Histone H2B (P10) polyclonal antibody

Catalog: BCP00873

BackGround:

believed

acetylated

BRE1A/BRE1B

RNF20/RNF40).

to

weaken

lysine

E3

Host: R

Rabbit

Reactivity: Human, Rat, Mouse

phorylated at irradiation-induced DNA damage foci in mouse embryonic fibroblasts. In this case, phosphorylation at Ser14 is rapid, depends on prior phosphorylation of H2AX Ser139, and occurs in the absence of apoptosis, suggesting that Ser14 phosphorylation may have distinct roles in DNA-damage repair and apoptosis.

Product:

Rabbit IgG, 1mg/ml in PBS with 0.02% sodium azide, 50% glycerol, pH7.4.

Molecular Weight:

~ 18 kDa

Swiss-Prot:

P33778

Purification&Purity:

The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen and the purity is > 95% (by SDS-PAGE).

Applications:

WB: 1:2000~1:5000

Storage&Stability:

Store at $4 \,^{\circ}{\rm C}$ short term. Aliquot and store at $-20 \,^{\circ}{\rm C}$ long term. Avoid freeze-thaw cycles.

Specificity:

Histone H2B (P10) polyclonal antibody detects endogenous levels of Histone H2B protein.

DATA:



Western blot (WB) analysis of Histone H2B (P10) polyclonal antibody at 1:2000 dilution

Lane1:EC9706 whole cell lysate(40ug) Lane2:HCT116 whole cell lysate(40ug) Lane3:C6 whole cell lysate(40ug) Lane4:BV2 whole cell lysate(40ug)

condensation. Interestingly, histone H2B is rapidly phos Complex biotech, co. Ltd.
Add: No 9, weidi road Qixia District Nanjing, 210046, P. R. China.

(H2A, H2B, H3, and H4), is the primary building block of chromatin. Originally thought to function as a static

The nucleosome, made up of four core histone proteins

scaffold for DNA packaging, histones have now been

shown to be dynamic proteins, undergoing multiple types of post-translational modifications, including acetylation,

phosphorylation, methylation, and ubiquitination. The

p300/CBP histone acetyltransferases acetylate multiple

lysine residues in the amino terminal tail of histone H2B

(Lys5, 12, 15, and 20) at gene promoters during transcrip-

tional activation. Hyper-acetylation of the histone tails

neutralizes the positive charge of these domains and is

some-nucleosome interactions, thereby destabilizing

chromatin structure and increasing the access of DNA to

various DNA-binding proteins. In addition, acetylation of

specific lysine residues creates docking sites that facilitate

recruitment of many transcription and chromatin regula-

tory proteins that contain a bromodomain, which binds to

residues.

mono-ubiquitinated at Lys120 during transcriptional ac-

tivation by the RAD6 E2 protein in conjunction with the

ligase

Lys120 is associated with the transcribed region of active

genes and stimulates transcriptional elongation by facilitating FACT-dependent chromatin remodeling. In addi-

tion, it is essential for subsequent methylation of histone

H3 Lys4 and Lys79, two additional histone modifications

that regulate transcriptional initiation and elongation. In

response to metabolic stress, AMPK is recruited to re-

sponsive genes and phosphorylates histone H2B at Lys36,

both at promoters and in transcribed regions of genes, and

may regulate transcriptional elongation. In response to

multiple apoptotic stimuli, histone H2B is phosphorylated

at Ser14 by the Mst1 kinase. Upon induction of apoptosis,

Mst1 is cleaved and activated by caspase-3, leading to

global phosphorylation of histone H2B during chromatin

histone-DNA

and

Histone

(also

Mono-ubiquitinated histone H2B

nucleo-

H2B

known

is

as



Note:

For research use only, not for use in diagnostic procedure.