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Citrulline-Histone H3 (Arg17) Recombinant Rabbit mAb

Catalog # AP99173

Product Information

Application	WB, IHC-P, IHC-F, IF, IP, E
Primary Accession	Q71DI3
Other Accession	Q71DI3
Reactivity	Rat, Human, Mouse
Host	Rabbit
Clonality	Recombinant
Calculated MW	15388
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the histone H3 family.
SUBUNIT	The nucleosome is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. During nucleosome assembly the chaperone ASF1A interacts with the histone H3-H4 heterodimer (via C-terminus of H3); this interaction is direct (PubMed:17292837). Interacts with DNAJC9, CHAF1A and CHAF1B (PubMed:33857403). Interacts with NASP; NASP is a histone chaperone that stabilizes and maintains a soluble pool of Histone H3-H4 dimers (PubMed:22195965).
Post-translational modifications	Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Arg-9 (H3R8me2s). Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me). Acetylation at Lys-123 (H3K122ac) by EP300/p300 plays a central role in chromatin structure: localizes at the surface of the histone octamer and stimulates transcription, possibly by promoting nucleosome instability. Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription. Asymmetric dimethylation at Arg-18 (H3R17me2a) by CARM1 is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8me2s) by PRMT5 is linked to gene repression. Asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation (H3K4me2 and H3K4me3). H3R2me2a is present at the 3' of genes regardless of their transcription state and is enriched on inactive promoters, while it is absent on active promoters. Methylation at Lys-5 (H3K4me), Lys-37 (H3K36me) and Lys-80 (H3K79me) are linked to gene activation. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation of H3 and H4. Methylation at Lys-80 (H3K79me) is associated with DNA double-strand break (DSB) responses and is a specific target for TP53BP1. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are linked to gene repression. Methylation at Lys-10 (H3K9me) is a specific target for HP1 proteins (CBX1, CBX3 and CBX5) and prevents subsequent phosphorylation at Ser-11 (H3S10ph) and acetylation of H3 and H4. Methylation at Lys-5 (H3K4me) and Lys-80 (H3K79me) require preliminary monoubiquitination of H2B at 'Lys-120'. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are enriched in inactive X chromosome chromatin.

Monomethylation at Lys-57 (H3K56me1) by EHMT2/G9A in G1 phase promotes interaction with PCNA and is required for DNA replication. Phosphorylated at Thr-4 (H3T3ph) by VRK1 (PubMed:31527692). Phosphorylated at Thr-4 (H3T3ph) by HASPIN during prophase and dephosphorylated during anaphase (PubMed:15681610, PubMed:16185088). Phosphorylation at Ser-11 (H3S10ph) by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. In addition phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes following external stimulation, like mitogens, stress, growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun. Phosphorylation at Ser-11 (H3S10ph), which is linked to gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 (H3S10ph) by AURKB mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 (H3S10ph) is also an essential regulatory mechanism for neoplastic cell transformation. Phosphorylated at Ser-29 (H3S28ph) by MAP3K20 isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation. Phosphorylation at Thr-7 (H3T6ph) by PRKCB is a specific tag for epigenetic transcriptional activation that prevents demethylation of Lys-5 (H3K4me) by LSD1/KDM1A. At centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, by DAPK3 and PKN1. Phosphorylation at Thr-12 (H3T11ph) by PKN1 or isoform M2 of PKM (PKM2) is a specific tag for epigenetic transcriptional activation that promotes demethylation of Lys-10 (H3K9me) by KDM4C/JMJD2C. Phosphorylation at Tyr-42 (H3Y41ph) by JAK2 promotes exclusion of CBX5 (HP1 alpha) from chromatin. Monoubiquitinated by RAG1 in lymphoid cells, monoubiquitination is required for V(D)J recombination. Ubiquitinated by the CUL4-DDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA and facilitate DNA accessibility to repair proteins. Lysine deamination at Lys-5 (H3K4all) to form allysine is mediated by LOXL2. Allysine formation by LOXL2 only takes place on H3K4me3 and results in gene repression. Crotonylation (Kcr) is specifically present in male germ cells and marks testis-specific genes in post-meiotic cells, including X-linked genes that escape sex chromosome inactivation in haploid cells. Crotonylation marks active promoters and enhancers and confers resistance to transcriptional repressors. It is also associated with post-meiotically activated genes on autosomes. Butyrylation of histones marks active promoters and competes with histone acetylation. It is present during late spermatogenesis. Succinylation at Lys-80 (H3K79succ) by KAT2A takes place with a maximum frequency around the transcription start sites of genes (PubMed:29211711). It gives a specific tag for epigenetic transcription activation (PubMed:29211711). Desuccinylation at Lys-123 (H3K122succ) by SIRT7 in response to DNA damage promotes chromatin condensation and double-strand breaks (DSBs) repair (PubMed:27436229). Serine ADP-ribosylation by PARP1 or PARP2 constitutes the primary form of ADP-ribosylation of proteins in response to DNA damage (PubMed:29480802, PubMed:34874266). Serine ADP-ribosylation at Ser-11 (H3S10ADPr) promotes recruitment of CHD1L (PubMed:34874266). H3S10ADPr is mutually exclusive with phosphorylation at Ser-11 (H3S10ph) and impairs acetylation at Lys-10 (H3K9ac) (PubMed:30257210). Serotonylated by TGM2 at Gln-6 (H3Q5ser) during serotonergic neuron differentiation (PubMed:30867594). H3Q5ser is associated with trimethylation of Lys-5 (H3K4me3) and enhances general transcription factor IID (TFIID) complex-binding to H3K4me3, thereby facilitating transcription (PubMed:30867594). Dopaminylated by TGM2 at Gln-6 (H3Q5dop) in ventral tegmental area (VTA) neurons (PubMed:32273471). H3Q5dop mediates neurotransmission-independent role of nuclear dopamine by regulating relapse-related transcriptional plasticity in the reward system (By similarity). Lactylated in macrophages by EP300/P300 by using lactoyl-CoA directly derived from endogenous or exogenous lactate,

	leading to stimulates gene transcription.
DISEASE	Showing features for natural variant, mutagenesis.
Background Descriptions	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped around a nucleosome, an octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless and encodes a replication-dependent histone that is a member of the histone H3 family. Transcripts from this gene lack polyA tails; instead, they contain a palindromic termination element. This gene is found in the large histone gene cluster on chromosome 6p22-p21.3. [provided by RefSeq, Aug 2015],

Additional Information

Gene ID	126961;333932;653604
Other Names	Histone H3.1/Histone H3.2/Histone H3.3;HIST1H3A;H3FA;HIST1H3B;H3FL;HIST1H3C;H3FC;HIST1H3D;H3FB;HIST1H3E;H3FD;HIST1H3F;H3FI;HIST1H3G;H3FH;HIST1H3H;H3FK;HIST1H3I;H3FF;HIST1H3J;H3FJ;Histone H3.1;Histone H3/a;Histone H3/b;Histone H3/c;Histone H3/d;Histone H3/f;Histone H3/h;Histone H3/i;Histone H3/j;Histone H3/k;Histone H3/l;HIST2H3A;HIST2H3C;H3F2;H3FM;HIST2H3D;Histone H3.2;Histone H3/m;Histone H3/o;H3F3A;H3.3A;H3F3;PP781;H3F3B;H3.3B;Histone H3.3
Dilution	IHC-P=1:50-200,IHC-F=1:50-200,WB=1:500-2000,IF=1:50-200,ELISA=1:5000-10000,IP=1:50-200
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name	H3C15 (HGNC:20505)
Function	Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling.
Cellular Location	Nucleus. Chromosome.

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