Product datasheet

Anti-Histone H3 antibody [mAbcam 24834] - Nuclear Loading Control and ChIP Grade ab24834

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Overview

Product name
Anti-Histone H3 antibody [mAbcam 24834] - Nuclear Loading Control and ChIP Grade

Description
Mouse monoclonal [mAbcam 24834] to Histone H3 - Nuclear Loading Control and ChIP Grade

Host species
Mouse

Tested applications
Suitable for: ChIP, WB

Species reactivity
Reacts with: Mouse, Rat, Human

Predicted to work with: a wide range of other species

Immunogen
Synthetic peptide corresponding to Human Histone H3 aa 100 to the C-terminus.
Database link: P68431
(Peptide available as ab12149)

Positive control
ChIP: Chromatin was prepared from HeLa cells. WB: HeLa histone prep. NIH/3T3 and PC-12 whole cell lysates. Mouse and rat testis tissue lysates.

General notes
This antibody clone is manufactured by Abcam.

If you require this antibody in a particular buffer formulation or a particular conjugate for your experiments, please contact orders@abcam.com or you can find further information here.

Properties

Form
Liquid

Storage instructions
Shipped at 4°C. Store at +4°C short term (1-2 weeks). Upon delivery aliquot. Store at -20°C or -80°C. Avoid freeze / thaw cycle.

Storage buffer
pH: 7.50
Preservative: 0.02% Sodium azide
Constituent: PBS

Purity
IgG fraction

Clonality
Monoclonal

Clone number
mAbcam 24834

Myeloma
Sp2/0-Ag14

Isotype
IgG3
Light chain type  
kappa

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.

Sequence similarities  
Belongs to the histone H3 family.

Developmental stage  
Expressed during S phase, then expression strongly decreases as cell division slows down during the process of differentiation.

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 (H3K4me 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. 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. 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

Applications

Our Abpromise guarantee covers the use of ab24834 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

<table>
<thead>
<tr>
<th>Application</th>
<th>Abreviews</th>
<th>Notes</th>
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<tbody>
<tr>
<td>ChIP</td>
<td></td>
<td>Use 5 µg for 25 µg of chromatin.</td>
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<tr>
<td>WB</td>
<td>★★★★★</td>
<td>Use a concentration of 0.5 - 1 µg/ml. Detects a band of approximately 18 kDa (predicted molecular weight: 15 kDa). Can be blocked with Human Histone H3 peptide (ab12149).</td>
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</table>

Target

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.

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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 PRKCB2 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. Monoubiquitinated by RAG1 in lymphoid cells, monoubiquitination is required for V(D)J recombination (By similarity). 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.

**Cellular localization**

Nucleus. Chromosome.

**Images**

Chromatin was prepared from HeLa cells according to the Abcam X-ChIP protocol. Cells were fixed with formaldehyde for 10 minutes. The ChIP was performed with 25µg of chromatin, 5µg of ab24834 (blue), and 20µl of Protein A/G sepharose beads. No antibody was added to the beads control (yellow). The immunoprecipitated DNA was quantified by real time PCR (Taqman approach for active and inactive loci, Sybr green approach for heterochromatic loci). Primers and probes are located in the first kb of the transcribed region.
Anti-Histone H3 antibody [mAbcam 24834] - Nuclear Loading Control and ChiP Grade (ab24834) at 1 µg/ml + HeLa histone prep at 1 µg/ml

**Secondary**
Rabbit Anti-Mouse IgG H&L (HRP) (ab6728) at 1/5000 dilution

**Predicted band size:** 15 kDa
**Observed band size:** 18 kDa

*why is the actual band size different from the predicted?*

All lanes: Anti-Histone H3 antibody [mAbcam 24834] - Nuclear Loading Control and ChiP Grade (ab24834) at 1 µg/ml

Lane 1: NIH/3T3 (Mouse embryonic fibroblast cell line) Whole Cell Lysate
Lane 2: Testis (Mouse) Tissue Lysate
Lane 3: PC12 (Rat adrenal pheochromocytoma cell line) Whole Cell Lysate
Lane 4: Testis (Rat) Tissue Lysate - normal tissue (ab29388)

Lysates/proteins at 10 µg per lane.

**Secondary**
All lanes: Goat Anti-Mouse IgG H&L (HRP) preadsorbed (ab97040) at 1/5000 dilution

Developed using the ECL technique.

Performed under reducing conditions.

**Predicted band size:** 15 kDa
**Observed band size:** 18 kDa

*why is the actual band size different from the predicted?*

**Exposure time:** 3 minutes

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