Revision 1

Store at -20C

#9783

Tri-Methyl Histone H3 Antibody Sampler Kit

1 Kit (6 x 20 microliters)

Cell Signaling TECHNOLOGY®

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Product Includes	Product #	Quantity	Mol. Wt	Isotype/Source
Tri-Methyl-Histone H3 (Lys4) (C42D8) Rabbit mAb	9751	20 µl	17 kDa	Rabbit IgG
Tri-Methyl-Histone H3 (Lys9) (D4W1U) Rabbit mAb	13969	20 µl	17 kDa	Rabbit IgG
Tri-Methyl-Histone H3 (Lys27) (C36B11) Rabbit mAb	9733	20 µl	17 kDa	Rabbit IgG
Tri-Methyl-Histone H3 (Lys36) (D5A7) XP® Rabbit mAb	4909	20 µl	17 kDa	Rabbit IgG
Tri-Methyl-Histone H3 (Lys79) Antibody	4260	20 µl	17 kDa	Rabbit
Histone H3 (D1H2) XP® Rabbit mAb	4499	20 µl	17 kDa	Rabbit IgG
Anti-rabbit IgG, HRP-linked Antibody	7074	100 µl		Goat

Please visit cellsignal.com for individual component applications, species cross-reactivity, dilutions, protocols, and additional product information.

Description

Tri-Methyl Histone H3 Antibody Sampler Kit offers an economical means to evaluate the tri-methylation of Histone H3 on multiple residues. The kit contains enough primary antibody to perform two western blot experiments per primary.

Storage

Supplied in 10 mM sodium HEPES (pH 7.5), 150 mM NaCl, 100 µg/ml BSA, 50% glycerol and less than 0.02% sodium azide. Store at –20°C. Do not aliquot the antibody.

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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8. Wysocka, J. et al. (2005) *Cell* 121, 859-72.
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