www.neobiolab.com
info@neobiolab.com
888.754.5670, +1 617.500.7103 United States
0800.088.5164, +44 020.8123.1558 United Kingdom

HIST1H2BA

Reactivity: Human Mouse Rat MonkeyZ

Tested applications:WB

Recommended Dilution:WB 1:500 - 1:2000

Calculated MW:14kDa

Observed MW: Refer to Figures

Immunogen:

A synthetic peptide of human HIST1H2BA

Storage Buffer:

Store at -20. Avoid freeze / thaw cycles. Buffer: PBS with 0.02% sodium azide, 50% glycerol, pH7.3.

Synonym:

STBP; H2BFU; TSH2B; bA317E16.3;

Catalog #:A2354

Antibody Type:

Monoclonal Antibody

Species: Mouse

Gene ID:255626

Isotype: IgG

Swiss Prot:Q96A08

Purity: Affinity purification

For research use only.

Background:

The nucleosome, made up of four core histone proteins (H2A, H2B, H3, and H4), is the primary building block of chromatin. Originally thought to function as a static 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 (1,2). 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 transcriptional activation (1-3). Hyper-acetylation of the histone tails neutralizes the positive charge of these domains and is believed to weaken histone-DNA and nucleosome-nucleosome interactions, thereby destabilizing chromatin structure and increasing the access of DNA to various DNA-binding proteins (4,5). In addition, acetylation of specific lysine residues creates docking sites that facilitate recruitment of many transcription and chromatin regulatory proteins that contain a bromodomain, which binds to acetylated lysine residues (6). Histone H2B is mono-ubiquitinated at Lys120 during transcriptional activation by the RAD6 E2 protein in conjunction with the BRE1A/BRE1B E3 ligase (also known as RNF20/RNF40) (7). Mono-ubiquitinated histone H2B Lys120 is associated with the transcribed region of active genes and stimulates transcriptional elongation by facilitating FACT-dependent chromatin remodeling (7-9). In addition, it is essential for subsequent methylation of histone H3 Lys4 and Lys79, two additional histone modifications that regulate transcriptional initiation and elongation (10).

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