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 SC330746

PSME3 (NM_001267045) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	PSME3 (NM_001267045) Human Untagged Clone
Tag:	Tag Free
Symbol:	PSME3
Synonyms:	HEL-S-283; Ki; PA28-gamma; PA28G; PA28gamma; REG-GAMMA
Vector:	pCMV6-Entry (PS100001)

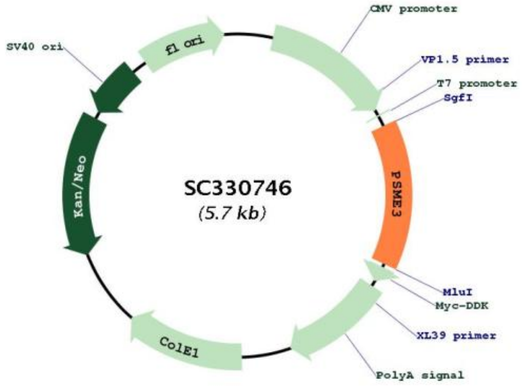
Fully Sequenced ORF:

```
>SC330746 representing NM_001267045.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGAAAAATGGATCCTCAAAAAAATAAAGTATTTGCAGTCTGGGGGCCTCTCAGCTTCTTATTACAGT
TACAAGGTTGATTCTTTCAGGGAGCGGATCACAAGTGAGGCAGAAGACTTGGTGGCAAATTTTTTCCCA
AAGAAGTTATTAGAACTTGATAGTTTTCTGAAGGAACCAATCTTAAACATCCATGACCTAACTCAGATC
CACTCTGACATGAATCTCCCAGTCCCTGACCCCATTCTTCTCACCAATAGCCATGATGGACTGGATGGT
CCCACTTATAAGAAGCGAAGGTTGGATGAGTGTGAAGAAGCCTTCCAAGGAACCAAGGTGTTTGTGATG
CCCAATGGGATGCTGAAAAGCAACCAGCAGCTGGTGGACATTATTGAGAAAGTGAAACCTGAGATCCGG
CTGTTGATTGAGAAATGTAACACGGTCAAAATGTGGGTACAGCTCCTGATTCCCAGGATAGAAGATGGA
AACAACTTTGGGGTGTCCATTCAGGAGGAAACAGTTGCAGAGCTAAGAACTGTTGAGAGTGAAGCTGCA
TCTTATCTGGACCAGATTTCTAGATATTATATTACAAGAGCCAAATTGGTTTCTAAAATAGCTAAATAT
CCCCATGTGGAGGACTATCGCCGCACCGTGACAGAGATTGATGAGAAAGAATATATCAGCCTTCGGCTC
ATCATATCAGAGCTGAGGAATCAATATGTCACTCTACATGACATGATCCTGAAAAATATCGAGAAGATC
AAACGGCCCCGGAGCAGCAATGCAGAGACTCTGTACTGA
```

Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN:	NM_001267045
Insert Size:	798 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_001267045.1
RefSeq Size:	3782 bp
RefSeq ORF:	798 bp
Locus ID:	10197
Cytogenetics:	17q21.31
Protein Families:	Stem cell - Pluripotency
Protein Pathways:	Antigen processing and presentation, Proteasome
MW:	30.9 kDa
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 gamma subunit of the 11S regulator. Six gamma subunits combine to form a homohexameric ring. Alternate splicing results in multiple transcript variants. [provided by RefSeq, May 2012] Transcript Variant: This variant (3) differs in the 5' UTR and 5' coding region, and initiates translation at an alternate start codon, compared to variant 1. The encoded isoform (3) has a distinct N-terminus and is longer than 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.