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HIST4H4

Reactivity: Human Mouse Rat

Tested applications:WB IHC IF IP

Recommended Dilution:WB 1:500 - 1:2000 IHC 1:50 - 1:200 IF 1:20 - 1:100 IP 1:20 - 1:100

Calculated MW:11kDa

Observed MW: Refer to Figures

Immunogen:

Recombinant protein of human HIST4H4

Storage Buffer:

Store at -20. Avoid freeze / thaw cycles. Buffer: PBS with 0.02% sodium azide, 50% glycerol, pH7.3.

Synonym:

HIST4H4;H4/p;HIST1H4A;HIST1H4B;HIST1H4C;HIST1H4D;HIST1H4E;HIST1H4F;HIST1H4H;HIST1H4I;HIST1H4J;HIST1H4K;HIST1H4L;HIST2H4A;HIST2H4B;MGC24116;Histone H4 ;

Catalog #:A1131

Antibody Type:

Polyclonal Antibody

Species: Rabbit

Gene ID:121504

Isotype: IgG

Swiss Prot:P62805

Purity: Affinity purification

For research use only.

Background:

The nucleosome, made up of four core histone proteins (H2A, H2B, H3, and H4), is the primary building block of chromatin. Originally thought to function as a static scaffold for DNA packaging, histones have now been shown to be dynamic proteins, undergoing multiple types of post-translational modifications, including acetylation, phosphorylation, methylation, and ubiquitination (1,2). Histone acetylation occurs mainly on the amino-terminal tail domains of histones H2A (Lys5), H2B (Lys5, 12, 15, and 20), H3 (Lys9, 14, 18, 23, 27, and 56), and H4 (Lys5, 8, 12, and 16) and is important for the regulation of histone deposition, transcriptional activation, DNA replication, recombination, and DNA repair (1-3). Hyper-acetylation of the histone tails neutralizes the positive charge of these domains and is believed to weaken histone-DNA and nucleosome-nucleosome interactions, thereby destabilizing chromatin structure and increasing the accessibility of DNA to various DNA-binding proteins (4,5). In addition, acetylation of specific lysine residues creates docking sites for a protein module called the bromodomain, which binds to acetylated lysine residues (6). Many transcription and chromatin regulatory proteins contain bromodomains and may be recruited to gene promoters, in part, through binding of acetylated histone tails. Histone acetylation is mediated by histone acetyltransferases (HATs), such as CBP/p300, GCN5L2, PCAF, and Tip60, which are recruited to genes by DNA-bound protein factors to facilitate transcriptional activation (3). Deacetylation, which is mediated by histone deacetylases (HDAC and sirtuin proteins), reverses the effects of acetylation and generally facilitates transcriptional repression (7,8). Histone H4 lysine 5 is acetylated by multiple HAT proteins. Acetylation by Esa1p in yeast, or Tip60 in mammalian cells, may contribute to both transcriptional activation and DNA repair, including non-homologous end joining and replication-coupled repair (9-12).

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