

Product datasheet for **SC126940**

Lipoamide Dehydrogenase (DLD) (NM_000108) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Lipoamide Dehydrogenase (DLD) (NM_000108) Human Untagged Clone
Tag:	Tag Free
Symbol:	Lipoamide Dehydrogenase
Synonyms:	DLDD; DLDH; E3; GCSL; LAD; OGDC-E3; PHE3
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC126940 sequence for NM_000108 edited (data generated by NextGen Sequencing)

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ATGCAGAGCTGGAGTCGTGTACTGCTCCTTGGCCAAGAGAGGCCATTTCAATCGAATA
TCTCATGGCCTACAGGGACTTTCTGCAGTGCCTCTGAGAACTTACGCAGATCAGCCGATT
GATGCTGATGTAACAGTTATAGGTTCTGGTCTGGAGGATATGTTGCTGTATTAAGCT
GCCCAGTTAGGCTTCAAGACAGTCTGCATTGAGAAAAATGAAACACTTGGTGAACATGC
TTGAATTTGGTTGTATTCTTTCTAAGGCTTTATTGAACAACTCTCATTATTACCATATG
GCCCATGGAAAAGATTTTGCATCTAGAGGAATTGAAATGTCCGAAGTTCGCTTGAATTTA
GACAAGATGATGGAGCAGAAGAGTACTGCAGTAAAAGCTTTAACAGGTGGAATTGCCAC
TTATTCAAACAGAATAAGGTTGTTTCATGTCAATGGATATGGAAAAGATAACTGGCAAAAAAT
CAAGTCACTGCTACGAAAGCTGATGGCGCACTCAGGTTATTGATACAAAGAACATTCTT
ATAGCCACGGGTTCAGAAGTTACTCCTTTTCTGGAATCACGATAGATGAAGATAACAATA
GTGTCATCTACAGGTGCTTTATCTTTAAAAAAGTTCCAGAAAAGATGGTTGTTATTGGT
GCAGGAGTAATAGGTGTAGAATTGGGTTTCAGTTTGGCAAAGACTTGGTGCAGATGTGACA
GCAGTTGAATTTTTAGGTCATGTAGGTGGAGTTGGAATTGATATGGAGATATCTAAAAAC
TTTCAACGCATCCTTCAAAAACAGGGGTTAAATTTAAATTTGAATACAAAGGTTACTGGT
GCTACCAAGAAGTCAGATGGAAAATTGATGTTTCTATTGAAGCTGCTTCTGGTGGTAAA
GCTGAAGTTATCACTTGTGATGACTCTTGGTTTGCATTGGCCGACGACCCTTTACTAAG
AATTTGGGACTAGAAGAGCTGGGAATTGAACTAGATCCCAGAGGTAGAATTCAGTCAAT
ACCAGATTTCAAATAAAATTCAAATATCTATGCCATTGGTGTAGTTGCTGGTCCA
ATGCTGGCTCACAAAGCAGAGGATGAAGGCATTATCTGTGTTGAAGGAATGGCTGGTGGT
GCTGTGCACATTGACTACAATTGTGTGCCATCAGTGATTACACACACCCTGAAGTTGCT
TGGGTTGGCAAAATCAGAAGAGCAGTTGAAAGAAGAGGGTATTGAGTACAAAGTTGGGAAA
TTCCATTTGCTGCTAACAGCAGAGCTAAGACAAATGCTGACACAGATGGCATGGTGAAG
ATCCTTGGGCAGAAATCGACAGACAGAGTACTGGGAGCACATATTCTTGGACCAGGTGCT
GGAGAAATGGTAAATGAAGCTGCTCTTGGTATGGAGCATCCTGTGAAGATATA
GCTAGAGTCTGTGCATGCACATCCGACCTTATCAGAAGCTTTTAGAGAAGCAAATCTTGT
GCGTCATTTGGCAAAATCAATCAACTTTTGA
    
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Clone variation with respect to NM_000108.3

5' Read Nucleotide Sequence:

