

Recombinant Histone H3 (Mono Methyl Lys36) Monoclonal Antibody

catalog number: AN302112L

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

Description

Reactivity Human;Rat;Mouse

Immunogen Monomethylated human histone H3 (Lys36) peptide

HostRabbitIsotypeIgG, κCloneA836

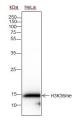
Purification Protein A purified

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

Applications Recommended Dilution

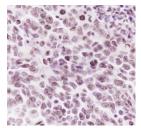
WB 1:500-1:2000
IHC 1:100-1:500
IF 1:50
IP 1:50-1:100

Data



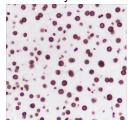
Western Blot with Histone H3 (Mono Methyl Lys36) Monoclonal Antibody at dilution of 1:2000. Lane 1: HeLa

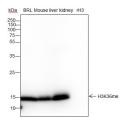
Observed-MW:17 kDa Calculated-MW:17 kDa



Immunohistochemistry of paraffin-embedded Human lung adenocarcinoma using Histone H3 (Mono Methyl Lys36)

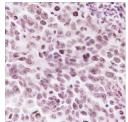
Monoclonal Antibody at dilution of 1:500.



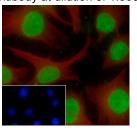


Western Blot with Histone H3 (Mono Methyl Lys36) Monoclonal Antibody at dilution of 1:2000. Lane 1: BRL, Mouse liver, Mouse kidney, Recombinant Histone H3

Observed-MW:17 kDa Calculated-MW:17 kDa



Immunohistochemistry of paraffin-embedded Mouse liver using Histone H3 (Mono Methyl Lys36) Monoclonal Antibody at dilution of 1:500.



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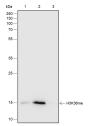
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Immunohistochemistry of paraffin-embedded Rat kidney Immunofluorescent analysis of (100% Ice-cold methanol) using Histone H3 (Mono Methyl Lys36) Monoclonal Antibody fixed HeLa cells using anti-Histone H3 (Mono Methyl Lys36) at dilution of 1:500.

Monoclonal Antibody at dilution of 1:50.



Immunoprecipitation analysis using anti-Histone H3 (Mono Methyl Lys36) Monoclonal Antibody. Western blot was performed from the immunoprecipitate using Histone H3 (Mono Methyl Lys36) Monoclonal Antibody at a dilution of 1:100. Lane 1:5% Input, Lane 2: Histone H3 Monoclonal Antibody, Lane 3: Rabbit monoclonal IgG Isotype

Observed-MW:17 kDa Calculated-MW:17 kDa

Preparation & Storage

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

Shipping Ice bag

Background

Histone post-translational modifications (PTMs) are key mechanisms of epigenetics that modulate chromatin structures, termed as "histone code". 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, gene transcription, etc. Histone methylation occurs primarily at lysine and arginine residues on the amino terminal of core histones. Methylation of histones can either increase or decrease transcription of genes, depending on which amino acids (Lys or Arg) in the histones are methylated and how many methyl groups are attached (mono-, di-, Trimethylation on Lys, mono-di-symmetric/asymmetric methylation on Arg). Mostly, lysine methylation occurs primarily on histone H3 Lys4, 9, 27, 36, 79 and H4 Lys20, while Arginine methylation occurs primarily on histone H3 Arg2, 8, 17, 26 and H4 Arg3. histone methyltransferases (HMTs) and histone demethylases (HDMs) are major regulating factors.

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