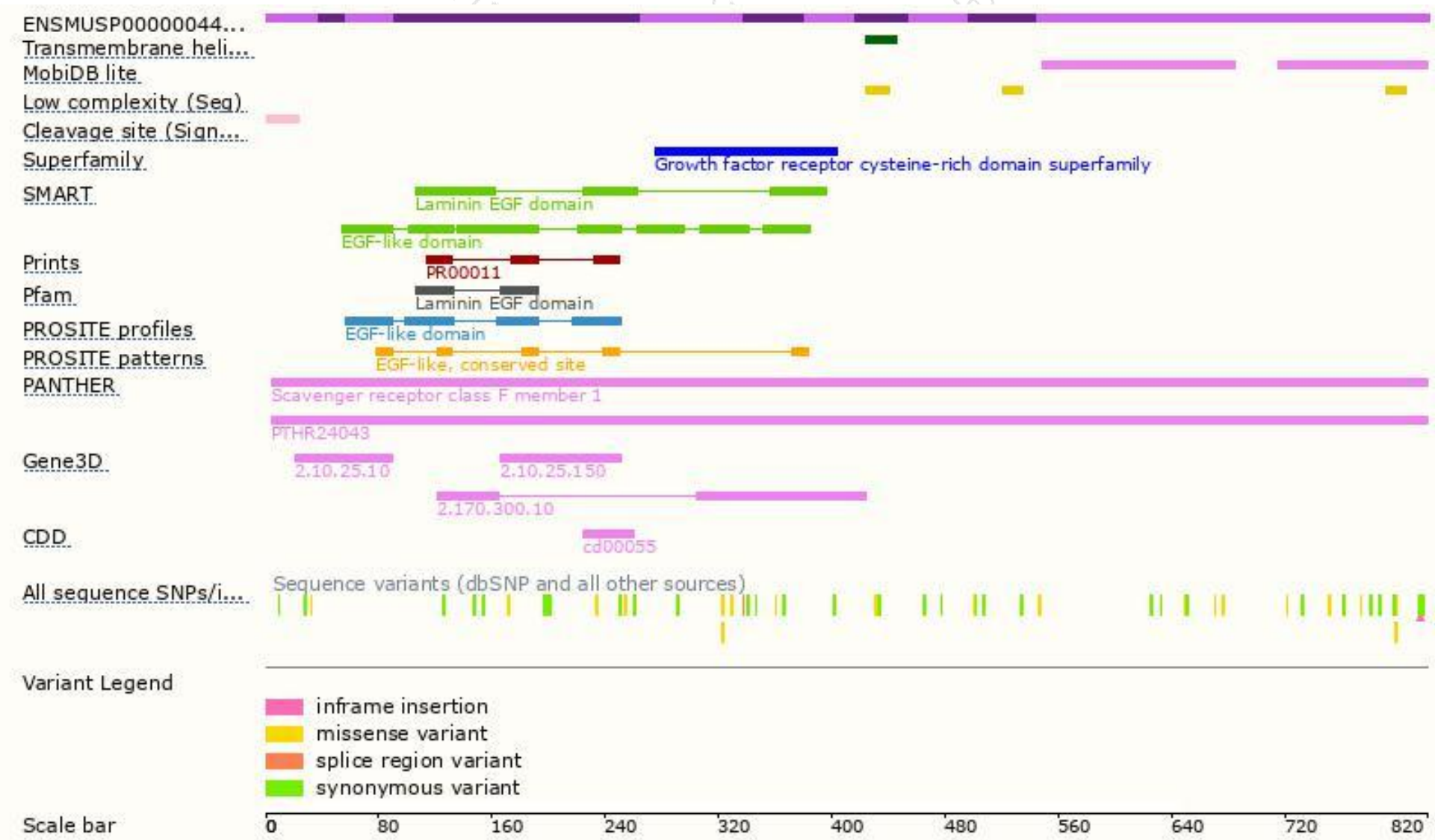




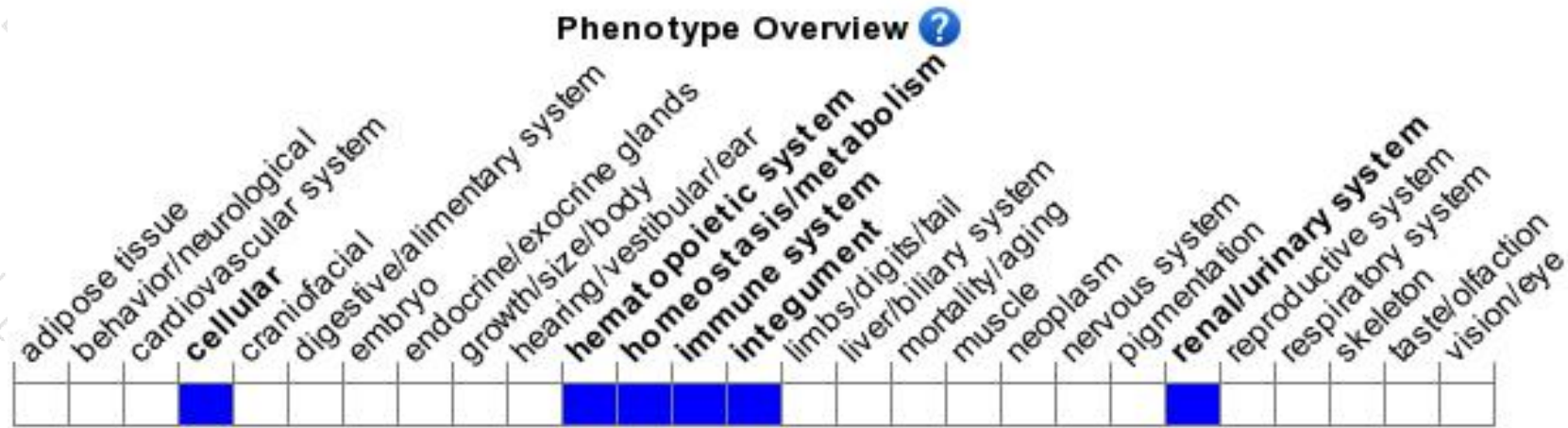
# Protein domain



集萃药康  
GemPharmatech



# 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 mice are viable and fertile with no abnormalities detected in plasma glucose, cholesterol, or triglycerides, or in the brain, lung, heart, kidney, liver, or testes. Mice homozygous for a targeted allele exhibit impaired clearance of apoptotic cells and autoimmune disease.

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

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