

Product datasheet for **MC225870**

Cd84 (NM_001252472) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Cd84 (NM_001252472) Mouse Untagged Clone
Tag: Tag Free
Symbol: Cd84
Synonyms: A130013D22Rik; CDw84; SLAMF5
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC225870 representing NM_001252472
Red=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGCCCCAGCGCCATCTGTGGATCTGGTTCCTTTGCCTACAAACCTGGTCTGAAGCAGCAGGAAAAGATG
CAGACCCGGTGGTAATGAATGGGATTCTGGGGAGTCAGTTACTTTCCTCTTAAATATTCAGAACCAAA
GAAAATTGACAACATTGCCTGGACTTCTCAATCATCTGTTGCTTTATAAAACCAGGAGTCAATAAAGCT
GAAGTTACCATAACCCAGGGCACTTATAAAGGACGAATAGAAATCATAGATCAGAAGTATGACCTGGTCA
TTAGAGACCTGAGGATGGAAGATGCAGGAATTACAAAGCAGACATCAATGAAGAGAATGAGGAAACCAT
CACCAAGATCTACTACCTTCATATCTACCGTAAGTTATGGCAGCACGGGGCCTTGGATTTACTTTTGATT
TGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001252472
Insert Size: 423 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).



[View online »](#)

OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<ol style="list-style-type: none">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:	<u>NM_001252472.1</u> , <u>NP_001239401.1</u>
RefSeq Size:	3520 bp
RefSeq ORF:	423 bp
Locus ID:	12523
UniProt ID:	<u>Q18PI6</u>
Cytogenetics:	1 79.54 cM

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 (PubMed:20962259). Can mediate natural killer (NK) cell cytotoxicity dependent on SH2D1A and SH2D1B (PubMed:20962259). Increases proliferative responses of activated T-cells and SH2D1A/SAP does not seem to be required for this process. Homophilic interactions enhance interferon gamma/IFNG secretion in lymphocytes and induce platelet stimulation via a SH2D1A/SAP-dependent pathway. May serve as a marker for hematopoietic progenitor cells (By similarity). Required for a prolonged T-cell:B-cell contact, optimal T follicular helper function, and germinal center formation (PubMed:20153220). In germinal centers involved in maintaining B cell tolerance and in preventing autoimmunity (PubMed:25801429). In mast cells negatively regulates high affinity immunoglobulin epsilon receptor signaling; independent of SH2D1A and SH2D1B but implicating FES and PTPN6/SHP-1 (By similarity). In macrophages enhances LPS-induced MAPK phosphorylation and NF-kappaB activation and modulates LPS-induced cytokine secretion; involving ITSM 2 (PubMed:20628063). Positively regulates macroautophagy in primary dendritic cells via stabilization of IRF8; inhibits TRIM21-mediated proteasomal degradation of IRF8 (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks several exons and its transcription extends past a splice site that is used in variant 1, resulting in a novel 3' coding region and 3' UTR compared to variant 1. It encodes isoform 2 which is shorter and has a distinct C-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.