

H3T3pK4ac polyclonal antibody - Classic

Cat. No. C15410279

Type: Polyclonal

Source: Rabbit

Lot #: 001

Size: 50 µg

Concentration: 0.57 µg/µl

Specificity: Human, mouse, *C. elegans*, rat, chicken, *Xenopus*, *Drosophila*, plant

Purity: Affinity purified

Storage: Store at -20°C; for long storage, store at -80°C. Avoid multiple freeze-thaw cycles.

Precautions: This product is for research use only. Not for use in diagnostic or therapeutic procedures.

Applications

	Suggested dilution	Results
ChIP	2-5 µg/million cells	
Immunohistochemistry	1:50	
IF	1:100	Figure 1
Western blot	1:500	Figure 2
Dot blot	1:1,000	Figure 3

Target description

Chromatin is the arrangement of DNA and proteins in which chromosomes are formed. Correspondingly, chromatin is formed from nucleosomes, which are comprised of a set of four histone proteins (H2A, H2B, H3, H4) wrapped with DNA. Chromatin is a very dynamic structure in which numerous post-translational modifications work together to activate or repress the availability of DNA to be copied, transcribed, or repaired. These marks decide which DNA will be open and commonly active (euchromatin) or tightly wound to prevent access and activation (heterochromatin). Common histone modifications include methylation of lysine and arginine, acetylation of lysine, phosphorylation of threonine and serine, and sumoylation, biotinylation, and ubiquitylation of lysine. Phosphorylation of threonine 3 (H3T3p) is a known mitotic marker and modified by the Haspin/Thr3 enzyme, while acetylation of lysine 4 (H3K4ac) on histone 3 is associated with transcriptional activation by Esa1. Methylation that occurs on H3K4 concurrently with acetylation seems to act as an adjuster to the activation effects of acetylation. Shugoshin protein cannot bind to the centromere of active cells when H3K4 is acetylated, which reduces dimethylation, and thus slows meiosis and mitosis. Usually, H3K4ac is a transitional modification, and will become further modified with methylation as transcription progresses, indicating complex transcriptional regulation.

