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#9753

Di-Methyl-Histone H3 (Lys9) Antibody

For Research Use Only. Not for Use in Diagnostic Procedures.

Applications: W, IP, ChIP	Reactivity: H M R Mk Dm	Sensitivity: Endogenous	MW (kDa): 17	Source/Isotype: Rabbit	UniProt ID: #P68431	Entrez-Gene Id: 8350
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Product Usage Information

For optimal ChIP results, use 20 µl of antibody and 10 µg of chromatin (approximately 4 x 10⁶ cells) per IP. This antibody has been validated using SimpleChIP[®] Enzymatic Chromatin IP Kits.

Application	Dilution
Western Blotting	1:1000
Immunoprecipitation	1:50
Chromatin IP	1:25

Storage

Supplied in 10 mM sodium HEPES (pH 7.5), 150 mM NaCl, 100 µg/ml BSA and 50% glycerol. Store at -20°C. Do not aliquot the antibody.

Specificity/Sensitivity

Di-Methyl-Histone H3 (Lys9) Antibody detects endogenous levels of histone H3 only when di-methylated on Lys9. The antibody does not cross-react with non-methylated, mono-methylated, or tri-methylated Lys9. In addition, the antibody does not cross-react with di-methylated or tri-methylated histone H3 Lys27.

Source / Purification

Polyclonal antibodies are produced by immunizing animals with a synthetic peptide corresponding to the amino terminus of histone H3 in which lysine 9 is di-methylated. Antibodies are purified by protein A and peptide affinity chromatography.

Background

The nucleosome, made up of four core histone proteins (H2A, H2B, H3, and H4), is the primary building block of chromatin. Originally thought to function as a static scaffold for DNA packaging, histones have now been shown to be dynamic proteins, undergoing multiple types of post-translational modifications, including acetylation, phosphorylation, methylation, and ubiquitination (1). Histone methylation is a major determinant for the formation of active and inactive regions of the genome and is crucial for the proper programming of the genome during development (2,3). Arginine methylation of histones H3 (Arg2, 17, 26) and H4 (Arg3) promotes transcriptional activation and is mediated by a family of protein arginine methyltransferases (PRMTs), including the co-activators PRMT1 and CARM1 (PRMT4) (4). In contrast, a more diverse set of histone lysine methyltransferases has been identified, all but one of which contain a conserved catalytic SET domain originally identified in the *Drosophila* Su(var)3-9, Enhancer of zeste, and Trithorax proteins. Lysine methylation occurs primarily on histones H3 (Lys4, 9, 27, 36, 79) and H4 (Lys20) and has been implicated in both transcriptional activation and silencing (4). Methylation of these lysine residues coordinates the recruitment of chromatin modifying enzymes containing methyl-lysine binding modules such as chromodomains (HP1, PRC1), PHD fingers (BPTF, ING2), tudor domains (53BP1), and WD-40 domains (WDR5) (5-8). The discovery of histone demethylases, such as PADI4, LSD1, JMJD1, JMJD2, and JHDM1, has shown that methylation is a reversible epigenetic marker (9).

Background References

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- Lee, D.Y. et al. (2005) *Endocr Rev* 26, 147-70.
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- Shi, X. et al. (2006) *Nature* 442, 96-9.
- Wysocka, J. et al. (2006) *Nature* 442, 86-90.
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Species Reactivity

Species reactivity is determined by testing in at least one approved application (e.g., western blot).

Western Blot Buffer

IMPORTANT: For western blots, incubate membrane with diluted primary antibody in 5% w/v BSA, 1X TBS, 0.1% Tween® 20 at 4°C with gentle shaking, overnight.

Applications Key

W: Western Blotting **IP:** Immunoprecipitation **ChIP:** Chromatin IP

Cross-Reactivity Key

H: Human **M:** Mouse **R:** Rat **Mk:** Monkey **Dm:** D. melanogaster

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