

MTOR Knockdown HeLa Cell Lysate, Heterozygous

Catalog No.: RM02015

Basic Information

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Category

Cell Lysate

Parental Cell line

HeLa

Genotype

Knockdown

Gene Information

Gene Symbol

MTOR

Species

Human

Gene ID

2475

Swiss Prot

P42345

Synonyms

FRAP; FRAP1; FRAP2; RAFT1; RAPT1; SKS

Contact

 | 400-999-6126

 | cn.market@abclonal.com.cn

 | www.abclonal.com.cn

Background

The protein encoded by this gene belongs to a family of phosphatidylinositol kinase-related kinases. These kinases mediate cellular responses to stresses such as DNA damage and nutrient deprivation. This protein acts as the target for the cell-cycle arrest and immunosuppressive effects of the FKBP12-rapamycin complex. The ANGPTL7 gene is located in an intron of this gene. [provided by RefSeq, Sep 2008]

Product Information

Description

MTOR Knockdown HeLa Cell Line is engineered from HeLa cell line with Gene-Editing technology.

Allele-1:121bp deletion in exon3

Allele-2:WT

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°C

Amount

50µL, 2µg/µL.

Storage

Lysate is stable for 12 months when stored at -20°C. Minimizing freeze-thaw cycles.

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 GGGAATGCCACCCG*****TACGTGGAATTTGA
Mut GGGAATGCCACCCG***Deletion***TACGTGGAATTTGA
Allele-1: 121bp deletion in exon3
WT GTGGAAGGTGGGAATGCCACCCGAATTGGCAGATTGC
Mut GTGGAAGGTGGGAATGCCACCCGAATTGGCAGATTGC
Allele-2: WT

Genome sequence analysis of PCR products from parental (WT) and MTOR Knockdown (KD) HeLa cells, using sanger sequencing.