

## BACKGROUND

The ubiquitin-proteasome system (UPS) is among others involved in the regulation of protein quality control in the cells. The UPS with the 26S proteasome as central proteolytic unit represents the major ATP-dependent degradation system in eukaryotes responsible for the maintenance of protein homeostasis. Short-lived regulatory proteins involved in cell differentiation, cell-cycle regulation, transcriptional regulation, or apoptosis, but also aberrant proteins are directed to proteasomal degradation through conjugation with the small protein modifier ubiquitin via a cascade of E1, E2, and E3 enzymes, thus forming poly-ubiquitinated (poly-ub) proteins. Poly-ub proteins are substrates for 26S proteasomes which are formed through the association of two 19S regulator complexes with the catalytic core complex, the 20S proteasome that hydrolyzes proteins into shorter peptide fragments. Peptide hydrolyzing activity of the 20S core is restricted to three  $\beta$ -subunits, i.e.  $\beta$ 1,  $\beta$ 2, and  $\beta$ 5, located in the two inner heptameric  $\beta$ -rings of the 20S proteasome. In infectious disease, cells activated by interferons (IFNs) express three unique catalytic subunits  $\beta$ 1i/LMP2,  $\beta$ 2i/MECL-1 and  $\beta$ 5i/LMP7 (PSMB8) forming an alternative proteasome isoform, the immunoproteasome (IP).<sup>1</sup> IP-mediated proteolysis is responsible for the generation of immunogenic epitopes presented by MHC class I molecules, which activate antigen-specific CD8<sup>+</sup> T cells.<sup>2</sup> Upon interferon (IFN)-exposure of cells or tissues, three alternative catalytically active  $\beta$  subunits are induced. These so called immunosubunits are incorporated into newly formed 20S immunoproteasomes (IP) in a process that is driven by  $\beta$ 5i/LMP7.  $\beta$ 1i/LMP2 and  $\beta$ 5i/LMP7 are encoded within the major histocompatibility II region and their incorporation into IPs induces altered proteolytic characteristics that result in many cases in more efficient liberation of MHC class I epitopes particularly within the early phase of antiviral immunity. This increase in MHC class I peptide supply by IPs appears to be important for triggering an effective early CD8 T cell response. However, an alternative physiological function of IPs has been demonstrated recently in that IPs protect cells against cytokine induced oxidative damage, thus preserving protein homeostasis. Substrate modification of oxidant-damaged proteins with poly-ubiquitin results in protein degradation particularly by IPs. Thus, a major innate function of IPs in viral infection is to stabilize cell viability in inflammatory tissue injury and prevent excessive inflammatory tissue damage in viral disease via preservation of protein homeostasis due to accelerated substrate turnover by IPs.<sup>3</sup>

### References:

1. Fehling, H.J. et al: Science 265:1234-7, 1994
2. Groettrup, M. et al: J. Biol. Chem. 270:23808-15, 1995
3. Opitz, E. et al: PLoS Pathog 7: e1002233, 2011

## TECHNICAL INFORMATION

### Source:

LMP7 Antibody is a mouse monoclonal antibody raised against recombinant human LMP7 fragments expressed in *E. coli*.

### Specificity and Sensitivity:

This antibody detects LMP7 proteins in various cell lysate.

**Storage Buffer:** PBS and 30% glycerol

### Storage:

Store at -20°C for at least one year. Store at 4°C for frequent use. Avoid repeated freeze-thaw cycles.

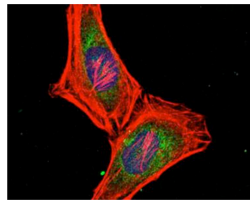
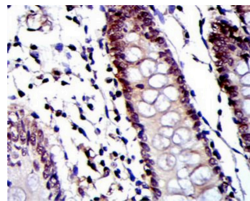
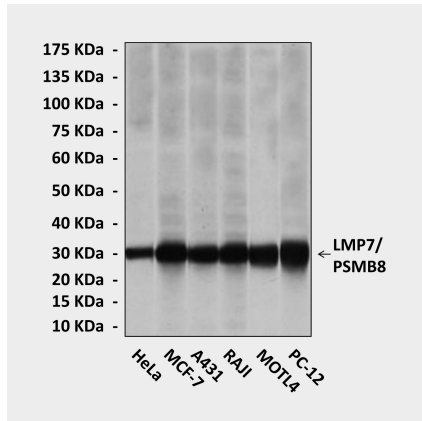
## APPLICATIONS

Application:	*Dilution:
WB	1:1000
IP	n/d
IHC (Paraffin)	1:50-200
ICC	1:50-200
FACS	n/d

*\*Optimal dilutions must be determined by end user.*



**QUALITY CONTROL DATA**



**Top:** Western blot detection of LMP7 proteins in various cell lysates using LMP7 Antibody. **Middle:** This antibody stains HeLa cells in confocal immunofluorescent testing LMP7 Antibody: Green; Actin filaments: Red; DRAQ5 DNA Dye: Blue). **Bottom:** It also stains paraffin-embedded human colon tissue in IHC analysis.

