Recombinant Human PSMD9, His-tagged

Cat. No. PSMD9-26023TH **Lot. No.** (See product label)

SPECIFICATION

Product Overview	Recombinant full length protein, corresponding to amino acids 1-223 of Human 26S Proteasome with N terminal His tag, 29kDa.
Species	Human
Source	E.coli
ProteinLength	1-223 a.a.
Description	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 a non-ATPase subunit of the 19S regulator.
Conjugation	HIS
Form	Lyophilised:Reconstitute with 58 µl aqua dest.
Storage buffer	Preservative: NoneConstituents: 0.5% Trehalose, 6M Urea, 100mM Sodium

	hydrogen phosphate, 10mM Sodium chloride, pH 4.5
Storage	Shipped at 4°C. Upon delivery aliquot and store at -80oC. Avoid freeze / thaw cycles.
Sequences of amino acids	MSDEEARQSGGSSQAGVVTVSDVQELMRRKEEIEAQIKAN YDVLESQKGIGMNEP LVDCEGYPRSDVDLYQVRTARHN IICLQNDHKAVMKQVEEALHQLHARDKEKQAR DMAEAH KEAMSRKLGQSESQGPPRAFAKVNSISPGSPASIAGLQ VDDEIVEFGSV NTQNFQSLHNIGSVVQHSEGKPLNVTVIR RGEKHQLRLVPTRWAGKGLLGCNIIPLQ R
Full Length	Full L.

GENE INFORMATION

Gene Name	PSMD9 proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 [Homo sapiens]
Official Symbol	PSMD9
Synonyms	PSMD9; proteasome (prosome, macropain) 26S subunit, non-ATPase, 9; 26S proteasome non-ATPase regulatory subunit 9; p27; Rpn4;
Gene ID	5715
mRNA Refseq	NM_002813
Protein Refseq	NP_002804
MIM	603146
Uniprot ID	O00233

Chromosome Location	12q24.31-q24.32
Pathway	APC/C-mediated degradation of cell cycle proteins, organism-specific biosystem; APC/C:Cdc20 mediated degradation of Securin, organism-specific biosystem; APC/C:Cdc20 mediated degradation of mitotic proteins, organism-specific biosystem; APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1, organism-specific biosystem; Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins, organism-specific biosystem;
Function	bHLH transcription factor binding; protein binding; transcription coactivator activity;