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# BAZ1B Knockout 293T Cell Line, Homozygous

**Catalog No.: RM02450**

## Basic Information

**Catalog No.**
RM02450

**Category**
Cell Line

**Parental Cell line**
293T

**Genotype**
Knockout

## Background

This gene encodes a member of the bromodomain protein family. The bromodomain is a structural motif characteristic of proteins involved in chromatin-dependent regulation of transcription. This gene is deleted in Williams-Beuren syndrome, a developmental disorder caused by deletion of multiple genes at 7q11.23. [provided by RefSeq, Jul 2008]

## Gene Information

**Gene Symbol**
BAZ1B

**Species**
Human

**Gene ID**
9031

**Swiss Prot**
Q9UIG0

**Synonyms**
WBSCR10; WBSCR9; WSTF

## Product Information

**Description**
BAZ1B Knockout 293T Cell line is engineered from 293T cell line with Gene-Editing Technology.
Allele-1:73bp deletion in exon1
Allele-2:73bp deletion in exon1
Mammalian cells such as human, rat and mouse cells are normally diploid with two alleles. Homozygote: both alleles were knocked out, mRNA has no signal, no expression of proteins. Heterozygote: only one allele was knocked out, the mRNA transcript levels was decreased compared to wild type, and the protein expression levels was also lower than that of the wild type.

**Packaging**
1 vial parental cell line and 1 vial knockout cell line

**Shipping Conditions**
Dry ice

**Amount**
1~5x$10^6$ cells/vial

**Storage**
Store at -20℃

**Protocol**
Upon arrival, it should be maintained in DMEM medium with 10%(v/v) fetal bovine serum and 100U penicillin-streptomycin, at 37℃ with 5% $CO_2$ condition.
1. Thaw the vial in 37℃ water bath ,and shake it to melt as soon as possible.
2. Transfer the cell suspension to a 15mL conical tube with pre-warmed 5mL complete medium and centrifuge 1000rpm for approximately 5 minutes at room temperature.
3. Remove and discard the supernatant.
4. Resuspend the cell pellet with 1mL pre-warmed complete medium and seed in 10cm dish.
5. Add 8-10mL of complete medium.
6. Incubate the culture at 37℃ incubator with 5% $CO_2$.
7. A subcultivation ratio of 1:2-1:4 is recommended.

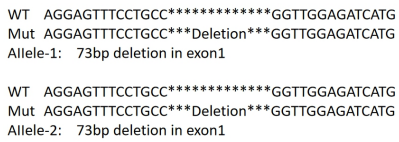
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## Sequencing data




Genome sequence analysis of PCR products from parental (WT) and BAZ1B knockout (KO) 293T cells, using sanger sequencing.



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