Rabbit Anti-Di-Methyl-Histone H3 (Lys36)antibody

SL60111R

Product Name	Di-Methyl-Histone H3 (Lys36)
Product Type	Methylated anti
Immunogen Species	Rabbit
Clonality	Polyclonal
React Species	Human,Mouse,Rat
Applications	WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,ICC/IF=1:50-200,IF=1:100-500（Paraffin sections need antigen repair） not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
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 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 either promote or 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 dimethylation). Histone lysine methylation usually occurs at lysine residues 4, 9, 27, 36, 79 of histone H3 and lysine 20 of histone H4; arginine methylation typically occurs at arginine residues 2, 8, 17, 26 of histone H3 and arginine 3 of histone H4. Histone methyltransferases (HMTs) and histone demethylases (HDMs) are the main regulatory factors for methylation modifications.