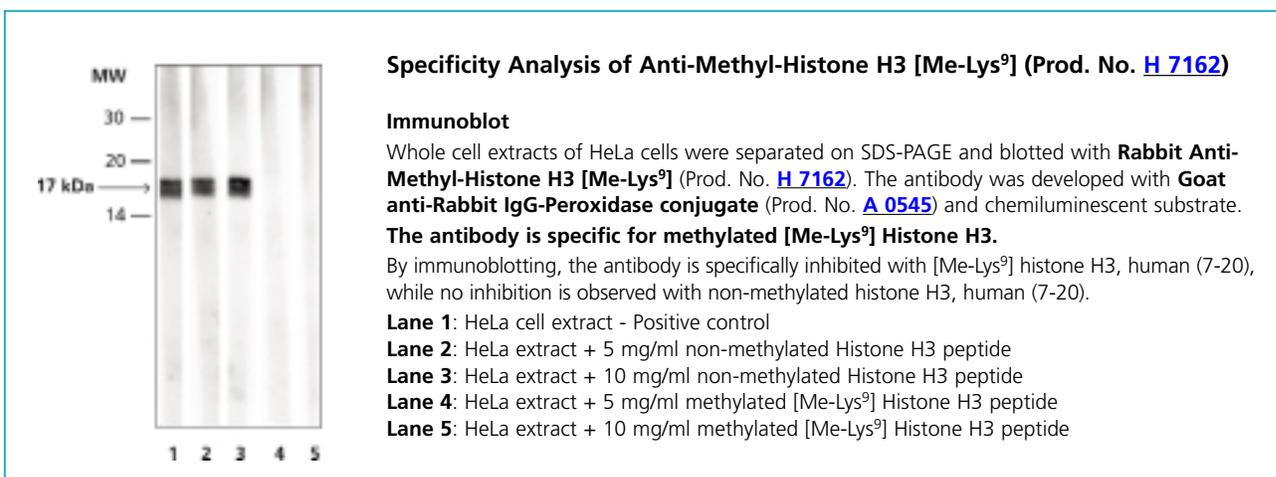


New Product Highlights

Anti-Methyl-Histone H3 [Me-Lys⁹]: Heterochromatin assembly marker

In eukaryotic cells, DNA associates with histones and other proteins to form chromatin. The basic unit of chromatin is the nucleosome, consisting of 140 base pairs of DNA wrapped around an octameric core of the four conserved histones H2A, H2B, H3 and H4. The relatively unstructured and highly charged N-terminal tail domains of histones are central to the processes that modulate chromatin structure. A diverse and elaborate array of post-translational modifications, including acetylation, phosphorylation and methylation, occurs on the N-terminal tail domains of histones, particularly of H3 and H4 [1-4]. These modifications alter chromatin structure and recruit downstream chromatin-associated proteins involved in transcription regulation.

Sigma-RBI is pleased to introduce **Anti-Methyl-Histone H3 [Me-Lys⁹]** (Prod. No. [H 7162](#)) that has been developed using a synthetic methylated peptide corresponding to amino acids 7-20 [Me-Lys⁹] of histone H3. This histone H3 sequence is identical in many species including mouse, rat, bovine, chicken, frog, *Drosophila*, and *C. elegans*, and is highly conserved (single amino acid substitution) in *Tetrahymena* histone H3. Anti-Methyl-Histone H3 [Me-Lys⁹] recognizes histone H3 methylated on Lys⁹. Applications include the detection of [Me-Lys⁹] histone H3 by immunoblotting (17 kDa). Staining of [Me-Lys⁹] histone H3 is specifically inhibited with [Me-Lys⁹] histone H3, human (7-20), while no inhibition is displayed with non-methylated histone H3, human (7-20).



Histone methylation, like acetylation, is a complex, dynamic process influencing a number of processes, including transcriptional regulation, chromatin condensation, mitosis and heterochromatin assembly. Conserved lysine residues in the N-terminal tail domains of histone H3, Lys⁴, Lys⁹ and Lys²⁷ are the preferred sites of methylation [1,4-6]. Methylation of H3 at Lys⁹ is a modification intrinsically linked to epigenetic silencing and heterochromatin assembly. Histone H3 is methylated at Lys⁹ by site-specific H3 methyltransferases (HMTases) encoded by the SUV39H1 gene family [7]. Methylation of H3 at Lys⁹ by SUV39H1 generates a binding site for HP1 proteins, a family of heterochromatic adaptor proteins implicated in both gene silencing and in the organization of higher order chromatin [8-11]. Methylation of Lys⁹ interferes with the phosphorylation of Ser¹⁰, but is also influenced by pre-existing modifications in the N-terminus of H3, such as H3 Ser¹⁰ phosphorylation itself [7]. Conversely, the *in vivo* deregulation or disruption of SUV39H1 activity modulates H3 Ser¹⁰ phosphorylation in native chromatin, leading to aberrant mitotic divisions.

Related Antibodies

[H 6409](#) **Monoclonal Anti-phospho-Histone H3 [pSer¹⁰]**, clone H3-P (mouse)

[H 9908](#) **Monoclonal Anti-phospho-Histone H3 [pSer²⁸]**, clone HTA28 (mouse)

[H 9286](#) **Anti-acetyl-Histone H3 [Ac-Lys⁹]** (rabbit)

[H 9161](#) **Anti-acetyl- and phospho-Histone H3 [Ac-Lys⁹, pSer¹⁰]** (rabbit)

[A 5463](#) **Anti-Acetylated Proteins** (rabbit)

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