

## **Product datasheet for TR519801**

## Ythdc1 Mouse shRNA Plasmid (Locus ID 231386)

**Product data:** 

**Product Type:** shRNA Plasmids

**Product Name:** Ythdc1 Mouse shRNA Plasmid (Locus ID 231386)

**Locus ID:** 231386

**Synonyms:** A730098D12Rik; C80342; mKIAA1966

**Vector:** pRS (TR20003)

E. coli Selection: Ampicillin

Mammalian Cell Puromycin

Selection:

Format: Retroviral plasmids

Components: Ythdc1 - Mouse, 4 unique 29mer shRNA constructs in retroviral untagged vector(Gene ID =

231386). 5µg purified plasmid DNA per construct

29-mer scrambled shRNA cassette in pRS Vector, TR30012, included for free.

RefSeq: NM 001347375, NM 001347376, NM 177680, NM 001359907, NM 001359908, NR 153372,

NM 177680.1, NM 177680.3, BC022697, BC037593, BC044650, BC048817, NM 177680.4

UniProt ID: <u>E9Q5K9</u>

**OriGene Technologies, Inc.** 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



## Summary:

Regulator of alternative splicing that specifically recognizes and binds N6-methyladenosine (m6A)-containing RNAs (By similarity). M6A is a modification present at internal sites of mRNAs and some non-coding RNAs and plays a role in the efficiency of mRNA splicing, processing and stability (By similarity). Acts as a key regulator of exon-inclusion or exonskipping during alternative splicing via interaction with mRNA splicing factors SRSF3 and SRSF10 (By similarity). Specifically binds m6A-containing mRNAs and promotes recruitment of SRSF3 to its mRNA-binding elements adjacent to m6A sites, leading to exon-inclusion during alternative splicing (By similarity). In contrast, interaction with SRSF3 prevents interaction with SRSF10, a splicing factor that promotes exon skipping: this prevents SRSF10 from binding to its mRNA-binding sites close to m6A-containing regions, leading to inhibit exon skipping during alternative splicing (By similarity). May also regulate alternative splice site selection (By similarity). Also involved in nuclear export of m6A-containing mRNAs via interaction with SRSF3: interaction with SRSF3 facilitates m6A-containing mRNA-binding to both SRSF3 and NXF1, promoting mRNA nuclear export (By similarity). Also recognizes and binds m6A on other RNA molecules (By similarity). Involved in random X inactivation mediated by Xist RNA: recognizes and binds m6A-containing Xist and promotes transcription repression activity of Xist (By similarity). Involved in S-adenosyl-L-methionine homeostasis by regulating expression of MAT2A transcripts, probably by binding m6A-containing MAT2A mRNAs (PubMed:29262316).[UniProtKB/Swiss-Prot Function]

## shRNA Design:

Performance Guaranteed:

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 <a href="mailto:techsupport@origene.com">techsupport@origene.com</a>. If you need a special design or shRNA sequence, please utilize our <a href="mailto:custom shRNA service">custom shRNA service</a>.

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).