

Product datasheet for SR417688

OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

Ythdf2 Mouse siRNA Oligo Duplex (Locus ID 213541)

Product data:

Product Type: siRNA Oligo Duplexes

Purity: HPLC purified

Quality Control: Tested by ESI-MS

Sequences: Available with shipment

Stability: One year from date of shipment when stored at -20°C.

of transfections: Approximately 330 transfections/2nmol in 24-well plate under optimized conditions (final

conc. 10 nM).

Note: Single siRNA duplex (10nmol) can be ordered.

RefSeq: <u>NM 145393</u>

UniProt ID: Q91YT7

Synonyms: 9430020E02Rik; HGRG8; NY-REN-2

Components: Ythdf2 (Mouse) - 3 unique 27mer siRNA duplexes - 2 nmol each (Locus ID 213541)

Included - SR30004, Trilencer-27 Universal Scrambled Negative Control siRNA Duplex - 2 nmol

Included - SR30005, RNAse free siRNA Duplex Resuspension Buffer - 2 ml



Summary:

Specifically recognizes and binds N6-methyladenosine (m6A)-containing RNAs, and regulates mRNA stability (PubMed:28867294, PubMed:29855337). M6A is a modification present at internal sites of mRNAs and some non-coding RNAs and plays a role in mRNA stability and processing (PubMed:28867294, PubMed:29855337). Acts as a regulator of mRNA stability by promoting degradation of m6A-containing mRNAs via interaction with the CCR4-NOT and ribonuclease P/MRP complexes, depending on the context (PubMed:30065315, PubMed:29855337). M6A-containing mRNAs containing a binding site for RIDA/HRSP12 (5'-GGUUC-3') are preferentially degraded by endoribonucleolytic cleavage: cooperative binding of RIDA/HRSP12 and YTHDF2 to transcripts leads to recruitment of the ribonuclease P/MRP complex (By similarity). Other m6A-containing mRNAs undergo deadenylation via direct interaction between YTHDF2 and CNOT1, leading to recruitment of the CCR4-NOT and subsequent deadenylation of m6A-containing mRNAs (By similarity). Required maternally to regulate oocyte maturation: probably acts by binding to m6A-containing mRNAs, thereby regulating maternal transcript dosage during oocyte maturation, which is essential for the competence of oocytes to sustain early zygotic development (PubMed:28867294). Also involved in hematopoietic stem cells specification by binding to m6A-containing mRNAs, leading to promote their degradation (PubMed:30065315, PubMed:30150673). Also acts as a regulator of neural development by promoting m6A-dependent degradation of neural development-related mRNA targets (PubMed:29855337). Regulates circadian regulation of hepatic lipid metabolism: acts by promoting m6A-dependent degradation of PPARA transcripts (By similarity). Regulates the innate immune response to infection by inhibiting the type I interferon response: acts by binding to m6A-containing IFNB transcripts and promoting their degradation (PubMed:30559377). Also acts as a promoter of cap-independent mRNA translation following heat shock stress: upon stress, relocalizes to the nucleus and specifically binds mRNAs with some m6A methylation mark at their 5'-UTR, protecting demethylation of mRNAs by FTO, thereby promoting cap-independent mRNA translation (By similarity). [UniProtKB/Swiss-Prot Function]

Performance Guaranteed:

OriGene guarantees that at least two of the three Dicer-Substrate duplexes in the kit will provide at least 70% or more knockdown of the target mRNA when used at 10 nM concentration by quantitative RT-PCR when the TYE-563 fluorescent transfection control duplex (cat# SR30002) indicates that >90% of the cells have been transfected and the HPRT positive control (cat# SR30003) provides 90% knockdown efficiency.

For non-conforming siRNA, requests for replacement product must be made within ninety (90) days from the date of delivery of the siRNA kit. To arrange for a free replacement with newly designed duplexes, 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 siRNA control (quantitative RT-PCR data required).