

# ZBTB7A Antibody

Rabbit mAb

Catalog # AP92326

## Product Information

<b>Application</b>	WB, IHC, IF, ICC, IP, IHF
<b>Primary Accession</b>	<a href="#">O95365</a>
<b>Reactivity</b>	Human
<b>Clonality</b>	Monoclonal
<b>Other Names</b>	FBI1; LRF; Pokemon; TIP21; ZBTB7; ZBTB7A; ZNF857A;
<b>Isotype</b>	Rabbit IgG
<b>Host</b>	Rabbit
<b>Calculated MW</b>	61439

## Additional Information

<b>Dilution</b>	WB 1:1000~1:5000 IHC 1:50~1:200 ICC/IF 1:50~1:200 IP 1:50
<b>Purification</b>	Affinity-chromatography
<b>Immunogen</b>	A synthesized peptide derived from human ZBTB7A
<b>Description</b>	Plays a key role in the instruction of early lymphoid progenitors to develop into B lineage by repressing T-cell instructive Notch signals (By similarity).
<b>Storage Condition and Buffer</b>	Rabbit IgG in phosphate buffered saline , pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol. Store at +4°C short term. Store at -20°C long term. Avoid freeze / thaw cycle.

## Protein Information

<b>Name</b>	ZBTB7A ( <a href="#">HGNC:18078</a> )
<b>Function</b>	<p>Transcription factor that represses the transcription of a wide range of genes involved in cell proliferation and differentiation (PubMed:<a href="#">14701838</a>, PubMed:<a href="#">17595526</a>, PubMed:<a href="#">20812024</a>, PubMed:<a href="#">25514493</a>, PubMed:<a href="#">26455326</a>, PubMed:<a href="#">26816381</a>). Directly and specifically binds to the consensus sequence 5'-[GA][CA]GACCCCCCCC-3' and represses transcription both by regulating the organization of chromatin and through the direct recruitment of transcription factors to gene regulatory regions (PubMed:<a href="#">12004059</a>, PubMed:<a href="#">17595526</a>, PubMed:<a href="#">20812024</a>, PubMed:<a href="#">25514493</a>, PubMed:<a href="#">26816381</a>). Negatively regulates SMAD4 transcriptional activity in the TGF-beta signaling pathway through these two mechanisms (PubMed:<a href="#">25514493</a>). That is, recruits the chromatin regulator HDAC1 to the SMAD4-DNA complex and in parallel prevents the recruitment of the transcriptional activators CREBBP and EP300 (PubMed:<a href="#">25514493</a>). Collaborates with transcription factors like RELA to modify the accessibility of gene transcription regulatory regions to secondary transcription factors (By similarity). Also directly interacts with transcription factors like SP1 to prevent their binding to DNA (PubMed:<a href="#">12004059</a>). Functions as an androgen</p>

receptor/AR transcriptional corepressor by recruiting NCOR1 and NCOR2 to the androgen response elements/ARE on target genes (PubMed:[20812024](#)). Thereby, negatively regulates androgen receptor signaling and androgen-induced cell proliferation (PubMed:[20812024](#)). Involved in the switch between fetal and adult globin expression during erythroid cells maturation (PubMed:[26816381](#)). Through its interaction with the NuRD complex regulates chromatin at the fetal globin genes to repress their transcription (PubMed:[26816381](#)). Specifically represses the transcription of the tumor suppressor ARF isoform from the CDKN2A gene (By similarity). Efficiently abrogates E2F1-dependent CDKN2A transactivation (By similarity). Regulates chondrogenesis through the transcriptional repression of specific genes via a mechanism that also requires histone deacetylation (By similarity). Regulates cell proliferation through the transcriptional regulation of genes involved in glycolysis (PubMed:[26455326](#)). Involved in adipogenesis through the regulation of genes involved in adipocyte differentiation (PubMed:[14701838](#)). Plays a key role in the differentiation of lymphoid progenitors into B and T lineages (By similarity). Promotes differentiation towards the B lineage by inhibiting the T-cell instructive Notch signaling pathway through the specific transcriptional repression of Notch downstream target genes (By similarity). Also regulates osteoclast differentiation (By similarity). May also play a role, independently of its transcriptional activity, in double-strand break repair via classical non-homologous end joining/cNHEJ (By similarity). Recruited to double-strand break sites on damage DNA, interacts with the DNA-dependent protein kinase complex and directly regulates its stability and activity in DNA repair (By similarity). May also modulate the splicing activity of KHDRBS1 toward BCL2L1 in a mechanism which is histone deacetylase-dependent and thereby negatively regulates the pro-apoptotic effect of KHDRBS1 (PubMed:[24514149](#)).

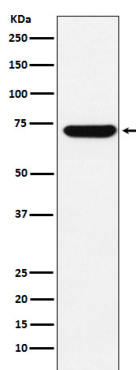
#### Cellular Location

Nucleus. Note=Recruited to double-strand break sites of damaged DNA. {ECO:0000250|UniProtKB:O88939}

#### Tissue Location

Widely expressed (PubMed:9927193). In normal thymus, expressed in medullary epithelial cells and Hassle's corpuscles (at protein level) (PubMed:15662416). In tonsil, expressed in squamous epithelium and germinal center lymphocytes (at protein level) (PubMed:15662416). Up-regulated in a subset of lymphomas, as well as in a subset of breast, lung, colon, prostate and bladder carcinomas (at protein level) (PubMed:15662416). Expressed in adipose tissues (PubMed:14701838).

## Images



Western blot analysis of ZBTB7A expression in HepG2 cell lysate.