

Product datasheet for **MC229447**

Prdm16 (NM_001291029) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Prdm16 (NM_001291029) 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: >MC229447 representing NM_001291029
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGCGATCCAAGGCGAGGGCGAGGAAGCTAGCCAAAAGTGACGGTGACGTTGTAATAATATGTATGAAC
 CTGACCCGGACCTGCTGGCCGGCCAGAGTGCCGAGGAGAGACCGAAGACGGCATCTGTCCCCATCCC
 CATGGGGCCACCGTCCCCCTTCCCACCCAGCGAGGACTTCACTCCAAGGAGGGCTCGCCCTATGAGGCT
 CCTGTCTACATTCCTGAAGACATTCCAATCCCACCCAGACTTCGAGCTACGAGAGTCTCCATACCAGGAG
 CTGGCCCTGGGGATCTGGGCCAAGCGGAAGATGGAATCGGGGAGAGGTTTGGCCCTACGTGGTGACGCC
 CCGGGCCGCACTGAAGGAGGCCGACTTTGGATGGGAGCAGATGCTGACGGATACAGAGGTGCATCCAG
 GAGAGTGCATCAAAAAGCAGATCTCTGAAGACTTGGGTAGCGAGAAGTTCTGCGTGGATGCCAATCAGG
 CGGGTCTGGCAGCTGGCTCAAGTACATCCGTGTAGCGTGTCTGTGATGACCAAAACCTCGCCATGTG
 TCAGATCAACGAACAGATTTACTATAAAGTCATTAAGGACATCGAGCCTGGAGAGGAAGTGTGGTGCAT
 GTGAAAGAAGGTGCCTACTCCTTGGGTGCATGGCCCCAGCTTGGATGAGGACCCACATTCCGCTGTG
 AGGAGCCAGCTCTACGAGGGCCTAGGGGAGGAACTCAAGCCGAGGGCCTTGGCGTGGCAGCGACGGG
 CAAGCGCATGAGTGCAAGGATTGCGAGCGGATGTTCCCAACAAGTACAGCTTGGAGCAACACATGATCG
 TCCACACGGAAGAGCGTGAGTACAAATGTGACCAAGTGTCCCAAGGCCCTCAACTGGAAGTCCAACCTCAT
 CCGCCACCCAGATGTCTACGACAGTGGCAAGCGCTTCAATGTGAAAAGTGTGTCAAGGTGTTACGGGAC
 CCCAGCAACCTCCAGCGTCACATCCGCTCACAGCATGTCGGTGCCCGGGCCCATGCCTGCCCTGACTGTG
 GCAAGACCTTCGCCACATCCTCTGGCCTCAAACAGCACAAGCATATCCACAGCACGGTGAAGCCATTTCAT
 ATGCGAGGTCTGCCACAAGTCTACACGAGTTCTCAACCTGTGCCGGCACAAGCGGATGCACGCCGAC
 TGCAGGACGCAGATCAAGTGCAAGGACTGTGGCAGATGTTGAGCACTACCTCCTCCTCAACAAGCATC
 GGAGATTCTGCGAGGGCAAGAACCATTACAGCCTGGCAGCATCTTACCCAGGCTGCCCTTGACCCC
 CAGCCCCATGATGGACAAGACAAAACCTCCCCGACCCTCAACCAGGGGGCCTAGGCTTACGCGAGTAC
 TTCCTCCAGACCTCATCTGGGAGCCTGCCCTTCTCGGCTGCTCCTCCGGCCTTCCCCGACTCACTC



[View online »](#)

