OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC328504

MINPP1 (NM_001178117) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MINPP1 (NM_001178117) Human Untagged Clone
Tag:	Tag Free
Symbol:	MINPP1
Synonyms:	HIPER1; MINPP2; MIPP
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328504 representing NM_001178117. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGGCTGCGGCGCTG CTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCTCGTCGCTCAGCCCCTAT TTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGTCGGGCCCCGAGGCTCCGTGGCGG GACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGCTGGTCGCCCTCATTCGCCACGGCACCCGC TACCCCACGGTCAAACAGATCCGCAAGCTGAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGG GATGGCGGGGCTAGTAGTACCGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTAC GCGGACTGGATGGACGGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTG GCCTCGCTCTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCCTGCGGCTCATCACCAGTTCCAAG CACCGCTGCATGGATAGCAGCGCCGCCTTCCTGCAGGGGCTGTGGCAGCACTACCACCCTGGCTTGCCG CCGCCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTGAT CACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAAATGCTACAGCTCTTTATCACGTGGAAGCCTTCAAA ACTGGACCAGAAATGCAGAACATTTTAAAAAAAGTTGCAGCTACTTTGCAAGTGCCAGTAAATGATTTA AATGCAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCAC TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

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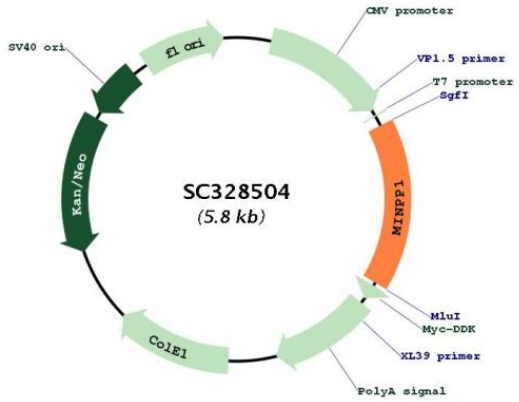
Plasmid Map:



ACCN:	NM_001178117
Insert Size:	939 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).
OTI Annotation:	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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_001178117.1
RefSeq Size:	2674 bp
RefSeq ORF:	939 bp

Locus ID:	9562
UniProt ID:	Q9UNW1
Cytogenetics:	10q23.2
Protein Families:	Druggable Genome
Protein Pathways:	Inositol phosphate metabolism
MW:	34.7 kDa
Gene Summary:	This gene encodes multiple inositol polyphosphate phosphatase; an enzyme that removes 3-phosphate from inositol phosphate substrates. It is the only enzyme known to hydrolzye inositol pentakisphosphate and inositol hexakisphosphate. This enzyme also converts 2,3 bisphosphoglycerate (2,3-BPG) to 2-phosphoglycerate; an activity formerly thought to be exclusive to 2,3-BPG synthase/2-phosphatase (BPGM) in the Rapoport-Luebering shunt of the glycolytic pathway.[provided by RefSeq, Sep 2009] Transcript Variant: This variant (2) lacks two alternate coding exons compared to variant 1, that causes a frameshift. The resulting isoform (2) has a shorter and distinct C-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.