Tri-Methyl-Histone H3 (Lys4) (C42D8) Rabbit mAb (Alexa Fluor® 647 Conjugate)



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Applications: IF-IC, FC-FP	Reactivity: H M R Mk Dm Sc	Sensitivity: Endogenous	Source/Isotype: Rabbit IgG	UniProt ID: #P68431	Entrez-Gene Id: 8350
Product Usage		Application			Dilution
Information		Immunofluorescence (Immunocytochemistry)			1:1600
		Flow Cytometry (Fixed/Permeabilized)			1:50
Storage		Supplied in PBS (pH 7.2), less than 0.1% sodium azide and 2 mg/ml BSA. Store at 4°C. Do not aliquot the antibody. Protect from light. Do not freeze.			
Specificity/Sensitivity		Tri-Methyl-Histone H3 (Lys4) (C42D8) Rabbit mAb (Alexa Fluor [®] 647 Conjugate) detects endogenous levels of histone H3 when tri-methylated on Lys4. This antibody shows some cross-reactivity with histone H3 that is di-methylated on Lys4, but does not cross-react with non-methylated or monomethylated histone H3 Lys4. In addition, the antibody does not cross-react with methylated histone H3 Lys9, Lys27, Lys36 or methylated histone H4 Lys20.			
Species predicted to react based on 100% sequence homology		Xenopus, Zebrafish			
Source / Purification		Monoclonal antibody is produced by immunizing animals with a synthetic peptide corresponding to amino terminus of histone H3 in which Lys4 is tri-methylated.			
Description		in-house for direct flow of	647 fluorescent dye and tested human cells. The antibody is ited Tri-Methyl-Histone H3 (Lys4		

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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- 7. Wysocka, J. et al. (2006) Nature 442, 86-90.
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Applications Key IF-IC: Immunofluorescence (Immunocytochemistry) FC-FP: Flow Cytometry (Fixed/Permeabilized)

Cross-Reactivity Key H: Human M: Mouse R: Rat Mk: Monkey Dm: D. melanogaster Sc: S. cerevisiae

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