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H3K27me2 polyclonal antibody
Rabbit Polyclonal Antibody
Catalog # ABV11351

Specification

H3K27me2 polyclonal antibody - Product Information

Application	**CHIP, DB, E, WB**
Primary Accession	P68431
Host	**Rabbit**
Clonality	**Polyclonal**
Isotype	**Rabbit IgG**
Calculated MW	**15404**

H3K27me2 polyclonal antibody - Additional Information

Gene ID 8350;8351;8352;8353;8354;8355;8356;8357;8358;8968

Positive Control	**Western blot: HeLa cells, IF: HeLa cells, ELISA: Antigen, ChIP: HeLa cells, Dot blot: Histone Peptides.**
Application & Usage	**WB: 1:1000, ELISA: 1:1000, Dot Blot: 1:50,000, IF: 1:500, ChIP: 2 µg/ChIP.**

Other Names
Histone H3

Target/Specificity
H3K27me2

Antibody Form
Liquid

Appearance
Colorless liquid

Formulation
In PBS with 0.05% sodium azide and 0.05% ProClin 300.

Handling
The antibody solution should be gently mixed before use.

Reconstitution & Storage
-20 °C

Background Descriptions

Precautions
H3K27me2 polyclonal antibody is for research use only and not for use in diagnostic or therapeutic procedures.

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H3K27me2 polyclonal antibody - Protein Information

Name H3C1 (HGNC:4766)

Synonyms H3FA, HIST1H3A

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.

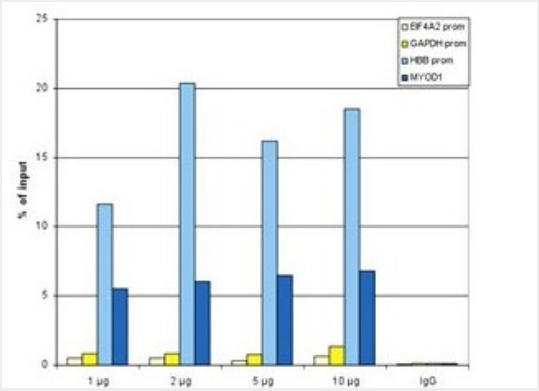
Cellular Location
Nucleus. Chromosome.

H3K27me2 polyclonal antibody - Protocols

Provided below are standard protocols that you may find useful for product applications.

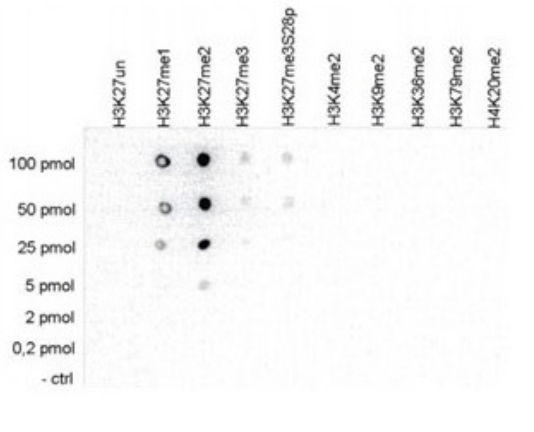
- Western Blot
- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

H3K27me2 polyclonal antibody - Images

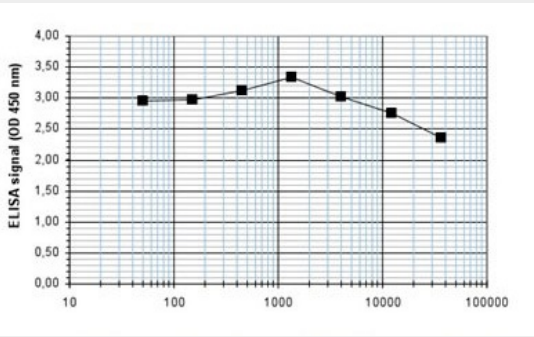


ChIP assays were performed using HeLa cells and the antibody and optimized PCR primer sets for qPCR. A titration of the antibody consisting of 1, 2, 5, and 10 µl per ChIP experiment was analysed. IgG (5 µg/IP) was used as negative control. The Fig shows the recovery, expressed as a % of input (the relative amount of IP DNA compared to input DNA after qPCR analysis).

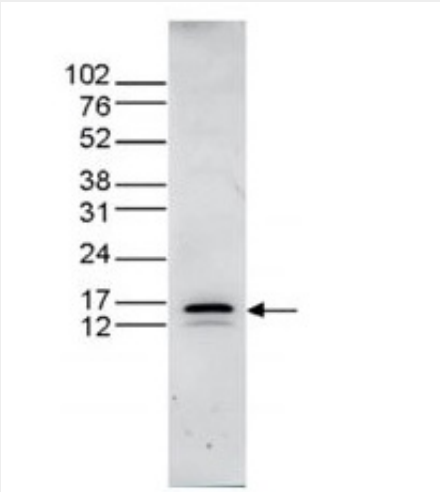
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A Dot Blot analysis was performed to test the cross reactivity of the antibody with peptides containing other modifications of histone H3 and the unmodified H3K9 sequence. 100 to 0.2 pmol of the peptide containing the respective histone modification were spotted on a membrane. The Fig shows a high specificity of the antibody for the modification of interest.



To determine the titer, an ELISA was performed using a serial dilution of the antibody. The antigen used was a peptide containing the histone modification of interest. By plotting the absorbance against the antibody dilution the titer of the antibody was estimated to be 1:480,000.



HeLa cells extracts (15 µg) were analysed by WB blot using the antibody. The molecular weight marker is shown on the left; the location of the protein of interest is indicated on the right.

H3K27me2 polyclonal antibody - Background

Histones are the main constituents of the protein part of chromosomes of eukaryotic cells. They are rich in the amino acids arginine and lysine and have been greatly conserved during evolution.

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Histones pack the DNA into tight masses of chromatin. Two core histones of each class H2A, H2B, H3 and H4 assemble and are wrapped by 146 base pairs of DNA to form one octameric nucleosome. Histone tails undergo numerous post-translational modifications, which either directly or indirectly alter chromatin structure to facilitate transcriptional activation or repression or other nuclear processes. In addition to the genetic code, combinations of the different histone modifications reveal the so-called “histone code”. Histone methylation and demethylation is dynamically regulated by respectively histone methyl transferases and histone demethylases. Levels of H3K27 dimethylation are higher in silent genes than in active genes suggesting that this histone modification is associated with transcriptional repression.