



**Synonyms:** AF9; YEATS3

**Locus ID:** 4300

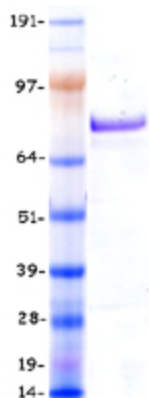
**UniProt ID:** [P42568](#), [A0A0S2Z448](#)

**Cytogenetics:** 9p21.3

**Summary:** 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 marked preference for histone H3 that is crotonylated (PubMed:25417107, PubMed:27105114, PubMed:27545619). 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 at 'Lys-9' (H3K9ac), but with lower affinity than crotonylated histone H3 (PubMed:25417107, PubMed:27105114). In the SEC complex, MLLT3 is required to recruit the complex to crotonylated histones (PubMed:27105114, PubMed:27545619).[UniProtKB/Swiss-Prot Function]

**Protein Families:** Transcription Factors

### Product images:



Coomassie blue staining of purified MLLT3 protein (Cat# [TP306283]). The protein was produced from HEK293T cells transfected with MLLT3 cDNA clone (Cat# [RC206283]) using MegaTran 2.0 (Cat# [TT210002]).