

Recombinant Histone H3 (Mono Methyl Arg2) Monoclonal Antibody

catalog number: AN302117L

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

Description

Reactivity	Human;Rat;Mouse;Monkey;Pig;Arabidopsis thaliana;Phaeodactylum tricornutum
Immunogen	Monomethylated human histone H3 (Arg2) peptide
Host	Rabbit
Isotype	Rabbit IgG
Clone	C171738
Purification	Protein A purified
Buffer	PBS, 50% glycerol, 0.05% Proclin 300, 0.05% protein protectant.

Applications

Recommended Dilution

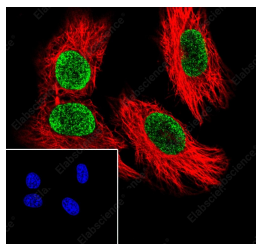
WB	1:1000-1:2000
IF	1:100-1:400

Data



Western Blot with Histone H3 (Mono Methyl Arg2) Monoclonal Antibody at dilution of 1:2000. Lane 1: HeLa, Lane 2: C2C12 nuclear, Lane 3: C2C12 cytoplasm, Lane 4: BRL, Lane 5: COS-7, Lane 6: Mouse liver, Lane 7: Rat kidney, Lane 8: Pig brain, Lane 9: Recombinant histone H3(20 ng)

Observed-MW:15 kDa
Calculated-MW:15 kDa

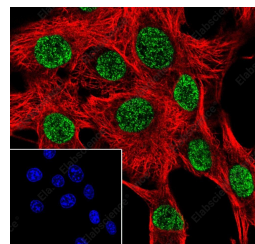


Immunofluorescent analysis of (100% Ice-cold methanol) fixed HeLa cells using anti-Histone H3 (Mono Methyl Arg2) Monoclonal Antibody at dilution of 1:400.



Western Blot with Histone H3 (Mono Methyl Arg2) Monoclonal Antibody at dilution of 1:500. Lane 1: Phaeodactylum tricornutum, Lane 2: Maize leaf

Observed-MW:15 kDa
Calculated-MW:15 kDa



Immunofluorescent analysis of (100% Ice-cold methanol) fixed C2C12 cells using anti-Histone H3 (Mono Methyl Arg2) Monoclonal Antibody at dilution of 1:400.

Preparation & Storage

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

Background

For Research Use Only

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Rev. V1.3

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.