

## **Product datasheet for SC204576**

## PSMA1 (NM 148976) Human 3' UTR Clone

**Product data:** 

**Product Type:** 3' UTR Clones

**Product Name:** PSMA1 (NM\_148976) Human 3' UTR Clone

Symbol: PSMA1

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

Mammalian Cell

Selection:

Neomycin

**Vector:** pMirTarget (PS100062)

**ACCN:** NM\_148976

**Insert Size:** 346 bp

Insert Sequence: >SC204576 3'UTR clone of NM\_148976

The sequence shown below is from the reference sequence of NM\_148976. The complete

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

Blue=Stop Codon Red=Cloning site

 ${\tt GGCAAGTTGGACGCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG}$ 

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

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 148976.3</u>



**OriGene Technologies, Inc.** 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



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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:** 13.6