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Product datasheet for MC226603

Mbnl1 (NM_001253711) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Mbnl1 (NM_001253711) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Mbnl1
Synonyms:	Mbnl; mKIAA0428
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226603 representing NM_001253711 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGCCATGCTGGCCCAGCAAATGCAGTTAGCCAATGCCATGATGCCCGGTGCCCCGTTGCAGCCCGTGC CAATGTTTTCAGTTGCACCAAGCTTAGCCACCAGTGCATCAGCAGCCTTTAACCCTTACCTGGGGCCTGT TTCCCCAAGCCTGGTTCCAGCAGAGATCTTGCCGACTGCACCAATGTTGGTCACGGGGAATCCTGGAGTT CCAGTGCCAGCAGCTGCCGCAGCTGCTGCACAGAAGTTAATGCGGACAGACAGACTGGAGGTGTGTCGAG AGTACCAGCGTGGCAATTGCAACAGAGGAGAAAATGACTGTCGGTTTGCTCATCCTGCTGACAGCACAAT GATTGATACCAATGACAACACAGTCACTGTCTGCATGGATTACATCAAGGGGAGATGCTCTCGGGAAAAG TGCAAATACTTCCATCCTCCCGCACACCTGCAAGCCAAGATCAAGGCTGCCCAATACCAGGTCAACCAGG CTGCAGCAGCACAGGCTGCAGCTACTGCAGCTGCCATGACTCAGTCGGCTGTCAAATCACTGAAGCGACC CCTCGAGGCAACCTTTGACCTGGGAATTCCTCAAGCTGTACTTCCCCCATTGCCAAAGAGGCCTGCTCTT GAAAAAACCAACGGTGCCACCGCAGTCTTTAACACTGGTATTTTCCAATACCAACAGGCTCTAGCCAACA TGCAGTTACAGCAGCATACAGCATTTCTCCCACCAGATACCCATAATATCTGCCGAACATCTGACTAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001253711
Insert Size:	768 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:	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_001253711.2, NP_001240640.1
RefSeq Size:	4547 bp
RefSeq ORF:	768 bp
Locus ID:	56758
Cytogenetics:	3 D
Gene Summary:	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] Transcript Variant: This variant (5) lacks the exon containing the start codon, contains an alternate in-frame exon, and lacks an alternate segment compared to variant 1, that causes a frameshift. The resulting isoform (5) is shorter at the N-terminus, contains an alternate internal segment, 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.