


Pan Methylated Lysine Monoclonal Antibody(Mix)

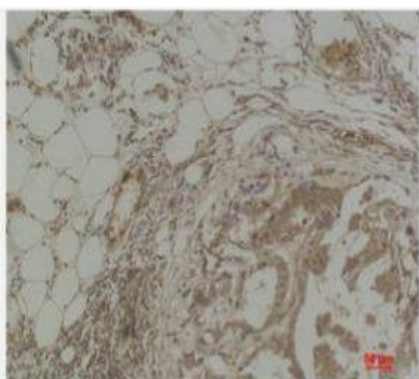
Catalog No.	IMB0159
Reactivity	Species independent
Applications	WB; IHC-p
Gene Name	-
Protein Name	-
Human Gene Id	-
Swiss-Prot	-
Formulation	PBS, pH 7.4, containing 0.5%BSA, 0.02% sodium azide as Preservative and 50% Glycerol.
Source	Monoclonal, Mouse
Dilution	WB: 1:1000-2000 IHC: 1:200-500
Purification	The antibody was affinity-purified from mouse ascites by affinity-chromatography using epitope-specific immunogen.
Concentration	-
Storage&Stability	-20°C/1 year
Background	Methylation of lysine residues is a common regulatory posttranslational modification (PTM) that results in the mono-, di-, or tri-methylation of lysine at ε-amine groups by protein lysine methyltransferases (PKMTs). Two PKMT groups are recognized based on structure and catalytic mechanism: class I methyltransferases or seven β strand enzymes, and SET domain-containing class V methyltransferases. Both use the methyl donor S-adenosyl-L-methionine to methylate histone and non-histone proteins. Class I methyltransferases methylate amino acids, DNA, and RNA. Six methyl-lysine-interacting protein families are distinguished based on binding domains: mBT, PHD finger, Tudor, PWWP, WD40 repeat, and chromodomains. Many of these display differential binding preferences based on lysine methylation state. KDM1 subfamily lysine demethylases catalyze demethylation of mono- and di-methyl lysines, while 2-oxoglutarate-dependent JmjC (KDM2-7) subfamily enzymes also modify tri-methyl lysine residues.
Subcellular Location.	-
BiowMW	-

Products Images:



94KD
66KD
45KD
35KD
26KD
14.4KD

Western blot analysis of Hela using Pan Methylated Lysine Monoclonal Antibody.



Immunohistochemical analysis of paraffin-embedded Human Breast Carcinoma using Pan Methylated Lysine Monoclonal Antibody.