

Product datasheet for **RC201734L3V**

ERAB (HSD17B10) (NM_004493) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	ERAB (HSD17B10) (NM_004493) Human Tagged ORF Clone Lentiviral Particle
Symbol:	ERAB
Synonyms:	17b-HSD10; ABAD; CAMR; DUPXp11.22; ERAB; HADH2; HCD2; HSD10MD; MHBD; MRPP2; MRX17; MRX31; MRXS10; SCHAD; SDR5C1
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-Myc-DDK-P2A-Puro (PS100092)
Tag:	Myc-DDK
ACCN:	NM_004493
ORF Size:	783 bp
ORF Nucleotide Sequence:	The ORF insert of this clone is exactly the same as(RC201734).
OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
RefSeq:	NM_004493.2
RefSeq Size:	963 bp
RefSeq ORF:	786 bp
Locus ID:	3028
UniProt ID:	Q99714
Cytogenetics:	Xp11.22
Domains:	adh_short



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Protein Families:	Druggable Genome
Protein Pathways:	Alzheimer's disease, Metabolic pathways, Valine, leucine and isoleucine degradation
MW:	26.9 kDa
Gene Summary:	<p>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]</p>