

PXN Knockout HeLa Cell Lysate, Homozygous

Catalog No.: RM02078

Basic Information

Catalog No.

RM02078

Category

Cell Lysate

Parental Cell line

HeLa

Genotype

Knockout

Gene Information

Gene Symbol

PXN

Species

Human

Gene ID

5829

Swiss Prot

P49023

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Background

This gene encodes a cytoskeletal protein involved in actin-membrane attachment at sites of cell adhesion to the extracellular matrix (focal adhesion). Alternatively spliced transcript variants encoding different isoforms have been described for this gene. These isoforms exhibit different expression pattern, and have different biochemical, as well as physiological properties (PMID:9054445). [provided by RefSeq, Aug 2011]

Product Information

Description

PXN Knockout HeLa Cell Line is engineered from HeLa cell line with Gene-Editing technology.

Allele-1:exon1 was deleted

Allele-2:exon1 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°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 CCCTCTGTCCTTT*****CCCTGGGGCAGGGT
Mut CCCTCTGTCCTTT***Deletion***CCCTGGGGCAGGGT
Allele-1: exon1 was deleted

WT CCTCTGTCCTTTG*****CCCTGGGGCAGGGT
Mut CCTCTGTCCTTTG***Deletion***CCCTGGGGCAGGGT
Allele-2: exon1 was deleted

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