Rabbit anti-Human, Mouse Histone H3K27me1 Polyclonal Antibody | anti-HIST3H3 antibody

Histone H3K27me1 Antibody

CATALOG #	HOST	REACTIVITY	APPLICATIONS
AAA326694	**Rabbit**	**Human, Mouse**	**ELISA, Immunocytochemistry, Immunofluorescence, Immunohistochemistry, Western Blot**

PRODUCT SYNONYMS

Histone H3K27me1; Polyclonal Antibody; Histone H3K27me1 Antibody; H3.3A; HIST1 cluster; H3E; H3 histone family; member A; H3.1; H3/l; H3F3; H3FF; H3FJ; H3FL; Histone gene cluster 1; member E; histone H3.1t; Histone H3/o; FLJ92264; H 3; H3; member B; member C; member D; member F; member H; member I; member J; member K; member L; member T; H3 histone; family 3A; H3/A; H3/b; H3/c; H3/d; h3/f; H3/h; H3/i; H3/j; H3/k; H3/t; H31_HUMAN; H3F1K; H3F3A; H3FA; H3FB; H3FC; H3FD; H3FH; H3FI; H3FK; H3A; H3B; H3C; H3D; H3F; H3G; H3H; H3I; H3J; HIST1H3A; HIST1H3B; HIST1H3C; HIST1H3D; HIST1H3E; HIST1H3F; HIST1H3G; HIST1H3H; HIST1H3I; HIST1H3J; HIST3H3; Histone 1; H3a; H3b; H3c; H3d; H3e; H3f; H3g; H3h; H3i; Histone 3; histone cluster 1 H3 family member a; histone cluster 1 H3 family member b; histone cluster 1 H3 family member c; histone cluster 1 H3 family member d; histone cluster 1 H3 family member e; histone cluster 1 H3 family member f; histone cluster 1 H3 family member g; histone cluster 1 H3 family member h; histone cluster 1 H3 family member i; histone cluster 1 H3 family member j; Histone cluster 1; H3j; member G; Histone H 3; Histone H3.1; Histone H3.2; Histone H3.3; 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; Histone H3/m; anti-HIST3H3 antibody

PRODUCT SPECIFICATIONS

Host	Rabbit
Reactivity	Human, Mouse
Clonality	Polyclonal
Isotype	IgG
Specificity	Histone H3K27me1 antibody detects endogenous levels of total Histone H3K27me1
Purity/Purification	The antiserum was purified by peptide affinity chromatography using SulfoLink Coupling Resin.
Form/Format	Liquid Phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Concentration	1mg/ml (varies by lot)
Sequence Length	136
Applicable Applications for anti-HIST3H3 antibody	ELISA, ICC (Immunocytochemistry), IF (Immunofluorescence), IHC (Immunohistochemistry), WB (Western Blot)
Immunogen	A synthetic methylated peptide corresponding to residues surrounding K27 of human histone H3
Subcellular Location	Nucleus
Tissue Specificity	Expressed in testicular cells.
Conjugation	Unconjugated
Preparation and Storage	Store at -20 degree C. Stable for 12 months from date of receipt.

IMAGES

IF (Immunofluorescence)
AAA326694 staining HepG2 by IF/ICC. The sample were fixed with PFA and permeabilized in 0.1% Triton X-100, then blocked in 10% serum for 45 minutes at 25 degree C. The primary antibody was diluted at 1/200 and incubated with the sample for 1 hour at 37 degree C. An Alexa Fluor 594 conjugated goat anti-rabbit IgG (H+L) Ab, diluted at 1/600, was used as the secondary antibody.

IHC (Immunohistochemistry)
AAA326694 at 1/100 staining Mouse lung tissue by IHC-P. The sample was formaldehyde fixed and a heat mediated antigen retrieval step in citrate buffer was performed. The sample was then blocked and incubated with the antibody for 1.5 hours at 22 degree C. An HRP conjugated goat anti-rabbit antibody was used as the secondary.

WB (Western Blot)
Western blot analysis of extracts of HeLa using H3K27me1 antibody. The lane on the left is treated with the antigen-specific peptide.

ADDITIONAL INFORMATION

Related Product Information for anti-HIST3H3 antibody	Description: Modulation of chromatin structure plays an important role in the regulation of transcription in eukaryotes. The nucleosome, made up of DNA wound around eight core histone proteins (two each of H2A, H2B, H3, and H4), is the primary building block of chromatin (1). The amino-terminal tails of core histones undergo various post-translational modifications, including acetylation, phosphorylation, methylation, and ubiquitination (2-5). These modifications occur in response to various stimuli and have a direct effect on the accessibility of chromatin to transcription factors and, therefore, gene expression (6). In most species, histone H2B is primarily acetylated at Lys5, 12, 15, and 20 (4, 7). Histone H3 is primarily acetylated at Lys9, 14, 18, 23, 27, and 56. Acetylation of H3 at Lys9 appears to have a dominant role in histone deposition and chromatin assembly in some organisms (2, 3). Phosphorylation at Ser10, Ser28, and Thr11 of histone H3 is tightly correlated with chromosome condensation during both mitosis and meiosis (8-10). Phosphorylation at Thr3 of histone H3 is highly conserved among many species and is catalyzed by the kinase haspin. Immunostaining with phospho-specific antibodies in mammalian cells reveals mitotic phosphorylation at Thr3 of H3 in prophase and its dephosphorylation during anaphase (11). 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. Subunit Structure: 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. 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 (By similarity). 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 (By similarity). 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 (By similarity). Phosphorylated at Thr-4 (H3T3ph) by HASPIN during prophase and dephosphorylated during anaphase. 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 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 (By similarity). Ubiquitinated. 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 (By similarity). 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. It gives a specific tag for epigenetic transcription activation. Similarity: Belongs to the histone H3 family.
References	Wu D, Huang CJ, Jiao XF, Ding ZM, Zhang JY, Chen F, Wang YS, Li X, Huo LJ; Journal: Oncotarget. Olaquindox disrupts tight junction integrity and cytoskeleton architecture in mouse Sertoli cells.

NCBI AND UNIPROT INFORMATION

NCBI GI #	4504299
NCBI GeneID	8290
NCBI Accession #	NP_003484.1
NCBI GenBank Nucleotide #	NM_003493.2
UniProt Accession #	Q16695; Q6FGU4; B2R5K3
Molecular Weight	Observed: 15 kDa Predicted: 16 kDa
NCBI Official Full Name	histone H3.1t
NCBI Official Synonym Full Names	histone cluster 3 H3
NCBI Official Symbol	HIST3H3
NCBI Official Synonym Symbols	H3t; H3.4; H3/g; H3FT
NCBI Protein Information	histone H3.1t
UniProt Protein Name	Histone H3.1t
UniProt Gene Name	**HIST3H3**
UniProt Synonym Gene Names	H3FT; H3/t; H3t

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