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IL23R Knockout HeLa Cell Lysate, Homozygous

Catalog No.: RM02260

Basic Information

Catalog No.

RM02260

Category

Cell Lysate

Parental Cell line

HeLa

Genotype

Knockout

Background

The protein encoded by this gene is a subunit of the receptor for IL23A/IL23. This protein pairs with the receptor molecule IL12RB1/IL12Rbeta1, and both are required for IL23A signaling. This protein associates constitutively with Janus kinase 2 (JAK2), and also binds to transcription activator STAT3 in a ligand-dependent manner. [provided by RefSeq, Jul 2008]

Gene Information

Gene Symbol

IL23R

Species

Human

Gene ID

149233

Swiss Prot

Q5VWK5

Contact

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Product Information

Description

IL23R Knockout HeLa Cell Line is engineered from HeLa cell line with Gene-Editing technology.

Allele-1:169bp deletion in exon2

Allele-2:169bp 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

Amount

4°C

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 $1\times$ 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 ATAAACTGCTCTGG*************TATAAAAACTTTCT
Mut ATAAACTGCTCTGG***Deletion***TATAAAAACTTTCT
Allele-1: 169bp deletion in exon2

WT ATAAACTGCTCTGG**************TATAAAAACTTTCT
Mut ATAAACTGCTCTGG***Deletion***TATAAAAACTTTCT
Allele-2: 169bp deletion in exon2

Genome sequence analysis of PCR products from parental (WT) and IL23R knockout (KO) HeLa cells, using sanger sequencing.