

## 32-2757: PSMD10 Recombinant Protein

**Alternative Name :** 26S proteasome non-ATPase regulatory subunit 10,26S proteasome regulatory subunit p28,Gankyrin,PSMD10,p28,dj889N15.2.

### Description

Source : Escherichia Coli. PSMD10 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 226 amino acids and having a molecular mass of 24.4 kDa. Gankyrin (proteasome 26S subunit) is a multicatalytic proteinase oncoprotein commonly overexpressed in most hepatocellular carcinomas. Proteasomes are found throughout eukaryotic cells at a high concentrations and cleave peptides in an ATP/ubiquitin-dependent process in a non-lysosomal pathway. Gankyrin interacts with S6 ATPase of the 19S regulatory particle of the 26S proteasome. Gankyrin is involved in the regulation of the phosphorylation of the retinoblastoma protein by CDK4, and to enhance the ubiquitinylation of p53 by MDM2. Gankyrin consists of 7 ankyrin repeats and is structurally similar to I kappa Bs. Gankyrin acts as a regulatory subunit of the 26s proteasome which is involved in the atp-dependent degradation of ubiquitinated proteins. Gankyrin is involved in progression of esophageal squamous cell carcinoma. gankyrin plays an oncogenic role especially in early stages of human epatocarcinogenesis. Gankyrin binds to NF-kappaB and suppresses its activity at the transcription level by modulating acetylation through SIRT1. Structural comparison between Gankyrin & p16(INK4A) identified numerous residues of gankyrin that are potentially important for CDK4 binding.

### Product Info

<b>Amount :</b>	25 µg
<b>Purification :</b>	Greater than 95.0% as determined by SDS-PAGE.
<b>Content :</b>	The PSMD10 protein solution (1mg/ml) contains 1x PBS pH-7.4 & 10% glycerol.
<b>Storage condition :</b>	PSMD10 although stable 4°C for 4 weeks, should be stored desiccated below -18°C. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA).Please prevent freeze-thaw cycles.
<b>Amino Acid :</b>	MEGCVSNLMV CNLAYSGLKLE ELKESILADK SLATRTDQDS RTALHWACSA GHTEIVEFLL QLGVNVNDKD DAGWSPLHIA ASAGRDEIVK ALLGKGAQVN AVNQNGCTPL HYAASKNRHE IAVMLLEGGA NPDAKDHYEA TAMHRAAAKG NLKMIHILLY YKASTNIQDT EGNTPHLAC DEERVEEAKL LVSQGASIYI ENKKEKTPLQ VAKGGLGLIL KRMVEG.