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Rabbit Anti-Mono-Methyl-Histone H4 (Arg23)antibody

SL60159R

Product Name	Mono-Methyl-Histone H4 (Arg23)
Product Type	Methylated anti
Immunogen Species	Rabbit
Clonality	Polyclonal
React Species	Human,Mouse,Rat,African Green Monkey
Applications	WB=1:500-2000 not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
Theoretical molecular weight	11kDa
Cellular localization	The nucleus
Form	Liquid
Concentration	1mg/ml
Lsotype	IgG
Purification	Antigen affinity purification
Buffer Solution	1M TBS(pH7.4) with 1% BSA, 3% Proclin300 and 50% Glycerol.
Storage	Shipped at 4℃. Store at -20 °C for one year. Avoid repeated freeze/thaw cycles.
Attention	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
PubMed	PubMed
Product Detail	Post-translational modifications (PTMs) of histones are a key mechanism 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 acylation 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 things. 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 well as the number of methyl groups (lysine can undergo mono-, di-, and tri-methylation, while arginine can undergo mono-, symmetric, and asymmetric di-methylation). 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.