

## Product datasheet for **SC116449**

### MEF2B (BORCS8-MEF2B) (NM\_005919) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	MEF2B (BORCS8-MEF2B) (NM_005919) Human Untagged Clone
Tag:	Tag Free
Symbol:	BORCS8-MEF2B
Synonyms:	LOC729991-MEF2B; MEF2B; MEF2BNB-MEF2B; RSRFR2
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Cell Selection:	None
Fully Sequenced ORF:	>NCBI ORF sequence for NM_005919, the custom clone sequence may differ by one or more nucleotides

```
ATGGGGAGGAAAAAATCCAGATCTCCCGCATCCTGGACCAAAGGAATCGGCAGGTGACGTTACCAAGC
GGAAGTTCGGGCTGATGAAGAAGGCCTATGAGCTGAGCGTGCTCTGTGACTGTGAGATAGCCCTCATCAT
CTTCAACAGCGCCAACCGCCTCTCCAGTATGCCAGCACGGACATGGACCGTGTGCTGCTGAAGTACACA
GAGTACAGCGAGCCCCACGAGAGCCGCACCAACTGACATCCTCGAGACGCTGAAGCGGAGGGGATTG
GCCTCGATGGGCCAGAGCTGGAGCCGGATGAAGGGCCTGAGGAGCCAGGAGAGAAGTTTCGGAGGCTGGC
AGGCGAAGGGGTGATCCGGCCTTGCCCGACCCCGGCTGTATCCTGCAGCTCCTGCTATGCCAGCCCA
GATGTGGTATACGGGGCCTTACCGCCACCAGGCTGTGACCCAGTGGGCTTGGGAAGCACTGCCCGCCC
AGAGCCGCCATCTCCCTTCGACCAGCAGCCCCAAAGCCGGGCCCCAGGCCTGGTGCACCCTCTCTT
CTACCAAGCCACCTACCAGCAAGACACCACCCCACTGTACCTGCCGACGGAAGGGCGGAGGTCAGAC
CTGCCTGGTGGCCTGGCTGGGCCCGAGGGGGACTAAACACCTCCAGAAGCCTCTACAGTGGCCTGCAGA
ACCCCTGCTCCACTGCAACTCCCGACCCCACTGGGGAGCTTCCCTTCCCTCCCGGAGGCCCCCACT
GGGGGCCGAAGCCTGGGCGAGGAGGGTCCCCAACCCGCGCGCCTCCCGCCGACCCCCCACTCAGCA
TCAAGTCTGAGCGCCTCTCCGGCCCCGGGGGCCCGGCGACTTTCCTAAGACCTTCCCTATCCCTT
GCTCCTCGCCCGTCCCTGGCAGAGCCTCTGCGCCTGGGCCCGCCTGCGCCGCTGCCCTTGGCCGAC
GGCTGGCCCCGGTAGGAGATCACCCGGTGGCACAGCCAGAGCGCTCGCCAGGTACGGCGAGGGCACGT
GGGGACCCACCTCCCTCCAGGCCTCTTCCAGAGAAGACCAACAGTGA
```



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**5' Read Nucleotide Sequence:**

>OriGene 5' read for NM\_005919 unedited  
 TAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGCGCTATGGAGGAGCCGGA  
 GATGCAGCTCAAGGGGAAGAAAGTACACGGACAGGTTCACTGAGAGCGTCTACGTCTGG  
 CCAACGAGCCATCCGTGGCCCTGTACCGGCTGCAGGAGCATGTGCGTCGCTCCCTCCCGG  
 AGCTGGCCAGCACAAGGCAGACATGCAGCGTTGGGAGGAGCAGAGCCAGGGAGCCATCT  
 ACACTGTGGAGTACGCTGCAGCGCCGTGAAGAACCTGGTGGACAGCAGCGTCTACTTCC  
 GCAGCGTGGAGGTTCTGCTCAAACAGGCCATCAGCATCCGGGACCATATGAATGCCAGTG  
 CCCAGGGCCACAGCCCGGAGGAACCCCGCCCTCCTCAGCCTGATCCTGGAAGAGAC  
 TCGGGGCCCCAGCCTCCGCCAACCCAGAGACGGGGTTTACCATGTTGGCTAGGCTGG  
 TCTCAAACCTCTGAGCTCGTGATCCTCCCGCTCAGCCTCCCAAAGTGCTGGGATTATAG  
 GTGTGAGCCACCCAGCCAGCCTTGGTTCTCCCTTTCTCATCTGGATAAGGAAGGCTGG  
 ACTGCACCTTCTCTACAGGCTGAGTTGGACATTCGAGATCTACCCTCCCAACCTGCATT  
 CTGCCTCAAGCAGCAACGCCACCCAGGCTCANGCCACATGGAGAAGCCACCCCTAGNT  
 CCAGTGGTGGATGTGGCACCTCGGCCTGGCCATCAGAGCTCCCTTGTCTAGTTCCTATG  
 ATGGTTNGAGATGGACACGTGACCCATGAGCGACCTTCTGGGAGTTCTCCAGGAACAC  
 AGGAAGGTGAGCTGGGTGTATGGGAACAGGCCCGCCAGGGGGTCCGGGGACCTGAAAA  
 CATGGGGAGCCCTGGATCACTGTACTGAACTA

