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TSC22D3 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM50025

Basic Information

Catalog No.
RM50025

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockout

Gene Information

Gene Symbol
TSC22D3

Species
Human

Gene ID
1831

Swiss Prot
Q99576

Synonyms
DIP; GILZ; DSIPI; TSC-22R; TSC22D3

Contact

400-999-6126

cn.market@abclonal.com.cn

www.abclonal.com.cn

Background

This gene encodes the anti-inflammatory protein glucocorticoid (GC)-induced leucine zipper. Expression of this gene stimulated by glucocorticoids and interleukin 10 and it appears to play a key role in the anti-inflammatory and immunosuppressive effects of this steroid. This protein has also been shown to inhibit pro-inflammatory molecules including nuclear factor κB. Alternate splicing results in multiple transcript variants.

Product Information

Description
TSC22D3 Knockout cell line is engineered from 293T cell line with Gene-Editing Technology.
Allele-1:exon2 was deleted
Allele-2:exon2 was deleted
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 Lysate and 1 vial knockout cell Lysate

Shipping Conditions
4℃

Amount
50μL, 2μg/μL.

Storage
Store at -20℃

Protocol
To be used as WB control. Lysate is supplied in 1× SDS sample buffer (2% SDS, 60 mM Tris-HCl pH 6.8, 10% Glycerol, 0.02% Bromophenol blue, 60 mM beta-mercaptoethanol). Lysate should be boiled for 3 - 5 minutes before loading onto gel.

Sequencing data

```
WT    ACTGCCATGTACTC**********GCACTGGAGGTGGA
Mut   ACTGCCATGTACTC***Deletion***GCACTGGAGGTGGA
Allele-1:    exon2 was deleted

WT    ACTGCCATGTACTC**********GCACTGGAGGTGGA
Mut   ACTGCCATGTACTC***Deletion***GCACTGGAGGTGGA
Allele-2:    exon2 was deleted
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Genome sequence analysis of PCR products from parental (WT) and TSC22D3 knockout (KO) 293T cells, using sanger sequencing.