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Product datasheet for SC336047

PMPCA (NM_001282946) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	PMPCA (NM_001282946) Human Untagged Clone
Tag:	Tag Free
Symbol:	PMPCA
Synonyms:	Alpha-MPP; CLA1; CPD3; INPP5E; MAS2; P-55; SCAR2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

Fully Sequenced ORF:

>SC336047 representing NM_001282946.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGAAGCGAAATACCTTAGTGGAATTGCTCACTTTTTGGAAAAATTGGCATTTTCGTCTACTGCTCGAT
TTGACAGCAAAGATGAAATTCTGCTTACGTTGGAAAAGCATGGGGGTATCTGTGACTGCCAGACATCAA
GACACCACCATGTATGCTGTGTCTGCTGATAGCAAAGGCTTGGACACGGTGGTTGCCTTACTGGCTGAT
GTGGTTCTGCAGCCCCGGCTAACAGATGAAGAAGTCGAGATGACGCGGATGGCGGTCCAGTTTGAGCTG
GAGGACCTGAACCTGCGGCCTGACCCAGAGCCACTTCTCACCGAGATGATTCATGAAGCGGCTTACAGG
GAGAACACAGTTGGCCTCCACCGTTTCTGCCCCACAGAAAACGTAGCAAAGATCAACCGAGAGGTGCTG
CATTCCTACCTGAGGAACTACTACACTCCCGACCGCATGGTGCTGGCCGGCGTGGGCGTGGAGCACGAG
CATCTGGTGGACTGTGCCCGGAAGTACCTCCTGGGGGTCCAGCCGGCCTGGGGGAGCGCAGAGGCCGTG
GATATTGACAGATCTGTGGCCCAGTACACTGGGGGGATTGCCAAGCTAGAAAGAGACATGTCCAATGTC
AGCCTGGGCCCGACCCCCATCCCCGAGCTCACGCACATCATGGTTGGACTGGAGAGCTGCTCCTTCCTG
GAGGAGGACTTCATCCCCTTTGCAGTGTTGAACATGATGATGGGCGGAGGTGGCTCCTTCTCGGCTGGT
GGGCCCGGCAAGGGCATGTTCTCCAGGCTCTACCTCAACGTGCTCAACAGGCACCACTGGATGTATAAC
GCGACCTCCTACCACCACAGCTACGAGGACACTGGCCTCCTTTGCATCCATGCCAGCGCCGACCCAAGA
CAGGTTCGAGAAATGGTAGAAATCATCACAAAGGAGTTTATTTTAATGGGCGGAACCGTGGACACGGTG
GAGCTGGAACGAGCCAAGACGCAGCTGACATCAATGCTCATGATGAACCTGGAATCCAGGCCTGTGATC
TTCGAGGATGTGGGGAGGCAGGTGCTGGCCACTCGCTCCAGAAAGCTGCCGCACGAGCTGTGCACGCTC
ATCCGCAACGTGAAGCCGGAAGATGTGAAGAGAGTCGCTTCTAAGATGCTCCGAGGGAAGCCGGCAGTG
GCCGCCCTGGGTGACCTGACTGACCTGCCCACGTATGAGCACATCCAGACCGCCCTGTCGAGTAAGGAC
GGGCGCCTGCCCAGGACGTACCGGCTCTTCCGGTAG
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

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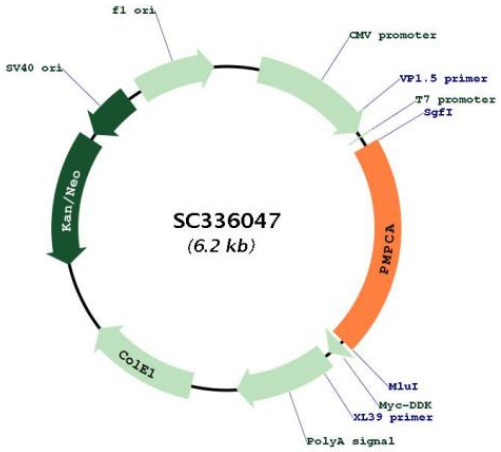
Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN: NM_001282946

Insert Size: 1278 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

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: NM_001282946.1

RefSeq Size: 2180 bp

RefSeq ORF: 1278 bp

Locus ID: 23203

UniProt ID: Q10713

Cytogenetics: 9q34.3

Protein Families: Druggable Genome, Protease

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MW: 48.1 kDa

Gene Summary: The protein encoded by this gene is found in the mitochondrion, where it represents the alpha subunit of a proteolytic heterodimer. This heterodimer is responsible for cleaving the transit peptide from nuclear-encoded mitochondrial proteins. Defects in this gene are a cause of spinocerebellar ataxia, autosomal recessive 2. [provided by RefSeq, Mar 2016]
Transcript Variant: This variant (3) uses an alternate splice site in the 5' coding region which results in the use of an alternate start codon compared to variant 1. The encoded isoform (3) is shorter and has a distinct N-terminus compared to isoform 1. 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.

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