Ablumir
Built Around Immunology

# Anti-Histone H2A Rabbit mAb [61G65]

**Catalog No.: A52147**

## Basic Information

| | |
|---|---|
| Catalog No. (Cat.No.) | A52147 |
| Host species | Rabbit |
| Reactivity | Human,Mouse,Rat |
| Applications | WB,IHC,IP,IF,ELISA,ChIP,Cut&Tag |
| Synonyms | Histone H2A,H2A,H2A1,H2A2,H2A.L1,H2A.P,H2A.J,H2AFJ,H2AFK,H2AFZ |

## Product Information

| | |
|---|---|
| Target | Histone H2A |
| Molecular Weight(Calculated) | 14 kDa |
| Molecular Weight(Observed) | 17 kDa |
| Isotype | IgG,Kappa |
| Conjugation | NA |
| Concentration | 0.2 mg/ml |
| Clonality | Monoclonal |
| Clone No. | 61G65 |
| 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 | 1:1000-1:5000 |
| IHC | 1:200-1:1000 |
| 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 |
| Gene Name | *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. |