

Recombinant Human KDM4A / JHDM3A / JMJD2A protein ab125541

画像数 1

製品の詳細

製品名	Recombinant Human KDM4A / JHDM3A / JMJD2A protein
精製度	> 90 % Densitometry. Purity was determined to be >90% by densitometry. Affinity purified.
発現系	Baculovirus infected Sf9 cells
アクセッション番号	<u>O75164</u>
タンパク質長	Protein fragment
Animal free	No
由来	Recombinant
生物種	Human
予測される分子量	150 kDa including tags
領域	1 to 886
タグ	GST tag N-Terminus

特性

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.

アプリケーション	Western blot SDS-PAGE
製品の状態	Liquid

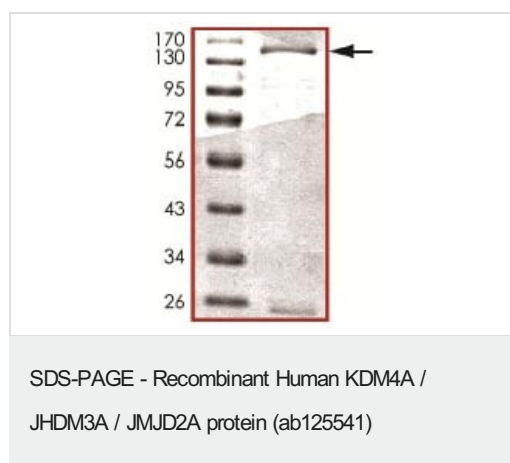
前処理および保存

保存方法および安定性	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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関連情報

機能	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.
組織特異性	Ubiquitous.
配列類似性	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.
ドメイン	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.
翻訳後修飾	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.
細胞内局在	Nucleus.

画像



SDS-PAGE analysis of ab125541.

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