

Rabbit Anti-Mono-Methyl-Histone H3 (Arg42)antibody

SL60096R

Product Name	Mono-Methyl-Histone H3 (Arg42)
Product Type	Methylated anti
Immunogen Species	Rabbit
Clonality	Polyclonal
React Species	Human,Mouse,Rat
Applications	WB=1:500-2000 not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
Theoretical molecular weight	17kDa
Cellular localization	The nucleus
Form	Liquid
Concentration	1mg/ml
Isotype	IgG
Purification	Antigen affinity purification
Buffer Solution	1M TBS(pH7.4) with 1% BSA, 3% Proclin300 and 50% Glycerol.
Storage	Shipped at 4°C. 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 epigenetics for regulating chromatin structure and are 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 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 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. Protein methyltransferases (HMTs) and histone demethylases (HDMs) are the main regulatory factors for methylation modifications.