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PXN Knockout HeLa Cell Lysate, Homozygous

Catalog No.: RM02078

Basic Information

Catalog No.
RM02078

Category
Cell Lysate

Parental Cell line
HeLa

Genotype
Knockout

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]

Gene Information

Gene Symbol
PXN

Species
Human

Gene ID
5829

Swiss Prot
P49023

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℃

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.

Contact

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Sequencing data

WT CCCTCTGTCCTCTT**********CCCTGGGGCAGGGT
Mut CCCTCTGTCCTCTT***Deletion***CCCTGGGGCAGGGT
Allele-1: exon1 was deleted

WT CCTCTGTCCTCTTG**********CCCTGGGGCAGGGT
Mut CCTCTGTCCTCTTG***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.