

Antibody Specification

Description	histone cluster 1 H3 family member a(HIST1H3A) Homo sapiens Histones are basic nuclear proteins that are the major components of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped around a histone core composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted by the linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene encodes a replication-dependent histone that is a member of the histone H3 family. Transcripts from this gene lack a poly(A) signal and a palindromic termination element. This gene is found in the large histone gene cluster on chromosome 12.
Cell Pathway/ Category	Systemic lupus erythematosus,
Protein Expression	Blood,Epithelium,Kidney,Lung,Ovary,Spleen,Uterus,
Subcellular Localization	nuclear chromosome,nuclear chromosome, telomeric region,nucleosome,nuclear nucleosome,extracellular space,plasma membrane, adherens junction,membrane,protein complex,extracellular exosome,

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Protein Function

caution:Was originally (PubMed:2587222) thought to originate from mouse.,developmental stage:Expression decreases as cell division slows down during the process of differentiation.,function:Core component of DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template for transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated by modifications of histones, also called histone code, and nucleosome remodeling.,mass spectrometry:Mass spectrometry:PubMed:16457589,miscellaneous:This histone is only present in mammals and is enriched in acetylated histones (H3K9me2).,PTM:Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation. Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me).,PTM:Asymmetric dimethylation at Arg-9 (H3R8me2) by CARM1 is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8me2) by PRMT6 is linked to gene repression and is mutually exclusive with H3K4me2 and H3K4me3. H3R2me2a is present at the 3' of genes regardless of their transcription status but it is absent on active promoters.,PTM:Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PAD14 is linked to transcription.,PTM:Deiminated on Arg-4 in granulocytes upon calcium entry.,PTM:Methylation at Lys-5 (H3K79me) are linked to gene activation. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation. Methylation at Lys-5 (H3K79me) is associated with DNA double-strand break (DSB) responses and is a specific target for TP53. Methylation at Lys-28 (H3K27me) are linked to gene repression. Methylation at Lys-10 (H3K9me) is a specific target for histone deacetylase and prevents subsequent phosphorylation at Ser-11 (H3S10ph) and acetylation of H3 and H4. Methylation at Lys-10 requires preliminary monoubiquitination of H2B at 'Lys-120'. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) on chromosome chromatin.,PTM:Monoubiquitination of Lys-120 by RING1 and RNF2/RING2 complex gives rise to gene repression and participates in X chromosome inactivation of female mammals. It is involved in the initiation of X chromosome inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A at Lys-27' of histone H3. Monoubiquitination of Lys-120 by RNF2/RING2 can also be induced by ultraviolet and DNA damage. Double-strand breaks (DSBs), it is ubiquitinated through 'Lys-63' linkage of ubiquitin moieties by the E2 ubiquitin ligase RNF168, leading to the recruitment of repair proteins to sites of DNA damage. Monoubiquitination and polyubiquitination are distinct events.,PTM:Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase. At centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably by DAPK3. Phosphorylation at Ser-11 (H3S10ph) by AURKB is crucial for chromosome condensation and cell-cycle progression. In addition phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase 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, which is linked to gene activation, prevents methylation at Lys-10 (H3K9me). 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 by MLTK isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation.,PTM:Phosphorylation on Ser-2 is enhanced during mitosis. Phosphorylation on Ser-2 by RPS6KA5/MSK1.,PTM:Acetylation of H3 inhibits Ser-2 phosphorylation by RPS6KA5/MSK1.,PTM:Symmetric dimethylation on Arg-9 is a crucial role in the germ-cell lineage.,PTM:The chromatin-associated form is phosphorylated on Thr-12 (H3T11ph) by CUL4-DDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histone and DNA accessibility to repair proteins.,similarity:Belongs to the histone H2A family.,similarity:Belongs to the histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterodimer. The octamer wraps approximately 147 bp of DNA.,subunit:The nucleosome is a histone octamer containing two molecules of H3 and H4 assembled in one H3-H4 heterodimer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. assembly the chaperone ASF1A interacts with the histone H3-H4 heterodimer.,

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