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Product datasheet for TL500635

Celf2 Mouse shRNA Plasmid (Locus ID 14007)

Product data:

Product Type:	shRNA Plasmids
Product Name:	Celf2 Mouse shRNA Plasmid (Locus ID 14007)
Locus ID:	14007
Synonyms:	B230218O03; B230345P09Rik; C88023; CELF-2; CUG-BP2; Cugbp2; D230046B21Rik; Etr-3; mETR-3; Napor
Vector:	pGFP-C-shLenti (TR30023)
E. coli Selection:	Chloramphenicol (34 ug/ml)
Mammalian Cell Selection:	Puromycin
Format:	Lentiviral plasmids
Components:	Celf2 - Mouse, 4 unique 29mer shRNA constructs in lentiviral GFP vector(Gene ID = 14007). 5µg purified plasmid DNA per construct 29-mer scrambled shRNA cassette in pGFP-C-shLenti Vector, TR30021, included for free.
RefSeq:	BC026856, NM_001110228, NM_001110229, NM_001110230, NM_001110231, NM_001110232, NM_001160292, NM_001160293, NM_001310447, NM_001347094, NM_010160, NM_001160292.1, NM_001160293.1, NM_010160.1, NM_010160.2, NM_001110229.1, NM_001110230.1, NM_001110232.1, NM_001110228.1, NM_001110231.1, BC033049, BC130235
UniProt ID:	Q9Z0H4

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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 TNNT2 in embryonic, but not adult, skeletal muscle (By similarity). Activates TNNT2 exon 5 inclusion by antagonizing the repressive effect of PTB (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). Promotes inclusion of exonS 21 and exclusion of exon 5 of the NMDA receptor R1 pre-mRNA (By similarity). Involved in the apoB RNA editing activity (By similarity). Increases COX2 mRNA stability and inhibits COX2 mRNA translation in epithelial cells after radiation injury. Modulates the cellular apoptosis program by regulating COX2-mediated prostaglandin E2 (PGE2) expression. Binds to (CUG)n triplet repeats in the 3' UTR of transcripts such as DMPK (By similarity). Binds to the muscle-specific splicing enhancer (MSE) intronic sites flanking the TNNT2 alternative exon 5 (By similarity). Binds preferentially to UG-rich sequences, in particular UG repeat and UGUU motifs (By similarity). Binds to apoB mRNA, specifically to AU-rich sequences located immediatly upstream of the edited cytidine (By similarity). Binds AU-rich sequences in the 3' UTR of COX2 mRNA. Binds to an intronic RNA element responsible for the silencing of exon 21 splicing. Binds to (CUG)n repeats. May be a specific regulator of miRNA biogenesis. Binds to primary microRNA pri-MIR140 and, with CELF1, negatively regulates the processing to mature miRNA (By similarity).[UniProtKB/Swiss-Prot Function]

shRNA Design:

These shRNA constructs were designed against multiple splice variants at this gene locus. To be certain that your variant of interest is targeted, please contact techsupport@origene.com. If you need a special design or shRNA sequence, please utilize our custom shRNA service.

Performance Guaranteed:

OriGene guarantees that the sequences in the shRNA expression cassettes are verified to correspond to the target gene with 100% identity. One of the four constructs at minimum are guaranteed to produce 70% or more gene expression knock-down provided a minimum transfection efficiency of 80% is achieved. Western Blot data is recommended over qPCR to evaluate the silencing effect of the shRNA constructs 72 hrs post transfection. To properly assess knockdown, the gene expression level from the included scramble control vector must be used in comparison with the target-specific shRNA transfected samples.

For non-conforming shRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the shRNA kit. To arrange for a free replacement with newly designed constructs, please contact Technical Services at techsupport@origene.com. Please provide your data indicating the transfection efficiency and measurement of gene expression knockdown compared to the scrambled shRNA control (Western Blot data preferred).