

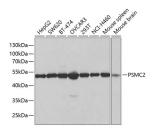
Tel:240-252-7368(USA) Fax: 240-252-7376(USA) techsupport@elabscience.com Website: www.elabscience.com

PSMC2 Polyclonal Antibody

Catalog No.E-AB-60540ReactivityH,M,RStorageStore at -20°C. Avoid freeze / thaw cycles.HostRabbitApplicationsWBIsotypeIgG

Note: Centrifuge before opening to ensure complete recovery of vial contents.

Images



Western blot analysis of extracts of various cell lines using PSMC2 Polyclonal Antibody at 1:1000 dilution.

Immunogen Information

Immunogen Recombinant fusion protein of human PSMC2

GeneID 5701 **Swissprot** P35998

Synonyms PSMC2,MSS1,Nbla10058,S7,ATPase 2

Product Information

Calculated MW 33kDa/48kDa

Observed MW 49kDa

Buffer PBS with 0.02% sodium azide,50% glycerol,pH7.3.

Purify Affinity purification
Dilution WB 1:500-1:2000

Background

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 one of the ATPase subunits, a member of the triple-A family of ATPases which have a chaperone-like activity. This subunit has been shown to interact with several of the basal transcription factors so, in addition to participation in proteasome functions, this subunit may participate in the regulation of transcription. This subunit may also compete with PSMC3 for binding to the HIV tat protein to regulate the interaction between the viral protein and the transcription complex. Alternative splicing results in multiple transcript variants encoding distinct isoforms.

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