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Product datasheet for SC310584

PSME3 (NM_176863) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	PSME3 (NM_176863) Human Untagged Clone
Tag:	Tag Free
Symbol:	PSME3
Synonyms:	HEL-S-283; Ki; PA28-gamma; PA28G; PA28gamma; REG-GAMMA
Mammalian Cell Selection:	None
Vector:	pCMV6-XL4
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF sequence for NM_176863 edited ATGGCCTCGTTGCTGAAGGTGGATCAGGAAGTGAAGCTCAAGGTTGATTCTTTCAGGGAG CGGATCACAAGTGAGGCAGAAGACTTGGTGGCAAATTTTTTCCCAAAGAAGTTATTAGAA CTTGATAGTTTTCTGAAGGAACCAATCTTAAACATCCATGACCTAACTCAGATCCACTCT GACATGAATCTCCCAGTCCCTGACCCCATTCTTCTCACCAATAGCCATGATGGACTGGAT GGTCCCACTTATAAGAAGCGAAGGTTGGATGAGTGTGAAGAAGCCTTCCAAGGAACCAAG GTGTTTGTGATGCCCAATGGGATGCTGAAAAGCAACCAGCAGCTGGTGGACATTATTGAG AAAGTGAAACCTGAGATCCGGCTGTTGATTGAGAAATGTAACACGCCTTCAGGCAAAGGT CCTCATATATGTTTTGACCTCCAGGTCAAAATGTGGGTACAGCTCCTGATTCCCAGGATA GAAGATGGAAACAACTTTGGGGTGTCCATTCAGGAGGAAACAGTTGCAGAGCTAAGAACT GTTGAGAGTGAAGCTGCATCTTATCTGGACCAGATTTCTAGATATTATATTACAAGAGCC AAATTGGTTTCTAAAATAGCTAAATATCCCCATGTGGAGGACTATCGCCGCACCGTGACA GAGATTGATGAGAAAGAATATATCAGCCTTCGGCTCATCATATCAGAGCTGAGGAATCAA TATGTCACTCTACATGACATGATCCTGAAAAATATCGAGAAGATCAAACGGCCCCGGAGC AGCAATGCAGAGACTCTGTACTGA

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5' Read Nucleotide Sequence:

>OriGene 5' read for NM_176863 unedited
TGCGTTTGTATACGACTCCTATAGGGCGGCCGCGTAATTCGGCACCAGGAGCGAGCGAGC
AGTGAGTAAGCCAGCAAGGGCGGTCGGGTCCCGAGGTCAGCCGAGATTTCTCAGGTCCCT
CCGGCCCCCTCCCTGGAGTCCACAGCGCCTCCGGTGTCCAGAGGATCGGACACGGCCCGG
CCCGGCCATGGCCTCGTTGCTGAAGGTGGATCAGGAAGTGAAGCTCAAGGTTGATTCTTT
CAGGGAGCGGATCACAAGTGAGGCAGAAGACTTGGTGGCAAATTTTTTCCCAAAGAAGTT
ATTAGAACTTGATAGTTTTCTGAAGGAACCAATCTTAAACATCCATGACCTAACTCAGAT
CCACTCTGACATGAATCTCCCAGTCCCTGACCCCATTCTTCTCACCAATAGCCATGATGG
ACTGGATGGTCCCACTTATAAGAAGCGAAGGTTGGATGAGTGTGAAGAAGCCTTCCAAGG
AACCAAGGTGTTTGTGATGCCCAATGGGATGCTGAAAAGCAACCAGCAGCTGGTGGACAT
TATTGAGAAAGTGAAACCTGAGATCCGGCTGTTGATTGAGAAATGTAACACGCCTTCAGG
CAAAGGTCCTCATATATGTTTTGACCTCCAGGTCAAAATGTGGGTACAGCTCCTGATTCC
CAGGATAGAAGATGGAAACAACTTTGGGGTGTCCATTCAGGAGGAAACAGTTGCAGAGCT
AAGAACTGTTGAGAGTGAAGCTGCATCTTATCTGGACCAGATTTCTAGATATTATATTAC
AAGAGCCAAATTGGTTTCTAAATAGCTAAATATCCCCATGTGGAGGACTATCGCCGCACC
GTGACAGAGATTGATGAGAAAGAATATATCAGCCCTTCGCTCATCATATCAGAGCTGAGA
TCAATATGTCACCTCTACATGAACATGATCCTGAAAAATTATCGGAGAGGATC

