

# Product datasheet for SC330848

# PSMD11 (NM 001270482) Human Untagged Clone

## **Product data:**

Tag:

Symbol:

Vector:

#### **Product Type: Expression Plasmids Product Name:** PSMD11 (NM 001270482) Human Untagged Clone Tag Free PSMD11 Synonyms: p44.5; Rpn6; S9 pCMV6-Entry (PS100001) >SC330848 representing NM\_001270482. **Fully Sequenced ORF:** Blue=Insert sequence Red=Cloning site Green=Tag(s) ATCGACATCCTCCACTCCATCGTGAAGCGTGACATTCAGGAAAACGATGAAGAGGCAGTGCAAGTCAAA GAGCAGAGCATCCTGGAACTGGGATCTCTCCTGGCAAAGACTGGACAAGCTGCAGAGCTTGGAGGACTC CTGAAGTATGTACGACCCTTCTTGAATTCCATCAGCAAGGCTAAAGCAGCTCGCCTGGTCCGATCTCTT CTTGATCTGTTTCTTGATATGGAAGCAGCTACAGGGCAGGAGGTCGAGCTGTGTTTAGAGTGCATCGAA TGGGCCAAGTCAGAGAAAAGAACTTTCTTACGCCAAGCTTTGGAGGCAAGACTGGTGTCTTTGTACTTT GATACCAAGAGGTACCAGGAAGCATTGCATTTGGGTTCTCAGCTGCTGCGGGAGTTGAAAAAGATGGAC GACAAAGCTCTTTTGGTGGAAGTACAGCTTTTAGAAAGCAAAACATACCATGCCCTGAGCAACCTGCCG AAAGCCCGAGCTGCCTTAACTTCTGCTCGAACCACAGCAAATGCCATCTACTGCCCCCCTAAATTGCAG GCCACCTTGGACATGCAGTCGGGTATTATCCATGCAGCAGAAGAAGGACTGGAAAACTGCGTACTCA TACTTCTATGAGGCATTTGAGGGTTATGACTCCATCGACAGCCCCAAGGCCATCACATCTCTGAAGTAC ATGTTGCTGTGCAAAATCATGCTCAACACCCCAGAAGATGTCCAGGCTTTGGTGAGCGGGAAGCTTGCA CTTCGGTATGCAGGGAGGCAGACAGAAGCATTAAAATGCGTGGCTCAGGCTAGCAAGAACAGATCACTG GCAGATTTTGAAAAGGCTCTGACAGATTACCGGGCAGAGCTCCGGGATGACCCAATCATCAGCACACAC TTGGCCAAGTTGTATGATAACTTACTAGAACAGAATCTGATCCGAGTCATTGAGCCTTTTTCCAGAGTA CAGATTGAACACATATCTAGTCTCATCAAACTCTCCAAGGCCGACGTGGAAAGGAAATTATCACAGATG CCAGTAGATAAAACTTACGAAGCTGCTCTGGAAACAATTCAGAACATGAGCAAAGTAGTGGATTCCCTC

**Restriction Sites:** 

Sgfl-Mlul

TACAACAAAGCCAAGAAACTGACATAG

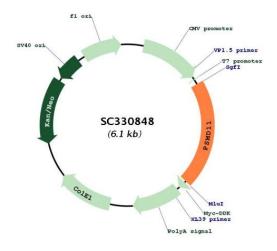


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### Plasmid Map:



ACCN:	NM_001270482
Insert Size:	1269 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:	<ol> <li>Centrifuge at 5,000xg for 5min.</li> <li>Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>Close the tube and incubate for 10 minutes at room temperature.</li> <li>Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
RefSeq:	<u>NM 001270482.1</u>
RefSeq Size:	4035 bp
RefSeq ORF:	1269 bp
Locus ID:	5717

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	PSMD11 (NM_001270482) Human Untagged Clone – SC330848
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UniProt ID:	<u>000231</u>
Cytogenetics:	17q11.2
Protein Families:	Stem cell - Pluripotency
Protein Pathways:	Proteasome
MW:	47.5 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. This gene encodes a member of the proteasome subunit S9 family that functions as a non-ATPase subunit of the 19S regulator and is phosphorylated by AMP-activated protein kinase. Alternatively spliced transcript variants have been observed for this gene. [provided by RefSeq, Jul 2012]

Transcript Variant: This variant (1) represents the longer transcript. Variants 1 and 2 encode the same protein. 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.

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