

Product datasheet for RC400448

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OriGene Technologies, Inc.

PTEN (NM_000314) Human Mutant ORF Clone

Product data:

Product Type: Mutant ORF Clones

Product Name: PTEN (NM 000314) Human Mutant ORF Clone

Mutation Description: Q214*

Affected Codon#: 214

Affected NT#: c.640

Nucleotide Mutation: PTEN Mutant (Q214*), Myc-DDK-tagged ORF clone of Homo sapiens phosphatase and tensin

homolog (PTEN) as transfection-ready DNA

Effect: Truncation

Symbol: PTEN

Synonyms: 10q23del; BZS; CWS1; DEC; GLM2; MHAM; MMAC1; PTEN1; PTENbeta; TEP1

E. coli Selection: Kanamycin (25 ug/mL)

Mammalian Cell Neomycin

Selection:

Vector: pCMV6-Entry (PS100001)

Tag: Myc-DDK
ACCN: NM 000314

ORF Size: 639 bp
Restriction Sites: Sgfl-Mlul



ORF Nucleotide Sequence:

>RC400448 representing NM_000314

Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATTACAAGGATGACGACGATAAGGTTTAA

Protein Sequence:

>RC400448 representing NM_000314
Red=Cloning site Green=Tags(s)

MTAIIKEIVSRNKRRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNL CAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAAIHCKAGKGRTGVMICAYLL HRGKFLKAQEALDFYGEVRTRDKKGVTIPSQRRYVYYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGT CNP

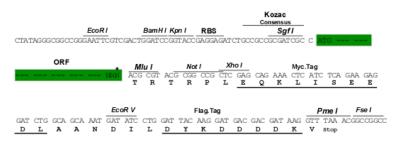
TRTRPLEQKLISEEDLAANDILDYKDDDDKV

Restriction Sites:

Sgfl-Mlul

Cloning Scheme:





^{*} The last codon before the Stop codon of the ORF



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. <u>More info</u>

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

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).

 RefSeq:
 NP 000305

 RefSeq Size:
 5572 bp

 RefSeq ORF:
 1212 bp

 Locus ID:
 5728

 Cytogenetics:
 10q23.31

Domains: PTPc_motif

Protein Families: Druggable Genome, Phosphatase

Protein Pathways: Endometrial cancer, Focal adhesion, Glioma, Inositol phosphate metabolism, Melanoma, p53

signaling pathway, Pathways in cancer, Phosphatidylinositol signaling system, Prostate cancer,

Small cell lung cancer, Tight junction

MW: 25 kDa





Gene Summary:

This gene was identified as a tumor suppressor that is mutated in a large number of cancers at high frequency. The protein encoded by this gene is a phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase. It contains a tensin like domain as well as a catalytic domain similar to that of the dual specificity protein tyrosine phosphatases. Unlike most of the protein tyrosine phosphatases, this protein preferentially dephosphorylates phosphoinositide substrates. It negatively regulates intracellular levels of phosphatidylinositol-3,4,5-trisphosphate in cells and functions as a tumor suppressor by negatively regulating AKT/PKB signaling pathway. The use of a non-canonical (CUG) upstream initiation site produces a longer isoform that initiates translation with a leucine, and is thought to be preferentially associated with the mitochondrial inner membrane. This longer isoform may help regulate energy metabolism in the mitochondria. A pseudogene of this gene is found on chromosome 9. Alternative splicing and the use of multiple translation start codons results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Feb 2015]