

Product datasheet for **RC400420**

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:	R142Q
Affected Codon#:	142
Affected NT#:	c.425
Nucleotide Mutation:	PTEN Mutant (R142Q), Myc-DDK-tagged ORF clone of Homo sapiens phosphatase and tensin homolog (PTEN) as transfection-ready DNA
Effect:	Missense
Symbol:	PTEN
Synonyms:	10q23del; BZS; CWS1; DEC; GLM2; MHAM; MMAC1; PTEN1; PTENbeta; TEP1
E. coli Selection:	Kanamycin (25 ug/mL)
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
Tag:	Myc-DDK
ACCN:	NM_000314
ORF Size:	1209 bp
Restriction Sites:	Sgfi-MluI



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ORF Nucleotide Sequence:

>RC400420 representing NM_000314
 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGACAGCCATCATCAAAGAGATCGTTAGCAGAAACAAAAGGAGATATCAAGAGGATGGATTCGACTTAG
 ACTTGACCTATATTTATCCAAACATTATTGCTATGGGATTTCTGCAGAAAGACTTGAAGGCGTATACAG
 GAACAATATTGATGATGTAGTAAGGTTTTGGATTCAAAGCATAAAAACCATTACAAGATATACAATCTT
 TGTGCTGAAAGACATTATGACACCGCCAAATTTAATTGCAGAGTTGCACAATATCCTTTTGAAGACCATA
 ACCCACCACAGCTAGAACTTATCAAACCCTTTTGTGAAGATCTTGACCAATGGCTAAGTGAAGATGACAA
 TCATGTTGCAGCAATTCAGTGTAAAGCTGAAAAGGGACGAACTGGTGTAAATGATATGTGCATATTTATTA
 CATCAGGGCAAATTTTTAAAGGCACAAGAGGCCCTAGATTTCTATGGGGAAGTAAAGACCAGAGACAAAA
 AGGGAGTAACTATCCAGTCAGAGGCGCTATGTGATTATTATAGCTACCTGTTAAAGAATCATCTGGA
 TTATAGACCAGTGGCACTGTTGTTTACAAGATGATGTTTGAAGTAACTTCCAATGTTCACTGGCGGAACT
 TGCAATCCTCAGTTTGGTCTGCCAGCTAAAGGTGAAGATATATTCCTCCAATTCAGGACCCACACGAC
 GGAAGACAAGTTCATGTACTTTGAGTCCCTCAGCCGTTACCTGTGTGTGGTATATCAAGTAGAGTT
 CTTCCACAAAACAGAAAGATGCTAAAAAGGACAAAATGTTTCACTTTTGGGTAATACATTCTTCATA
 CCAGGACCAGAGGAACTCAGAAAAAGTAGAAAATGGAAGTCTATGTGATCAAGAAATCGATAGCATT
 GCAGTATAGAGCGTGCAGATAATGACAAGGAATATCTAGTACTTACTTTAACAAAAATGATCTTGACAA
 AGCAAAATAAGACAAAGCCAACCGATACTTTTCTCAAATTTAAGGTGAAGCTGACTTACAAAAACA
 GTAGAGGAGCCGTCAAATCCAGAGGCTAGCAGTTCAACTTCTGTAACACCAGATGTTAGTGACAATGAAC
 CTGATCATTATAGATTTCTGACACCACTGACTCTGATCCAGAGAATGAACCTTTTGATGAAGATCAGCA
 TACACAAATTACAAAAGTC

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Protein Sequence:

>RC400420 representing NM_000314
 Red=Cloning site Green=Tags(s)

MTAIIKEIVSRNKRRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNL
 CAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCELDQWLSDDNHVAAIHCKAGKGRGVMICAYLL
 HQGKFLKAQEALDFYGEVTRDKKGVIPSQRRYVYYSYLLKNHLDYRPVALLFHKMMFETIPMFSGGT
 CNPQFVVCQLKVKIYSSNSGPTRRREDKFMFEFPQPLVCGDIKVEFFHKQNKMLKKDKMFHFWNTFFI
 PGPEETSEKVENGSLCDQEIDSICSIERADNDKEYLVLTLTKNDLKDANKDKANRYFSPNFKVKLYFTKT
 VEEPSNPEASSSTSVTPDVSDNEPDHYRYSDDTSDPENEPFDEDQHTQITKV

TRTRPLEQ**KL**ISEEDLAANDILDYKDDDDKV

Restriction Sites:

Sgfl-MluI

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:	47 kDa
Gene Summary:	<p>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]</p>