

## Immunotag™ Histone H3 Polyclonal Antibody

Antibody Specification	
Catalog No.	ITT5434
Product Description	Immunotag™ Histone H3 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
Clonality	Polyclonal
Storage/Stability	-20°C/1 year
Application	WB,ELISA
Recommended Dilution	Western Blot: 1/500 - 1/2000. ELISA: 1/20000. 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 non-methylation site of K27
Specificity	Histone H3 Polyclonal Antibody detects endogenous levels of Histone H3 protein only when non-methylated.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific antigen.
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
Accession No.	P68431/Q71DI3/P84243/Q6NXT2 Q6LED0/P84245
Alternate Names	HIST1H3A; H3FA; HIST1H3B; H3FL; HIST1H3C; H3FC; HIST1H3D; H3FB; HIST1H3E; H3FD; HIST1H3F; H3FF; HIST1H3G; H3FG; HIST1H3H; H3FH; HIST1H3I; H3FI; HIST1H3J; H3FJ; Histone H3.1; Histone H3.1; Histone H3.2; Histone H3/m; Histone H3/o; H3F3A; H3F3B; 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 major components of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped around a core of eight nucleosomes, each consisting of two pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted by 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 polyA signal sequence. 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 junction,membrane,protein complex,extracellular exosome,

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<p>Protein Function</p>	<p>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 that packages DNA into chromatin, 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 acetylation of histones, also called histone code, and nucleosome remodeling.,mass spectrometry:Monoisotopic with molecular weight of 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. Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me).,PTM:Asymmetric methylation on Lys-9 (H3R8me) linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8sme2) by PRMT5 is linked to gene repression. Symmetric dimethylation at Arg-27 (H3R26sme2) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation. Methylation at Arg-27 (H3R26me) at the 3' of genes regardless of their transcription state and is enriched on inactive promoters, while it is enriched on active promoters. Methylation at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription.,PTM:Asymmetric methylation on Lys-9 (H3K9me) 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. 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 is a tag for epigenetic transcriptional repression and participates in X chromosome inactivation of female mammals. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A is linked to X chromosome inactivation. 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 H2A and H2B ubiquitination are distinct events.,PTM:Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase I. Phosphorylation at Thr-11 (H3S10ph) 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 Thr-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes. Phosphorylation at Thr-11 (H3S10ph) by mitogens, stress, growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun. Phosphorylation at Thr-11 (H3S10ph) by AURKB gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Thr-11 (H3S10ph) mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Thr-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 I. Phosphorylation at Thr-11 (H3S10ph) 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 Thr-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes. Phosphorylation at Thr-11 (H3S10ph) by mitogens, stress, growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun. Phosphorylation at Thr-11 (H3S10ph) gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Thr-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/MSK1. 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). Phosphorylation at Thr-121 (H3T11ph) by RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA. Ubiquitination of H2A and H2B ubiquitination are distinct events.,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 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. During transcription, it interacts with the histone H3-H4 heterodimer.,</p>
<p>Usage</p>	<p>For Research Use Only! Not for diagnostic or therapeutic procedures.</p>

