Recombinant Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody

catalog number: **AN302118L**

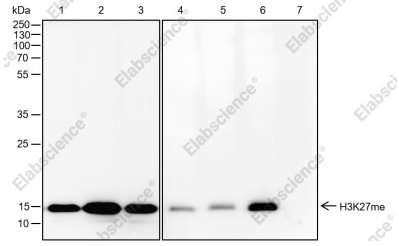
Note: *Centrifuge before opening to ensure complete recovery of vial contents.*

Description

Reactivity	Human;Rat;Mouse;Corn
Immunogen	Monomethylated human histone H3 (Lys27) peptide
Host	Rabbit
Isotype	Rabbit IgG
Clone	C111739
Purification	Protein A purified
Buffer	PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications	Recommended Dilution
WB	1:1000-1:2000
IHC	1:1000-1:3000
IF	1:500-1:1000
ChIP	6 μg/5×10^6 cells

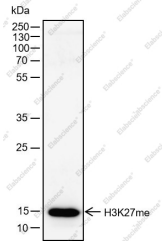
Data



Western Blot with Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody at dilution of 1:2000. Lane 1: HeLa, Lane 2: Neuro-2a, Lane 3: BRL, Lane 4: Mouse liver, Lane 5: Rat brain, Lane 6: Pig brain, Lane 7: Recombinant histone H3(50ng)

Observed-MW:15 kDa

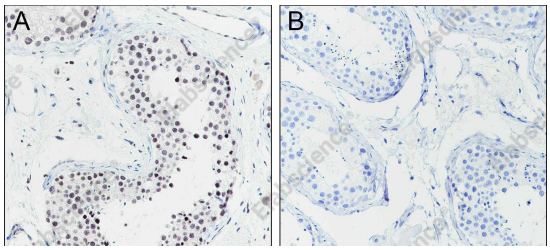
Calculated-MW:15 kDa



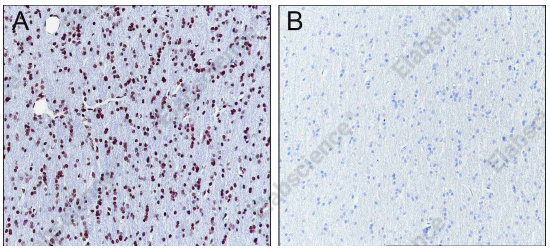
Western Blot with Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody at dilution of 1:1000. Lane 1: Maize leaves

Observed-MW:15 kDa

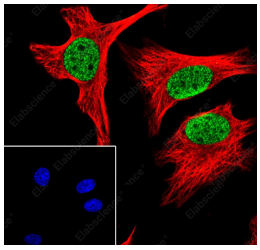
Calculated-MW:15 kDa



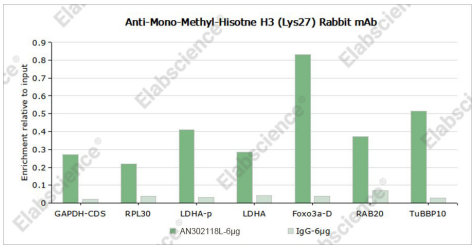
Immunohistochemistry of paraffin-embedded Human testis using Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody at dilution of 1:3000.



Immunohistochemistry of paraffin-embedded Mouse cerebrum using Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody at dilution of 1:3000.



Immunofluorescent analysis of (100% Ice-cold methanol) fixed HeLa cells using anti-Hisotne H3 (Mono Methyl Lys27) Monoclonal Antibody at dilution of 1:1000.



Chromatin immunoprecipitation analysis of HeLa immunoprecipitated DNA by real-time PCR using primers specific for the human GAPDH-CDS, RPL30, LDHA-P, LDHA-CDS, 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	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 gene s, 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.