

Product datasheet for **MC227944**

Celf1 (NM_001244891) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Celf1 (NM_001244891) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Celf1
Synonyms:	1600010O03Rik; AA407467; Brunol2; CUG-BP; CUG-BP1; CUGBP; Cugbp1; D2Wsu101e; HNAB50; NAB50
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC227944 representing NM_001244891
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGCATCGCC**

ATGAACGGCACCCCTGGACCACCCAGACCAACCAGATCTTGATGCTATCAAGATGTTTGTGGCCAGGTTCC
 CAAGGACCTGGTCTGAGAAAAGACTTGAGGGAGCTTTTTGAGCAGTATGGTGTCTATGAAATCAACAT
 CCTAAGGGATAGGAGCCAAAACCTCCTCAGAGCAAAGGGTGCTGTTTTGTTACATTTTACACCCGTAAA
 GCTGCATTAGAAGCTCAGAATGCTCTCCATAACATGAAGGTCCTCCCTGGGATGCATCACCTATACAGA
 TGAAGCCTGTGACAGTAAAAGAACAATGCTGTGGAAGACAGGAAGCTCTTTATTGGTATGATTTCCAA
 GAAGTGTACTGAAAATGACATCCGAGTCATGTTTTCTTCGTTTGGACAGATTGAAGAGTGCCGGATATTG
 CGGGGACCTGATGGCTTGAGCAGAGTTGTGCATTTGTGACTTTACTACAAGAACCATGGCACAGACAG
 CTATCAAAGCAATGCACCAAGCACAAACCATGGAGGGTTGCTCATCCCCAATGGTGGTAAAGTTTGCCGA
 CACCCAGAAGGACAAAGAACAGAAGAGAATGGCCAGCAGCTCCAGCAGCAGATGCAGCAGATCAGTGCA
 GGGTCTGTGTGGGAAACCTGGCTGGTCTGAACACACTTGGACCCAGTACTTAGCACTTTATTTGCAGC
 TCCTACAGCAGACTGCCTCCTCTGGGAACCTCAACACCCTGAGCAGCCTCCACCCAAATGGGAGGGTTAAA
 TGCAATGCAGCTACAGAAATTTGGCTGCACTAGCTGCTGCAGCTAGTGCAGCTCAGAACACACCAAGTGGT
 ACCAATGCTCTCACTACATCCAGCAGTCCCCTCAGCGTACTCACCAGTTCAGGGTCTTCACCGAGCTCCA
 GCAGCAGTAATTTGTCAACCCCATAGCCTCACTTGGAGCCCTGCAAACATTGGCCGGAGCAACAGCTGG
 CCTCAACGTTGGCTCATTGGCAGGGATGGCTGCTTTGAATGGTGGTCTGGGCAGCAGTGGCCTTTCCAAT
 GGCCTGGGAGTACCATGGAAGCCCTCACCCAGGCGTATTCTGGTATCCAGCAATATGCTGCTGCAGCCC
 TCCCACCTGTACAACCAGAATTTATTGACACAGCAGAGTATTGGTGTCTGCTGGAAGCCAGAAGGAAGG
 TCCAGAAGGAGCCAACCTGTTTCTATCACCTGCCCCAGGAGTTTGGAGACCAGGACTTACTGCAGATG
 TTTATGCCCTTTGGGAATGTCGTGTCGGCCAAGGTTTTTCATAGACAAGCAGACAAACCTGAGCAAGTGT
 TTGGTTTTGTAAGTTATGACAATCCTGTCTCAGCTCAAGCTGCCATCCAGTCCATGAACGGCTTTCAAAT
 TGGAAATGAAGAGGCTTAAAGTGCAGCTCAAACGTTCAAGAATGATAGTAAGCCCTACTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM_001244891
- Insert Size:** 1461 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_001244891.1](#), [NP_001231820.1](#)

RefSeq Size: 7849 bp

RefSeq ORF: 1461 bp

Locus ID: 13046

UniProt ID: [P28659](#)

Cytogenetics: 2 50.44 cM

Gene Summary:

RNA-binding protein implicated in the regulation of several post-transcriptional events. Involved in pre-mRNA alternative splicing, mRNA translation and stability. Mediates exon inclusion and/or exclusion in pre-mRNA that are subject to tissue-specific and developmentally regulated alternative splicing (By similarity). Specifically activates exon 5 inclusion of cardiac isoforms of TNNT2 during heart remodeling at the juvenile to adult transition (By similarity). Acts as both an activator and repressor of a pair of coregulated exons: promotes inclusion of the smooth muscle (SM) exon but exclusion of the non-muscle (NM) exon in actinin pre-mRNAs (By similarity). Activates SM exon 5 inclusion by antagonizing the repressive effect of PTB (By similarity). Promotes exclusion of exon 11 of the INSR pre-mRNA (By similarity). Inhibits, together with HNRNPH1, insulin receptor (IR) pre-mRNA exon 11 inclusion in myoblast (By similarity). Increases translation and controls the choice of translation initiation codon of CEBPB mRNA (By similarity). Increases mRNA translation of CEBPB in aging liver. Increases translation of CDKN1A mRNA by antagonizing the repressive effect of CALR3 (By similarity). Mediates rapid cytoplasmic mRNA deadenylation (By similarity). Recruits the deadenylase PARN to the poly(A) tail of EDEN-containing mRNAs to promote their deadenylation (By similarity). Required for completion of spermatogenesis. Binds to (CUG)_n triplet repeats in the 3' UTR of transcripts such as DMPK and to Bruno response elements (BREs) (By similarity). Binds to muscle-specific splicing enhancer (MSE) intronic sites flanking the alternative exon 5 of TNNT2 pre-mRNA (By similarity). Binds to AU-rich sequences (AREs or EDEN-like) localized in the 3' UTR of JUN and FOS mRNAs. Binds to the IR RNA (By similarity). Binds to the 5'-region of CDKN1A and CEBPB mRNAs (By similarity). Binds with the 5'-region of CEBPB mRNA in aging liver. May be a specific regulator of miRNA biogenesis. Binds to primary microRNA pri-MIR140 and, with CELF2, negatively regulates the processing to mature miRNA (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) has an alternate exon in the 5' region, which results in a downstream AUG start codon, and has an additional segment in the 3' UTR, compared to variant 1. The resulting isoform (2) is shorter at the N-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.