

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 nucleosome core particle, the basic unit of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped twice around a core of eight histone molecules, two molecules of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted by the association of linker histones with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless. HIST1H3A is a member of the histone H3 family. Transcripts from this gene lack polyA tails; instead, they contain a polyU tail. HIST1H3A is found in the large histone gene cluster on chromosome 6p22-p21.3. [provided by RefSeq, Aug 2015],
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,cell-cell junction,membrane,protein complex,extracellular exosome,

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	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 nucleosome which packages DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. involved in gene expression regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via acetylation of histones, also called histone code, and nucleosome remodeling.,mass spectrometry:Monoisotopic with molecular weight 16 kDa.,PubMed:16457589,miscellaneous:This histone is only present in mammals and is enriched in acetylated chromatin (H3K9me2).,PTM:Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me).,PTM:Asymmetric dimethylation is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8sme2) by PRMT5 is linked to gene repression. Symmetric dimethylation (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation. Methylation at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription.,PTM:Hydroxylation entry.,PTM:Methylation at Lys-5 (H3K4me), Lys-37 (H3K36me) and Lys-80 (H3K79me) are linked to gene repression. Methylation facilitates subsequent acetylation of H3 and H4. Methylation at Lys-80 (H3K79me) is associated with DNMT3A specific target for TP53BP1. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are linked to gene repression. DNMT3A specific target for HP1 proteins (CBX1, CBX3 and CBX5) and prevents subsequent phosphorylation at Ser-11. Methylation at Lys-5 (H3K4me) and Lys-80 (H3K79me) require preliminary monoubiquitination of H2B and H2A. Methylation at Lys-28 (H3K27me) are enriched in inactive X chromosome chromatin.,PTM:Monoubiquitination of Lys-120 by UBR1 is a ubiquitin tag for epigenetic transcriptional repression and participates in X chromosome inactivation of female mammals through both imprinted and random X inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Methylation of 'Lys-27' of histone H3. Monoubiquitination of Lys-120 by RNF2/RING2 can also be induced by DNA damage. Following DNA double-strand breaks (DSBs), it is ubiquitinated through 'Lys-63' linkage of ubiquitin moiety by E3 complex of RNF8 and 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 I of meiosis centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably mediated by AURKB. Phosphorylation at Ser-11 (H3S10ph) by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. Phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes responsive to 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 mediates gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 is a regulatory mechanism for neoplastic cell transformation. Phosphorylated at Ser-29 (H3S28ph) by MLTK isoform 1 upon ultraviolet B irradiation.,PTM:Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase I of meiosis centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably mediated by AURKB. Phosphorylation at Ser-11 (H3S10ph) by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. Phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes responsive to 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 mediates gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 is a regulatory mechanism for neoplastic cell transformation. Phosphorylated at Ser-29 by MLTK isoform 1, RPS6KA5 or RPS6KA4 upon ultraviolet B irradiation.,PTM:Phosphorylation on Ser-2 is enhanced during mitosis. Phosphorylation on Ser-2 by RPS6KA5 or RPS6KA4 inhibits acetylation of H3.,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-121 (H3T11ph) by RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and other nuclear proteins.,similarity:Belongs to the histone H2A family.,similarity:Belongs to the histone H3 family.,subunit: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.,subunit:The nucleosome is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. During DNA replication, it interacts with the histone H3-H4 heterodimer.,
Protein Function	
Usage	For Research Use Only! Not for diagnostic or therapeutic procedures.

