

ARG66753 anti-Histone H3 phospho (Ser10) antibody [SQab20186]

Package: 100 μl Store at: -20°C

Summary

Product Description	Recombinant Rabbit Monoclonal antibody [SQab20186] recognizes Histone H3 phospho (Ser10)
Tested Reactivity	Hu
Tested Application	IHC-P
Host	Rabbit
Clonality	Monoclonal
Clone	SQab20186
Isotype	lgG
Target Name	Histone H3
Species	Human
Immunogen	Phosphospecific peptide within aa. 1-100 of Human Histone H3. (phosphorylated at Ser10)
Conjugation	Un-conjugated
Alternate Names	H3F3; H3-3B; H3.3A; H3F3A

Application Instructions

Application table	Application	Dilution
	IHC-P	1:100 - 1:200
Application Note	0	nediation was performed in Tris/EDTA buffer (pH 9.0). nended starting dilutions and the optimal dilutions or concentrations ientist.
Positive Control	Tonsil tissue.	

Properties

Form	Liquid
Purification	Purification with Protein A.
Buffer	PBS, 0.01% Sodium azide, 40% Glycerol and 0.05% BSA.
Preservative	0.01% Sodium azide
Stabilizer	40% Glycerol and 0.05% BSA
Storage instruction	For continuous use, store undiluted antibody at 2-8°C for up to a week. For long-term storage, aliquot and store at -20°C. Storage in frost free freezers is not recommended. Avoid repeated freeze/thaw cycles. Suggest spin the vial prior to opening. The antibody solution should be gently mixed before use.
Note	For laboratory research only, not for drug, diagnostic or other use.

Bioinformation

Gene Symbol	НЗ-ЗА
Gene Full Name	H3.3 histone A
Background	Histones are basic nuclear proteins that are responsible for the nucleosome structure of 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. [UniProt]
ΡΤΜ	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). Acetylation at Lys-123 (H3K122ac) by EP300/p300 plays a central role in chromatin structure: localizes at the surface of the histone octamer and stimulates transcription, possibly by promoting nucleosome instability.
	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. Monomethylation at Lys-57 (H3K56me1) by EHMT2/G9A in G1 phase promotes interaction with PCNA and is required for DNA replication.
	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 MAP3K20 isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation. Phosphorylation at Thr-7 (H3T6ph) by PRKCB 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.

Ubiquitinated. Monoubiquitinated by RAG1 in lymphoid cells, monoubiquitination is required for V(D)J recombination (By similarity).

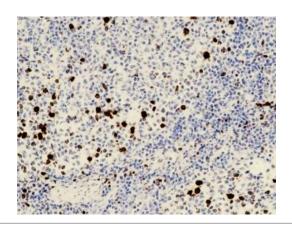
Lysine deamination at Lys-5 (H3K4all) to form allysine is mediated by LOXL2. Allysine formation by LOXL2 only takes place on H3K4me3 and results in gene repression (PubMed:22483618).

Crotonylation (Kcr) is specifically present in male germ cells and marks testis-specific genes in postmeiotic cells, including X-linked genes that escape sex chromosome inactivation in haploid cells. Crotonylation marks active promoters and enhancers and confers resistance to transcriptional repressors. It is also associated with post-meiotically activated genes on autosomes. [UniProt]

Cellular Localization

Nucleus. Chromosome. [UniProt]

Images



ARG66753 anti-Histone H3 phospho (Ser10) antibody [SQab20186] IHC-P image

Immunohistochemistry: Formalin/PFA-fixed and paraffin-embedded Human tonsil tissue. Antigen Retrieval: Heat mediation was performed in Tris/EDTA buffer (pH 9.0). The tissue section was stained with ARG66753 anti-Histone H3 phospho (Ser10) antibody [SQab20186] at 18°C - 25°C for 30 minutes.