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Anti-Histone H2A (Ubiquityl Lys119) Rabbit mAb [78H93]

Catalog No.: A52146

Basic Information

Catalog No. (Cat.No.)	A52146
Host species	Rabbit
Reactivity	Human,Mouse,Rat
Applications	WB,IHC,IP,IF,ELISA,ChIP,Cut&Tag
Synonyms	Histone H2A (Ubiquityl Lys119),Ubi-H2A(Lys119),H2A,H2A1,H2A2,H2AFJ,H2AFK,H2AFZ

Product Information

Target	Histone H2A (Ubiquityl Lys119)
Molecular Weight(Calculated)	14 kDa
Molecular Weight(Observed)	23 kDa
Isotype	IgG,Kappa
Conjugation	NA
Concentration	0.2 mg/ml
Clonality	Monoclonal
Clone No.	78H93
RRID	NA
Storage buffer	50% Glycerol, 0.05% BSA and 0.05% preservative in PBS (pH 7.2-7.4)
Storage	Stored at -20°C for 1 year. Avoid repeated freeze / thaw cycles.
Shipped at conditions	Frozen
Form	Liquid

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Product Usage Information

Application	Dilution
WB	1:2000-1:10000
IHC	1:1000-1:4000
IP	1:50-1:200
IF	1:200-1:1000
ELISA	1:5000-1:20000
ChIP	1:50-1:100
Cut&Tag	1:50-1:100

Target Information

Protein Name	Histone H2A (Ubiquityl Lys119)
Gene Name	*H2AFX*□*H2A*
Domain	NA
Background	Histones are basic core proteins of eukaryotic nucleosomes. Two copies each of H2A, H2B, H3 and H4 assemble into a histone octamer wrapped by DNA to form nucleosomes, the fundamental repeating unit of chromatin. The N-terminal tails of histones undergo diverse post-translational modifications, including ubiquitylation, phosphorylation, acetylation and mono/di/trimethylation. These epigenetic marks do not alter DNA sequence, but modulate chromatin compaction, governing DNA damage repair, gene transcription, cell cycle and other biological events.Ubiquitylation of H2A at Lys119 mediates transcriptional repression and DNA damage response. Phosphorylation of H2A.X at Ser139 (γH2AX) serves as a canonical marker for DNA double-strand breaks. H2A acetylation relaxes chromatin and facilitates transcription. H3 carries the most abundant modifications: phosphorylation at Thr3 and Ser10/Thr11 drives mitotic chromosome condensation. Acetylation at H3K9/K14/K18/K27/K36 generally activates transcription. H3K4 methylation (me1/me2/me3) marks active promoters, whereas H3K9 and H3K27 methylation are linked to heterochromatin formation and gene silencing. H3K36me2/me3 regulates transcriptional elongation, and H3K79 methylation controls DNA damage checkpoints. H4K16 acetylation counteracts chromatin compaction.