

Product datasheet for SC323057

p73 (TP73) (NM_001126242) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: p73 (TP73) (NM_001126242) Human Untagged Clone

Tag: Tag Free

Symbol: p73

Synonyms: P73

Mammalian Cell

Neomycin

Selection:

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Fully Sequenced ORF: >SC323057 representing NM_001126242.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

GTTACAGAGCATTTACCACCTGCAGAACCTGACCATTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC



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Restriction Sites: Sgfl-Mlul

ACCN: NM_001126242

Insert Size: 1281 bp

OTI Disclaimer: Due to the inherent nature of this plasmid, standard methods to replicate additional amounts

of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at customercom or by

calling 301.340.3188 option 3 for pricing and delivery.

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning

into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube

containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method: 1. Centrifuge at 5,000xg for 5min.

2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.

3. Close the tube and incubate for 10 minutes at room temperature.

4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid

at the bottom.

5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of

shipping when stored at -20°C.

RefSeq: <u>NM 001126242.2</u>

 RefSeq Size:
 4982 bp

 RefSeq ORF:
 1281 bp

 Locus ID:
 7161

 UniProt ID:
 015350

Cytogenetics: 1p36.32

Protein Families: Druggable Genome, Transcription Factors

Protein Pathways: Neurotrophin signaling pathway, p53 signaling pathway

MW: 47.7 kDa



Gene Summary:

This gene encodes a member of the p53 family of transcription factors involved in cellular responses to stress and development. It maps to a region on chromosome 1p36 that is frequently deleted in neuroblastoma and other tumors, and thought to contain multiple tumor suppressor genes. The demonstration that this gene is monoallelically expressed (likely from the maternal allele), supports the notion that it is a candidate gene for neuroblastoma. Many transcript variants resulting from alternative splicing and/or use of alternate promoters have been found for this gene, but the biological validity and the full-length nature of some variants have not been determined. [provided by RefSeq, Feb 2011] Transcript Variant: This variant (4) differs in the 5' UTR and coding sequence and lacks an alternate coding exon compared to variant 1, that causes a frameshift. The resulting isoform (d, also known as deltaN p73 gamma) has a shorter and distinct N-terminus and a shorter and distinct C-terminus compared to isoform a. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.