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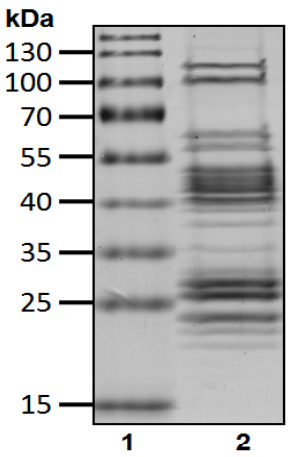
Bovine 26S proteasome

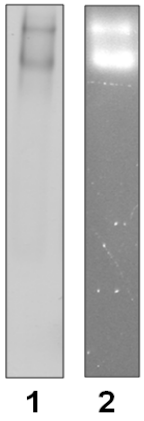
Cat. # A1200, A1201

Also Known as: 26S proteasome
NCBI Reference: N/A
MW (no tag): ~2500 kDa
Species: Bovine
Source: Bovine red blood cells
Tag: No
Stock Buffer: 20 mM Tris, pH 7.6, 40 mM NaCl, 2 mM βME, 2 mM ATP, 5 mM $MgCl_2$, 10% Glycerol
Concentration: See tube label
Quality Assurance: At least 90% by native-PAGE

Image



Coomassie-stained SDS-PAGE
Lane 1: Molecular weight markers
Lane 2: 5 µg purified Bovine 26S proteasome



3 µg purified bovine 26S proteasome was resolved by 4% native-PAGE. The protein was visualized by Coomassie-staining (lane 1); or the proteasome activity was determined by an overlay assay using Suc-LLVY-AMC as the substrate (lane 2).

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Description: The 26S proteasome is an approximately 2.5 mDa large complex composed of the 20S proteasome and the 19S regulatory particle (also called PA700 in mammals). The 20S proteasome has 28 subunits that form a barrel – shaped structure arranged as four heptomeric ring of αββα. Three β subunits have peptidase activities that hydrolyze proteins. Either one or both ends of the 20S proteasome can associate with PA700 to form the 26S proteasome. PA700 contains 19 different proteins that have the ability to bind, deubiquitinate and unfold polyubiquitinated proteins with the consumption of ATP hydrolysis. The 26S proteasome degrades polyubiquitinated proteins, which plays essential roles in regulating various cellular events including protein quality control, gene transcription and signal transduction.

Storage: Store at -80°C; avoid multiple freeze-thaw cycles

Note: N/A

Literature:

1. Waxman L, *et al* . (1987) J Biol Chem 262(6), 2451 – 2457.
2. Pickart CM (1997) FASEB J 11(13), 1055 – 1066.
3. Xie Y (2010) J Mol Cell Biol 2(6), 308 – 317.