Data Sheet (Cat.No.TMAB-04696)

Anti-Crotonyl-Histone H2B (Lys11) Antibody (6G247)

Product Details

Ig Type:	IgG
Reactivity:	Human,Mouse,Rat
Clone:	6G247
Purification:	Protein A purified

Applications

Verified Activity:

1. Blocking buffer: 5% NFDM/TBST
Primary ab dilution: 1: 2000
Primary ab incubation condition: 2 hours at room temperature
Secondary ab: Goat Anti-Rabbit IgG H&L (HRP)
Lysate: (-) HeLa, (+) HeLa+crotonic acid (100 ng/ml, 18 hr)
Protein loading quantity: 20 μg
Exposure time: 60 s
Predicted MW: 14 kDa
Observed MW: 14 kDa
2. Blocking buffer: 5% NFDM/TBST
Primary ab dilution: 1: 2000
Primary ab incubation condition: 2 hours at room temperature
Secondary ab: Goat Anti-Rabbit IgG H&L (HRP)
Lysate: 1: HeLa, 2: NIH-3T3, 3: BRL, 4: Rat kidney, 5: Mouse kidney
Protein loading quantity: 20 μg
Exposure time: 60 s
Predicted MW: 14 kDa
Observed MW: 14 kDa
3. Tissue: Rat liver
Section type: Formalin fixed & Paraffin-embedded section
Retrieval method: High temperature and high pressure
Retrieval buffer: Tris/EDTA buffer, pH 9.0 Primary ab dilution: 1:100
Primary ab incubation condition: 1 hour at room temperature
Secondary ab: SP Kit (Rabbit)
Counter stain: Hematoxylin (Blue)
Comment: Color brown is the positive signal for TMAB-04696
4. Tissue: Mouse small intestine
Section type: Formalin fixed & Paraffin-embedded section
Retrieval method: High temperature and high pressure
Retrieval buffer: Tris/EDTA buffer, pH 9.0 Primary ab dilution: 1:100
Primary ab incubation condition: 1 hour at room temperature
Secondary ab: SP Kit (Rabbit)
Counter stain: Hematoxylin (Blue)
Comment: Color brown is the positive signal for TMAB-04696
5. Tissue: Human breast
Section type: Formalin fixed & Paraffin-embedded section
Retrieval method: High temperature and high pressure
Retrieval buffer: Tris/EDTA buffer, pH 9.0 Primary ab dilution: 1:100

Primary ab incubation condition: 1 hour at room temperature
Secondary ab: SP Kit (Rabbit)
Counter stain: Hematoxylin (Blue)
Comment: Color brown is the positive signal for TMAB-04696

Application: WB,IHC-P,IHC-Fr,IF

Recommended: WB: 1:500-2000; IHC-P: 1:100-500; IHC-Fr: 1:100-500; IF: 1:100-500

Properties

Stability & Storage: Store at 2°C-8°C for 1 month. Store at -20°C or -80°C for 12 months. Avoid repeated freeze-thaw cycles.

Shipping: Shipping with blue ice.

Research Background

Histone post-translational modifications (PTMs) are key mechanisms in epigenetic regulation of chromatin structure, often referred to as the "histone code." PTMs on histones include acetylation, methylation, phosphorylation, and several novel acylation modifications discovered in recent years. These histone modifications directly influence chromatin structure and the binding of transcription factors or other epigenetic regulators, thereby altering genomic stability and gene transcription. Histone methylation typically occurs on lysine and arginine residues of core histones. It can either promote or inhibit gene transcription, depending on whether methylation occurs on lysine or arginine residues and the number of methyl groups present (lysines can be mono-, di-, or trimethylated, while arginines can undergo mono-, symmetric, or asymmetric dimethylation). Lysine methylation in histones commonly occurs at lysine residues 4, 9, 27, 36, and 79 of histone H3, and at lysine 20 of histone H4. Arginine methylation typically occurs at arginine residues 2, 8, 17, and 26 of histone H3, and at arginine 3 of histone H4. Histone methyltransferases (HMTs) and histone demethylases (HDMs) are the primary regulators of methylation modifications.

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