53BP1 (Phospho Ser1778) Rabbit pAb

CatalogNo: YP1254 **Orthogonal Validated**

Key Features

Host Species	Reactivity	Applications
Rabbit	Human,Mouse,Rat	WB
MW	**Isotype**	
213kD (Observed)	IgG	

Storage

Storage*	-15°C to -25°C/1 year(Do not lower than -25°C)
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.

Recommended Dilution Ratios

WB 1:1000-2000

Basic Information

Clonality	Polyclonal

Immunogen Information

Immunogen	Synthesized phosho peptide around human 53BP1 (Ser1778)
Specificity	This antibody detects endogenous levels of Human 53BP1 (phospho-Ser1778).The name of modified sites may be influenced by many factors, such as species (the modified site was not originally found in human samples) and the change of protein sequence (the previous protein sequence is incomplete, and the protein sequence may be prolonged with the development of protein sequencing technology). When naming, we will use the "numbers" in historical reference to keep the sites consistent with the reports. The antibody binds to the following modification sequence (lowercase letters are modification sites):TEsQL

Target Information

Gene name TP53BP1

Protein Name 53BP1 (Ser1778)

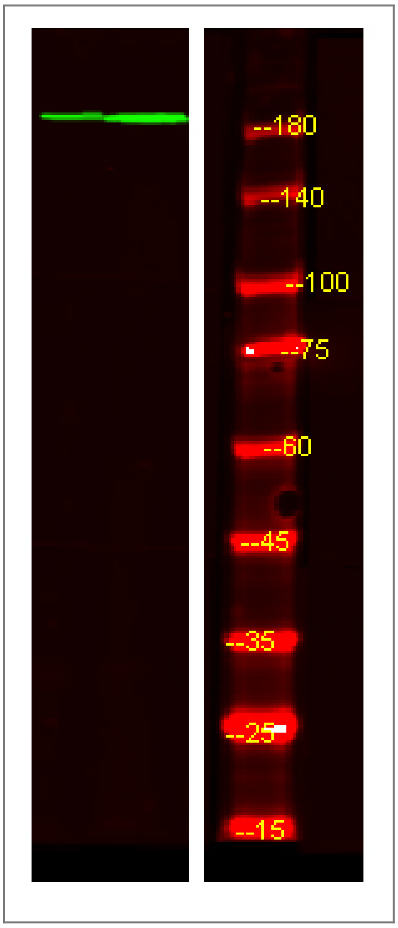
Organism	Gene ID	UniProt ID
Human	7158;	Q12888;
Mouse	27223;	P70399;

Cellular Localization Nucleus

Tissue specificity Cerebellum,Cervix,Epithelium,Myeloid leukemia cell,Skeletal muscle,

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 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.,

Validation Data



Western Blot analysis of Hela treated or untreated by LPS lysis, using primary antibody at 1:1000 dilution. Secondary antibody (catalog#:RS23920) was diluted at 1:10000

Contact information

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