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Product datasheet for SC100435

PMPCA (NM_015160) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	PMPCA (NM_015160) Human Untagged Clone
Tag:	Tag Free
Symbol:	PMPCA
Synonyms:	Alpha-MPP; CLA1; CPD3; INPP5E; MAS2; P-55; SCAR2
Mammalian Cell Selection:	None
Vector:	pCMV6-XL4
E. coli Selection:	Ampicillin (100 ug/mL)

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Fully Sequenced ORF:

>OriGene ORF within SC100435 sequence for NM_015160 edited (data generated by NextGen Sequencing)

ATGGCGGCTGTGGTGCTGGCGGCGACGCGGTTGCTGCGGGGCTCGGGTTCTTGGGGCTGT
TCGCGGCTGAGGTTTGGACCTCCTGCGTACAGACGGTTTAGTAGTGGTGGTGCCTATCCC
AACATCCCCCTCTCTTCTCCCTTACCTGGAGTACCCAAGCCTGTTTTTGCTACAGTTGAT
GGACAGGAAAAGTTTGAAACCAAAGTAACCACATTGGATAATGGGCTTCGCGTGGCATCT
CAGAATAAGTTTGGACAGTTTTGTACAGTAGGAATTCTTATCAATTCAGGATCGAGATAT
GAAGCGAAATACCTTAGTGGAATTGCTCACTTTTTGGAAAAATTGGCATTTTCGTCTACT
GCTCGATTTGACAGCAAAGATGAAATTCTGCTTACGTTGGAAAAGCATGGGGGTATCTGT
TACTGCCAGACATCAAGAGACACCACCATGTATGCTGTGTCTGCTGATAGCAAAGGCTTG
GACACGGTGGTTGCCTTACTGGCTGATGTGGTTCTGCAGCCCCGGCTAACAGATGAAGAA
GTCGAGATGACGCGGATGGCGGTCCAGTTTGAGCTGGAGGACCTGAACCTGCGGCCTGAC
CCAGAGCCACTTCTCACCGAGATGATTCATGAAGCGGCTTACAGGGAGAACACAGTTGGC
CTCCACCGTTTCTGCCCCACAGAAAACGTAGCAAAGATCAATCGAGAGGTGCTGCATTCC
TACCTGAGGAACTACTACACTCCCGACCGCATGGTGCTGGCCGGCGTGGGCGTGGAGCAC
GAGCATCTGGTGGACTGTGCCCGGAAGTACCTCCTGGGGGTCCAGCCGGCCTGGGGGAGC
GCAGAGGCCGTGGATATTGACAGATCTGTGGCCCAGTACACTGGGGGGATTGCCAAGCTA
GAAAGAGACATGTCCAATGTCAGCCTGGGCCCGACCCCCATCCCCGAGCTCACGCACATC
ATGGTTGGACTGGAGAGCTGCTCCTTCCTGGAGGAGGACTTCATCCCCTTTGCAGTGTTG
AACATGATGATGGGCGGAGGTGGCTCCTTCTCGGCTGGTGGGCCCGGCAAGGGCATGTTC
TCCAGGCTCTACCTCAACGTGCTCAACAGGCACCACTGGATGTATAACGCGACCTCCTAC
CACCACAGCTACGAGGACACTGGCCTCCTTTGCATCCATGCCAGCGCCGACCCAAGACAG
GTTCGAGAAATGGTAGAAATCATCACAAAGGAGTTTATTTTAATGGGCGGAACCGTGGAC
ACGGTGGAGCTGGAACGAGCCAAGACGCAGCTGACATCAATGCTCATGATGAACCTGGAA
TCCAGGCCTGTGATCTTCGAGGATGTGGGGAGGCAGGTGCTGGCCACTCGCTCCAGAAAG
CTGCCGCACGAGCTGTGCACGCTCATCCGCAACGTGAAGCCGGAAGATGTGAAGAGAGTC
GCTTCTAAGATGCTCCGAGGGAAGCCGGCAGTGGCCGCCCTGGGTGACCTGACTGACCTG
CCCACGTATGAGCACATCCAGACCGCCCTGTCGAGTAAGGACGGGCGCCTGCCCAGGACG
TACCGGCTCTTCCGGTAG

Clone variation with respect to NM_015160.1
421 g=>t;702 c=>t

5' Read Nucleotide Sequence:

