

Product datasheet for SC310599

PSME1 (NM 176783) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: PSME1 (NM_176783) Human Untagged Clone

Tag: Tag Free PSME1 Symbol:

Synonyms: HEL-S-129m; IFI5111; PA28A; PA28alpha; REGalpha

Vector: pCMV6 series

>NCBI ORF sequence for NM_176783, the custom clone sequence may differ by one or more **Fully Sequenced ORF:**

nucleotides

CTCTGTACCAAGACAGAGAACCTGCTCGGGAGCTATTTCCCCAAGAAGATTTCTGAGCTG GATGCATTTTTAAAGGAGCCAGCTCTCAATGAAGCCAACTTGAGCAATCTGAAGGCCCCA TTGGACATCCCAGTGCCTGATCCAGTCAAGGAGAAAGAGAGAAGAGGAGCGGAAGAAACAG CAGGAGAAGGAAGACAAGGATGAAAAGAAGAAGGGGGGAGGATGAAGACAAAGGTCCTCCC TGTGGCCCAGTGAACTGCAATGAAAAGATCGTGGTCCTTCTGCAGCGCTTGAAGCCTGAG ATCAAGGATGTCATTGAGCAGCTCAACCTGGTCACCACCTGGTTGCAGCTGCAGATACCT CGGATTGAGGATGGTAACAATTTTGGAGTGGCTGTCCAGGAGAAGGTGTTTGAGCTGATG ACCAGCCTCCACACCAAGCTAGAAGGCTTCCACACTCAAATCTCTAAGTATTTCTCTGAG CGTGGTGATGCAGTGACTAAAGCAGCCCAAGCAGCCCCATGTGGGTGATTATCGGCAGCTG GTGCACGAGCTGGATGAGGCAGAGTACCGGGACATCCGGCTGATGGTCATGGAGATCCGC

ACCCACTCCCTGACCCTGCAGGCTAGGGGTTAA

Restriction Sites: Please inquire ACCN: NM 176783

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.

The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube Components:

containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).



OriGene Technologies, Inc. 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



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 176783.1</u>, <u>NP 788955.1</u>

RefSeq Size: 1187 bp
RefSeq ORF: 753 bp
Locus ID: 5720
Cytogenetics: 14q12

Protein Pathways: Antigen processing and presentation, Proteasome

Gene Summary: The 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure

composed of 2 complexes, a 20S core and a 19S regulator. The 20S core is composed of 4 rings of 28 non-identical subunits; 2 rings are composed of 7 alpha subunits and 2 rings are composed of 7 beta subunits. The 19S regulator is composed of a base, which contains 6 ATPase subunits and 2 non-ATPase subunits, and a lid, which contains up to 10 non-ATPase subunits. Proteasomes are distributed throughout eukaryotic cells at a high concentration and cleave peptides in an ATP/ubiquitin-dependent process in a non-lysosomal pathway. An essential function of a modified proteasome, the immunoproteasome, is the processing of class I MHC peptides. The immunoproteasome contains an alternate regulator, referred to as the 11S regulator or PA28, that replaces the 19S regulator. Three subunits (alpha, beta and gamma) of the 11S regulator have been identified. This gene encodes the alpha subunit of the 11S regulator, one of the two 11S subunits that is induced by gamma-interferon. Three alpha and three beta subunits combine to form a heterohexameric ring. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2013]

Transcript Variant: This variant (2) contains an alternate 3' structure, and thus differs in the 3' coding region and 3' UTR, compared to variant 1. The encoded isoform (3) has a distinct and longer C-terminus, compared to isoform 1.