SANTA CRUZ BIOTECHNOLOGY, INC.

PSMD1 (C-7): sc-166038

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

In eukaryotic cells, selective breakdown of cellular proteins is ensured by their ubiquitination and subsequent degradation by the 26S Proteasome. The 26S Proteasome is a protease complex that selectively breaks down proteins that have been modified by polyubiquitin chains. It is made up of two multisubunit complexes: the 20S Proteasome chamber, which serves as the proteolytic core of the complex, and two 19S regulatory particles which recognize and unfold ubiquitinated proteins. PSMD1 (proteasome (prosome, macropain) 26S subunit, non-ATPase 1), also known as S1 or p112, is a regulatory component of the 26S Proteasome. It is widely expressed with highest expression levels found in skeletal muscle and heart. PSMD1 is the largest of at least 11 non-ATPase regulatory subunits of the 19S regulator lid and is implicated in substrate recognition and binding.

CHROMOSOMAL LOCATION

Genetic locus: PSMD1 (human) mapping to 2q37.1; Psmd1 (mouse) mapping to 1 C5.

SOURCE

PSMD1 (C-7) is a mouse monoclonal antibody raised against amino acids 91-390 mapping near the N-terminus of PSMD1 of human origin.

PRODUCT

Each vial contains 200 µg IgG_{2b} kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

PSMD1 (C-7) is available conjugated to agarose (sc-166038 AC), 500 µg/ 0.25 ml agarose in 1 ml, for IP; to HRP (sc-166038 HRP), 200 µg/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-166038 PE), fluorescein (sc-166038 FITC), Alexa Fluor® 488 (sc-166038 AF488), Alexa Fluor® 546 (sc-166038 AF546), Alexa Fluor® 594 (sc-166038 AF594) or Alexa Fluor® 647 (sc-166038 AF647), 200 µg/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor® 680 (sc-166038 AF680) or Alexa Fluor® 790 (sc-166038 AF790), 200 µg/ml, for Near-Infrared (NIR) WB, IF and FCM.

APPLICATIONS

PSMD1 (C-7) is recommended for detection of PSMD1 of mouse, rat and human origin by Western Blotting (starting dilution 1:100, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Suitable for use as control antibody for PSMD1 siRNA (h): sc-62898, PSMD1 siRNA (m): sc-62899, PSMD1 shRNA Plasmid (h): sc-62898-SH, PSMD1 shRNA Plasmid (m): sc-62899-SH, PSMD1 shRNA (h) Lentiviral Particles: sc-62898-V and PSMD1 shRNA (m) Lentiviral Particles: sc-62899-V.

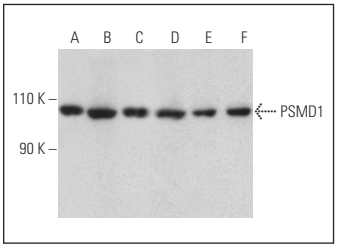
Molecular Weight of PSMD1: 106 kDa.

Positive Controls: Sol8 cell lysate: sc-2249, HeLa whole cell lysate: sc-2200 or K-562 whole cell lysate: sc-2203.

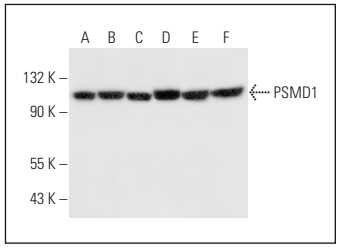
STORAGE

Store at 4° C, **DO NOT FREEZE**. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

DATA



PSMD1 (C-7): sc-166038. Western blot analysis of PSMD1 expression in Hep G2 (**A**), K-562 (**B**), Jurkat (**C**), JAR (**D**), HeLa (**E**) and Sol8 (**F**) whole cell lysates. Detection reagent used: m-IgG_{2b} BP-HRP: sc-542741.



PSMD1 (C-7): sc-166038. Western blot analysis of PSMD1 expression in Sol8 (**A**), K-562 (**B**), HEK293 (**C**), Jurkat (**D**), HeLa (**E**) and Hep G2 (**F**) whole cell lysates.

SELECT PRODUCT CITATIONS

1. Guo, X., et al. 2016. Site-specific proteasome phosphorylation controls cell proliferation and tumorigenesis. Nat. Cell Biol. 18: 202-212.
2. Jia, X., et al. 2017. Label-free proteomic analysis of exosomes derived from inducible hepatitis B virus-replicating HepAD38 cell line. Mol. Cell. Proteomics 16: S144-S160.
3. Kim, H.T. and Goldberg, A.L. 2017. The deubiquitinating enzyme Usp14 allosterically inhibits multiple proteasomal activities and ubiquitin-independent proteolysis. J. Biol. Chem. 292: 9830-9839.
4. Ben-David, U., et al. 2018. Genetic and transcriptional evolution alters cancer cell line drug response. Nature 560: 325-330.
5. Katz, C., et al. 2018. Wild-type and cancer-related p53 proteins are preferentially degraded by MDM2 as dimers rather than tetramers. Genes Dev. 32: 430-447.
6. Cheng, Z.L., et al. 2020. The Zscan4-Tet2 transcription nexus regulates metabolic rewiring and enhances proteostasis to promote reprogramming. Cell Rep. 32: 107877.
7. VerPlank, J.J.S., et al. 2022. Raising cGMP restores proteasome function and myelination in mice with a proteotoxic neuropathy. Brain 145: 168-178.
8. Liu, L., et al. 2022. Proteasome 26S subunit, non-ATPase 1 (PSMD1) facilitated the progression of lung adenocarcinoma by the de-ubiquitination and stability of PTEN-induced kinase 1 (PINK1). Exp. Cell Res. 413: 113075.
9. Kim, M.Y., et al. 2024. Depletion of proteasome subunit PSMD1 induces cancer cell death via protein ubiquitination and DNA damage, irrespective of p53 status. Sci. Rep. 14: 7997.

RESEARCH USE

For research use only, not for use in diagnostic procedures.