Product name:	53BP1 Rabbit Polyclonal Antibody
Cat number:	ABN06336
Conjugate:	Unconjugated
Size:	100µL
Clone:	Polyclonal
Concentration:	1mg/ml
Host:	Rabbit
Isotype:	IgG
Immunogen:	The antiserum was produced against synthesized peptide derived from human 53BP1. AA range:1-50
Reactivity:	Human,Mouse,Rat
Applications:	WB 1:500-1:2000,IHC 1:100-1:300,ICC/IF 1:200-1:1000,ELISA 1:5000-1:20000
Molecular Weight:	213kDa
Purification:	Affinity purification
Form:	Liquid
Buffer:	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% New type preservative N.
Storage:	Store at 4°C short term. Aliquot and store at -20°C for 12 months. Avoid freeze/thaw cycles.

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: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.,