SunLong Biotech Co.,LTD
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[Primary Antibody]

Mouse Anti-Mono-Methyl-Histone H3 (Arg8)antibody

Catalog Number: SLM-60160M

FOR RESEARCH USE ONLY

[DATASHEET]

Host:	Mouse
Isotype:	IgG
Clonality:	Monoclonal
Clone No.:	C12C11
Target:	Mono-Methyl-Histone H3 (Arg8)
Purification:	Antigen affinity purification
Concentration:	1mg/ml
Storage:	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol. Shipped at 4℃. Store at -20 °C for one year. Avoid repeated freeze/thaw cycles.
Applications:	WB (1:500-2000) IHC-P (1:50-200) IHC-F (1:50-200) IF (1:50-200) ICC/IF (1:50-200) IP (1:25-100) Not yet tested in other applications. Optimal working dilutions must be determined by the end user.
Reactivity:	Human,Mouse(predicted:Rat,Monkey)
Predicted MW.:	17kDa
Subcellular Location:	The nucleus
Background:	Post-translational modifications (PTMs) of histones are key mechanisms in the epigenetic regulation of chromatin structure, known as the 'histone code.' Post-translational modifications on histones include acetylation, methylation, phosphorylation, and some newly discovered acyl modifications in recent years. These histone modifications directly affect the binding of chromatin to transcription factors or other epigenetic regulators, altering genome stability and gene transcription, among other processes. Histone methylation typically occurs on lysine and arginine residues of core histones. Histone methylation can both promote and inhibit gene transcription, depending on whether the histone methylation occurs on lysine or arginine, as

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	well as the number of methyl groups (lysine can undergo mono-, di-, and tri-methylation, while arginine can undergo mono-, symmetric, and asymmetric dimethylation). Histone lysine methylation usually occurs on lysine residues at positions 4, 9, 27, 36, 79 of histone H3 and position 20 of histone H4; arginine methylation typically occurs on arginine residues at positions 2, 8, 17, 26 of histone H3 and position 3 of histone H4. Protein methyltransferases (HMTs) and histone demethylases (HDMs) are the main regulatory factors for methylation modifications.

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