

Product datasheet for MC207523

PPP4c (NM_019674) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
 Product Name: PPP4c (NM_019674) Mouse Untagged Clone
 Tag: Tag Free
 Symbol: PPP4c
 Synonyms: 1110002D08Rik; AU016079; Ppx
 Vector: pCMV6-Entry (PS100001)
 E. coli Selection: Kanamycin (25 ug/mL)
 Cell Selection: Neomycin
 Fully Sequenced ORF: >MC207523 representing NM_019674
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGGATCGCC**

ATGGCGGAGATCAGCGACCTGGACCGGCAGATCGAGCAGCTACGGCGCTGCGAGCTGATCAAAGAGAGCG
 AAGTCAAGGCCCTGTGCGCCAAGGCCAGAGAAATCTTGGTAGAAGAGAGCAACGTGCAGAGGGTGGACTC
 GCCAGTACAGTATGCGGTGACATCCATGGACAATTCTATGACCTCAAGGAGCTGTTAGAGTAGGTGGC
 GATGTCCCTGAGACCAACTACCTTTCATGGGAGACTTTGTGGACCGTGGTTTCTACAGTGTGAAACCT
 TCCTCCTCCTGCTGGCTCTTAAGTTTCGCTATCCTGACAGAATCACTTTGATCCGGGGCAATCATGAGAG
 TCGCCAGATTACCCAGGTCTATGGGTTCTATGATGAGTGCTTACGGAAATATGGTTCAGTACTGTATGG
 CGCTACTGTACTGAGATCTTTGACTACCTCAGCCTGTCTGCCATCATTGATGGCAAGATCTTCTGTGTGC
 ATGGAGGTCTTTCCCTTCCATCCAGACCTTGGACCAGATCCGGACAATTGACCGAAAGCAAGAGGTACC
 CCATGATGGACCCATGTGCGACCTCCTGTGGTCTGACCCTGAAGACACAACAGGCTGGGGAGTGAGCCCC
 CGCGGGCAGGTTACCTGTTTGGCAGTGACGTGGTCCGCCAGTTCAATGCAGCCAACGACATTGATATGA
 TCTGCCGTGCCACCAATTAGTGATGGAAGGCTACAAGTGGCACTTCAATGAGACCGTGTACTGTGTG
 GTCAGCGCCTAATTACTGCTACCGCTGTGGCAATGTGGCAGCCATCTTAGAACTGGATGAGCACCTCCAG
 AAAGATTTTCATCATCTTCGAGGCTGCACCCCAAGAGACACGTGGCATCCCTCCAAAAAGCCAGTGGCCG
 ACTATTTCTGTGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
 ACCN: NM_019674
 Insert Size: 924 bp



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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:	<ol style="list-style-type: none">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_019674.3 , NP_062648.1
RefSeq Size:	1332 bp
RefSeq ORF:	924 bp
Locus ID:	56420
UniProt ID:	P97470
Cytogenetics:	7 F3
Gene Summary:	<p>Protein phosphatase that is involved in many processes such as microtubule organization at centrosomes, maturation of spliceosomal snRNPs, apoptosis, DNA repair, tumor necrosis factor (TNF)-alpha signaling, activation of c-Jun N-terminal kinase MAPK8, regulation of histone acetylation, DNA damage checkpoint signaling, NF-kappa-B activation and cell migration. The PPP4C-PPP4R1 PP4 complex may play a role in dephosphorylation and regulation of HDAC3. The PPP4C-PPP4R2-PPP4R3A PP4 complex specifically dephosphorylates H2AFX phosphorylated on Ser-140 (gamma-H2AFX) generated during DNA replication and required for DNA double strand break repair (By similarity). Dephosphorylates NDEL1 at CDK1 phosphorylation sites and negatively regulates CDK1 activity in interphase. In response to DNA damage, catalyzes RPA2 dephosphorylation, an essential step for DNA repair since it allows the efficient RPA2-mediated recruitment of RAD51 to chromatin (By similarity).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (2) differs in the 5' UTR compared to variant 1. Variants 1 and 2 both encode the same protein. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>