

# Product datasheet for SC325599

## PSMB5 (NM\_001144932) Human Untagged Clone

### **Product data:**

#### OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	PSMB5 (NM_001144932) Human Untagged Clone
Tag:	Tag Free
Symbol:	PSMB5
Synonyms:	LMPX; MB1; X
Vector:	pCMV6 series
Fully Sequenced ORF:	<pre>&gt;NCBI ORF sequence for NM_001144932, the custom clone sequence may differ by one or more nucleotides ATGGCGCTTGCCAGCGTGTTGGAGAGACCGCTACCGGTGAACCAGCGCGGGTTTTTCGGA CTTGGGGGTCGTGCAGATCTGCTGGATCTAGGTCCAGGGAGTCTCAGTGATGGTCTGAGC CTGGCCGCGCCAGGCTGGGGTGTCCCAGAAGAGCCAGGAATCGAAATGCTTCATGGAACA ACCACCCTGGCCTTCAAGTTCCGCCATGGAGTCATAGTTGCAGCTGACTCCAGGGCTACA GCGGGTGCTTACATTGCCTCCCAGACGGTGAAGAAGGTGATAGAGATCAACCCATACCTG CTAGGCACCATGGCTGGGGGCGCAGCGGATTGCAGCTTCTGGGAACGGCTGTTGGCTCGG CAATGTCGAATCTATGAGCTTCGAAATAAGGAACGCATCTCTGTAGCAGCTGCTTCCAAA CTGCTTGCCAACATGGTGTATCAGTACAAAGGCATGGGGCTGTCCATGGGCACCATGATC TGTGGCTGGGATAAGAGAGGCCCTGTGTCTGAAGTCCTGGGCACCATGATC TGTGGCTGGGATAAGAGAGGCCCTGTGTCTGAAGTCCTGGCAACAGGCCTCTACTA CGTGGACAG</pre>
<b>Restriction Sites:</b>	Please inquire
ACCN:	NM_001144932
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.
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).



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#### SMB5 (NM\_001144932) Human Untagged Clone – SC325599

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 001144932.1, NP 001138404.1</u>
RefSeq Size:	1379 bp
RefSeq ORF:	612 bp
Locus ID:	5693
UniProt ID:	<u>P28074</u>
Cytogenetics:	14q11.2
Protein Families:	Protease
Protein Pathways:	Proteasome
Gene Summary:	The proteasome is a multicatalytic proteinase complex with a highly ordered ring-shaped 20S core structure. The core structure is composed of 4 rings of 28 non-identical subunits; 2 rings are composed of 7 beta subunits. Proteasomes

core structure. The core structure 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. 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. This gene encodes a member of the proteasome B-type family, also known as the T1B family, that is a 20S core beta subunit in the proteasome. This catalytic subunit is not present in the immunoproteasome and is replaced by catalytic subunit 3i (proteasome beta 8 subunit). Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jan 2009]

Transcript Variant: This variant (3) includes an alternate exon, compared to variant 1, that causes a frameshift. The resulting protein (isoform 3) has a distinct C-terminus, compared to isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.

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