

Immunotag™ Histone H3 (Di Methyl Lys27) Polyclonal Antibody

Antibody Specification	
Catalog No.	ITH0009
Product Description	Immunotag™ Histone H3 (Di Methyl Lys27) Polyclonal Antibody
Size	50 µg, 100 µg
Conjugation	HRP, Biotin, FITC, Alexa Fluor® 350, Alexa Fluor® 405, Alexa Fluor® 488, Alexa Fluor® 555, Alexa Fluor® 647
IMPORTANT NOTE	This product is custom manufactured with a lead time of 3-4 weeks. Once in production, this item cannot be returned.
Target Protein	Histone H3 (D-Lys27)
Clonality	Polyclonal
Storage/Stability	-20°C/1 year
Application	WB,ELISA
Recommended Dilution	Western Blot: 1/500 - 1/2000. ELISA: 1/10000. Not yet tested in other applications.
Concentration	1 mg/ml
Reactive Species	Human,Mouse,Rat
Host Species	Rabbit
Immunogen	Synthesized peptide derived from human Histone H3 around the di-methylation site of K27
Specificity	Di-Methyl-Histone H3 (K27) Polyclonal Antibody detects endogenous levels of Histone H3 around the methylation site of K27
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific resin
Form	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Gene Name	HIST1H3A/HIST1H3/HIST1H3C/HIST1H3D/HIST1H3E/HIST1H3F/HIST1H3G/HIST1H3H/HIST1H3I/HIST1H3J/HIST1H3K/HIST1H3L/HIST1H3M/HIST1H3N/HIST1H3O/HIST1H3P/HIST1H3Q/HIST1H3R/HIST1H3S/HIST1H3T/HIST1H3U/HIST1H3V/HIST1H3W/HIST1H3X/HIST1H3Y/HIST1H3Z/HIST2H3A/HIST2H3B/HIST2H3C/HIST2H3D/HIST2H3E/HIST2H3F/HIST2H3G/HIST2H3H/HIST2H3I/HIST2H3J/HIST2H3K/HIST2H3L/HIST2H3M/HIST2H3N/HIST2H3O/HIST2H3P/HIST2H3Q/HIST2H3R/HIST2H3S/HIST2H3T/HIST2H3U/HIST2H3V/HIST2H3W/HIST2H3X/HIST2H3Y/HIST2H3Z/HIST3H3A/HIST3H3B/HIST3H3C/HIST3H3D/HIST3H3E/HIST3H3F/HIST3H3G/HIST3H3H/HIST3H3I/HIST3H3J/HIST3H3K/HIST3H3L/HIST3H3M/HIST3H3N/HIST3H3O/HIST3H3P/HIST3H3Q/HIST3H3R/HIST3H3S/HIST3H3T/HIST3H3U/HIST3H3V/HIST3H3W/HIST3H3X/HIST3H3Y/HIST3H3Z
Accession No.	P68431 P68433 Q6LED0
Alternate Names	HIST1H3A; H3FA; HIST1H3B; H3FL; HIST1H3C; H3FC; HIST1H3D; H3FB; HIST1H3E; H3FD; HIST1H3F; H3FE; HIST1H3G; H3FG; HIST1H3H; H3FH; HIST1H3I; H3FI; HIST1H3J; H3FJ; Histone H3.1; Histone H3/a; Histone H3/b; Histone H3/c; Histone H3/d; Histone H3/e; Histone H3/f; Histone H3/g; 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/n; Histone H3/o; Histone H3/p; Histone H3/q; Histone H3/r; Histone H3/s; Histone H3.3; H3F3C; Histone H3.3C; Histone H3.5

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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 organization. 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. HIST1H3A is a member of the histone H3 family. Transcripts from this gene lack polyA tails; instead, they contain a polyA signal. 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:Expression decreases as cell division slows down during the process of differentiation.,function:Core component of nucleosome, limiting DNA accessibility to the cellular machineries which require DNA as a template. Involved in gene regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a number of 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 nucleosomes (H3K9me2).,PTM:Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impacts transcription on 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 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation. Methylation at the 3' of genes regardless of their transcription state and is enriched on inactive promoters, while it is enriched on 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 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-28 (H3K27me) is a specific target for HP1 proteins (CBX1, CBX3 and CBX5) and prevents subsequent phosphorylation at Ser-2. 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 RNF2/RING2 tag for epigenetic transcriptional repression and participates in X chromosome inactivation of female mammals. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination is involved in X chromosome inactivation, imprinted and random X inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of Lys-120 by RNF2/RING2 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 of Lys-120 by RNF2/RING2 ubiquitination are distinct events.,PTM:Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase I. Phosphorylation at centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. 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. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 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, RPS6KA5 or RPS6KA4 upon ultraviolet B irradiation.,PTM:Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase I. Phosphorylation at centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, probably by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. Phosphorylation at Ser-11 (H3S10ph) by AURKB by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-2 by RPS6KA4 and RPS6KA5 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 RPS6KA4 and RPS6KA5 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. Phosphorylation at Thr-121 (H3T11ph) by RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA. Ubiquitination of Lys-120 by RNF2/RING2 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.,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 DNA replication, it interacts with the histone H3-H4 heterodimer.,
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