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SET2 Antibody (N-term)

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP1196a

Product Information

Application	IHC-P, E
Primary Accession	Q9BYW2
Other Accession	E9Q5F9
Reactivity	Human
Predicted	Mouse
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit IgG
Clone Names	RB2780
Calculated MW	287597
Antigen Region	21-50

Additional Information

Gene ID	29072
Other Names	Histone-lysine N-methyltransferase SETD2, HIF-1, Huntingtin yeast partner B, Huntingtin-interacting protein 1, HIP-1, Huntingtin-interacting protein B, Lysine N-methyltransferase 3A, SET domain-containing protein 2, hSET2, p231HBP, SETD2, HIF1, HYPB, KIAA1732, KMT3A, SET2
Target/Specificity	This SET2 antibody is generated from rabbits immunized with a KLH conjugated synthetic peptide between 21~50 amino acids from the N-terminal region of human SET2.
Dilution	IHC-P~~1:100~500 E~~Use at an assay dependent concentration.
Format	Purified polyclonal antibody supplied in PBS with 0.09% (W/V) sodium azide. This antibody is prepared by Saturated Ammonium Sulfate (SAS) precipitation followed by dialysis against PBS.
Storage	Maintain refrigerated at 2-8°C for up to 2 weeks. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	SET2 Antibody (N-term) is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	SETD2

Function	Histone methyltransferase that specifically trimethylates 'Lys-36' of histone H3 (H3K36me3) using dimethylated 'Lys-36' (H3K36me2) as substrate (PubMed:16118227, PubMed:19141475, PubMed:21526191, PubMed:21792193, PubMed:23043551, PubMed:27474439). It is capable of trimethylating unmethylated H3K36 (H3K36me0) in vitro (PubMed:19332550). Represents the main enzyme generating H3K36me3, a specific tag for epigenetic transcriptional activation (By similarity). Plays a role in chromatin structure modulation during elongation by coordinating recruitment of the FACT complex and by interacting with hyperphosphorylated POLR2A (PubMed:23325844). Acts as a key regulator of DNA mismatch repair in G1 and early S phase by generating H3K36me3, a mark required to recruit MSH6 subunit of the MutS alpha complex: early recruitment of the MutS alpha complex to chromatin to be replicated allows a quick identification of mismatch DNA to initiate the mismatch repair reaction (PubMed:23622243). Required for DNA double-strand break repair in response to DNA damage: acts by mediating formation of H3K36me3, promoting recruitment of RAD51 and DNA repair via homologous recombination (HR) (PubMed:24843002). Acts as a tumor suppressor (PubMed:24509477). H3K36me3 also plays an essential role in the maintenance of a heterochromatic state, by recruiting DNA methyltransferase DNMT3A (PubMed:27317772). H3K36me3 is also enhanced in intron-containing genes, suggesting that SETD2 recruitment is enhanced by splicing and that splicing is coupled to recruitment of elongating RNA polymerase (PubMed:21792193). Required during angiogenesis (By similarity). Required for endoderm development by promoting embryonic stem cell differentiation toward endoderm: acts by mediating formation of H3K36me3 in distal promoter regions of FGFR3, leading to regulate transcription initiation of FGFR3 (By similarity). In addition to histones, also mediates methylation of other proteins, such as tubulins and STAT1 (PubMed:27518565, PubMed:28753426). Trimethylates 'Lys-40' of alpha-tubulins such as TUBA1B (alpha- TubK40me3); alpha-TubK40me3 is required for normal mitosis and cytokinesis and may be a specific tag in cytoskeletal remodeling (PubMed:27518565). Involved in interferon-alpha-induced antiviral defense by mediating both monomethylation of STAT1 at 'Lys-525' and catalyzing H3K36me3 on promoters of some interferon-stimulated genes (ISGs) to activate gene transcription (PubMed:28753426).
Cellular Location	Nucleus {ECO:0000250|UniProtKB:E9Q5F9}. Chromosome {ECO:0000250|UniProtKB:E9Q5F9}
Tissue Location	Ubiquitously expressed.

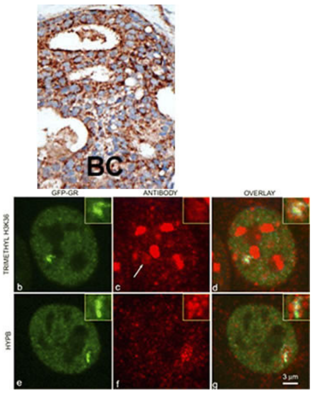
Background

SET2 is a histone methyltransferase that methylates 'Lys-36' of histone H3. H3 'Lys-36' methylation represents a specific tag for epigenetic transcriptional activation. This protein probably plays a role in chromatin structure modulation during elongation via its interaction with hyperphosphorylated POLR2A. SET2 binds DNA at promoters, and may act as a transcription activator. SET2 binds to the promoters of adenovirus 12 E1A gene in case of infection, possibly leading to regulate its expression. Huntington's disease (HD), a neurodegenerative disorder characterized by loss of striatal neurons, is caused by an expansion of a polyglutamine tract in the HD protein huntingtin. SET2 belongs to a class of huntingtin interacting proteins characterized by WW motifs.

References

Rega, S., et al., Mol. Cell. Neurosci. 18(1):68-79 (2001).
Passani, L.A., et al., Hum. Mol. Genet. 9(14):2175-2182 (2000).
Faber, P.W., et al., Hum. Mol. Genet. 7(9):1463-1474 (1998).

Images



Formalin-fixed and paraffin-embedded human cancer tissue reacted with the primary antibody, which was peroxidase-conjugated to the secondary antibody, followed by DAB staining. This data demonstrates the use of this antibody for immunohistochemistry; clinical relevance has not been evaluated. BC = breast carcinoma; HC = hepatocarcinoma.

Citations

- Organization of chromatin and histone modifications at a transcription site.