

53BP1 (PT0456R) PT® Rabbit mAb

Catalog No :	YM8293
Reactivity :	Human;
Applications :	WB;IF;IP;ELISA
Target :	53BP1
Fields :	>>NOD-like receptor signaling pathway
Gene Name :	TP53BP1
Protein Name :	Tumor suppressor p53-binding protein 1
Human Gene Id :	7158
Human Swiss Prot No :	Q12888
Mouse Gene Id :	27223
Mouse Swiss Prot No :	P70399
Specificity :	endogenous
Formulation :	PBS, 50% glycerol, 0.05% Proclin 300, 0.05%BSA
Source :	Monoclonal, rabbit, IgG, Kappa
Dilution :	WB 1:2000-1:10000;IF 1:200-1:1000;ELISA 1:5000-1:20000;IP 1:50-1:200;
Purification :	Protein A
Storage Stability :	-15°C to -25°C/1 year(Do not lower than -25°C)
Molecularweight :	214kD
Observed Band :	450kD

Background : function:May have a role in checkpoint signaling during mitosis (By similarity). Enhances TP53-mediated transcriptional activation. Plays a role in the response to DNA damage.,PTM:Asymmetrically dimethylated on Arg residues by PRMT1. Methylation is required for DNA binding.,PTM:Phosphorylated at basal level in the absence of DNA damage. Hyper-phosphorylated in an ATM-dependent manner in response to DNA damage induced by ionizing radiation. Hyper-phosphorylated in an ATR-dependent manner in response to DNA damage induced by UV irradiation.,similarity:Contains 2 BRCT domains.,subcellular location:Associated with kinetochores. Both nuclear and cytoplasmic in some cells. Recruited to sites of DNA damage, such as double stand breaks. Methylation of histone H4 at 'Lys-20' is required for efficient localization to double strand breaks.,subunit:Interacts with IFI202A (By similarity). Binds to the central domain of TP53/p53. May form homo-oligomers. Interacts with DCLRE1C. Interacts with histone H2AFX and this requires phosphorylation of H2AFX on 'Ser-139'. Interacts with histone H4 that has been dimethylated at 'Lys-20'. Has low affinity for histone H4 containing monomethylated 'Lys-20'. Does not bind histone H4 containing unmethylated or trimethylated 'Lys-20'. Has low affinity for histone H3 that has been dimethylated on 'Lys-79'. Has very low affinity for histone H3 that has been monomethylated on 'Lys-79' (in vitro). Does not bind unmethylated histone H3.,

Function : function:May have a role in checkpoint signaling during mitosis (By similarity). Enhances TP53-mediated transcriptional activation. Plays a role in the response to DNA damage.,PTM:Asymmetrically dimethylated on Arg residues by PRMT1. Methylation is required for DNA binding.,PTM:Phosphorylated at basal level in the absence of DNA damage. Hyper-phosphorylated in an ATM-dependent manner in response to DNA damage induced by ionizing radiation. Hyper-phosphorylated in an ATR-dependent manner in response to DNA damage induced by UV irradiation.,similarity:Contains 2 BRCT domains.,subcellular location:Associated with kinetochores. Both nuclear and cytoplasmic in some cells. Recruited to sites of DNA damage, such as double stand breaks. Methylation of histone H4 at 'Lys-20' is required for efficient localization to double strand breaks.,subunit:Interacts with IFI202A (By similarity). Binds to th

Subcellular Location : Nucleus

Expression : Cerebellum,Cervix,Epithelium,Myeloid leukemia cell,Skeletal muscle,

Tag : hot,recombinant

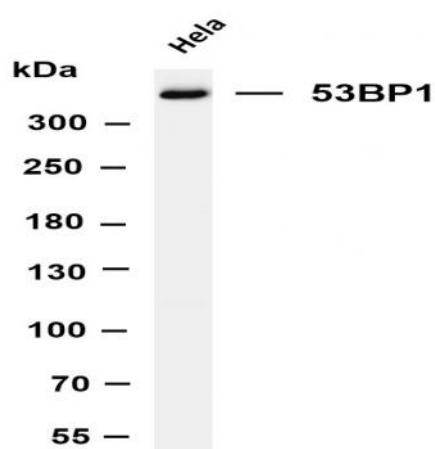
Sort : 1532

No4 : 1

Host : Rabbit

Modifications : Unmodified

Products Images



Various whole cell lysates were separated by 4-8% SDS-PAGE, and the membrane was blotted with anti-53BP1 (PT0456R) antibody. The HRP-conjugated Goat anti-Rabbit IgG(H + L) antibody was used to detect the antibody. Lane 1: HeLa Predicted band size: 214kDa Observed band size: 450kDa