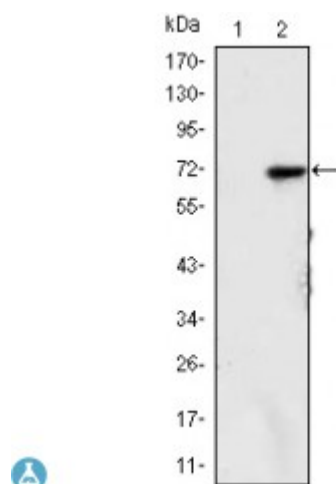


Anti-JMJD2A antibody



Description	Mouse monoclonal to JMJD2A.
Model	STJ98191
Host	Mouse
Reactivity	Human
Applications	ELISA, IF, IHC, WB
Immunogen	Purified recombinant fragment of human JMJD2A expressed in E. Coli.
Gene ID	9682
Gene Symbol	KDM4A
Dilution range	WB 1:500-1:2000IHC 1:200-1:1000IF 1:200-1:1000ELISA 1:10000
Specificity	JMJD2A Monoclonal Antibody detects endogenous levels of JMJD2A protein.
Tissue Specificity	Ubiquitous.
Purification	Affinity purification
Clone ID	5H1
Note	For Research Use Only (RUO).
Protein Name	Lysine-specific demethylase 4A JmjC domain-containing histone demethylation protein 3A Jumonji domain-containing protein 2A
Clonality	Monoclonal
Conjugation	Unconjugated

Isotype	IgG1
Formulation	Ascitic fluid containing 0.03% sodium azide.
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:22978OMIM:609764
Alternative Names	Lysine-specific demethylase 4A JmjC domain-containing histone demethylation protein 3A Jumonji domain-containing protein 2A
Function	Histone demethylase that specifically demethylates 'Lys-9' and 'Lys-36' residues of histone H3, thereby playing a central role in histone code. Does not demethylate histone H3 'Lys-4', H3 'Lys-27' nor H4 'Lys-20'. Demethylates trimethylated H3 'Lys-9' and H3 'Lys-36' residue, while it has no activity on mono- and dimethylated residues. Demethylation of Lys residue generates formaldehyde and succinate. Participates in transcriptional repression of ASCL2 and E2F-responsive promoters via the recruitment of histone deacetylases and NCOR1, respectively.; Isoform 2: Crucial for muscle differentiation, promotes transcriptional activation of the Myog gene by directing the removal of repressive chromatin marks at its promoter. Lacks the N-terminal demethylase domain.
Sequence and Domain Family	The 2 Tudor domains recognize and bind methylated histone H3 'Lys-4' residue (H3K4me). Double Tudor domain has an interdigitated structure and the unusual fold is required for its ability to bind methylated histone tails. Trimethylated H3 'Lys-4' (H3K4me3) is bound in a cage of 3 aromatic residues, 2 of which are from the Tudor domain 2, while the binding specificity is determined by side-chain interactions involving residues from the Tudor domain 1. The Tudor domains are also able to bind trimethylated histone H3 'Lys-9' (H3K9me3), di- and trimethylated H4 'Lys-20' (H4K20me2 and H4K20me3). Has high affinity for H4K20me2, blocking recruitment of proteins such as TP53BP1.
Cellular Localization	Nucleus
Post-translational Modifications	Ubiquitinated by RNF8 and RNF168 following DNA damage, leading to its degradation. Degradation promotes accessibility of H4K20me2 mark for DNA repair protein TP53BP1, which is then recruited.