

Product datasheet for **SC300504**

C18orf1 (LDLRAD4) (NM_001003674) Human Untagged Clone

Product data:

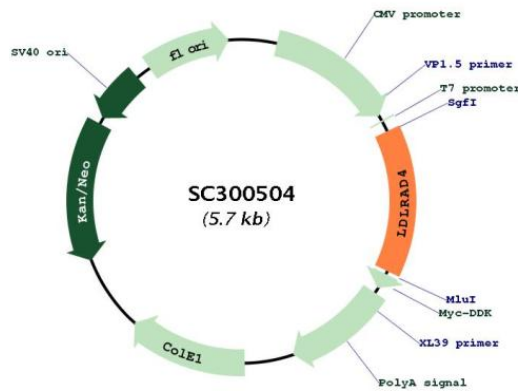
Product Type:	Expression Plasmids
Product Name:	C18orf1 (LDLRAD4) (NM_001003674) Human Untagged Clone
Tag:	Tag Free
Symbol:	LDLRAD4
Synonyms:	C18orf1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC300504 representing NM_001003674. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGTCCAGTGACCACCTGAACAACAGCACACTGAAGGAGGCTCAGTTCAAAGACCTGTTCTTAAAAAAA
GCGGAGCTGGAGTTCGCCAAATCATCATCATCGTCGTGGTGGTACGGTGATGGTGGTGGTGCATCGTC
TGCCTGCTGAACCACTACAAAGTCTCCACGCGGTCCTTCATCAACCGCCGAACCCAGAGCCGGAGGCGG
GAGGACGGGCTGCCGCAGGAAGGGTGCCTGTGGCCTTCAGACAGCGCCGACCCGGGCTGGGCGCCTCG
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GAACTCAACCGAGAGTCCGTGAGGGCCCCACCCAACCGAACCATATTTGACAGTGATTTAATAGACATT
GCTATGTATAGCGGGGGTCCATGCCACCAGCAGCAACTCGGGCATCAGTGCAAGCACCTGCAGCAGT
AACGGGAGGATGGAGGGGCCACCCCCACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTC
CTCCATCACCAGCGCAGCAACGCACACAGGGGCAGCAGACTGCAGTTTCAGCAGAACAATGCAGAGAGC
ACAATAGTACCCATCAAAGGCAAAGATAGGAAGCCTGGGAACCTGGTCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
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Restriction Sites: Sgfl-MluI



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Plasmid Map:


ACCN: NM_001003674

Insert Size: 810 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).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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_001003674.3](#)

RefSeq Size: 9148 bp

RefSeq ORF:	810 bp
Locus ID:	753
UniProt ID:	O15165
Cytogenetics:	18p11.21
Protein Families:	Druggable Genome, Transmembrane
MW:	30.1 kDa
Gene Summary:	<p>Functions as a negative regulator of TGF-beta signaling and thereby probably plays a role in cell proliferation, differentiation, apoptosis, motility, extracellular matrix production and immunosuppression. In the canonical TGF-beta pathway, ZFYVE9/SARA recruits the intracellular signal transducer and transcriptional modulators SMAD2 and SMAD3 to the TGF-beta receptor. Phosphorylated by the receptor, SMAD2 and SMAD3 then form a heteromeric complex with SMAD4 that translocates to the nucleus to regulate transcription. Through interaction with SMAD2 and SMAD3, LDLRAD4 may compete with ZFYVE9 and SMAD4 and prevent propagation of the intracellular signal.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (c1) contains an alternate 5' terminal exon, differs in its 5' UTR, lacks a portion of the 5' coding region, and initiates translation at an alternate start codon, compared to variant a1. The encoded isoform (gamma 1) is shorter and has a distinct N-terminus, compared to isoform alpha 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.</p>