

**AF9 (MLLT3) Antibody (Center V422)**  
**Purified Rabbit Polyclonal Antibody (Pab)**  
**Catalog # AP6190b**

**Specification**

**AF9 (MLLT3) Antibody (Center V422) - Product Information**

Application	WB,E
Primary Accession	<a href="#">P42568</a>
Reactivity	Human, Mouse
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit Ig
Antigen Region	407-438

**AF9 (MLLT3) Antibody (Center V422) - 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 407-438 amino acids from the Central region of human AF9 (MLLT3).

**Dilution**

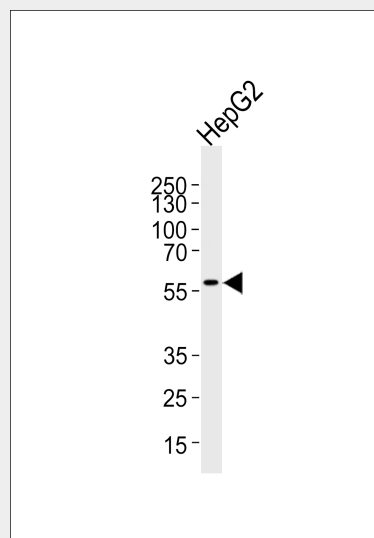
WB~~1:1000

**Format**

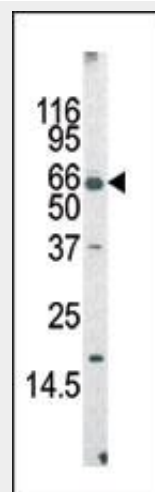
Purified polyclonal antibody supplied in PBS with 0.09% (W/V) sodium azide. This antibody is prepared by Saturated Ammonium Sulfate (SAS) precipitation followed by dialysis against PBS.

**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.



Western blot analysis of lysate from HepG2 cell line, using MLLT3 C-term Antibody(Cat. #AP6190b). AP6190b was diluted at 1:1000 at each lane. A goat anti-rabbit IgG H&L(HRP) at 1:5000 dilution was used as the secondary antibody. Lysate at 35ug per lane.



The anti-MLLT3 Pab (Cat. #AP6190b) is used in Western blot to detect MLLT3 in mouse cerebellum tissue lysate

**AF9 (MLLT3) Antibody (Center V422) - Background**

## Precautions

AF9 (MLLT3) Antibody (Center V422) is for research use only and not for use in diagnostic or therapeutic procedures.

## AF9 (MLLT3) Antibody (Center V422) - 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:<a href="http://www.uniprot.org/citations/20159561" target="\_blank">20159561</a>, PubMed:<a href="http://www.uniprot.org/citations/20471948" target="\_blank">20471948</a>, PubMed:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>, PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/27545619" target="\_blank">27545619</a>). Specifically recognizes and binds acylated histone H3, with a preference for histone H3 that is crotonylated (PubMed:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>, PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/27545619" target="\_blank">27545619</a>, PubMed:<a href="http://www.uniprot.org/citations/30374167" target="\_blank">30374167</a>, PubMed:<a href="http://www.uniprot.org/citations/30385749" target="\_blank">30385749</a>). Crotonylation marks active promoters and enhancers and confers resistance to transcriptional repressors (PubMed:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>, PubMed:<a href="http://www.uniprot.org/citations/20471948" target="\_blank">20471948</a>, PubMed:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>, PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/27545619" target="\_blank">27545619</a>).

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 I 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 cell 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.

## AF9 (MLLT3) Antibody (Center V422) - 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).

PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/27545619" target="\_blank">27545619</a>). Recognizes and binds histone H3 crotonylated at 'Lys-9' (H3K9cr), and with slightly lower affinity histone H3 crotonylated at 'Lys-18' (H3K18cr) (PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>). 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:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>, PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/30385749" target="\_blank">30385749</a>). In the SEC complex, MLLT3 is required to recruit the complex to crotonylated histones (PubMed:<a href="http://www.uniprot.org/citations/27105114" target="\_blank">27105114</a>, PubMed:<a href="http://www.uniprot.org/citations/27545619" target="\_blank">27545619</a>). Recruitment of the SEC complex to crotonylated histones promotes recruitment of DOT1L on active chromatin to deposit histone H3 'Lys-79' methylation (H3K79me) (PubMed:<a href="http://www.uniprot.org/citations/25417107" target="\_blank">25417107</a>). Plays a key role in hematopoietic stem cell (HSC) maintenance by preserving, rather than conferring, HSC stemness (PubMed:<a href="http://www.uniprot.org/citations/31776511" target="\_blank">31776511</a>). Acts by binding to the transcription start site of active genes in HSCs and sustaining level of H3K79me2, probably by recruiting DOT1L (PubMed:<a href="http://www.uniprot.org/citations/31776511" target="\_blank">31776511</a>).

### 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

**AF9 (MLLT3) Antibody (Center V422) - Protocols**

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)