CGGGCTTCCC GGGCATCTTTCCTCCATCCCTGTACCCACGACCACCTCTGCTACCTCCCACGCCGCTGCT
 CAAGAGCCCCCTGAACCACGCGCAGGACGCCAAGCTACCCAGCCCCTGGGAAACCCAGCCCTGCCCTT
 GTCTCCGCGGT CAGCAATAGCAGCCAGGGTGCCACAGCGGCCACCGGGT CAGAGGAGAAATTTGATGGCC
 GCTTGGAAAGCGCATATGCGGAGAAGGTCAAAAATAGGAGCCCTGACATGTCGGATGGCAGTGACTTTGA
 GGATATCAACACCACGACCGGGACAGACTTGGACACTACCACGGGCACGGGGT CAGACCTGGACAGCGAC
 CTGGACAGTGACAGAGACAAAGGCAAGGACAAGGGGAAGCCAGTGGAGAGCAAACCTGAGTTTGGGGGTG
 CATCTGTGCCCCCTGGGGCCATGAACAGTGTGGCCGAGGTACCGCCTTCTACTCACAGATTCCCTTCT
 CCCGCCACCCGAGGAACAGCTGCTGACGGCCTCGGGAGCTGCCGGCGACTCCATCAAGGCCATCGCGTCC
 ATCGCGGAGAAATACTTCGGTCTCGCTTCATGAGCATGCAGGAGAAGAAGCTGGGCTACTACCCTACC
 ACTCCGTGTTCCCTTCCAGTTCCTGCCTAACTTTCCCCTACTCCCTTACCCCTTTACGGACCGAGCCCT
 CGCCACAACCTTGTGGTCAAGGCTGAGCAAAGTCAACCCGGGATGCCCTCAAGGTGGGCGGCCCAAGT
 GCGGAGTGCCCTTTCAGCTCACCACCAAACAAAAGAGGCCAAACCCGCCCTGCTCGCACCCAAGTCC
 CCCTCATCCCCTCATCTGGCGAGGAACAGCCACTGGACCTGAGCATCGGCAGCAGGGCCAGGGCAAGCCA
 GAACGGAGGTGGCCGTGAGCCGCGGAAGAACCAGTCTACGGTGAACGGAAGCCGGGGT CAGCGAGGGG
 CTGCCTAAGGTGTGCCACAGCTGCCCCAGCAGCCCTCCTTGCAATTGCTAAGCCTTACCCTTCT
 TCATGGATCCCATCTACAGCAGGGTAGAAAAGCGGAAGGTGGCAGACCCTGTGGGAGTCCGAAAGAGAA
 GTACCTGCGGCCGTCCTCCACTTCTGTTCCACCCCAAGATGTCAGCCATAGAAACCATGACGGAGAAGCTG
 GAGAGCTTTGAGCCATGAAGGCCGACTCAGGCAGCTCCCTGCAGCCCCTGCCTCACCACCGTTCAACT
 TCCGCTCCCCACCCCAACGCTCTCGGATCCCATCCTCAGGAAGGGGAAGGAGAGATACACGTGCAGGTA
 CTGTGGCAAGATCTTCCCAGATCTGCAAACTCAACAAGACATCTGAGGACACACAGGGGAGCAGCCA
 TACAGGTGCAAGTACTGTGACCGGTCATTCAGCATCTCCTCAACCTCCAGCGGCACGTGAGGAACATCC
 ACAACAAAGAGAAGCCGTTCAAGTGCCATCTGTGCAACCGCTGCTTCGGGCAGCAGACCAACCTAGACCG
 GCACCTGAAGAAGCACGAACACGAGGGCGCACCAGTGGCCAGCACTCCGGGGTGT CACGAACCCACCTG
 GGCACCAGCGCCTCCTCCCCACCTCCGAGTCGGACAACCATGCACTTTTAGATGAGAAGGAAGATTCTT
 ACTTCTCCGAGATCCGAACTTCAATCGCCAACAGCGAGATGAACCAGGCATCCACTCGAATTGGACAAACG
 GCCTGAGATCCAAGACCTGGACAGCAACCCACCGTGTCCAGGCTCAGCCAGTGC AAAGCCAGAGGACGTA
 GAGGAGGAGGAAGAGGAGGAGCTGGAGGAAGAGGATGATGACAGCTTAGCCGGGAAGT CACAGGAGGACA
 CGGTGTCCCCACACCTGAGCCCCAAGGAGTCTATGAAGATGAAGAGGATGAGGAACCCACCGCTGAC
 CATGGGCTTTGACCATAACCCGGAGGCATATGCAATGA

ACGGGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGA
 TTACAAGGATGACGACGATAAAGGTTAA

- Restriction Sites:** SgfI-NotI
- ACCN:** NM_001291029
- Insert Size:** 3537 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_001291029.1](#), [NP_001277958.1](#)

RefSeq Size: 8436 bp

RefSeq ORF: 3537 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 (4) uses an alternate in-frame splice site each in the 5' and 3' coding regions, and lacks an alternate exon in the 3' coding region, compared to variant 1. It encodes isoform 4, which is shorter and has a 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.