

Product datasheet for SC201342

OriGene Technologies, Inc.

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ERAB (HSD17B10) (NM_001037811) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: ERAB (HSD17B10) (NM_001037811) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: HSD17B10

Synonyms: 17b-HSD10; ABAD; CAMR; DUPXp11.22; ERAB; HADH2; HCD2; HSD10MD; MHBD; MRPP2;

MRX17; MRX31; MRXS10; SCHAD; SDR5C1

ACCN: NM_001037811

Insert Size: 176 bp

Insert Sequence: >SC201342 3'UTR clone of NM_001037811

The sequence shown below is from the reference sequence of NM_001037811. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GCCCTCTGTGCCTAATAAAGTCTCTTTTTCTCACAGAG

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a

point of reference. Note that the complete sequence of this clone is largely the same as the

reference sequence but may contain minor differences, e.g., single nucleotide

polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The

package also includes 100 pmols of both the corresponding 5' and 3' vector primers in

separate vials.

RefSeq: NM 001037811.2





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Summary:

This gene encodes 3-hydroxyacyl-CoA dehydrogenase type II, a member of the short-chain dehydrogenase/reductase superfamily. The gene product is a mitochondrial protein that catalyzes the oxidation of a wide variety of fatty acids and steroids, and is a subunit of mitochondrial ribonuclease P, which is involved in tRNA maturation. The protein has been implicated in the development of Alzheimer disease, and mutations in the gene are the cause of 17beta-hydroxysteroid dehydrogenase type 10 (HSD10) deficiency. Several alternatively spliced transcript variants have been identified, but the full-length nature of only two transcript variants has been determined. [provided by RefSeq, Aug 2014]

Locus ID: 3028

MW: 6.5