

Product datasheet for **MC227817**

Mid1 (NM_001290512) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Mid1 (NM_001290512) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Mid1
Synonyms:	61B3-R; DXHXS1141; Fxy; Trim18
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >MC227817 representing NM_001290512
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGCATCGCC**

ATGACCTTGCACAAGGATGCATTTTCAAAGCTTGACACTGAGCAAACTTGGAGAGTAATCTCACCAATC
 TTATTAAGAGAAAACAGAACTGGAGACTCTTTTGGCTAAACTCATCCAACTTGTCAACATGTTGAAGT
 CAATGCATCCCGTCAAGAAGCCAACTGACAGAAGAATGTGATCTTCTCATTGAAATCATTACAGCAACGA
 AGACAAATTATTGGAACAAAGATTAAGAAGGCAAGGTGATCAGGCTCCGCAAGTTAGCTCAGCAGATTG
 CAAACTGTAAACAGTGCCTTGAGAGGTCTGCATCGCTCATCTCGCAAGCGGAGCACTCGTGAAAGAAAA
 TGACCACGCCGTTTTCTACAGACAGCAAGAATATCACTGAGAGAGTCTCCATGGCAACTGCATCTCTCC
 CAGGTCCTAATCCCGAAATCAACCTCAATGACACGTTTGACACTTTTGCCTTGGATTTTCCCGGGAGA
 AGAAACTGCTAGAATGTCTGGATTACCTAACAGCTCCCAACCCTCCCGCATTAGAGAAGAGCTCTGCAC
 CGTTTCTACGACACCATCACCGTCCACTGGACCTCAGAGGACGAGTTTCAGCGTGGTCTCCTACGAGCTC
 CAGTACACCATATTCACCGGACAAGCCAATGTTGTGAGTCTGTGTAACCTCGGCGGACAGCTGGATGATCG
 TGCCCAACATCAAGCAGAACCACTACACCGTGCACGGCCTGCAAAGTGGACCAAGTATATCTTACCGGT
 GAAGGCCATCAACCAGGCGGGCAGCCGTAGCAGCGAGCCCGAAAAGCTGAAGACCAACAGTCAGCCGTTT
 AGACTGGATCCCAATCGGCTCATCGCAAGCTGAAGGTGTCCCACGACAACCTGACTGTCGAGCGCGACG
 AGTCGTCCTCTAAGAAGAGTCACGCGCCGGAGCGCTTCGCTGGTCAAGGGAGCTACGGAGTGGCTGGCAA
 CGTGTTCATCGACAGCGCCGCTCACTACTGGGAAGTGGTACCAGCGGAAGCACATGGTACGCCATCGGC
 CTGGCGTACAGATCGGCGCCGAAACACGAGTGGATCGGAAGAACGCGGCGTCTGGGCCCTCTGCCGCT
 GCCACAACCCTGGGCGGTGCGACACGAGGCAAGGAGACCCCATCGGCGCGCCCTCACCTCAGGCG
 CGTCGGCGTCTGCTGGACTACGACAACGCTCCATCGCCTTCTACGACGCTCTGAGCTCCGTCACCTC
 CACACCTTCCACGCGGCGCTCGCGCAGCCCGTGTGCCCACTTACCGTGTGGAACAAGTGTCTGACCA
 TCGTCACGGGTCTGCCATCCCGGACCATCTGGACTGTACGGAGCAGCGACCT**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001290512

Insert Size: 1386 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_001290512.1](#), [NP_001277441.1](#)

RefSeq Size: 3158 bp

RefSeq ORF: 1386 bp

Locus ID: 17318

Cytogenetics: X 79.19 cM

Gene Summary: Has E3 ubiquitin ligase activity towards IGBP1, promoting its monoubiquitination, which results in deprotection of the catalytic subunit of protein phosphatase PP2A, and its subsequent degradation by polyubiquitination.[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (6) differs in the 5' UTR, lacks a portion of the 5' coding region, and uses an alternate in-frame splice site, compared to variant 1. It initiates translation at an alternate start codon. The encoded isoform (4) has a distinct N-terminus and is shorter than isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.