>OriGene 5' read for NM_015160 unedited
TTTGTAATACGACTCACTATAGGGCGGCCGCGAATTCGGCACCAGGCAAGATGGCGGCTG
TGGTGCTGGCGGCGACGCGGTTGCTGCGGGGCTCGGGTTCTTGGGGCTGTTCGCGGCTGA
GGTTTGGACCTCCTGCGTACAGACGGTTTAGTAGTGGTGGTGCCTATCCCAACATCCCCC
TCTCTTCTCCCTTACCTGGAGTACCCAAGCCTGTTTTTGCTACAGTTGATGGACAGGAAA
AGTTTGAAACCAAAGTAACCACATTGGATAATGGGCTTCGCGTGGCATCTCAGAATAAGT
TTGGACAGTTTTGTACAGTAGGAATTCTTATCAATTCAGGATCGAGATATGAAGCGAAAT
ACCTTAGTGGAATTGCTCACTTTTTGGAAAAATTGGCATTTTCGTCTACTGCTCGATTTG
ACAGCAAAGATGAAATTCTGCTTACGTTGGAAAAGCATGGGGGTATCTGTTACTGCCAGA
CATCAAGAGACACCACCATGTATGCTGTGTCTGCTGATAGCAAAGGCTTGGACACGGTGG
TTGCCTTACTGGCTGATGTGGTTCTGCAGCCCCGGCTAACAGATGAAGAAGTCGAGATGA
CGCGGATGGCGGTCCAGTTTGAGCTGGAGGACCTGAACCTGCGGCCTGACCCAGAGCCAC
TTCTCACCGAGATGATTCATGAAGCGGCTTACAGGGAGAACACAGTTGGCCTNCACCGTT
TCTGCCCCACAGAANACGTAGCANAGATCAATCGAGAGGTGCTGCATTCCTACCTNGAGA
ACTACTACACTCCCGACCGCATGGTGCTGNCCNGCGTGGGCGTGNAGACGAGCATCTGGT
GGACTGTGCCCGGAAGTCCCTNCTGGGGTCCAGCCNGNCTGNGGGACGCANAGCCGTGNT
ATTGACAGACTGTGCCCATACCTGGGGGGGATGCAGCTAGAGAGACTGTCATGTCAGCTG
GCCCGACCCATNCCGACTCGCCANATGGTGGACTGAACTGCTCCCTGAGAG

3' Read Nucleotide Sequence:

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>OriGene 3' read for NM_015160 unedited
GTACCGCGGCCGCAATCTAGAGTCGAGTTTTTTTTTTTTTTTTTTAAGAAAGATGCCGC
TCTTTATTACCAGGGAAGCTGTGTGCACGCGCGTGGAGCGCGCTCCTTGGAGCTGACCGG
GCCCTTACCTTCTCCTGCTTGTCAGAGGTGAGTCCTGGTACCCAGCACGGTGGCCTCTGG
GAGGCTCTGATAGGTCAGCCTTTGCTGCCTCCCAGCTCAGGGCTCCTCCAAGGAACCTGC
GGGGCCCCATGTGCCCACAGCCCGAGGAGGGAAGCACCGACCGCCCTCCTCGTGGCACGC
TGCACTCCAGCGCTGGGCACTTCACCTGCTTCCTGGCTTGCGGTGGTCAGGCTCGATACT
GACTCCACTGATCGGCACATTGAGTTCCGAAAGAATGCAAACCGCGTGGGTGCTGTGGCG
ACATTGTTTGCACCGTTTATACAACCAGACAGCTTTTTAGACTAAATTCGTGTCCAAACT
AACACGCACGGGAACGGGCTCCAGCTGCAGCTCCCTGGGTCTGTCAGGCCGGGGAGCGGT
TCTACCGGAAGAGCCGGTACGTCCTGGGCAGGCGCCCGTCCTTACTCGACAGGGCGGTCT
GGATGTGCTCATACGTGGGCAGGTCAGTCAGGTCACCCAGGGGCGGCCACTGCCGGCTTC
CCTCGGAGCATCTTAGAAGCGACTCTCTTCACATCTTCCGGGCTCACGTTTGCGATGAGC
GTGCACAGCTCGTGCGGGAGCTTTCTGGAGCGAGTGGCCAGCACCTGCCTCCCCAATCCT
CGAAGATAACAGGCCTGGATTCAGGTTCATCATGAGCATTGATGTCAGCTGCGTCTGGCC
TCGTTCCAGCTTACCCGGGTCCCGGGTCCGCCCATAAAATAAACCCCTTGGGAAGAATCT
TACCATTTTCCAACCTGCTTTGGTCCGCCCTGGCCTGATACCAAGAAGCCCTGTCCTCTT
ACTTGGTGGTAGGAGGCCCCGTTATCATCCGGGGGG
```

Restriction Sites: NotI-NotI

ACCN: NM_015160

Insert Size: 2300 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_015160.1, NP_055975.1

RefSeq Size: 2097 bp

RefSeq ORF: 1578 bp

Locus ID: 23203

UniProt ID: Q10713

Cytogenetics: 9q34.3

Domains: Peptidase_M16, Peptidase_M16_C

Protein Families: Druggable Genome, Protease

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 (1) represents the longest transcript and encodes the longest 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.