

Recombinant Histone H3 (Di Methyl Lys14) Monoclonal Antibody

catalog number: **AN302108L**

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

Description

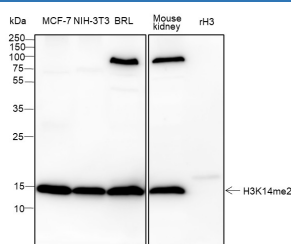
Reactivity	Human;Rat;Mouse
Immunogen	Dimethylated human histone H3 (Lys 14) peptide
Host	Rabbit
Isotype	IgG, κ
Clone	A832
Purification	Protein A purified
Buffer	PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications

Recommended Dilution

WB	1:500-1:2000
IHC	1:100-1:500
IF	1:50
ChIP	6 μ g/5 \times 10 ⁶ cells

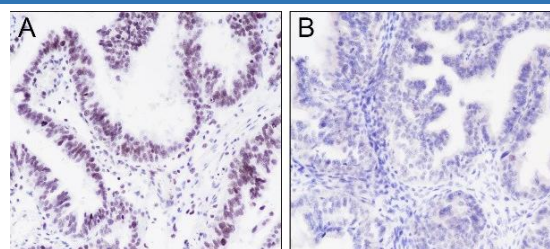
Data



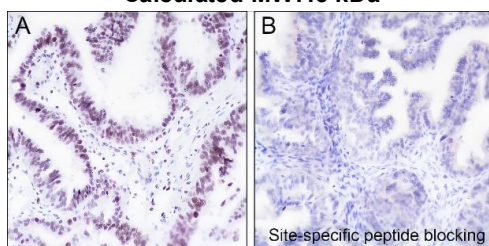
Western Blot with Histone H3 (Di Methyl Lys14) Monoclonal Antibody at dilution of 1:2000. Lane 1: MCF-7, Lane 2: NIH-3T3, Lane 3: BRL, Lane 4: Mouse kidney, Lane 5: rH3

Observed-MW:15 kDa

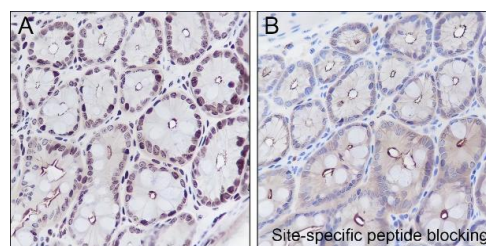
Calculated-MW:15 kDa



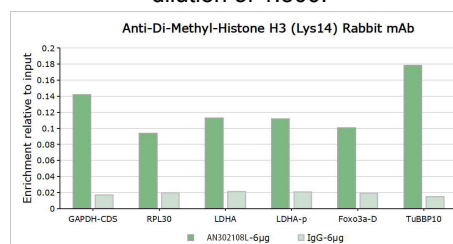
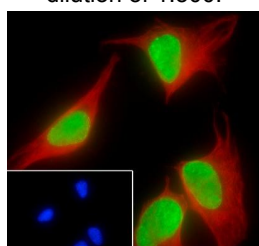
Immunohistochemistry of paraffin-embedded Human ovarian cancer using Histone H3 (Di Methyl Lys14) Monoclonal Antibody at dilution of 1:500.



Immunohistochemistry of paraffin-embedded Mouse colon using Histone H3 (Di Methyl Lys14) Monoclonal Antibody at dilution of 1:500.



Immunohistochemistry of paraffin-embedded Rat liver using Histone H3 (Di Methyl Lys14) Monoclonal Antibody at dilution of 1:500.



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Rev. V1.1

Immunofluorescent analysis of (100% Ice-cold methanol) fixed HeLa cells using anti-Histone H3 (Di Methyl Lys14) Monoclonal Antibody at dilution of 1:50.

Chromatin immunoprecipitation analysis of MCF-7 immunoprecipitated DNA by real-time PCR using primers specific for the human GAPDH-CDS, RPL30, LDHA-P, LDHA-CDS, FOXO3a-D 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	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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