3' Read Nucleotide Sequence:

>Forward primer walk for NM_176863 unedited
TGTTCGAAGAGAACAGGAAAATCCCAGGATAGAAGATGGAAACAACTTTGGGGTGTCCAT
TCAGGAGGAAACAGTTGCAGAGCTAAGAACTGTTGAGAGTGAAGCTGCATCTTATCTGGA
CCAGATTTCTAGATATTATATTACAAGAGCCAAATTGGTTTCTAAAATAGCTAAATATCC
CCATGTGGAGGACTATCGCCGCACCGTGACAGAGATTGATGAGAAAGAATATATCAGCCT
TCGGCTCATCATATCAGAGCTGAGGAATCAATATGTCACTCTACATGACATGATCCTGAA
AAATATCGAGAAGATCAAACGGCCCCGGAGCAGCAATGCAGAGACTCTGTACTGAGGCCA
GGGCCAGGGCCAGGGGACTCTGTGAGTCTGGCTCAAGACCGACATTGCCTTGGTTTGTTA
CATGACTATCGTGATGGGGAAACTGGCTGGAAATAGTAATCACACCTCTCTGTTTTTAGT
TAGAGTCTAATGAAACTCTCATCTAGTTCTGTGATGTGTTTACCTCTTTTTTCAGGCCTC
AGGAACTCTTCTATTTCCTTCCCTAATACCCCACACCCAACCTGTCGTAATTTCTGGAGA
ACTCCAGGTTTGTGTGTGCAGGATGTTGGCACAAAAATACCTGTGTTTTCATTCTCCCCC
TCTCTCCCTCCTGTGTCTTGCGCTTTATGTTTTCTTCCGTTTGATAATTAGTTGGTTAAA
AGCTGAGGGAACCCGGAAGGAAAGTGCTAGGTGTTTTTTAGGAACTAGGGTGGCGGGGGG
ACGAACTTCTCTTCCTCACATGAGGTTACTGTTTCTTTCCTCTGGTGGGGCATTGGATCC
TCCCCACAGTTGCCCTGGTGATGACTTAGGCTTTCCAATCTGTGTACATCCCACTTTGAA
TCTTGATCGGTGGACAAGAAAATAACCTTAGGCCTTTCAGTC

Restriction Sites: Please inquire

ACCN: NM_176863

Insert Size: 2500 bp

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: The open reading frame of this TrueClone was fully sequenced and found to be a perfect match to the protein associated to this reference.

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:	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_176863.1, NP_789839.1
RefSeq Size:	3228 bp
RefSeq ORF:	804 bp
Locus ID:	10197
UniProt ID:	P61289
Cytogenetics:	17q21.31
Protein Families:	Stem cell - Pluripotency
Protein Pathways:	Antigen processing and presentation, Proteasome
Gene Summary:	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. The immunoproteasome contains an alternate regulator, referred to as the 11S regulator or PA28, that replaces the 19S regulator. Three subunits (alpha, beta and gamma) of the 11S regulator have been identified. This gene encodes the gamma subunit of the 11S regulator. Six gamma subunits combine to form a homohexameric ring. Alternate splicing results in multiple transcript variants. [provided by RefSeq, May 2012] Transcript Variant: This variant (2), uses ans alternate in-frame splice site, compared to variant 1. The resulting isoform (2) is longer than 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.