

## **Product datasheet for SC205221**

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## PSMA1 (NM\_001143937) Human 3' UTR Clone

**Product data:** 

**Product Type:** 3' UTR Clones

Product Name: PSMA1 (NM 001143937) Human 3' UTR Clone

**Vector:** pMirTarget (PS100062)

Symbol: PSMA1

Synonyms: HC2; HEL-S-275; NU; PROS30

**ACCN:** NM\_001143937

**Insert Size:** 473 bp

Insert Sequence: >SC205221 3'UTR clone of NM\_001143937

The sequence shown below is from the reference sequence of NM\_001143937. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

**ACGCGT**AAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

**Restriction Sites:** Sgfl-Mlul

**OTI Disclaimer:** 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).

**Components:** 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.

**RefSeq:** <u>NM 001143937.2</u>





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**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 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 peptidase T1A family, that is a 20S core alpha subunit. Alternative splicing results in multiple transcript variants encoding distinct isoforms.[provided by RefSeq, Jan 2009]

**Locus ID:** 5682

MW: 18