

Histone H4 (Acetyl Lys16) Rabbit pAb

CatalogNo: YK0014

Key Features

Host Species

- Rabbit

Reactivity

- Human, Mouse, Rat

Applications

- WB, IHC, IF, ELISA

MW

- 11kD (Observed)

Isotype

- IgG

Storage

Storage* -15°C to -25°C/1 year (Do not lower than -25°C)

Formulation Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.

Recommended Dilution Ratios

WB 1:500-2000

IHC 1:50-300

IF 1:50-300

ELISA 1:5000-20000

Basic Information

Clonality Polyclonal

Immunogen Information

Immunogen The antiserum was produced against synthesized peptide derived from human Histone H4 around the acetylated site of Lys16. AA range: 1-50

Specificity

Acetyl-Histone H4 (K16) Polyclonal Antibody detects endogenous levels of Histone H4 protein only when acetylated at K16. The name of modified sites may be influenced by many factors, such as species (the modified site was not originally found in human samples) and the change of protein sequence (the previous protein sequence is incomplete, and the protein sequence may be prolonged with the development of protein sequencing technology). When naming, we will use the "numbers" in historical reference to keep the sites consistent with the reports. The antibody binds to the following modification sequence (lowercase letters are modification sites):GAKRH

Target Information

Gene name HIST1H4A/HIST1H4B/HIST1H4C/HIST1H4D/HIST1H4E/HIST1H4F/HIST1H4H/HIST1H4I/HIST1H4J/HIST1H4K/HIST1H4L/HIST2H4A/HIST2H4B/HIST4H4

Protein Name Histone H4

Organism	Gene ID	UniProt ID
Human	121504 ; 554313 ; 8294 ; 8359 ; 8360 ; 8361 ; 8362 ; 8363 ; 8364 ; 8365 ; 8366 ; 8367 ; 8368 ; 8370 ;	P62805 ;
Mouse	100041230 ;	P62806 ;
Rat	100360950 ;	P62804 ;

Cellular Localization Nucleus. Chromosome.

Tissue specificity B-cell lymphoma, Bone marrow, Brain, Clones donated by HIP, Corpus call

Function 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. PTM: Acetylation at Lys-6, Lys-9, Lys-13 and Lys-17 occurs in coding regions of the genome but not in heterochromatin. PTM: Citrullination at Arg-4 by PADI4 impairs methylation. PTM: Monomethylated, dimethylated or trimethylated at Lys-21. Monomethylation is performed by SET8. Trimethylation is performed by SUV420H1 and SUV420H2 and induces gene silencing. PTM: Monomethylation at Arg-4 by PRMT1 favors acetylation at Lys-9 and Lys-13. Demethylation is performed by JMJD6. PTM: Sumoylated, which is associated with transcriptional repression. PTM: 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. Similarity: Belongs to the histone H4 family. subunit: The nucleosome is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA.

Validation Data

Contact information

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