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Product datasheet for SC335770

LASS3 (CERS3) (NM_001290342) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: LASS3 (CERS3) (NM_001290342) Human Untagged Clone

Tag: Tag Free

Symbol: CERS3

Synonyms: ARCI9; LASS3

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF:

>SC335770 representing NM_001290342.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGTTTTGGACGTTTAAAGAATGGTTCTGGTTGGAAAGATTCTGGCTTCCTCCAACAATAAAGTGGTCA
GATCTTGAGGATCACGATGGACTCGTCTTTGTAAAACCTTCTCATTTATACGTGACAATTCCATATGCT
TTTCTCTTGCTGATTATCAGACGTGTATTTGAAAAATTTGTTGCTTCACCTCTAGCAAAATCATTTGGC
ATTAAAGAGACAGTTCGAAAGGTTACACCAAATACTGTCTTAGAGAATTTTTTCAAACATTCCACAAGG
CAACCATTGCAAACTGATATTTATGGACTGGCAAAGAAGTGTAACTTGACGGAGCGCCAGGTGGAAAGA
TGGTTTAGGAGTCGGCGGAATCAAGAGAGGCCTTCCAGGCTGAAGAAATTCCAGGAAGCTTGCTGGAGA
TTTGCATTTTACTTAATGATCACTGTTGCTGGAATTGCGTTTCTTTATGATAAACCTTGGCTATATGAC
TTATGGGAGGTTTGGAATGGCTATCCCAAACAGCCCCTGCTGCCATCCCAGTACTGGTACTACATTTTA
GAAATGAGTTTTTATTGGTCTCTGTTATTTAGACTTGGCTTTGATGTCAAGAGAAAGGATTTTCTAGCT
CATATCATCCACCACCTGGCTGCTATTAGTCTGATGAGCTTCTCTTGGTGTGCTAATTATATTCGCAGT
GGGACCCTCGTGATGATTGTACACGATGTGGCTGACATTTGGCTGGAGTCTGCTAAGATGTTTTCTTAT
GCTGGATGGACGCAGACCTGTAACACCCTGTTTTTCATCTTCTCCACCATATTTTTCATCAGCCGCCTC
ATTGTTTTTCCTTTCTGGATTTTATATTGCACGCTGATCTTGCCTATGTATCACCTCGAGCCTTTCTTT
TCATACATCTTCCTCAACCTACAGCTCATGATCTTGCAGGTCCTTCACCTTTACTGGGGTTATTACATC
TTGAAGATGCTCAACAGATGTATATTCATGAAGAGCATCCAGGATGTGAGGAGTGATGACGAGGATTAT
GAAGAGGAAGAGGAAGAGGAAGAAGAAGAGGCTACCAAAGGCAAAGAGATGGATTGTTTAAAGAACGGC
CTCAGGGCTGAGAGGCACCTCATTCCCAATGGCCAGCATGGCCATTAG

Restriction Sites: SgfI-MluI

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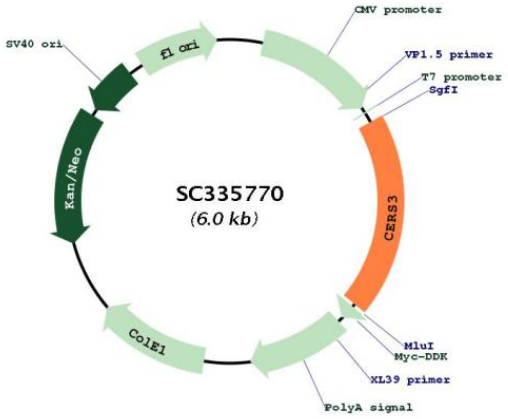
Plasmid Map:



ACCN:	NM_001290342
Insert Size:	1152 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:	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_001290342.1
RefSeq Size:	4042 bp

RefSeq ORF:	1152 bp
Locus ID:	204219
UniProt ID:	Q8IU89
Cytogenetics:	15q26.3
Protein Families:	Transcription Factors, Transmembrane
MW:	46.3 kDa
Gene Summary:	This gene is a member of the ceramide synthase family of genes. The ceramide synthase enzymes regulate sphingolipid synthesis by catalyzing the formation of ceramides from sphingoid base and acyl-coA substrates. This family member is involved in the synthesis of ceramides with ultra-long-chain acyl moieties (ULC-Cers), important to the epidermis in its role in creating a protective barrier from the environment. The protein encoded by this gene has also been implicated in modification of the lipid structures required for spermatogenesis. Mutations in this gene have been associated with male fertility defects, and epidermal defects, including ichthyosis. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Aug 2015] Transcript Variant: This variant (2) differs in the 5' UTR and the 5' coding region and initiates translation at a downstream start codon, compared to variant 1. Variants 2, 3 and 4 encode the same isoform (2), which has a shorter N-terminus, compared to 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.