

**SATB1 Antibody (Internal)**  
**Goat Polyclonal Antibody**  
**Catalog # ALS15368****Specification**

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**SATB1 Antibody (Internal) - Product Information**

Application	WB, IHC
Primary Accession	<a href="#">Q01826</a>
Reactivity	Human, Mouse, Rat, Rabbit, Hamster, Monkey
Host	Goat
Clonality	Polyclonal
Calculated MW	86kDa KDa

**SATB1 Antibody (Internal) - Additional Information****Gene ID** 6304**Other Names**

DNA-binding protein SATB1, Special AT-rich sequence-binding protein 1, SATB1

**Target/Specificity**

Human SATB1. Reported variants NP\_001124482.1 and NP\_002962.1 represent identical protein.

**Reconstitution & Storage**

Store at -20°C. Minimize freezing and thawing.

**Precautions**

SATB1 Antibody (Internal) is for research use only and not for use in diagnostic or therapeutic procedures.

**SATB1 Antibody (Internal) - Protein Information****Name** SATB1 ([HGNC:10541](#))**Function**

Crucial silencing factor contributing to the initiation of X inactivation mediated by Xist RNA that occurs during embryogenesis and in lymphoma (By similarity). Binds to DNA at special AT-rich sequences, the consensus SATB1-binding sequence (CSBS), at nuclear matrix- or scaffold-associated regions. Thought to recognize the sugar-phosphate structure of double-stranded DNA. Transcriptional repressor controlling nuclear and viral gene expression in a phosphorylated and acetylated status-dependent manner, by binding to matrix attachment regions (MARs) of DNA and inducing a local chromatin-loop remodeling. Acts as a docking site for several chromatin remodeling enzymes (e.g. PML at the MHC-I locus) and also by recruiting corepressors (HDACs) or coactivators (HATs) directly to promoters and enhancers. Modulates genes that are essential in the maturation of the immune T-cell CD8SP from thymocytes. Required for the switching of fetal globin species, and beta- and gamma-globin genes regulation during erythroid differentiation. Plays a role in chromatin organization and nuclear architecture during

apoptosis. Interacts with the unique region (UR) of cytomegalovirus (CMV). Alu-like motifs and SATB1-binding sites provide a unique chromatin context which seems preferentially targeted by the HIV-1 integration machinery. Moreover, HIV-1 Tat may overcome SATB1-mediated repression of IL2 and IL2RA (interleukin) in T-cells by binding to the same domain than HDAC1. Delineates specific epigenetic modifications at target gene loci, directly up-regulating metastasis-associated genes while down-regulating tumor-suppressor genes. Reprograms chromatin organization and the transcription profiles of breast tumors to promote growth and metastasis. Promotes neuronal differentiation of neural stem/progenitor cells in the adult subventricular zone, possibly by positively regulating the expression of NEUROD1 (By similarity).

#### **Cellular Location**

Nucleus matrix. Nucleus, PML body. Note=Organized into a cage-like network anchoring loops of heterochromatin and tethering specialized DNA sequences (PubMed:12692553). When sumoylated, localized in promyelocytic leukemia nuclear bodies (PML NBs) (PubMed:18408014)

#### **Tissue Location**

Expressed predominantly in thymus.

### **SATB1 Antibody (Internal) - Protocols**

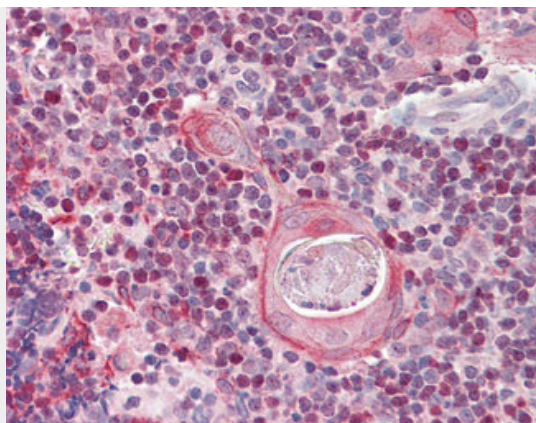
Provided below are standard protocols that you may find useful for product applications.

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

### **SATB1 Antibody (Internal) - Images**



SATB1 antibody (0.3 ug/ml) staining of MOLT4 lysate (35 ug protein/ml in RIPA buffer).



Anti-SATB1 antibody IHC of human thymus.

### **SATB1 Antibody (Internal) - Background**

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### **SATB1 Antibody (Internal) - References**

Dickinson L.A.,et al.Cell 70:631-645(1992).  
Ota T.,et al.Nat. Genet. 36:40-45(2004).  
Totoki Y.,et al.Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.  
Muzny D.M.,et al.Nature 440:1194-1198(2006).  
Mural R.J.,et al.Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.