

Product datasheet

Recombinant Human KDM4A / JHDM3A / JMJD2A protein ab125541

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Description

Product name	Recombinant Human KDM4A / JHDM3A / JMJD2A protein
Purity	> 90 % Densitometry. Purity was determined to be >90% by densitometry. Affinity purified.
Expression system	Baculovirus infected Sf9 cells
Accession	<u>O75164</u>
Protein length	Protein fragment
Animal free	No
Nature	Recombinant
Species	Human
Predicted molecular weight	150 kDa including tags
Amino acids	1 to 886
Tags	GST tag N-Terminus

Specifications

Our **Abpromise guarantee** covers the use of **ab125541** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	Western blot SDS-PAGE
Form	Liquid

Preparation and Storage

Stability and Storage	Shipped on dry ice. Upon delivery aliquot and store at -80°C. Avoid freeze / thaw cycles. pH: 7.50 Constituents: 0.31% Glutathione, 0.002% PMSF, 0.004% DTT, 0.79% Tris HCl, 0.003% EDTA, 25% Glycerol (glycerin, glycerine), 0.88% Sodium chloride
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General Info

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.

Tissue specificity

Ubiquitous.

Sequence similarities

Belongs to the JHDM3 histone demethylase family.

Contains 1 C2HC pre-PHD-type zinc finger.

Contains 1 JmjC domain.

Contains 1 JmjN domain.

Contains 2 PHD-type zinc fingers.

Contains 2 Tudor domains.

Domain

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.

Post-translational modifications

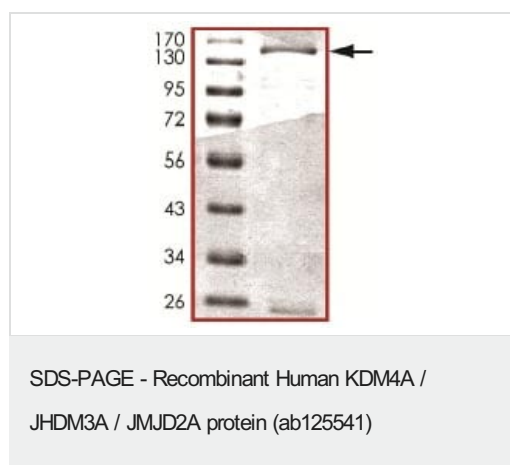
Ubiquitinated by RNF8 and RNF168 following DNA damage, leading to its degradation.

Degradation promotes accessibility of H4K20me2 mark for DNA repair protein TP53BP1, which is then recruited.

Cellular localization

Nucleus.

Images



SDS-PAGE analysis of ab125541.

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