

## Product datasheet for **SC334420**

### SLAMF7 (NM\_001282595) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	SLAMF7 (NM_001282595) 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:	>NCBI ORF sequence for NM_001282595, the custom clone sequence may differ by one or more nucleotides

```
ATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAG
AGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCC
CATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAAAC
TTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCC
TCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGACTGGGGCTATTTCTTTGGTTTCTGAA
GAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAAACTCCTAACATA
TGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAG
ATCCAGCAAATACGGTTTACTCCACTGTGAAAATACCGAAAAAGATGAAAATCCCCACTCACTGCTCAC
GATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAG
```

Restriction Sites:	Sgfl-MluI
ACCN:	NM_001282595
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).



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**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\\_001282595.1](#), [NP\\_001269524.1](#)

**RefSeq Size:** 2369 bp

**RefSeq ORF:** 606 bp

**Locus ID:** 57823

**UniProt ID:** [Q9NQ25](#)

**Cytogenetics:** 1q23.3

**Protein Families:** Druggable Genome, Transmembrane

**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 (9) lacks a portion of the 5' UTR and 5' coding region, and uses a downstream in-frame translational start codon, compared to variant 1. The encoded isoform (i) is shorter at the N-terminus, compared to 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.