

Product datasheet for SC322079

Proteasome 20S alpha 5 (PSMA5) (NM_002790) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Proteasome 20S alpha 5 (PSMA5) (NM_002790) Human Untagged Clone
Tag:	Tag Free
Symbol:	Proteasome 20S alpha 5
Synonyms:	PSC5; ZETA
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-AC (PS100020)
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for SC322079
 GTGGGTGAGTTGGCTGCCGGTGAGTTGGGTGCCGGTGGAGTCGTGTTGGTCCCTCAGAATC
 CCCGCGTAGCCGCTGCCCTCCTACCCTCGCCATGTTTCTTACCCGGTCTGAGTACGAC
 AGGGGCGTGAATACTTTTTCTCCGAAGGAAGATTATTTCAAGTGAATATGCCATTGAG
 GCTATCAAGCTTGGTTCTACAGCCATTGGGATCCAGACATCAGAGGGTGTGTGCCTAGCT
 GTGAGAAAGAAATTACTTCCCCACTGATGGAGCCAGCAGCATTGAGAAAATTGTAGAG
 ATTGATGCTCACATAGTTGTGCCATGAGTGGGCTAATTGCTGATGCTAAGACTTTAATT
 GATAAAGCCAGAGTGGAGACACAGAACCCTGGTTCACCTACAATGAGACAATGACAGTG
 GAGAGTGTGACCCAAGCTGTGTCCAATCTGGCTTTCAGTTTGGAGAAGAAGATGCAGAT
 CCAGGTGCCATGTCTCGTCCCTTTGGAGTAGCATTATTATTTGGAGGAGTTGATGAGAAA
 GGACCCAGCTGTTTCATATGGACCCATCTGGGACCTTTGTACAGTGTGATGCTCGAGCA
 ATTTGGCTCTGCTCAGAGGGTGCCAGAGCTCCTTGCAAGAAGTTTACCACAAGTCTATG
 ACTTTGAAAGAAGCCATCAAGTCTTCACTCATCATCTCCTCAAACAAGTAATGGAGGAGAAG
 CTGAATGCAACAAACATTGAGCTAGCCACAGTGCAGCCTGGCCAGAAATTTCCACATGTTT
 ACAAAGGAAGAAGCTTGAAGAGGTTATCAAGGACATTTAAGGAATCCTGATCCTCAGAACT
 TCTCTGGGACAATTTTCAGTTCTAATAATGTCCTTAAATTTTATTTCCAGCTCCTGTTCTCT
 TGGAAAATCTCCATTGTATGTGCATTTTTTAAATGATGTCTGTACATAAAGGCAGTTCTG
 AAATAAAGAAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Restriction Sites:	Please inquire
ACCN:	NM_002790
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).



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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).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. 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.
RefSeq:	NM_002790.2 , NP_002781.2
RefSeq Size:	1023 bp
RefSeq ORF:	726 bp
Locus ID:	5686
UniProt ID:	P28066
Cytogenetics:	1p13.3
Domains:	proteasome
Protein Families:	Druggable Genome, Protease
Protein Pathways:	Proteasome
Gene Summary:	<p>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. Multiple alternatively spliced transcript variants encoding two distinct isoforms have been found for this gene. [provided by RefSeq, Dec 2010]</p> <p>Transcript Variant: This variant (1) is the predominant transcript and encodes the longer isoform (1). 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.</p>