abcam

## Product datasheet

# Recombinant human KAT3B / p300 protein ab198138

2 Images

### Description

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| **Product name** | Recombinant human KAT3B / p300 protein |
| **Biological activity** | Specific Activity: ≥357 pmole/min/µg |
| **Purity** | >= 50 % SDS-PAGE. |
| **Expression system** | Baculovirus infected Sf9 cells |
| **Accession** | Q09472 |
| **Protein length** | Protein fragment |
| **Animal free** | No |
| **Nature** | Recombinant |
| **Species** | Human |
| **Sequence** | QAIAEKQPSQEVKMEAKMEVDQPEPADTQPEDISESKVE<br>DCKMESTETEE<br>RSTELKTEIKEEEDQPSTSATQSSPAPGQSKKKIFKPEEL<br>RQALMPTLEA<br>LYRQDPESLPFRQPVDPQLLGIPDYFDIVKSPMDLSTIKRK<br>LDTGQYQEP<br>WQYVDDIWLMFNNAWLYNRKTSRVYKYCSKLSEVFEQEI<br>DPVMQSLGYCC<br>GRKLEFSPQTLCCYGKQLCTIPRDATYYSYQNRYHFCEKC<br>FNEIQGESVS<br>LGDDPSQPQTTINKEQFSKRKNDTLDPELFVECTECGRK<br>MHQICVLHHEI<br>IWPAGFVCDGCLKKSARTRKENKFSAKRLPSTRLGTFLEN<br>RVNDFLRRQN<br>HPESGEVTVRVVHASDKTVEVKPGMKARFVDSGEMAES<br>FPYRTKALFAFE<br>EIDGVDLCFFGMHVQEYGSDCPPPNQRRVYISYLDSVHFF<br>RPKCLRTAVY<br>HEILIGYLEYVKKLGYTTGHIWACPPSEGDDYIFHCHPPDQK<br>IPKPKRLQ<br>EWYKKMLDKAVSERIVHDYKDIFKQATEDRLTSAKELPYF<br>EGDFWPNVLE<br>ESIKELEQEEEERKREENTSNESTDVTKGDSKNAKKKNN |

KKTSKNKSSLS
RGNKKKPGMPNVSNDLSQKLYATMEKHKEVFFVIRLIAGP
AANSLPPIVD
PDPLIPCDLMDGRDAFLTLARDKHLEFSSLRRAQWSTMC
MLVELHTQSQD
RFVYTCNECKHHVETRWHCTVCEDYDLCITCYNTKNHDH
KMEKLGLGLDD
ESNNQQAAATQSPGDSRRLSIQRCIQSLVHACQCRNANC
SLPSCQKMKRV
VQHTKGCKRKTNGGCPICKQLIALCCYHAKHCQENKCPV
PFCLNIK

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| **Molecular weight information** | 125 kDa by SDS-PAGE |
| **Amino acids** | 985 to 1810 |
| **Additional sequence information** | N-terminal His-GST tag NM_001429 |

## Specifications

Our Abpromise guarantee covers the use of **ab198138** in the following tested applications.

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

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| **Applications** | SDS-PAGE<br>Functional Studies |
| **Form** | Liquid |

## Preparation and Storage

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| **Stability and Storage** | Shipped on Dry Ice. Store at -80°C. Avoid freeze / thaw cycle.<br>pH: 8.00<br>Preservative: 1.36% Imidazole<br>Constituents: 20% Glycerol, 0.63% Tris HCl, 0.64% Sodium chloride, 0.02% Potassium chloride<br>This product is an active protein and may elicit a biological response in vivo, handle with caution. |

## General Info

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| **Function** | Functions as histone acetyltransferase and regulates transcription via chromatin remodeling. Acetylates all four core histones in nucleosomes. Histone acetylation gives an epigenetic tag for transcriptional activation. Mediates cAMP-gene regulation by binding specifically to phosphorylated CREB protein. Mediates acetylation of histone H3 at 'Lys-122' (H3K122ac), a modification that localizes at the surface of the histone octamer and stimulates transcription, possibly by promoting nucleosome instability. Mediates acetylation of histone H3 at 'Lys-27' (H3K27ac). Also functions as acetyltransferase for nonhistone targets. Acetylates 'Lys-131' of ALX1 and acts as its coactivator. Acetylates SIRT2 and is proposed to indirectly increase the transcriptional activity of TP53 through acetylation and subsequent attenuation of SIRT2 deacetylase function. Acetylates HDAC1 leading to its inactivation and modulation of transcription. Acts as a TFAP2A-mediated transcriptional coactivator in presence of CITED2. Plays a role as a coactivator of NEUROD1-dependent transcription of the secretin and p21 genes and controls terminal differentiation of cells in the intestinal epithelium. Promotes cardiac myocyte |

