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Product datasheet for SC307282

C18orf1 (LDLRAD4) (NM_181482) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	C18orf1 (LDLRAD4) (NM_181482) Human Untagged Clone
Tag:	Tag Free
Symbol:	C18orf1
Synonyms:	C18orf1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC307282 representing NM_181482. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGCCGGAAGCTGGTTTTCAGGCCACAAATGCTTTCACAGAGTGCAAATTCACCTGCACCAGTGGTAAA TGCTTGTATCTTGGTTCGCTGGTCTGTAACCAACAGAACGACTGTGGGGACAACAGTGACGAAGAGAAC TGTCTCCTGGTGACCGAGCACCCGCCTCCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAAATCATC ATCATCGTCGTGGTGGTCACGGTGATGGTGGTGGTCATCGTCTGCCTGCTGAACCACTACAAAGTCTCC ACGCGGTCCTTCATCAACCGCCCGAACCAGAGCCGGAGGCGGGAGGACGGGCTGCCGCAGATCATGCAT GCCCCGCGGTCCAGGGACAGGTTCACAGCGCCGTCCTTCATCCAGAGGGATCGCTTCAGCCGCTTCCAG CCCACCTACCCCTATGTGCAGCACGAGATTGATCTTCCTCCCACCATCTCCCTGTCCGACGGTGAAGAG CCACCTCCTTACCAGGGGCCCTGCACCCTGCAGCTCCGGGACCCTGAACAGCAGATGGAACTCAACCGA GAGTCCGTGAGGGCCCCACCCAACCGAACCATATTTGACAGTGATTTAATAGACATTGCTATGTATAGC GGGGGTCCATGCCCACCCAGCAGCAACTCGGGCATCAGTGCAAGCACCTGCAGCAGTAACGGGAGGATG GAGGGGCCACCCCCCACATACAGCGAGGTGATGGGCCACCACCCAGGCGCCTCTTTCCTCCATCACCAG CGCAGCAACGCACACAGGGGCAGCAGACTGCAGTTTCAGCAGAACAATGCAGAGAGCACAATAGTACCC ATCAAAGGCAAAGATAGGAAGCCTGGGAACCTGGTCTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI
ACCN:	NM_181482
Insert Size:	867 bp

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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_181482.4
RefSeq Size:	8689 bp
RefSeq ORF:	867 bp
Locus ID:	753
UniProt ID:	O15165
Cytogenetics:	18p11.21
Protein Families:	Druggable Genome, Transmembrane
MW:	32.1 kDa
Gene Summary:	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] Transcript Variant: This variant (a2) differs in its 5' UTR and lacks an alternate in-frame exon in the central coding region, compared to variant a1, resulting in an isoform (alpha 2) that is shorter than 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.