abcam

Product datasheet

Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade ab181447



2 References 6 Images

Overview

Product name Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade

Description Rabbit monoclonal [EPR17588] to Histone H2A (phospho S129) - ChIP Grade

Host species Rabbit

Tested applications

Suitable for: PepArr, Dot blot, ChIP, WB, ELISA

Species reactivity

Reacts with: Human, Saccharomyces cerevisiae

Immunogen Synthetic peptide. This information is proprietary to Abcam and/or its suppliers.

Positive control WB: Saccharomyces cerevisiae treated with 0.2% Methyl methanesulfonate for 1 hour lysate.

ChIP: Chromatin prepared from Saccharomyces cerevisiae cells.

General notesThis product is a recombinant monoclonal antibody, which offers several advantages including:

- High batch-to-batch consistency and reproducibility

- Improved sensitivity and specificity

Long-term security of supplyAnimal-free production

For more information see here.

Our RabMAb[®] technology is a patented hybridoma-based technology for making rabbit monoclonal antibodies. For details on our patents, please refer to **RabMAb**[®] **patents**.

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 long

term. Avoid freeze / thaw cycle.

Storage buffer Preservative: 0.01% Sodium azide

Constituents: 59% PBS, 40% Glycerol (glycerin, glycerine), 0.05% BSA

Purity Protein A purified

ClonalityMonoclonalClone numberEPR17588

Isotype IgG

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Applications

The Abpromise guarantee

Our Abpromise guarantee covers the use of ab181447 in the following tested applications.

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

Application	Abreviews	Notes
PepArr		Use at an assay dependent concentration.
Dot blot		1/1000.
ChIP		Use 2 µg for 25 µg of chromatin.
WB		1/5000. Detects a band of approximately 14 kDa (predicted molecular weight: 14 kDa).
ELISA		Use at an assay dependent concentration.

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.

Sequence similarities

Post-translational modifications

Belongs to the histone H2A family.

The chromatin-associated form is phosphorylated on Thr-121 during mitosis.

Deiminated on Arg-4 in granulocytes upon calcium entry.

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.

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.

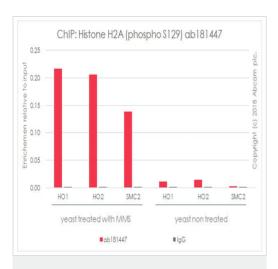
Symmetric dimethylation on Arg-4 by the PRDM1/PRMT5 complex may play a crucial role in the

germ-cell lineage.

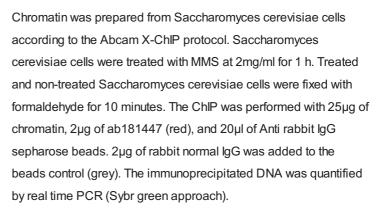
Cellular localization

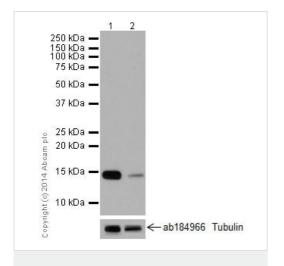
Nucleus. Chromosome.

Images



ChIP - Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447)





Western blot - Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447)

All lanes : Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447) at 1/5000 dilution

Lane 1 : Saccharomyces cerevisiae treated with 0.2% Methyl methanesulfonate for 1 hour lysate

Lane 2: Untreated Saccharomyces cerevisiae whole cell lysate

Lysates/proteins at 10 µg per lane.

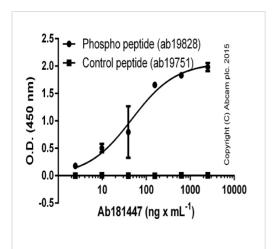
Secondary

All lanes : Goat Anti-Rabbit lgG, (H+L), Peroxidase conjugated at 1/1000 dilution

Predicted band size: 14 kDa **Observed band size:** 14 kDa

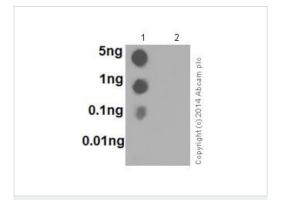
Exposure time: 3 minutes

Blocking/Dilution buffer: 5% NFDM/TBST.



ELISA - Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447)

Serially diluted ab181447 was bound to immobilised phospho (ab19828) - or control (ab19751) peptides (1 microgram x mL-1). The antibody was detected by HRP-labelled goat anti-rabbit lgG (ab97080; diluted 50000 times) and signal was developed with TMB substrate.

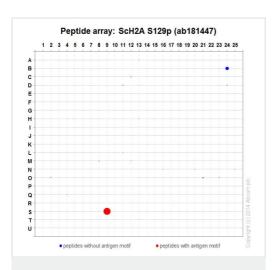


Dot Blot - Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447)

Dot blot analysis of Histone H2A (phospho S129) peptide (Lane 1), and non-phospho peptide (Lane 2), labeled using ab181447 at 1/1000 dilution, followed by Goat Anti-Rabbit lgG, (H+L), Peroxidase conjugated secondary antibody at 1/1000 dilution.

Blocking/Dilution buffer: 5% NFDM/TBST.

Exposure time: 3 minutes



Peptide Array - Anti-Histone H2A (phospho S129) antibody [EPR17588] - ChIP Grade (ab181447) ab181447 was tested in Peptide Array against 501 different modified and unmodified histone peptides; each peptide is printed on the array at six concentrations (each in triplicate).

Circle area represents affinity between the antibody and a peptide: all antigen-containing peptides are displayed as red circles, all other peptides as blue circles. The affinity is calculated as area under curve when antibody binding values are plotted against the corresponding peptide concentration. Each circle area is normalized to the peptide with the strongest affinity.

The complete dataset, including full list of all peptides and information on the position of each peptide in the diagram, can be downloaded here.



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