

Product datasheet for **MC226564**

Mbnl1 (NM_001253710) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Mbnl1 (NM_001253710) Mouse Untagged Clone
Tag: Tag Free
Symbol: Mbnl1
Synonyms: Mbnl; mKIAA0428
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC226564 representing NM_001253710
Red=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGGCCATGCTGGCCAGCAAATGCAGTTAGCCAATGCCATGATGCCCGGTGCCCGTTGCAGCCCGTGC
CAATGTTTTAGTTGCACCAAGCTTAGCCACCAGTGCATCAGCAGCCTTTAACCCCTACCTGGGGCCTGT
TTCCCAAGCCTGGTTCCAGCAGAGATCTTCCGACTGCACCAATGTTGGTCACGGGGAATCCTGGAGTT
CCAGTGCCAGCAGCTGCCGAGCTGCTGCACAGAAGTTAATGCGGACAGACAGACTGGAGGTGTGTGCGAG
AGTACCAGCGTGGCAATTGCAACAGAGGAGAAAATGACTGTCGGTTTGTCTCATCTGCTGACAGCACAAT
GATTGATACCAATGACAACACAGTCACTGTCTGCATGGATTACATCAAGGGGAGATGCTCTCGGGAAAAG
TGCAAATACTTCCATCTCCCGCACACCTGCAAGCCAAGATCAAGGCTGCCCAATACCAGGTCAACCAGG
CTGCAGCAGCACAGGCTGCAGCTACTGCAGTGCCATGGGAATTCCTCAAGCTGTACTTCCCCATTGCC
AAAGAGGCCTGCTCTTGAATAAACAACGGTGCCACCGCAGTCTTAACTGTTATTTTCCAATACCAA
CAGGCTTAGCCAACATGCAGTTACAGCAGCATAACAGCATTCTCCACCAGGCTCAATATTGTGCATGA
CACCCGCTACAAGTGTGATACCCATAATATCTGCCGAACATCTGACTAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001253710
Insert Size: 750 bp



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| 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: | <ol style="list-style-type: none"> 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: | <u>NM_001253710.2, NP_001240639.1</u> |
| RefSeq Size: | 4529 bp |
| RefSeq ORF: | 750 bp |
| Locus ID: | 56758 |
| Cytogenetics: | 3 D |
| Gene Summary: | <p>Mediates pre-mRNA alternative splicing regulation. Acts either as activator or repressor of splicing on specific pre-mRNA targets. Inhibits cardiac troponin-T (TNNT2) pre-mRNA exon inclusion but induces insulin receptor (IR) pre-mRNA exon inclusion in muscle. Antagonizes the alternative splicing activity pattern of CELF proteins. Regulates the TNNT2 exon 5 skipping through competition with U2AF2. Inhibits the formation of the spliceosome A complex on intron 4 of TNNT2 pre-mRNA. Binds to the stem-loop structure within the polypyrimidine tract of TNNT2 intron 4 during spliceosome assembly. Binds to the 5'-YGCU(U/G)Y-3'consensus sequence. Binds to the IR RNA. Binds to CUG triplet repeat expansion in myotonic dystrophy muscle cells by sequestering the target RNAs (By similarity). [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (4) lacks the exon containing the start codon and lacks an alternate exon in the 3' end compared to variant 1 that causes a frameshift. The resulting isoform (4) is shorter at the N-terminus and has a shorter and 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.</p> |