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Anti-Histone H2B (C-terminus) Antibody

Catalog # AN1809

Product Information

Application	WB, ICC
Primary Accession	P33778
Reactivity	Rat
Host	Rabbit
Clonality	Rabbit Polyclonal
Isotype	IgG
Calculated MW	13950

Additional Information

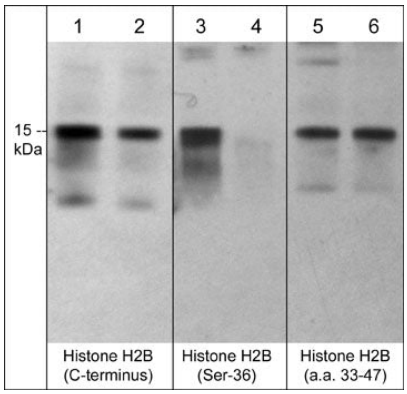
Gene ID	3018
Other Names	HIST1H2BB, H2BFF, Histone H2B type1B, H2B/f
Target/Specificity	The nucleosome is a protein complex consisting of four core histones (H2A, H2B, H3, and H4). Two molecules of each histone forms an octamer that makes up the nucleosome. DNA wraps around repeating nucleosome units to generate chromatin structures. The structure of chromatin determines the accessiblity to transcription factors. Post-translational modification of the amino-terminal tail of histones in nucleosomes alters chromatin structure to promote or inhibit transcription. Complex alterations in acetylation, methylation, ubiquination, and/or phosphorylation determine the chromatin structural changes that occur during specific phases of the cell cycle or in response to cell stimuli. One mode of regulating histone H2B activity is through phosphorylation in the amino terminal region. Important sites of phosphorylation include Ser-14, Ser-32, and Ser-36. AMPK phosphorylates Ser-36 on histone H2B during cell stress leading to increased transcription and cell survival, while ectopic expression of an unphosphorylatable histone H2B during cell stress reduces transcription of AMPK-dependent genes and lowers cell survival.
Dilution	WB~~1:1000 ICC~~N/A
Storage	Maintain refrigerated at 2-8°C for up to 6 months. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	Anti-Histone H2B (C-terminus) Antibody is for research use only and not for use in diagnostic or therapeutic procedures.
Shipping	Blue Ice

Background

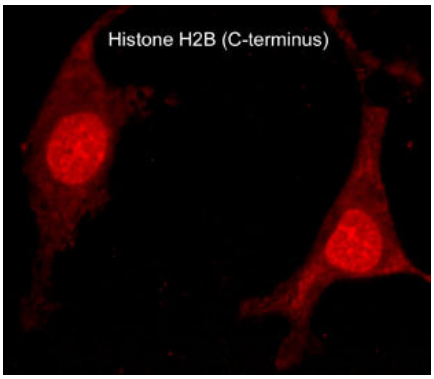
The nucleosome is a protein complex consisting of four core histones (H2A, H2B, H3, and H4). Two molecules of each histone forms an octamer that makes up the nucleosome. DNA wraps around repeating

nucleosome units to generate chromatin structures. The structure of chromatin determines the accessiblity to transcription factors. Post-translational modification of the amino-terminal tail of histones in nucleosomes alters chromatin structure to promote or inhibit transcription. Complex alterations in acetylation, methylation, ubiquination, and/or phosphorylation determine the chromatin structural changes that occur during specific phases of the cell cycle or in response to cell stimuli. One mode of regulating histone H2B activity is through phosphorylation in the amino terminal region. Important sites of phosphorylation include Ser-14, Ser-32, and Ser-36. AMPK phosphorylates Ser-36 on histone H2B during cell stress leading to increased transcription and cell survival, while ectopic expression of an unphosphorylatable histone H2B during cell stress reduces transcription of AMPK-dependent genes and lowers cell survival.

Images



Western blot analysis of human Jurkat cells treated with calyculin A (100 nM) for 30 min. (lanes 1, 3, & 5) then the blots were treated with lambda phosphatase (lanes 2, 4, & 6). The blots were probed with anti-Histone H2B (C-terminus) (lanes 1 & 2), anti-Histone H2B (Ser-36) (lanes 3 & 4), and anti-Histone H2B (a.a. 33-47) (lanes 5 & 6).



Immunocytochemical labeling of Histone H2B in methanol and acetone fixed rat A7r5 cells. The cells were labeled with rabbit polyclonal Histone H2B (C-terminus) antibody (AN1809), then the antibody was detected using appropriate secondary antibody conjugated to DyLight® 594.