

## Histone H3 (Tri Methyl Lys4) Rabbit pAb

CatalogNo: YH0029

### Key Features

#### Host Species

- Rabbit

#### Reactivity

- Human, Mouse, Rat

#### Applications

- WB

#### MW

- 15-17kD (Observed)

#### Isotype

- IgG

### Storage

**Storage\*** -15°C to -25°C/1 year (Do not lower than -25°C)

**Formulation** PBS, pH 7.4, containing 0.5%BSA, 0.02% sodium azide as Preservative and 50% Glycerol.

### Recommended Dilution Ratios

WB 1:500-1000

### Basic Information

**Clonality** Polyclonal

### Immunogen Information

**Immunogen** Synthetic Peptide of Histone H3 (Tri Methyl Lys4)

**Specificity** The antibody detects endogenous Histone H3 (Tri Methyl Lys4) protein.

### Target Information

**Gene name** HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4

**Protein Name** Histone H3.1/Histone H3.2/Histone H3.3

<b>Organism</b>	<b>Gene ID</b>	<b>UniProt ID</b>
Human	<a href="#">8350</a> ; <a href="#">8351</a> ; <a href="#">8352</a> ; <a href="#">8353</a> ; <a href="#">8354</a> ; <a href="#">8355</a> ; <a href="#">8356</a> ; <a href="#">8357</a> ; <a href="#">8358</a> ; <a href="#">8968</a> ;	<a href="#">P68431</a> ; <a href="#">Q71DI3</a> ; <a href="#">P84243</a> ;
Mouse	<a href="#">319152</a> ; <a href="#">15077</a> ; <a href="#">15078</a> ;	<a href="#">P68433</a> ;
Rat	<a href="#">291159</a> ; <a href="#">100361558</a> ;	<a href="#">Q6LED0</a> ; <a href="#">P84245</a> ;

**Cellular Localization** Nucleus. Chromosome.

**Tissue specificity** Blood ,Epithelium ,Kidney ,Lung ,Ovary ,Spleen ,Uterus ,

## Function

Caution: Was originally (PubMed:2587222) thought to originate from mouse. ,developmental stage: Expressed during S phase , then expression strongly decreases as cell division slows down during the process of differentiation. ,Function: Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin , limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation , DNA repair , DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones , also called histone code , and nucleosome remodeling. ,mass spectrometry: Monoisotopic with N-acetylserine PubMed:16457589 ,miscellaneous: This histone is only present in mammals and is enriched in acetylation of Lys-15 and dimethylation of Lys-10 (H3K9me2) . ,PTM: Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Arg-9 (H3R8sme2) . Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me) . ,PTM: Asymmetric dimethylation at Arg-18 (H3R17me2a) by CARM1 is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8sme2) by PRMT5 is linked to gene repression. Asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation (H3K4me2 and H3K4me3) . H3R2me2a is present at the 3' of genes regardless of their transcription state and is enriched on inactive promoters , while it is absent on active promoters. ,PTM: Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription. ,PTM: Deiminated on Arg-4 in granulocytes upon calcium entry. ,PTM: Methylation at Lys-5 (H3K4me) , Lys-37 (H3K36me) and Lys-80 (H3K79me) are linked to gene activation. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation of H3 and H4. Methylation at Lys-80 (H3K79me) is associated with DNA double-strand break (DSB) responses 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) and acetylation of H3 and H4. Methylation at Lys-5 (H3K4me) and Lys-80 (H3K79me) require preliminary monoubiquitination of H2B at 'Lys-120'. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are enriched in inactive X chromosome chromatin. ,PTM: Monoubiquitination of Lys-120 by RING1 and RNF2/RING2 complex gives a specific tag for epigenetic transcriptional repression and participates in X chromosome inactivation of female mammals. It is involved in the initiation of both imprinted and random X inactivation. Ubiquitinated H2A is enriched in inactive X chromosome chromatin. Ubiquitination of H2A functions downstream of methylation of 'Lys-27' of histone H3. Monoubiquitination of Lys-120 by RNF2/RING2 can also be induced by ultraviolet and may be involved in DNA repair. Following DNA double-strand breaks (DSBs) , it is ubiquitinated through 'Lys-63' linkage of ubiquitin moieties by the E2 ligase UBE2N and the E3 ligases RNF8 and RNF168 , leading to the recruitment of repair proteins to sites of DNA damage. Monoubiquitination and ionizing radiation-induced 'Lys-63'-linked ubiquitination 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 (By similarity) . 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 , 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 (H3S28ph) by MLTK isoform 1 , RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation. ,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 RPS6KA5/MSK1 directly represses transcription. Acetylation of H3 inhibits Ser-2 phosphorylation by RPS6KA5/MSK1. ,PTM: Symmetric dimethylation on Arg-4 by the PRDM1/PRMT5 complex may play a crucial role in the germ-cell lineage. ,PTM: The chromatin-associated form is phosphorylated on Thr-121 during mitosis. ,PTM: Ubiquitinated by the CUL4-DDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA and facilitate DNA accessibility to repair proteins. ,similarity: Belongs to the histone H2A family. ,similarity: Belongs to the histone H3 family. ,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. ,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 nucleosome assembly the chaperone ASF1A interacts with the histone H3-H4 heterodimer. ,

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## | Validation Data

## | Contact information

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Please scan the QR code to access additional product information:  
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