

Recombinant Histone H3 (Mono Methyl Lys79) Monoclonal Antibody

catalog number: **AN302072L**

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

Description

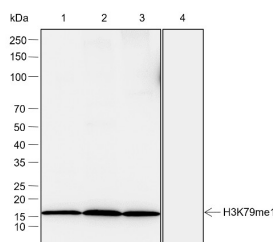
Reactivity	Human;Rat;Mouse
Immunogen	Peptide. This information is proprietary to PTMab.
Host	Rabbit
Isotype	IgG, κ
Clone	A792
Purification	Protein A purified
Buffer	PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications

Recommended Dilution

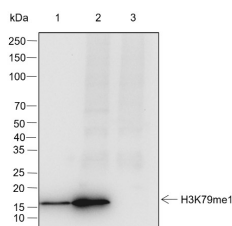
WB	1:1000-1:2000
ChIP	6 μ g antibody/100 μ g chromatin
IP	1:50-1:100

Data



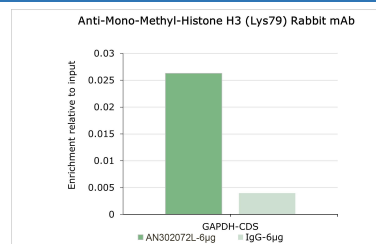
Western Blot with Histone H3 (Mono Methyl Lys79) Monoclonal Antibody at dilution of 1:2000. Lane 1: HeLa, Lane 2: Neuro-2a, Lane 3: BRL, Lane 4: Recombinant Histone H3

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



Immunoprecipitation analysis using anti-Histone H3 (Mono Methyl Lys79) Monoclonal Antibody. Western blot was performed from the immunoprecipitate using Histone H3 (Mono Methyl Lys79) 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



Chromatin immunoprecipitation analysis of HeLa immunoprecipitated DNA by real-time PCR using primers specific for the human GAPDH-CDS. 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.

For Research Use Only

Toll-free: 1-888-852-8623
Web: www.elabscience.com

Tel: 1-832-243-6086
Email: techsupport@elabscience.com

Fax: 1-832-243-6017

Rev. V1.1

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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