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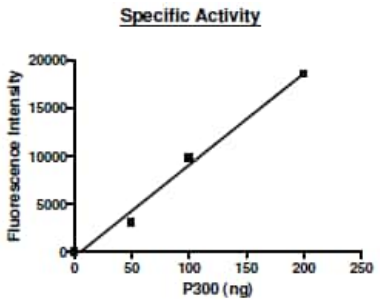
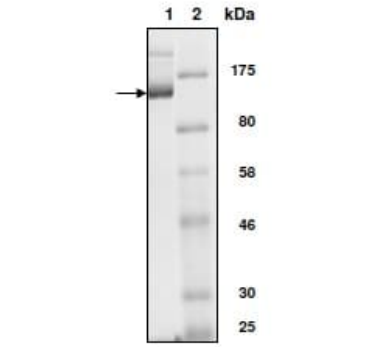
| | enlargement. Can also mediate transcriptional repression. Binds to and may be involved in the transforming capacity of the adenovirus E1A protein. In case of HIV-1 infection, it is recruited by the viral protein Tat. Regulates Tat's transactivating activity and may help inducing chromatin remodeling of proviral genes. Acetylates FOXO1 and enhances its transcriptional activity. Acetylates BCL6 wich disrupts its ability to recruit histone deacetylases and hinders its transcriptional repressor activity. Participates in CLOCK or NPAS2-regulated rhythmic gene transcription; exhibits a circadian association with CLOCK or NPAS2, correlating with increase in PER1/2 mRNA and histone H3 acetylation on the PER1/2 promoter. Acetylates MTA1 at 'Lys-626' which is essential for its transcriptional coactivator activity (PubMed:10733570, PubMed:11430825, PubMed:11701890, PubMed:12402037, PubMed:12586840, PubMed:12929931, PubMed:14645221, PubMed:15186775, PubMed:15890677, PubMed:16617102, PubMed:16762839, PubMed:18722353, PubMed:18995842, PubMed:23415232, PubMed:23911289, PubMed:23934153, PubMed:8945521). Acetylates XBP1 isoform 2; acetylation increases protein stability of XBP1 isoform 2 and enhances its transcriptional activity (PubMed:20955178). Acetylates PCNA; acetylation promotes removal of chromatin-bound PCNA and its degradation during nucleotide excision repair (NER) (PubMed:24939902). Acetylates MEF2D. |
| **Involvement in disease** | Defects in EP300 may play a role in epithelial cancer.<br>Chromosomal aberrations involving EP300 may be a cause of acute myeloid leukemias. Translocation t(8;22)(p11;q13) with KAT6A.<br>Rubinstein-Taybi syndrome 2 |
| **Sequence similarities** | Contains 1 bromo domain.<br>Contains 1 CBP/p300-type HAT (histone acetyltransferase) domain.<br>Contains 1 KIX domain.<br>Contains 2 TAZ-type zinc fingers.<br>Contains 1 ZZ-type zinc finger. |
| **Domain** | The CRD1 domain (cell cycle regulatory domain 1) mediates transcriptional repression of a subset of p300 responsive genes; it can be de-repressed by CDKN1A/p21WAF1 at least at some promoters. It conatins sumoylation and acetylation sites and the same lysine residues may be targeted for the respective modifications. It is proposed that deacetylation by SIRT1 allows sumoylation leading to suppressed activity. |
| **Post-translational modifications** | Acetylated on Lys at up to 17 positions by intermolecular autocatalysis. Deacetylated in the transcriptional repression domain (CRD1) by SIRT1, preferentially at Lys-1020. Deacetylated by SIRT2, preferentially at Lys-418, Lys-423, Lys-1542, Lys-1546, Lys-1549, Lys-1699, Lys-1704 and Lys-1707.<br>Citrullinated at Arg-2142 by PADI4, which impairs methylation by CARM1 and promotes interaction with NCOA2/GRIP1.<br>Methylated at Arg-580 and Arg-604 in the KIX domain by CARM1, which blocks association with CREB, inhibits CREB signaling and activates apoptotic response. Also methylated at Arg-2142 by CARM1, which impairs interaction with NCOA2/GRIP1.<br>Sumoylated; sumoylation in the transcriptional repression domain (CRD1) mediates transcriptional repression. Desumoylated by SENP3 through the removal of SUMO2 and SUMO3. Probable target of ubiquitination by FBXO3, leading to rapid proteasome-dependent degradation.<br>Phosphorylated by HIPK2 in a RUNX1-dependent manner. This phosphorylation that activates EP300 happens when RUNX1 is associated with DNA and CBFB. Phosphorylated by ROCK2 and this enhances its activity. Phosphorylation at Ser-89 by AMPK reduces interaction with nuclear receptors, such as PPARG. |
| **Cellular localization** | Cytoplasm. Nucleus. In the presence of ALX1 relocalizes from the cytoplasm to the nucleus. Colocalizes with ROCK2 in the nucleus. |

## Images




Functional Studies - Active human KAT3B / p300 protein fragment (ab198138)

Specific activity of ab198138 was ≥357 pmole/min/µg.




SDS-PAGE - Recombinant human KAT3B / p300 protein (ab198138)

SDS-PAGE analysis of ab198138.

**Please note:** All products are "FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC PROCEDURES"

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