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AF9 (MLLT3) Antibody (C-term K486)

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP6190a

Product Information

Application	WB, IHC-P, E
Primary Accession	P42568
Other Accession	A2AM29
Reactivity	Human, Mouse
Predicted	Mouse, Rat, Bovine, Canine, Rabbit, Chicken
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit IgG
Calculated MW	63351
Antigen Region	471-502

Additional Information

Gene ID	4300
Other Names	Protein AF-9, ALL1-fused gene from chromosome 9 protein, Myeloid/lymphoid or mixed-lineage leukemia translocated to chromosome 3 protein, YEATS domain-containing protein 3, MLLT3, AF9, YEATS3
Target/Specificity	This AF9 (MLLT3) antibody is generated from rabbits immunized with a KLH conjugated synthetic peptide between 471-502 amino acids from the C-terminal region of human AF9 (MLLT3).
Dilution	WB~~1:1000 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	AF9 (MLLT3) Antibody (C-term K486) is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	MLLT3 {ECO:0000303|PubMed:16001262, ECO:0000312|HGNC:HGNC:7136}
Function	Chromatin reader component of the super elongation complex (SEC), a complex required to increase the catalytic rate of RNA polymerase II

	transcription by suppressing transient pausing by the polymerase at multiple sites along the DNA (PubMed:20159561, PubMed:20471948, PubMed:25417107, PubMed:27105114, PubMed:27545619). Specifically recognizes and binds acylated histone H3, with a preference for histone H3 that is crotonylated (PubMed:25417107, PubMed:27105114, PubMed:27545619, PubMed:30374167, PubMed:30385749). Crotonylation marks active promoters and enhancers and confers resistance to transcriptional repressors (PubMed:25417107, PubMed:27105114, PubMed:27545619). Recognizes and binds histone H3 crotonylated at 'Lys-9' (H3K9cr), and with slightly lower affinity histone H3 crotonylated at 'Lys-18' (H3K18cr) (PubMed:27105114). Also recognizes and binds histone H3 acetylated and butyrylated at 'Lys-9' (H3K9ac and H3K9bu, respectively), but with lower affinity than crotonylated histone H3 (PubMed:25417107, PubMed:27105114, PubMed:30385749). In the SEC complex, MLLT3 is required to recruit the complex to crotonylated histones (PubMed:27105114, PubMed:27545619). Recruitment of the SEC complex to crotonylated histones promotes recruitment of DOT1L on active chromatin to deposit histone H3 'Lys-79' methylation (H3K79me) (PubMed:25417107). Plays a key role in hematopoietic stem cell (HSC) maintenance by preserving, rather than conferring, HSC stemness (PubMed:31776511). Acts by binding to the transcription start site of active genes in HSCs and sustaining level of H3K79me2, probably by recruiting DOT1L (PubMed:31776511). Required for DOT1L-mediated H3K79 hypermethylation at the SCNN1A promoter, resulting in transcriptional repression (By similarity). May play a role in leukemogenic gene transcription (PubMed:39794553).
Cellular Location	Nucleus {ECO:0000255|PROSITE-ProRule:PRU00376, ECO:0000269|PubMed:27105114}. Chromosome. Note=Colocalizes with acylated histone H3 (PubMed:25417107, PubMed:27105114). Colocalizes with histone H3 crotonylated at 'Lys-18' (H3K18cr) (PubMed:27105114)
Tissue Location	Enriched in undifferentiated hematopoietic stem cells in fetal liver, cord blood and bone marrow

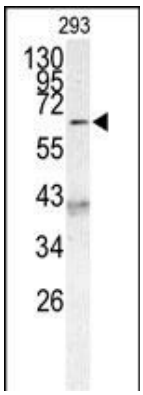
Background

The human AF9 gene is one of the most common fusion partner genes with the ALL1 gene at 11q23 (also called MLL), resulting in the t(9;11)(p22;q23). The AF9 gene is more than 100 kb, and 2 patient breakpoint cluster regions (BCRs) have been identified; BCR1 is within intron 4, previously called site A, whereas BCR2 or site B spans introns 7 and 8. Several different structural elements have been identified in AF9, including a colocalizing in vivo DNA topo II cleavage site and an in vitro DNase I hypersensitive (DNase 1 HS) site in intron 7 in BCR2. Reversibility experiments demonstrated a religation of the topo II cleavage sites. In addition, 2 scaffold associated regions (SARs) are located centromeric to the topo II and DNase I HS cleavage sites and border breakpoint regions in 2 leukemic cells lines: SAR1 is located in intron 4, whereas SAR2 encompasses parts of exons 5-7. The patient breakpoint regions of AF9 share the same structural elements as the MLL BCR. A DNA breakage and repair model for nonhomologous recombination between MLL and its partner genes, particularly AF9, has been proposed.

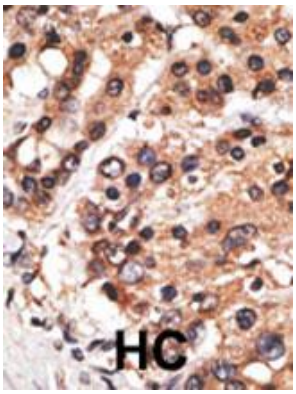
References

Iida, S., et al., Oncogene 8(11):3085-3092 (1993).
Nakamura, T., et al., Proc. Natl. Acad. Sci. U.S.A. 90(10):4631-4635 (1993).
Strissel, P. L., et al., Hum. Molec. Genet. 9: 1671-1679 (2000).

Images



Western blot analysis of AF9 (MLLT3) Antibody (C-term K486) (Cat.#AP6190a) in 293 cell line lysates (35ug/lane). MLLT3(arrow) was detected using the purified Pab.



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

Citations

- The leukemogenic AF4-MLL fusion protein causes P-TEFb kinase activation and altered epigenetic signatures.
- The mixed-lineage leukemia fusion partner AF4 stimulates RNA polymerase II transcriptional elongation and mediates coordinated chromatin remodeling.

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