OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC333968

SLAMF7 (NM_001282593) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	SLAMF7 (NM_001282593) Human Untagged Clone
Tag:	Tag Free
Symbol:	SLAMF7
Synonyms:	19A; CD319; CRACC; CS1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC333968 representing NM_001282593. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGCTGGTTCCCCAACATGCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGAGCACCTGTCAAAG CCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAAT GGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAAC CCTGTCAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGAGAACAATCCTAAAGGA AGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCACTGCT CACGATGCCAGACACACCAAGGCTATTTGCCTATGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

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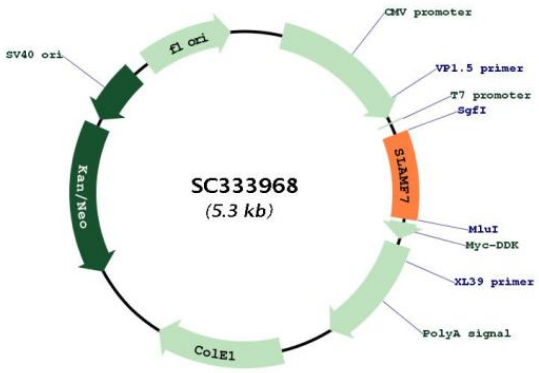
Plasmid Map:



ACCN:	NM_001282593
Insert Size:	450 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_001282593.1

RefSeq Size:	2363 bp
RefSeq ORF:	450 bp
Locus ID:	57823
Cytogenetics:	1q23.3
Protein Families:	Druggable Genome, Transmembrane
MW:	16.5 kDa
Gene Summary:	Self-ligand receptor of the signaling lymphocytic activation molecule (SLAM) family. SLAM receptors triggered by homo- or heterotypic cell-cell interactions are modulating the activation and differentiation of a wide variety of immune cells and thus are involved in the regulation and interconnection of both innate and adaptive immune response. Activities are controlled by presence or absence of small cytoplasmic adapter proteins, SH2D1A/SAP and/or SH2D1B/EAT-2. Isoform 1 mediates NK cell activation through a SH2D1A-independent extracellular signal-regulated ERK-mediated pathway (PubMed:11698418). Positively regulates NK cell functions by a mechanism dependent on phosphorylated SH2D1B. Downstream signaling implicates PLCG1, PLCG2 and PI3K (PubMed:16339536). In addition to heterotypic NK cells-target cells interactions also homotypic interactions between NK cells may contribute to activation. However, in the absence of SH2D1B, inhibits NK cell function. Acts also inhibitory in T-cells (By similarity). May play a role in lymphocyte adhesion (PubMed:11802771). In LPS-activated monocytes negatively regulates production of proinflammatory cytokines (PubMed:23695528).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (7) lacks an alternate in-frame exon in the 5' coding region, and also lacks two alternate exons that result in a frameshift in the 3' coding region, compared to variant 1. The encoded isoform (g) has a distinct C-terminus and is shorter than isoform a. 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.