

Product datasheet for SC334813

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Slap (SLA) (NM_001282964) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: Slap (SLA) (NM_001282964) Human Untagged Clone

Tag: Tag Free

Symbol: Slap

Synonyms: SLA1; SLAP

Mammalian Cell Neomycin

Selection:

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Fully Sequenced ORF: >NCBI ORF sequence for NM_001282964, the custom clone sequence may differ by one or

more nucleotides

Restriction Sites: Sgfl-Mlul

ACCN: NM 001282964

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: <u>NM 001282964.1</u>, <u>NP 001269893.1</u>

 RefSeq Size:
 3065 bp

 RefSeq ORF:
 750 bp

 Locus ID:
 6503

 UniProt ID:
 Q13239

 Cytogenetics:
 8q24.22

Protein Families: Druggable Genome

Gene Summary: Adapter protein, which negatively regulates T-cell receptor (TCR) signaling. Inhibits T-cell

antigen-receptor induced activation of nuclear factor of activated T-cells. Involved in the negative regulation of positive selection and mitosis of T-cells. May act by linking signaling proteins such as ZAP70 with CBL, leading to a CBL dependent degradation of signaling

proteins.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (4) differs in the 5' UTR and lacks an in-frame exon in the centtral coding region compared to variant 1. These differences result in the use of an upstream start codon compared to varian 1. The encoded isoform (d) is shorter but has an extended N-terminus compare 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.