

## Product datasheet for **SC201792**

### PSMC2 (NM\_002803) Human 3' UTR Clone

#### Product data:

**Product Type:** 3' UTR Clones  
**Product Name:** PSMC2 (NM\_002803) Human 3' UTR Clone  
**Vector:** pMirTarget (PS100062)  
**Symbol:** PSMC2  
**Synonyms:** MSS1; Nbla10058; RPT1; S7  
**ACCN:** NM\_002803  
**Insert Size:** 1371 bp  
**Insert Sequence:** >SC201792 3'UTR clone of NM\_002803  
The sequence shown below is from the reference sequence of NM\_002803. The complete sequence of this clone may contain minor differences, such as SNPs.  
**Blue**=Stop Codon **Red**=Cloning site

```
GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
GCTACTCCTCGTTACATGACATACAACTGAACCCTGAAGGCTTTCAGTGA AAACTTTAAATTTGGAATC
CTAACCTTATAGACTTGTTAATAACCAATTCATAACAAATAAATGGCTTCAAATTTGTATGCTTTT
TTCCATATCTCTTCTGTAAATATAATAAAAGGTGATTTCTAATGTTATTAGGCAGAAAAGCTTGTTAGA
ATATATTTTGACTATTTTTTTGACCCACACCCGTTTAAGGATTTACATCATAACAAGCGCTTGCTTAG
ATGGCTTCTATCCTAGGCATATGCTGGCCGGTCTCTACATATAAATTTCTATTGTATCCTCCCATCT
GTCCACTGAGGAAGATTATCAAATGGATCTTCATCCAATGGATGCATAAACTTTCCTACTTACTGTAG
TGGCAAAGCTGGCTTCAAGTACAAGTTTGTGGCTCCATTACCTATGCTCCTATTATCCGCTTCTGTC
CCGCAACAAAGTAGCTCACTTAGCGTATGACCACATGCATTATGATAGTTTCCACCACCATATTGAA
TAATAAAAGCTTTGGCCAAAGCTTTTTAAAGTAGGAGAAACATTGGATGTATATGTTTTGCATTGCCA
TTTGATTTCAAATTAATCAGGAAGAATTAGTGATTTTAAATGAGCAGTAAAGTGGTGAATAAAGCAGAA
AGAAAAATGTTTCAGCCAGAAGTAAAGACTAGTAAAAAAGAAAAAATATTTGTACATATGATCTA
ATTTAGAAAGTCCAGAATTGGCTTCATACAGAAAAGTGATTACTTTTCATTTTACA AATTACTTTAAAT
TTTGGTAAAGTTTCTGTTAGGCTTCTGGTCTACAGTGAGGTATTTAAAAATAAAGGTTATATTAGAAT
CCTCAACATCTCTTTAAATTTACCTCCTGTGTAACCACCACCAAAATCCTATCTTCTACCACAATTACCC
CTTCCCCAATGCCAAGACCAAAGCACAATAATGAATATTTTTATTGAAGTTTCGATATTCATAAATAAG
TTGCAAAAATAAGAGTTGGATATATTTTTAATTCACAATAGAAAAGTTGACAACATAGAAAATGCTGCT
TTGCACTGAAACTTAAAATTTATGAAAGTTTTCAAGTAAAGAAATTAAGCCCTTTTATAAAATCCAAC
CAACATTTCTGATTTTTTCATTTTATGAACTTGTATCAGAAAAATTCATCTTTTTTAAACCCTGCCATAAT
TTTTCTTGAGGAATTAATAGAGCAAACTATTTTCAGGTTATGCTTACAATAAAATATACTTAAGAAAA
TGACTGAAGATGTATGTTTTTGAATGTTTTGATTAATAAATGTACACATTTAGAACACA
ACGCGTAAGCGGCCGCGCATCTAGATTGAAAGAAATGACCGACCAAGCGACGCCAACCTGCCATCA
CGAGATTTGATTCACCGCCGCTTCTATGAAAGG
```



[View online »](#)

<b>Restriction Sites:</b>	Sgfl-Mlul
<b>OTI Disclaimer:</b>	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
<b>Components:</b>	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
<b>RefSeq:</b>	<a href="#">NM_002803.4</a>
<b>Summary:</b>	<p>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. This gene encodes one of the ATPase subunits, a member of the triple-A family of ATPases which have a chaperone-like activity. This subunit has been shown to interact with several of the basal transcription factors so, in addition to participation in proteasome functions, this subunit may participate in the regulation of transcription. This subunit may also compete with PSMC3 for binding to the HIV tat protein to regulate the interaction between the viral protein and the transcription complex. Alternative splicing results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Mar 2011]</p>
<b>Locus ID:</b>	5701
<b>MW:</b>	53.7