

**H3K9acS10p Antibody**  
**Rabbit Polyclonal Antibody**  
**Catalog # ABV11344****Specification**

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**H3K9acS10p Antibody - Product Information**

Application	<b>CHIP, DB, E, WB</b>
Primary Accession	<a href="#">P68431</a>
Host	<b>Rabbit</b>
Clonality	<b>Polyclonal</b>
Isotype	<b>Rabbit IgG</b>
Calculated MW	<b>15404</b>

**H3K9acS10p Antibody - Additional Information****Gene ID** 8350;8351;8352;8353;8354;8355;8356;8357;8358;8968

Positive Control	<b>IF: HeLa cells, WB: HeLa cells, ELISA: Antigen, ChIP: Human osteosarcoma cells, Dot blot: Histone peptides</b>
Application & Usage	<b>IF: 1:500, WB: 1:250, ELISA: 1:1000 - 1:4000, Dot Blot: 1:20000, ChIP: 15 µl/ChIP.</b>

**Other Names**

Histone H3

**Target/Specificity**

H3K9acS10p

**Antibody Form**

Liquid

**Appearance**

Colorless liquid

**Formulation**

In PBS with 0.05% (W/V) sodium azide.

**Handling**

The antibody solution should be gently mixed before use.

**Reconstitution & Storage**

-20 °C

**Background Descriptions****Precautions**

H3K9acS10p Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

## H3K9acS10p 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

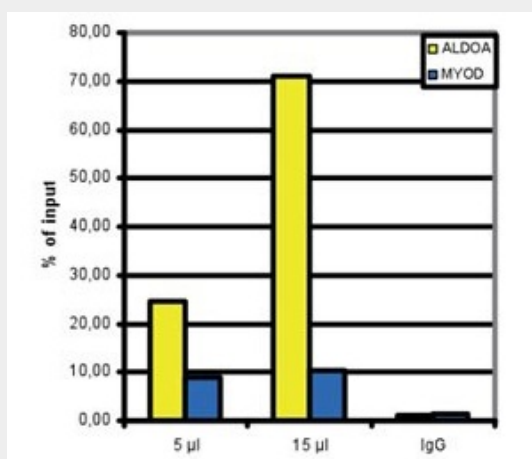
Nucleus. Chromosome.

## H3K9acS10p Antibody - Protocols

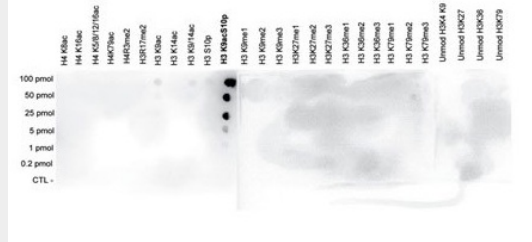
Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

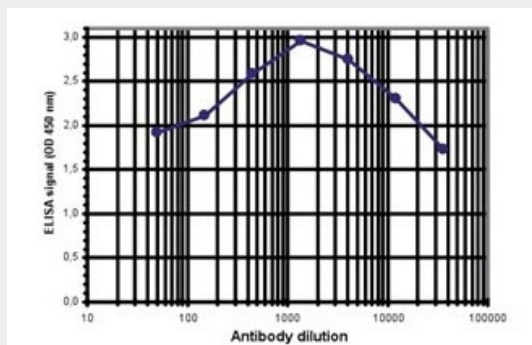
## H3K9acS10p Antibody - Images



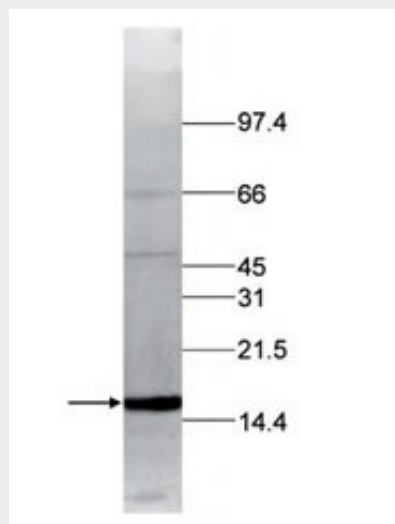
ChIP assays were performed using human osteosarcoma (U2OS) cells and the antibody and optimized PCR primer sets for qPCR. A titration of the antibody consisting of 2, 5, 10 and 15 µl per ChIP experiment was analysed. IgG (5 µg/IP) was used as negative control. The Fig shows the recovery, expressed as a % of input (the relative amount of IP DNA compared to input DNA after qPCR analysis).



A Dot Blot analysis was performed to test the cross reactivity of the antibody with peptides containing other modifications of histone H4 and H3 and unmodified H3 sequences. 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 1:89,000.



HeLa cells extracts (15 µg) were analysed by WB blot using the antibody.

### H3K9acS10p 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. Histones pack the DNA into tight masses of chromatin. 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. Acetylation of K9 and phosphorylation of S10 of histone H3 are associated with active gene transcription.