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

Product datasheet for SC204313

BCKDHB (NM_000056) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	BCKDHB (NM_000056) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	BCKDHB
Synonyms:	BCKDE1B; BCKDH E1-beta; E1B
ACCN:	NM_000056
Insert Size:	334 bp
Insert Sequence:	>SC204313 3'UTR clone of NM_000056 The sequence shown below is from the reference sequence of NM_000056. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC GATGCCCTTCGAAAAATGATCAACTATTGACCATATAGAAAAGCTGGAAGATTATGACTAGATATGGAA ATATTTTTTCTGAATTTTTTTTTATATTTCCTCCGACTTACCTCTTTTTGAAAAGAGAGTTTTTATTAA GTGAACCATCACGATATTGGCTGAAAAGTTCTACATTCTATTATTGTATTGTAACACACATGTATTGAT GATTTTCATTAAGAGTTTCAGATTAACTTTGAAAAATATTCCACATGGTAATCTTATAAATTCTGTTTA ATTACATCTGTAAATATTATGTGTGTGATAGTATTCAATAAAGTAAAATCAAATTGTC ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-MluI
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_000056.5

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Summary: This gene encodes the E1 beta subunit of branched-chain keto acid dehydrogenase, which is a multienzyme complex associated with the inner membrane of mitochondria. This enzyme complex functions in the catabolism of branched-chain amino acids. Mutations in this gene have been associated with maple syrup urine disease (MSUD), type 1B, a disease characterized by a maple syrup odor to the urine in addition to mental and physical retardation and feeding problems. Alternative splicing at this locus results in multiple transcript variants. [provided by RefSeq, Jan 2016]

Locus ID: 594

MW: 13.4