

Recombinant Histone H3 (Acetyl Lys64) Monoclonal Antibody

catalog number: AN301413L

Note: Centrifuge before opening to ensure complete recovery of vial contents.

Description

Reactivity Human; Rat; Mouse

Immunogen Acetylated human histone H3 (Lys64) peptide

HostRabbitIsotype IgG, κ CloneA108

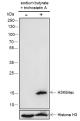
Purification Protein Apurified

Buffer PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications Recommended Dilution

WB 1:500-1:1000
IHC 1:50-1:200
ChIP $6 \mu g/5 \times 10^6 \text{ cells}$

Data

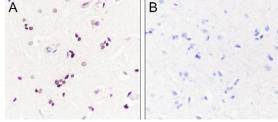


Western Blot with Histone H3 (Acetyl Lys64) Monoclonal Antibody at dilution of 1:1000. (-): MCF-7, (+): MCF-7 + sodium butyrate (50mM, 24hr) + trichostatin A (500ng/ml, 4

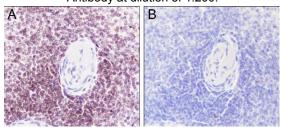
В

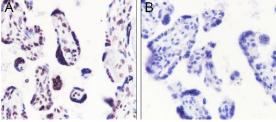
Immunohistochemistry of paraffin-embedded Mouse testis using Histone H3 (Acetyl Lys64) Monoclonal Antibody at dilution of 1:200.

hr) Observed-MW:15 kDa Calculated-MW:15 kDa

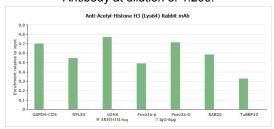


Immunohistochemistry of paraffin-embedded Human cerebrum using Histone H3 (Acetyl Lys64) Monoclonal Antibody at dilution of 1:200.





Immunohistochemistry of paraffin-embedded Human placenta using Histone H3 (Acetyl Lys64) Monoclonal Antibody at dilution of 1:200.



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Immunohistochemistry of paraffin-embedded Human spleen
using Histone H3 (Acetyl Lys64) Monoclonal Antibody at
dilution of 1:200.
Chromatin immunoprecipitation analysis of MCF-7+Sodium
butyrate (50 mM, 24 hr)+trichostatin A (500 ng/ml, 4 hr)
immunoprecipitated DNA by real-time PCR using primers

Chromatin immunoprecipitation analysis of MCF-7+Sodium butyrate (50 mM, 24 hr)+trichostatin A (500 ng/ml, 4 hr) immunoprecipitated DNA by real-time PCR using primers specific for the human GAPDH-CDS, RPL30, LDHA-CDS, FOXO3a-P, FOXO3a-D, RAB20 and TuBBP10. The data are presented as enrichment of each sample relative to the total amount of input chromatin at each amplicon.

Preparation & Storage

Storage Storage Store at -20°C Valid for 12 months. Avoid freeze / thaw cycles.

Shipping Ice bag

Background

Histone post-translational modifications (PTMs), known as the "histone code", are key mechanisms of epigenetics that modulate chromatin structures. The PTMs on histone including acetylation, methylation, phosphorylation, and novel acylations directly affect the accessibility of chromatin to transcription factors and other epigenetic regulators, altering genome stability and gene transcription. Histone acetylation, tightly controlled by the opposing action of histone acetyltransferases (HATs) and histone deacetylases (HDACs), occurs primarily at lysine residues on the N-terminal tails of histones H2A (Lys5, 9, and 15), H2B (Lys5, 12, 15, 16, and 20), H3 (Lys4, 9, 14, 18, 23, 27, and 36), and H4 (Lys5, 8, 12, 16, and 20), and plays vital roles in the regulation of gene expression, DNA damage repair, chromatin dynamics, etc.

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