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Product datasheet for SC333070

LASP1 (NM_001271608) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	LASP1 (NM_001271608) Human Untagged Clone
Tag:	Tag Free
Symbol:	LASP1
Synonyms:	Lasp-1; MLN50
Vector:	pCMV6-Entry (PS100001)
Fully Sequenced ORF:	>SC333070 representing NM_001271608. Blue=Insert sequence Red=Cloning site Green=Tag(s) ATGCTTCCATTGCGAGACCTGCAAGATGACACTGAACATGAAGAACTACAAGGGCTACGAGAAGAAGCC CTACTGCAACGCGTGCGCTACAAGGAGGAGTTTGAGAAGAACAAGGGCAAAGGTTTCAGCGTAGTGGCA GACACGCCCGAGCTCCAGAGAATCAAGAAGACCCAGGACCAGATCAGTAACATAAAATACCATGAGGAG TTTGAGAAGAGCCGCATGGGCCCTAGCGGGGGCGAGGGCATGGAGCCAGAGCGTCGGGATTCACAGGAC GGCAGCAGCTACCGGCGGCCCCTGGAGCAGCAGCAGCCTCACCACATCCCGACCAGTGCCCCGGTTTAC CAGCAGCCCCAGCAGCAGCCGGTGGCCCAGTCCTATGGTGGCTACAAGGAGCCTGCAGCCCCAGTCTCC ATACAGCGCAGCGCCCCAGGTGGTGGCGGGAAGCGGTACCGCGCGGTGTATGACTACAGCGCCGCCGAC GAGGACGAGGTCTCCTTCCAGGACGGGGACACCATCGTCAACGTGCAGCAGATCGACGACGGCTGGATG TACGGGACGGTGGAGCGCACCGGCGACACGGGGATGCTGCCGGCCAACTACGTGGAGGCCATCTGA
Restriction Sites:	SgfI-RsrII
ACCN:	NM_001271608
Insert Size:	618 bp

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OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery. 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
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:	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:	NM_001271608.1
RefSeq Size:	4050 bp
RefSeq ORF:	618 bp
Locus ID:	3927
UniProt ID:	Q14847
Cytogenetics:	17q12
Protein Families:	Druggable Genome
MW:	23.2 kDa

Gene Summary: This gene encodes a member of a subfamily of LIM proteins, characterized by a LIM motif and a domain of Src homology region 3, and also a member of the nebulin family of actin-binding proteins. The encoded protein is a cAMP and cGMP dependent signaling protein and binds to the actin cytoskeleton at extensions of the cell membrane. The encoded protein has been linked to metastatic breast cancer, hematopoetic tumors such as B-cell lymphomas, and colorectal cancer. [provided by RefSeq, Oct 2012]
Transcript Variant: This variant (2) lacks an exon in the 5' coding region compared to variant 1. This variant represents translation initiation at an alternate AUG compared to variant 1; the 5'-most initiation codon, as used in variant 1, is associated with a weak Kozak sequence and a truncated ORF that would render the transcript a candidate for nonsense-mediated decay (NMD). Leaky scanning may allow translation initiation at the downstream AUG, which results in an isoform (2) that has a distinct N-terminus and is shorter than 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.