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>OriGene 5' read for NM_000108 unedited
TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGGCCCAGCGGAGGT
GAAAGTTTGGCGGAAAGGAAAAACAGCGGAAAAAGCAGAGCTGGAGTCGTGTACTGCT
CCTTGGCCAAGAGAGGCCATTTCAATCGAATATCTCATGGCCTACAGGGACTTTCTGCAG
TGCCCTCTGAGAACTTACGCAGATCAGCCGATTGATGCTGATGTAACAGTTATAGGTTCTG
TTCCTGGAGGATATGTTGCTGCTATTAAGCTGCCAGTTAGGCTTCAAGACAGTCTGCA
TTGAGAAAAATGAAACACTTGGTGAACATGCTTGAATGTTGGTTGATTCTTCTAAGG
CTTTATTGAACAACTCTCATTATTACCATATGGCCCATGGAAAAGATTTTGCATCTAGAG
GAATTGAAATGTCCGAAGTTCGCTTGAATTTAGACAAGATGATGGAGCAGAAGAGTACTG
CAGTAAAAGCTTTAACAGGTGGAATTGCCCACTTATTCAAACAGAATAAGGTTGTTTCATG
TCAATGGATATGGAAAAGATAACTGGCAAAAATCAAGTCACTGCTACGAAAGCTGATGGCG
GCACTCAGGTTATTGATACAAAGAACATTCTTATAGCCACGGGTTCAGAAGTTACTCCTT
TTCTGGAATCACGATAGATGAAGATAACAATAGTGTATCTACAGGTGCTTTATCTTTAA
AAAAAGTTCCAGAAAAGATGGTTGTTATTGGTGCAGGAGTAATAGGTGTAGAAAATGGGT
TCAGTTTGGCAAAGACTTGGTGCAGATGTGACAGCAGTTGAATTTTTAGGTCATGTAGGT
GGGAGTGGNAATGATATGGNAGATATCTAAAACTTACN
    
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3' Read Nucleotide Sequence:	>OriGene 3' read for NM_000108 unedited TTTTTTTTTTTTTTTTTAACCAGTAAATGAATATTTAAGACGTTTATTTTCAGTATCTTCA TTCCCCACTGTAATACATTTGAATGCCACGTATTTGAGTTCCGTAATAGACTCTTCA ATTTGGGTAACATATAATTACCCTTCAGAGTTGCAGACAACAATGGAAGCTTTAAAACC TCTTCAACACAAATGCTACCCCTAAAATGAAAGAATTTAGAGGTTAAATAAAAACAAGTGA GAGACCATTTACTTACATCAGTTCGGTTTATAGACATTTGAATCATATCTGAATGACTGA CTTGTTTCCAATGTGAAAACCAAATTAATAAATACTTGATCACTGTGCTTCAAACACAAC TGTTACATATCAAATTCTAGCTCCAGCCATGTAAAATTCACCTTTTCTGTATCAGAGAA AAAAGCTATTTAAATTCAGGGGCATTGAATCTTTCATGAACAGCATGAAAATATGAGTTG ACGGAGATATCCAGGATGCTACAATAAGTAGCTTTTTGTCTTACATATTAGTGCCTGA AACAAAATACTAAATTTATGTAAAATATAGATATAAGAGTATTCATTTGTCCAAACCT ATTAATACCTTCCAAA
Restriction Sites:	NotI-NotI
ACCN:	NM_000108
Insert Size:	2190 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none"> 1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	<u>NM_000108.2</u> , <u>NP_000099.1</u>
RefSeq Size:	2320 bp
RefSeq ORF:	1530 bp
Locus ID:	1738
UniProt ID:	<u>P09622</u>
Cytogenetics:	7q31.1
Domains:	pyr_redox, pyr_redox_dim
Protein Families:	Druggable Genome
Protein Pathways:	Citrate cycle (TCA cycle), Glycine, serine and threonine metabolism, Glycolysis / Gluconeogenesis, Metabolic pathways, Pyruvate metabolism, Valine, leucine and isoleucine degradation

Gene Summary:

This gene encodes a member of the class-I pyridine nucleotide-disulfide oxidoreductase family. The encoded protein has been identified as a moonlighting protein based on its ability to perform mechanistically distinct functions. In homodimeric form, the encoded protein functions as a dehydrogenase and is found in several multi-enzyme complexes that regulate energy metabolism. However, as a monomer, this protein can function as a protease. Mutations in this gene have been identified in patients with E3-deficient maple syrup urine disease and lipoamide dehydrogenase deficiency. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2014]

Transcript Variant: This variant (1) represents the longest transcript and encodes the longest isoform (1). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.