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Product datasheet for AP03036BT-N

Methylated Lysine Rabbit Polyclonal Antibody

Product data:

Product Type:	Primary Antibodies
Applications:	ELISA, IP, WB
Recommended Dilution:	**ELISA:** 1/1000. **Western blot:** 1/2000-1/5000 (4). 0.2-0.5 µg/ml of this Biotin conjugated antibody was sufficient for detection of the methylated histone by western blot analysis using melanoma cells in TBSt. **Immunoprecipitation.**
Host:	Rabbit
Isotype:	IgG
Clonality:	Polyclonal
Immunogen:	Methylated KLH
Specificity:	This antibody detects proteins containing Methylated Lysine residues in SDS-PAGE immunoblots.
Formulation:	PBS Label: Biotin State: Aff - Purified State: Liquid purified Ig fraction Stabilizer: 50% Glycerol Preservative: 0.09% Sodium Azide
Concentration:	lot specific
Purification:	Affinity Chromatography
Conjugation:	Biotin
Storage:	Store undiluted at 2-8°C for one month or (in aliquots) at -20°C for longer. Avoid repeated freezing and thawing.
Stability:	Shelf life: one year from despatch.

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Background:

Post-translational modifications of proteins play critical roles in the regulation and function of many known biological processes. Proteins can be post-translationally modified in many different ways, and a common posttranscriptional modification of Lysine involves methylation (1). Lysine can be methylated once, twice or three times by lysine methyltransferases. The transfer of methyl groups from S-adenosyl methionine to histones is catalyzed by enzymes known as histone methyltransferases. Histones which are methylated on certain residues can act epigenetically to repress or activate gene expression (1, 2).
The transcriptional repressor SUV39H1 can encode novel enzymes which selectively methylate histone H3 at lysine 9. SUV39H1 places a methyl marker on histone H3, which is then recognized by HP1 through its chromo domain. This model may also explain the stable inheritance of the heterochromatic state (3). Some studies have also speculated a stimulatory role for transcription by methylated histone lyside 4 due to its presence at active transcription sites (4-6).

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