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Product datasheet for MC212466

Pld6 (NM_183139) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Pld6 (NM_183139) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Pld6
Synonyms:	4933433K01Rik; Gm10; mitoPLD; mZuc; Zuc
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC212466 representing NM_183139 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGGGCGCTCGAGTTGGCGGTTGGTGTTCGCGGCTGGTGCGGGTCTCGCGCTGGCCCTAGAGGCACTGC CGTGGCTGATGCGTTGGCTGCTGGCTGGGCGGCGGCCAAGGCGCGAGGTGCTCTTCTTCCCCTCACAGGT GACCTGCACCGAGGCTTTACTGCAGGCCCCAGGGTTGCCTCCCGGGCCCTCGGGCTGCCCGTGTAGCCTC CCCCACAGCGAGAGTTCACTGAGCCGCCTGCTGCGCGCGCTGTTGGCCGCCCGCTCCAGCTTGGAGCTCT GCCTCTTCGCCTTCTCCAGCCCGCAGCTGGGGCGTGCAGTGCAGCTGCTGCATCAGCGTGGGGTGCGCGT GCGGGTCATCACTGACTGCGACTACATGGCCCTCAACGGCTCTCAGATCGGCCTGCTGCGCAAGGGATAC AGGTACGGCACGACCAGGACCTAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_183139
Insert Size:	444 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).

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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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	NM_183139.2, NP_898962.2
RefSeq Size:	1769 bp
RefSeq ORF:	444 bp
Locus ID:	194908
UniProt ID:	Q5SWZ9
Cytogenetics:	11 B1.3
Gene Summary:	Endonuclease that plays a critical role in PIWI-interacting RNA (piRNA) biogenesis during spermatogenesis. piRNAs provide essential protection against the activity of mobile genetic elements. piRNA-mediated transposon silencing is thus critical for maintaining genome stability, in particular in germline cells when transposons are mobilized as a consequence of wide-spread genomic demethylation (PubMed:23064227, PubMed:23064230). Has been proposed to act as a cardiolipin hydrolase to generate phosphatidic acid at mitochondrial surface (PubMed:21397847, PubMed:21397848). Although it cannot be excluded that it can act as a phospholipase in some circumstances, it should be noted that cardiolipin hydrolase activity is either undetectable in vitro, or very low. In addition, cardiolipin is almost exclusively found on the inner mitochondrial membrane, while PLD6 localizes to the outer mitochondrial membrane, facing the cytosol. Has been shown to be a backbone-non-specific, single strand-specific nuclease, cleaving either RNA or DNA substrates with similar affinity (PubMed:23064227, PubMed:23064230). Produces 5' phosphate and 3' hydroxyl termini, suggesting it could directly participate in the processing of primary piRNA transcripts (PubMed:23064230). Also acts as a regulator of mitochondrial shape through facilitating mitochondrial fusion (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (2) uses an alternate splice site that results in a frameshift in the 3' coding region, compared to variant 1. The encoded isoform (b) has a distinct C-terminus and is shorter than isoform a. 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.