

Rabbit Anti-phospho-Histone H3 (Thr45) antibody

SL17442R

when kept at -20°C. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of		
Histone H3 (phospho T45); p-Histone H3 (phospho T45); H3 3 like sequence MH921; H3 3 like sequence MH921; H3 3A; H3 a; H3 b; H3 c; H3 d; H3 f; H3 h; H3 histone family member E pseudogene; H3 histone family member E pseudogene; H3 i; H3 j; H3 k; H3 l; H33_HUMAN; H3F3; H3F3; H3f3b; Histone H3 3 pseudogene; Histone H3 3 pseudogene; Histone H3.3.Organism Species:Rabbit Clonality: Polyclonal React Species:Human,Mouse,Rat,Chicken,Dog,Cow,Rabbit,Firefly, WB=1:500-2000ELISA=1:500-1000HHC-P=1:400-800HC-F=1:400-800ICC=1:100- 500IF=1:100-500 (Paraffin sections need antigen repair) not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.Molecular weight:17kDaCellular localization:The nucleus Hg nucleusForm:Lyophilized or Liquid Concentration: the phosphorylation site of Thr45:41-136/136Lsotype:IgG Purification: affinity purified by Protein A StorageStorage:Storage C °C on one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of	Product Name:	
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PubMed: PubMed	PubMed:	
Product Detail: Histones are basic nuclear proteins that are responsible for the nucleosome structure of	Product Detail:	

the chromosomal fiber in eukaryotes. Two molecules of each of the four core histones (H2A, H2B, H3, and H4) form an octamer, around which approximately 146 bp of DNA is wrapped in repeating units, called nucleosomes. The linker histone, H1, interacts with linker DNA between nucleosomes and functions in the compaction of chromatin into higher order structures. This gene contains introns and its mRNA is polyadenylated, unlike most histone genes. The protein encoded is a replication-independent member of the histone H3 family. [provided by RefSeq, Jul 2008]

Function:

Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active genes. Constitutes the predominant form of histone H3 in non-dividing cells and is incorporated into chromatin independently of DNA synthesis. Deposited at sites of nucleosomal displacement throughout transcribed genes, suggesting that it represents an epigenetic imprint of transcriptionally active chromatin. 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.

Subcellular Location: Nucleus. Chromosome.

Post-translational modifications:

Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Arg-9 (H3R8me2s). Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me).

Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PADI4 impairs methylation and represses transcription.

Asymmetric dimethylation at Arg-18 (H3R17me2a) by CARM1 is linked to gene activation. Symmetric dimethylation at Arg-9 (H3R8me2s) 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. Specifically enriched in modifications associated with active chromatin such as methylation at Lys-5 (H3K4me), Lys-37 and Lys-80. 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), which are linked to gene repression, are underrepresented. 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. Phosphorylated at Thr-4 (H3T3ph) by

GSG2/haspin during prophase and dephosphorylated during anaphase. 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 (H3S28ph) by MLTK isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation. Phosphorylation at Thr-7 (H3T6ph) by PRKCBB is a specific tag for epigenetic transcriptional activation that prevents demethylation of Lys-5 (H3K4me) by LSD1/KDM1A. At centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, by DAPK3 and PKN1. Phosphorylation at Thr-12 (H3T11ph) by PKN1 is a specific tag for epigenetic transcriptional activation that promotes demethylation of Lys-10 (H3K9me) by KDM4C/JMJD2C. Phosphorylation at Tyr-42 (H3Y41ph) by JAK2 promotes exclusion of CBX5 (HP1 alpha) from chromatin. Phosphorylation on Ser-32 (H3S31ph) is specific to regions bordering centromeres in metaphase chromosomes. Ubiguitinated. Monoubiguitinated by RAG1 in lymphoid cells, monoubiguitination is required for V(D)J recombination.

Similarity: Belongs to the histone H3 family.

SWISS: P84243

Gene ID: 3020

Database links:

Entrez Gene: 326601 Cow

Entrez Gene: 31848 Fruit fly (Drosophila melanogaster)

Entrez Gene: 33736 Fruit fly (Drosophila melanogaster)

Entrez Gene: 3020 Human

Entrez Gene: 3021 Human

Entrez Gene: 15078 Mouse

Entrez Gene: 15081 Mouse

Entrez Gene: 100361558 Rat

Entrez Gene: 100365096 Rat

Entrez Gene: 117056 Rat

Entrez Gene: 289314 Rat

Omim: 601128 Human

SwissProt: P02299 Fruit fly (Drosophila melanogaster)

SwissProt: P84249 Fruit fly (Drosophila melanogaster) ,gr

SwissProt: P84243 Human

SwissProt: Q16695 Human

SwissProt: Q93081 Human

SwissProt: P84244 Mouse

SwissProt: P84245 Rat

Unigene: 2931 Fruit fly (Drosophila melanogaster)

Unigene: 35099 Fruit fly (Drosophila melanogaster)

Unigene: 7418 Fruit fly (Drosophila melanogaster)

Unigene: 180877 Human

Unigene: 533624 Human

Unigene: 726012 Human

Unigene: 138832 Mouse

Unigene: 18516 Mouse

Unigene: 315189 Mouse

Unigene: 316825 Mouse

Unigene: 322735 Mouse

Unigene: 371563 Mouse

Unigene: 442502 Mouse
<u>Unigene: 106155</u> Rat
<u>Unigene: 124815</u> Rat
<u>Unigene: 198918</u> Rat
Unigene: 29857 Rat
Important Note:
This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.

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