

Antibody Specification

Description	histone cluster 1 H3 family member a(HIST1H3A) Homo sapiens Histones are basic nuclear proteins that are the main component of the nucleosome, the basic unit of chromatin. They are also involved in the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped 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 and encodes a protein that is a member of the histone H3 family. Transcripts from this gene lack polyA tails; instead, they contain a polyU tail. This gene 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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Protein Function	caution:Was originally (PubMed:2587222) thought to originate from mouse.,developmental stage:Expresses in embryonic stem cells and decreases as cell division slows down during the process of differentiation.,function:Core component of nucleosome, involved in DNA packaging into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histone H3 is involved in gene regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a number of post-translational modifications on histones, also called histone code, and nucleosome remodeling.,mass spectrometry:Monoisotopic with molecular weight 14.7 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 at Lys-9 (H3R8sme2) linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8sme2) by PRMT5 is linked to gene repression. Symmetric dimethylation at Lys-9 (H3R8sme2) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation. Symmetric dimethylation at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription.,PTM:Hydroxylation at Lys-9 (H3R8ci) entry.,PTM:Methylation at Lys-5 (H3K4me), Lys-37 (H3K36me) and Lys-80 (H3K79me) are linked to gene repression. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation of H3 and H4. Methylation at Lys-80 (H3K79me) is associated with DNA damage 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). Methylation at Lys-5 (H3K4me) and Lys-80 (H3K79me) require preliminary monoubiquitination of H2B and H28 (H3K27me) are enriched in inactive X chromosome chromatin.,PTM:Monoubiquitination of Lys-120 by RNF2/RING2 is a tag for epigenetic transcriptional repression and participates in X chromosome inactivation of female mammals. Ubiquitinated H2A is enriched in imprinted and random X inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A and 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 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 of mitosis and centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably 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. Growth factors, 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) prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 (H3S10ph) mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 (H3S10ph) 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 of mitosis and centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably 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. Growth factors, 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) prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 (H3S10ph) mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 (H3S10ph) 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. Acetylation of H3 inhibits Ser-2 phosphorylation by RPS6KA5/MSK1.,PTM:Symmetric dimethylation on Arg-9 (H3R8sme2) is a crucial role in the germ-cell lineage.,PTM:The chromatin-associated form is phosphorylated on Thr-121 (H3T11ph) by AURKB. RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA. Ubiquitination of H2A and proteins.,similarity:Belongs to the histone H2A family.,similarity:Belongs to the histone H3 family.,subunit:Histone H3 is composed of 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 DNA replication, the octamer interacts with the histone H3-H4 heterodimer.,
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