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Product datasheet for MC229536

Prdm16 (NM_001291026) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Prdm16 (NM_001291026) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Prdm16
Synonyms:	5730557K01Rik; csp1; mel1
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

Fully Sequenced ORF:

>MC229536 representing NM_001291026
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCCGCGATCGCC

ATGCGATCCAAGGCGAGGGCGAGGAAGCTAGCCAAAAGTGACGGTGACGTTGTAAATAATATGTATGAAC
CTGACCCGGACCTGCTGGCCGGCCAGAGTGCCGAGGAGGAGACCGAAGACGGCATCCTGTCCCCCATCCC
CATGGGGCCACCGTCCCCCTTCCCCACCAGCGAGGACTTCACTCCCAAGGAGGGCTCGCCCTATGAGGCT
CCTGTCTACATTCCTGAAGACATTCCAATCCCACCAGACTTCGAGCTACGAGAGTCCTCCATACCAGGAG
CTGGCCTGGGGATCTGGGCCAAGCGGAAGATGGAAATCGGGGAGAGGTTTGGCCCCTACGTGGTGACGCC
CCGGGCCGCACTGAAGGAGGCCGACTTTGGATGGGAGATGCTGACGGATACAGAGGTGTCATCCCAGGAG
AGCTGCATCAAAAAGATCTCTGAAGACTTGGGTAGCGAGAAGTTCTGCGTGGATGCCAATCAGGCGGGGT
CTGGCAGCTGGCTCAAGTACATCCGTGTAGCGTGTTCCTGTGATGACCAAAACCTCGCCATGTGTCAGAT
CAACGAACAGATTTACTATAAAGTCATTAAGGACATCGAGCCTGGAGAGGAACTGTTGGTGCATGTGAAA
GAAGGTGCCTACTCCTTGGGTGTCATGGCCCCCAGCTTGGATGAGGACCCCACATTCCGCTGTGATGAGT
GTGATGAGCTCTTCCAGTGCAGGCTGGACCTGAGGCGCCACAAGAAGTACGCGTGCAGCTCTGCAGGAGC
CCAGCTCTACGAGGGCCTAGGGGAGGAACTCAAGCCCGAGGGCCTTGGCGTGGGCAGCGACGGGCAAGCG
CATGAGTGCAAGGATTGCGAGCGGATGTTCCCCAACAAGTACAGCTTGGAGCAACACATGATCGTCCACA
CGGAAGAGCGTGAGTACAAATGTGACCAGTGTCCCAAGGCCTTCAACTGGAAGTCCAACCTCATCCGCCA
CCAGATGTCTCACGACAGTGGCAAGCGCTTCGAATGTGAAAACTGTGTCAAGGTGTTCACGGACCCCAGC
AACCTCCAGCGTCACATCCGCTCACAGCATGTCGGTGCCCGGGCCCATGCCTGCCCTGACTGTGGCAAGA
CCTTCGCCACATCCTCTGGCCTCAAACAGCACAAGCATATCCACAGCACGGTGAAGCCATTCATATGCGA
GGTCTGCCACAAGTCCTACACGCAGTTCTCCAACCTGTGCCGGCACAAGCGGATGCACGCCGACTGCAGG
ACGCAGATCAAGTGCAAGGACTGTGGGCAGATGTTCAGCACTACCTCCTCCCTCAACAAGCATCGGAGAT
TCTGCGAGGGCAAGAACCATTACACGCCTGGCAGCATCTTCACCCCAGGCCTGCCCTTGACCCCCAGCCC
CATGATGGACAAGACAAAACCCTCCCCGACCCTCAACCACGGGGGCCTAGGCTTCAGCGAGTACTTCCCC
TCCAGACCTCATCCTGGGAGCCTGCCCTTCTCGGCTGCTCCTCCGGCCTTCCCCGCACTCACTCCGGGCT