**3' Read Nucleotide Sequence:**

>OriGene 3' read for NM\_005919 unedited  
 GCCGCAATCTAGAGTCGAGTTTTTTTTTTTTTTTTTCCATGAAACTGAAGAAATGAAAT  
 TGGCTAGTGTCAGGTACAGTTGGATCCAGGGCTCCACACAATGTTCTCAGGTCCCCCGG  
 AACCCCTCGCCCCGGCTGGTTCCCATACCCAGCTCAACCTTCTGATGCTCCTGGTA  
 GAACTCCCAGGAAAGGTCGTCATTGGGTACGTGTCCATCTCAAACCAATCACTAGGAA  
 CCTAGGACAAGGGAGCTCTGATTGGCCAGGCCGAGGTGCCACATCCACCACTGGAAGT  
 GGGTGGCTTCTCCATGTGGCCTGAGCCTGGGGTGGGCGTTGCTGCTTGAGGCAGAATGCA  
 GGTGGGAGGGTAGATCTGCGAATGTCCAACCTCAGCCTGTAGAGAAGGTGCAGTCCAGCC  
 TTCTTATCCAGATGAAGAAAGGGAACCAAGGCTGGGTGCGGTGGCTCACACCTATAA  
 TCCCAGCACTTTGGGAGGCTGAGGCGGGAGGATCACGAGCTCAGGAGTTTGAGACCAGCC  
 TAGCCAACATGGTGAAACCCCGTCTCTGGGTTGGCGGAGGCTGGGGGGCCCCGAGTCTCT  
 TCCAGGATCAGGCTGAGGAGGGCGGGGGTGGTTCTCCGGGCTGTGGCCCTNNGCACTGG  
 CATTATATGGTCCCGGATGCTGATGGCCTGTTTGAGCAGACCTCCACGCTGCGGAAGT  
 AGACGCTGCTGTCCACCANGTTCTTACGGCGCTGCAGGCGTACTCCACAGTGTAGATGG  
 CTCCCTGGCTCTGCTCCTCCAACGCTGCATGTNTGCCTTGTGCTGGGCCAGCTCGGGGAA  
 GGAGCGACCCCATGCTCCTGCANCCGTACAGGGCCACGNATGGGCTCGTGCCCAAGCCT  
 AAACCCTCTCATGAAACTGCNCGGACTTTCTCCCTTGACTGATTTCCGGCTCTCCTAG  
 CGCCTTGTGCCGAATCCCGG

**Restriction Sites:**

NotI-NotI

**ACCN:**

NM\_005919

**Insert Size:**

1050 bp

**OTI Disclaimer:**

The sequence of an 'OriGene Unique Variant' differs significantly from the associated reference. It represents a novel splice variant from the same gene locus of the reference. Although such variants are true transcripts and present opportunity for discoveries, they are not yet curated by NCBI and should not be used if the exact reference accession sequence is required.

<b>OTI Annotation:</b>	This TrueClone was found to represent an alternative form of the specific reference to which it is associated. Its Open Reading Frame (ORF) may represent a novel form or alternative splice variant. By virtue of it being a true transcript (cDNA clone not PCR product), it provides a biologically relevant copy of its mRNA template. For more details, please evaluate the sequence information provided on this website or contact our customer care specialists.
<b>RefSeq:</b>	<a href="#">NM_005919.1</a> , <a href="#">NP_005910.1</a>
<b>RefSeq Size:</b>	1671 bp
<b>RefSeq ORF:</b>	1098 bp
<b>Locus ID:</b>	4207
<b>UniProt ID:</b>	<a href="#">Q02080</a> , <a href="#">A0A024R7N0</a>
<b>Domains:</b>	MADS
<b>Protein Families:</b>	Transcription Factors
<b>Gene Summary:</b>	<p>This gene represents numerous read-through transcripts that span GeneID:729991 and 100271849. Many read-through transcripts are predicted to be nonsense-mediated decay (NMD) candidates, and are thought to be non-coding. Some transcripts are predicted to be capable of translation reinitiation at a downstream AUG, resulting in expression of at least one isoform of myocyte enhancer factor 2B (MEF2B) from this read-through locus. At least one additional MEF2B variant and isoform can be expressed from a downstream promoter, and is annotated on GeneID:100271849. [provided by RefSeq, Oct 2010]</p> <p>Transcript Variant: This variant (1) lacks two alternate exons in the 5' region and one alternate exon in the 3' region, compared to variant 2. This variant is thought to be protein coding because translation can reinitiate at the downstream AUG, resulting in expression of an isoform of MEF2B (geneID:100271849). Isoform b has a shorter and distinct C-terminus, compared to MEF2A isoform a (NP_001139257.1). 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>