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Product datasheet for SC215523

MPP8 (MPHOSPH8) (NM_017520) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	MPP8 (MPHOSPH8) (NM_017520) Human 3' UTR Clone
Symbol:	MPP8
Synonyms:	HSMPP8; mpp8; TWA3
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_017520
Insert Size:	1596 bp

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Insert Sequence:

>SC215523 3'UTR clone of NM_017520
The sequence shown below is from the reference sequence of NM_017520. The complete sequence of this clone may contain minor differences, such as SNPs.
Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
ATAGGTGCATACAGAGTGCAGCTGCAGTGACCAAACAGAAGGGACTGGGCGGAGTTCTCTTCAGACCGA
TTCCTATACTCTCTTTGACAGCAGTTTGGAATTCTTCTAGCACATCTATGTAAAGTTTTGTCTGTAAAC
CTCTTGCAGTTAAGCCTGTTGTCTGTTGTAGTCTGTAAGATGCGACATAGCTGTGTCTGTGCCAGTATG
CCGGAATCTCAGTGCAGTGTCCAGACTGCGTATTTCAGTTTTTCCACAATGTGGATAGTACATATGAGG
ATTATTTAAGAAAATTAAAGACTTCACTTTCTTTTTTCTGGAGACGGAGTTTCGCTCTTGTTGCCCAGG
CTGGAGTGCAATGGTGCGATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGCC
TCAGCCTCCTGAGTAGCTGGGATTACAGACACCCGCCATGGCACCCAGCTAATTTTGTATTTTTAGTAG
AGATGGGGTTTATCCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCGCCCGCCTCGG
CCTCCCAAAGTGCTTGGATTACAGGCATGAGCCACCGCACCCAGCAAGAGTTATTTTCTTAACTTGAAA
TTTTCTACTAGCCCTGGTGAACTTCTGTGCTTAAAAAAAAAAAAAAAAAAAAGGAAAAATTCAGCTCTAA
AACATTTGCTTACAGCAAGGGAGCCATGTTATATTCAAGTTACCCAAGCACCAAATAAAGTGTGGGTTT
GCTGCCCTTGAAAGGGTTGGGAGGCCTGATCTTTTTCTAGTAGACAGTTGCCACACATTCCCCAAGCAC
AAAAGGTGGAGATGGCAGTCACTTTGTAAATATGCTGTAGTCACTTATCATCTTTTCAAAGGGTAACAA
GAGAATCTAAGATGTAGTAAGAATGTAAACCAGTACACTATGAGACCTAAAAGAGAGTATTAAATGTGA
ACTTTTAGCAGAGCGTGGTGGCTCACACCTATAATCCCAGCGCTTTGGAGGCTGAGGTTGGAGGATTGC
TTAAGTCCAGGAGTTCAAGACCAGCCTGGGTAACATGGGGTGGAACAAGCCTGTAGTCCCAGATACTCA
GGAGGCTGAGGTGAAAGGATTGCTTGAGCCAGGGAGGTCAAGGCTGCAGTGAGCCGTGAAAGGCCACTG
CACTCCAGCCTGAGTGACAGAATGAGACCTTGTCTCAAAAAAAAAAAAAAAGTTTCTTGGAACCTATACG
GTTTTTTTTTGTTTTTTTTTTTTGAAAAGCCAGACCTTGTGCCCTTGTTTTGAACACCGACTGGGAAGA
TGGGGCTTAGGTAACAGCCAAACCTGGCTGTCAGCTGTGTGGGAGCCACCACCCTCTCTGGGAAGAGTT
CCTGCTTCTGTATGGCAAGCATAAATCAAGCTCAGTCTGGGTTATGGAGAAGTTGAAAATTGTTTTGTT
CCTCATTAGTTTATAATTGTATGAAATACGATTTTAATGAAAACTTTTCAGAATTCACGTTTGTGTAGA
TATTTCAGAGAACCATTTTTACTTTACATCCTAAAACTGCCTTTTCCTATGGTTTTGTCAATAAAACAC
TATGATGTT
ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: SgfI-MluI

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

RefSeq: NM_017520.4

Summary: Heterochromatin component that specifically recognizes and binds methylated 'Lys-9' of histone H3 (H3K9me) and promotes recruitment of proteins that mediate epigenetic repression (PubMed:20871592, PubMed:26022416). Mediates recruitment of the HUSH complex to H3K9me3 sites: the HUSH complex is recruited to genomic loci rich in H3K9me3 and is required to maintain transcriptional silencing by promoting recruitment of SETDB1, a histone methyltransferase that mediates further deposition of H3K9me3, as well as MORC2 (PubMed:26022416, PubMed:28581500). Binds H3K9me and promotes DNA methylation by recruiting DNMT3A to target CpG sites; these can be situated within the coding region of the gene (PubMed:20871592). Mediates down-regulation of CDH1 expression (PubMed:20871592). Also represses L1 retrotransposons in collaboration with MORC2 and, probably, SETDB1, the silencing is dependent of repressive epigenetic modifications, such as H3K9me3 mark. Silencing events often occur within introns of transcriptionally active genes, and lead to the down-regulation of host gene expression (PubMed:29211708). The HUSH complex is also involved in the silencing of unintegrated retroviral DNA by being recruited by ZNF638: some part of the retroviral DNA formed immediately after infection remains unintegrated in the host genome and is transcriptionally repressed (PubMed:30487602). [UniProtKB/Swiss-Prot Function]

Locus ID: 54737

MW: 60.9