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TCCCGGGCATCTTTCCTCCATCCCTGTACCCACGACCACCTCTGCTACCTCCCACGCCGCTGCTCAAGAG
CCCCCTGAACCACGCGCAGGACGCCAAGCTACCCAGCCCGCTGGGAAACCCAGCCCTGCCCCTTGTCTCC
GCGGTCAGCAATAGCAGCCAGGGTGCCACAGCGGCCACCGGGTCAGAGGAGAAATTTGATGGCCGCTTGG
AAGACGCATATGCGGAGAAGGTCAAAAATAGGAGCCCTGACATGTCGGATGGCAGTGACTTTGAGGATAT
CAACACCACGACCGGGACAGACTTGGACACTACCACGGGCACGGGGTCAGACCTGGACAGCGACCTGGAC
AGTGACAGAGACAAAGGCAAGGACAAGGGGAAGCCAGTGGAGAGCAAACCTGAGTTTGGGGGTGCATCTG
TGCCCCCTGGGGCCATGAACAGTGTGGCCGAGGTACCGGCCTTCTACTCACAGCATTCCTTCTTCCCGCC
ACCCGAGGAACAGCTGCTGACGGCCTCGGGAGCTGCCGGCGACTCCATCAAGGCCATCGCGTCCATCGCG
GAGAAATACTTCGGTCCTGGCTTCATGAGCATGCAGGAGAAGAAGCTGGGCTCACTACCCTACCACTCCG
TGTTCCCCTTCCAGTTCCTGCCTAACTTTCCCCACTCCCTCTACCCCTTTACGGACCGAGCCCTCGCCCA
CAACTTGCTGGTCAAGGCTGAGCCAAAGTCACCCCGGGATGCCCTCAAGGTGGGCGGCCCCAGTGCGGAG
TGCCCCTTCGACCTCACCACCAAACCAAAAGAGGCCAAACCCGCCCTGCTCGCACCCAAGGTCCCCCTCA
TCCCCTCATCTGGCGAGGAACAGCCACTGGACCTGAGCATCGGCAGCAGGGCCAGGGCAAGCCAGAACGG
AGGTGGCCGTGAGCCGCGGAAGAACCACGTCTACGGTGAACGGAAGCCGGGGGTCAGCGAGGGGCTGCCT
AAGGTGTGCCCAGCACAGCTGCCCCAGCAGCCCTCCTTGCATTATGCTAAGCCTTCACCGTTCTTCATGG
ATCCCATCTACAGGGTAGAAAAGCGGAAGGTGGCAGACCCTGTGGGAGTCCTGAAAGAGAAGTACCTGCG
GCCGTCCCCACTTCTGTTCCACCCCCAGATGTCAGCCATAGAAACCATGACGGAGAAGCTGGAGAGCTTT
GCAGCCATGAAGGCCGACTCAGGCAGCTCCCTGCAGCCCCTGCCTCACCACCCGTTCAACTTCCGCTCCC
CACCCCCAACGCTCTCGGATCCCATCCTCAGGAAGGGGAAGGAGAGATACACGTGCAGGTACTGTGGCAA
GATCTTCCCCAGATCTGCAAATCTCACAAGACATCTGAGGACACACACAGGGGAGCAGCCATACAGGTGC
AAGTACTGTGACCGGTCATTCAGCATCTCCTCCAACCTCCAGCGGCACGTGAGGAACATCCACAACAAAG
AGAAGCCGTTCAAGTGCCATCTGTGCAACCGCTGCTTCGGGCAGCAGACCAACCTAGACCGGCACCTGAA
GAAGCACGAACACGAGGGCGCACCAGTGAGCCAGCACTCCGGGGTGCTCACGAACCACCTGGGCACCAGC
GCCTCCTCCCCCACCTCCGAGTCGGACAACCATGCACTTTTAGATGAGAAGGAAGATTCTTACTTCTCCG
AGATCCGAAACTTCATCGCCAACAGCGAGATGAACCAGGCATCCACTCGAATGGACAAACGGCCTGAGAT
CCAAGACCTGGACAGCAACCCACCGTGTCCAGGCTCAGCCAGTGCAAAGCCAGAGGACGTAGAGGAGGAG
GAAGAGGAGGAGCTGGAGGAAGAGGATGATGACAGCTTAGCCGGGAAGTCACAGGAGGACACGGTGTCCC
CCACACCTGAGCCCCAAGGAGTCTATGAAGATGAAGAGGATGAGGAACCACCCAGCCTGACCATGGGCTT
TGACCATACCCGGAGGTGTGTTGAGGAGCGAGGAGGCGGCCTGTTAGCTTTGGAGCCGACGCCGACCTTT
GGGAAGGGGCTGGATCTCCGCAGAGCAGCTGAGGAAGCATTTGAAGTTAAAGATGTGCTTAATTCCACCT
TAGATTCTGAGGTTTTAAAACAAACCCTGTACAGGCAGGCTAAGAACCAGGCATATGCAATGATGCTGTC
CCTCTCTGAAGACACTCCTCTCCACGCCCCCTCCCAGAGCTCACTGGATGCTTGGTTGAACATCACAGGA
CCCTCGTCAGAGTCCGGAGCCTTTAACCCCATCAACCACCTCTGA

ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGA
TTACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-NotI

ACCN: NM_001291026

Insert Size: 3825 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: Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.

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_001291026.1, NP_001277955.1
RefSeq Size:	8602 bp
RefSeq ORF:	3825 bp
Locus ID:	70673
UniProt ID:	A2A935
Cytogenetics:	4 E2
Gene Summary:	Binds DNA and functions as a transcriptional regulator (PubMed:18483224). Displays histone methyltransferase activity and monomethylates 'Lys-9' of histone H3 (H3K9me1) in vitro (PubMed:22939622). Probably catalyzes the monomethylation of free histone H3 in the cytoplasm which is then transported to the nucleus and incorporated into nucleosomes where SUV39H methyltransferases use it as a substrate to catalyze histone H3 'Lys-9' trimethylation (PubMed:22939622). Likely to be one of the primary histone methyltransferases along with MECOM/PRDM3 that direct cytoplasmic H3K9me1 methylation (PubMed:22939622). Functions in the differentiation of brown adipose tissue (BAT) which is specialized in dissipating chemical energy in the form of heat in response to cold or excess feeding while white adipose tissue (WAT) is specialized in the storage of excess energy and the control of systemic metabolism (PubMed:17618855, PubMed:18483224). Together with CEBPB, regulates the differentiation of myoblastic precursors into brown adipose cells (PubMed:18719582, PubMed:19641492). Functions as a repressor of TGF-beta signaling. [UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) uses an alternate in-frame splice site in the 5' coding region, compared to variant 1. It encodes isoform 3, which is shorter by an amino acid, 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.