

Immunotag™ Histone H3 Polyclonal Antibody

Antibody Specification	
Catalog No.	ITT2166
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 and is not eligible for return.
Target Protein	Histone H3
Clonality	Polyclonal
Storage/Stability	-20°C/1 year
Application	WB,IHC-p,ELISA
Recommended Dilution	Western Blot: 1/500 - 1/2000. Immunohistochemistry: 1/100 - 1/300. ELISA: 1/5000. Not yet tested in other applications.
Concentration	1 mg/ml
Reactive Species	Human,Mouse,Rat
Host Species	Rabbit
Immunogen	Synthesized peptide derived from Histone H3, at AA range: 1-80
Specificity	Histone H3 Polyclonal Antibody detects endogenous levels of Histone H3 protein.
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/HIST1H3B/HIST1H3C/HIST1H3D/HIST1H3E/HIST1H3F/HIST1H3G/HIST1H3H/HIST1H3I/HIST1H3J/HIST1H3K/HIST1H3L/HIST1H3M/HIST1H3N/HIST1H3O/HIST1H3P/HIST1H3Q/HIST1H3R/HIST1H3S/HIST1H3T/HIST1H3U/HIST1H3V/HIST1H3W/HIST1H3X/HIST1H3Y/HIST1H3Z
Accession No.	P68431/Q71DI3/P84243 Q6LED0/P84245
Alternate Names	HIST1H3A; H3FA; HIST1H3B; H3FL; HIST1H3C; H3FC; HIST1H3D; H3FB; HIST1H3E; H3FD; HIST1H3F; H3FE; HIST1H3G; H3GB; HIST1H3H; H3HB; HIST1H3I; H3IB; HIST1H3J; H3JB; HIST1H3K; H3KB; HIST1H3L; H3LB; HIST1H3M; H3MB; HIST1H3N; H3NB; HIST1H3O; H3OB; HIST1H3P; H3PB; HIST1H3Q; H3QB; HIST1H3R; H3RB; HIST1H3S; H3SB; HIST1H3T; H3TB; HIST1H3U; H3UB; HIST1H3V; H3VB; HIST1H3W; H3WB; HIST1H3X; H3XB; HIST1H3Y; H3YB; HIST1H3Z; H3ZB; 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; Histone H3/m; Histone H3/n; Histone H3/o; Histone H3/p; Histone H3/q; Histone H3/r; Histone H3/s; Histone H3/t; Histone H3/u; Histone H3/v; Histone H3/w; Histone H3/x; Histone H3/y; Histone H3/z

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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 histone proteins, 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	Protein_Acetylation
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:Expresses at embryonic stages.,expression pattern:Expression decreases as cell division slows down during the process of differentiation.,function:Core component of nucleosome, packaging 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 histone modifications of histones, also called histone code, and nucleosome remodeling.,mass spectrometry:Mass spectrometry analysis of H3K9me2 (PubMed:16457589),miscellaneous:This histone is only present in mammals and is enriched in acetylated chromatin.,PTM:Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Arg-18 (H3R17me). Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me). PTM:Hydroxylation of Arg-18 (H3R17me2a) by CARM1 is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8sme2) by PRMT6 is linked to gene repression and is mutually exclusive with asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6. Asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with symmetric dimethylation at Arg-9 (H3R8sme2). H3R2me2a is present at the 3' end of genes regardless of their transcription status. It is absent on active promoters.,PTM:Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PAD14 is linked to gene repression. Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PAD14 is linked to gene repression.,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 at Lys-9 (H3K9ac). Methylation at Lys-9 (H3K79me) is associated with DNA double-strand break (DSB) responses and is a specific target for TP53-mediated apoptosis. Methylation at Lys-28 (H3K27me) are linked to gene repression. Methylation at Lys-10 (H3K9me) is a specific target for DNMT3A and DNMT3B. Methylation prevents subsequent phosphorylation at Ser-11 (H3S10ph) and acetylation of H3 and H4. Methylation at Lys-10 (H3K9me) requires preliminary monoubiquitination of H2B at 'Lys-120'. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are linked to gene repression. Monoubiquitination of Lys-120 by RING1 and RNF2/RING2 complex gives rise to a repressed state. Repression and participates in X chromosome inactivation of female mammals. It is involved in the initial steps of X chromosome inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A at Lys-120 is required for the 27' of histone H3. Monoubiquitination of Lys-120 by RNF2/RING2 can also be induced by ultraviolet and oxidative stress. In response to double-strand breaks (DSBs), it is ubiquitinated through 'Lys-63' linkage of ubiquitin moieties by the E2 ubiquitin-conjugating enzyme UBE2A 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. 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. Phosphorylation at Ser-11 (H3S10ph) is enhanced during mitosis and upon ultraviolet B irradiation.,PTM:Hydroxylation of Ser-11 (H3S10ph) by MLTK isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation.,PTM:Monoubiquitination of Lys-120 by RING1 and RNF2/RING2 complex gives rise to a repressed state. Repression and participates in X chromosome inactivation of female mammals. It is involved in the initial steps of X chromosome inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A at Lys-120 is required for the 27' of histone H3. Monoubiquitination of Lys-120 by RNF2/RING2 can also be induced by ultraviolet and oxidative stress. In response to double-strand breaks (DSBs), it is ubiquitinated through 'Lys-63' linkage of ubiquitin moieties by the E2 ubiquitin-conjugating enzyme UBE2A 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 and dephosphorylated during anaphase. 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 during mitosis and meiosis. In addition phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes 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 (H3S10ph), which is linked to gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. 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 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) but facilitates acetylation of H3 and H4. 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:Acetylation of H3 inhibits Ser-2 phosphorylation by RPS6KA5/MSK1.,PTM:Symmetric dimethylation on Arg-9 (H3R8sme2) by PRMT6 is linked to gene repression and is mutually exclusive with asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6. Asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with symmetric dimethylation at Arg-9 (H3R8sme2). The chromatin-associated form is phosphorylated on Thr-12 (H3T11ph) from prophase to early anaphase, probably by DAPK3. CUL4-DDDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histone octamer and DNA, increasing 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 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.,assembly:The chaperone ASF1A interacts with the histone H3-H4 heterodimer.,
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Antibody Specification

Usage

For Research Use Only! Not for diagnostic or therapeutic procedures.