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Acetyl-Histone H3 (Lys27) Mouse mAb

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Catalog # AP94537

Product Information

Application	WB, IHC-P, IHC-F, IF
Reactivity	Human
Predicted	Mouse, Rat
Host	Mouse
Clonality	Monoclonal
Physical State	Liquid
Isotype	IgG
Purity	Antigen affinity purification
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SUBCELLULAR LOCATION	Nucleus. Chromosome. Note=Localizes to both the large, transcriptionally active, somatic macronucleus (MAC) and the small, transcriptionally inert, germ line micronucleus (MIC).
SIMILARITY	Belongs to the histone H3 family.
SUBUNIT	The nucleosome is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. Interacts with GCN5, whereby H3S10ph increases histone-protein interactions. Interacts with PDD1 and PDD3.
Post-translational modifications	Phosphorylated to form H3S10ph. H3S10ph promotes subsequent H3K14ac formation by GCN5. H3S10ph is only found in the mitotically dividing MIC, but not in the amitotically dividing MAC. H3S10ph is correlated with chromosome condensation during mitotic or meiotic micronuclear divisions. Acetylation of histone H3 leads to transcriptional activation. H3K14ac formation by GCN5 is promoted by H3S10ph. H3K9acK14ac is the preferred acetylated form of newly synthesized H3. Acetylation occurs almost exclusively in the MAC. Methylated to form H3K4me. H3K4me is only found in the transcriptionally active MAC. Methylated to form H3K9me in developing MACs during conjugation, when genome-wide DNA elimination occurs. At this stage, H3K9me specifically occurs on DNA sequences being eliminated (IES), probably targeted by small scan RNAs (scnRNAs) bound to IES, and is required for efficient IES elimination. H3K9me is required for the interaction with the chromodomains of PDD1 and PDD3. The full-length protein H3S (slow migrating) is converted to H3F (fast migrating) by proteolytic removal of the first 6 residues. H3F is unique to MIC, and processing seems to occur regularly each generation at a specific point in the cell cycle.
DISEASE	Expressed during S phase, then expression strongly decreases as cell division slows down during the process of differentiation.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	Modulation of the chromatin structure plays an important role in the regulation of transcription in eukaryotes. The nucleosome, made up of four core histone proteins (H2A, H2B, H3 and H4), is the primary building block of chromatin. The N-terminal tail of core histones undergoes different

posttranslational modifications including acetylation, phosphorylation and methylation. These modifications occur in response to cell signal stimuli and have a direct effect on gene expression. In most species, the histone H2B is primarily acetylated at lysines 5, 12, 15 and 20. Histone H3 is primarily acetylated at lysines 9, 14, 18 and 23. Acetylation at lysine 9 appears to have a dominant role in histone deposition and chromatin assembly in some organisms. Phosphorylation at Ser10 of histone H3 is tightly correlated with chromosome condensation during both mitosis and meiosis.

Additional Information

Target/Specificity	Expressed in testicular cells.Expressed during S phase, then expression strongly decreases as cell division slows down during the process of differentiation.
Dilution	WB=1:500-1000,IHC-P=1:50-200,IHC-F=1:50-200,ICC/IF=1:50-100,IF=1:50-200
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Background

Modulation of the chromatin structure plays an important role in the regulation of transcription in eukaryotes. The nucleosome, made up of four core histone proteins (H2A, H2B, H3 and H4), is the primary building block of chromatin. The N-terminal tail of core histones undergoes different posttranslational modifications including acetylation, phosphorylation and methylation. These modifications occur in response to cell signal stimuli and have a direct effect on gene expression. In most species, the histone H2B is primarily acetylated at lysines 5, 12, 15 and 20. Histone H3 is primarily acetylated at lysines 9, 14, 18 and 23. Acetylation at lysine 9 appears to have a dominant role in histone deposition and chromatin assembly in some organisms. Phosphorylation at Ser10 of histone H3 is tightly correlated with chromosome condensation during both mitosis and meiosis.

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