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SQSTM1 Knockout 293T Cell Lysate, Homozygous

Catalog No.: RM50134

Basic Information

Catalog No.
RM50134

Category
Cell Lysate

Parental Cell line
293T

Genotype
Knockout

Gene Information

Gene Symbol
SQSTM1

Species
Human

Gene ID
8878

Swiss Prot
Q13501

Synonyms
p60; p62; A170; DMRV; OSIL; PDB3; ZIP3; p62B; NADGP; FTDALS3; SQSTM1/p62

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Background

This gene encodes a multifunctional protein that binds ubiquitin and regulates activation of the nuclear factor kappa-B (NF-kB) signaling pathway. The protein functions as a scaffolding/adaptor protein in concert with TNF receptor-associated factor 6 to mediate activation of NF-kB in response to upstream signals. Alternatively spliced transcript variants encoding either the same or different isoforms have been identified for this gene. Mutations in this gene result in sporadic and familial Paget disease of bone.

Product Information

Description
SQSTM1 Knockout cell line is engineered from 293T cell line with Gene-Editing Technology.
Allele-1:1bp insertion and 3bp deletion in exon2
Allele-2:1bp insertion and 17bp deletion in exon2
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

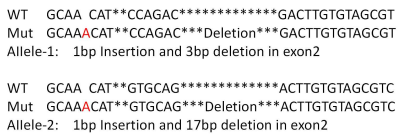
Shipping Conditions
4℃

Amount
50μL, 2μg/μL.

Storage
Lysate is stable for 12 months when stored at -20℃. 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



Genome sequence analysis of PCR products from parental (WT) and SQSTM1 knockout (KO) 293T cells, using sanger sequencing.