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SUPT16H Rabbit pAb

Catalog # AP100219

Product Information

Application	WB, IHC-P, IHC-F, IF
Primary Accession	Q9Y5B9
Other Accession	Q9Y5B9
Reactivity	Mouse
Predicted	Rat, Pig, Human, Rabbit, Dog, Horse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	119914
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human SUPT16H/CDC68
Epitope Specificity	601-700/1047
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the peptidase M24 family. SPT16 subfamily.
SUBUNIT	Component of the FACT complex, a stable heterodimer ofSSRP1 and SUPT16H. Also component of a CK2-SPT16-SSRP1 complexwhich forms following UV irradiation, composed of SSRP1, SUPT16H,CSNK2A1, CSNK2A2 and CSNK2B. Component of the WINAC complex, atleast composed of SMARCA2, SMARCA4, SMARCB1, SMARCC1, SMARCC2,SMARCD1, SMARCE1, ACTL6A, BAZ1B/WSTF, ARID1A, SUPT16H, CHAF1A andTOP2B. Interacts with NEK9. Binds to histone H2A-H2B. Interactswith GTF2E2.
Post-translational modifications	ADP-ribosylated. ADP-ribosylation by PARP1 is induced bygenotoxic stress and correlates with dissociation of FACT fromchromatin.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. The FACT complex is probably also involved in phosphorylation of 'Ser-392' of p53/TP53 via its association with CK2 (casein kinase II). Also involved in vitamin D-coupled transcription regulation via its association with the WINAC complex, a chromatin-remodeling complex recruited by vitamin D receptor (VDR), which is required for the ligand-bound VDR-mediated transrepression of the CYP27B1 gene.

Additional Information

Gene ID	11198
Other Names	CDC68; FACTP140; NEDDFAC; SPT16; SPT16/CDC68; Fact140; Supt16h; E1BNP8_BOVIN; SP16H_HUMAN; Chromatin-specific transcription elongation factor 140 kDa subunit; FACT 140 kDa subunit; Facilitates chromatin transcription complex subunit SPT16 (hSPT16); SP16H_MOUSE; Facilitates chromatin transcription complex subunit SPT16; Supt16; SPT16 homolog, facilitates chromatin remodeling subunit; suppressor of Ty (S.cerevisiae) 16 homolog; suppressor of Ty 16 homolog (S. cerevisiae); facilitates chromatin remodeling 140 kDa subunit
Dilution	WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name	SUPT16H
Synonyms	FACT140, FACTP140
Function	Component of the FACT complex, a general chromatin factor that acts to reorganize nucleosomes. The FACT complex is involved in multiple processes that require DNA as a template such as mRNA elongation, DNA replication and DNA repair. During transcription elongation the FACT complex acts as a histone chaperone that both destabilizes and restores nucleosomal structure. It facilitates the passage of RNA polymerase II and transcription by promoting the dissociation of one histone H2A-H2B dimer from the nucleosome, then subsequently promotes the reestablishment of the nucleosome following the passage of RNA polymerase II. The FACT complex is probably also involved in phosphorylation of 'Ser-392' of p53/TP53 via its association with CK2 (casein kinase II).
Cellular Location	Nucleus. Chromosome. Note=Colocalizes with RNA polymerase II on chromatin. Recruited to actively transcribed loci
Tissue Location	Ubiquitous..

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