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Runx1/AML1-ETO polyclonal antibody
Rabbit Polyclonal Antibody
Catalog # ABV11364

Specification

Runx1/AML1-ETO polyclonal antibody - Product Information

Application	**CHIP, E**
Primary Accession	Q01196
Host	**Rabbit**
Clonality	**Polyclonal**
Isotype	**Rabbit IgG**
Calculated MW	**48737**

Runx1/AML1-ETO polyclonal antibody - Additional Information

Gene ID 861

Positive Control — **Western blot: SKNO-1 cells, ELISA: Peptides, ChIP: Kasumi cells.**

Application & Usage — **ChIP: 4 µg/ChIP, WB: 1:1000, ELISA: 1:500**

Other Names
AML1-ETO

Target/Specificity
Runx1/AML1-ETO

Antibody Form
Liquid

Appearance
Colorless liquid

Formulation
In PBS with 0.05% (W/V) sodium azide.

Handling
The antibody solution should be gently mixed before use.

Reconstitution & Storage
-20 °C

Background Descriptions

Precautions
Runx1/AML1-ETO polyclonal antibody is for research use only and not for use in diagnostic or therapeutic procedures.

Runx1/AML1-ETO polyclonal antibody - Protein Information

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Name RUNX1

Synonyms AML1, CBFA2

Function
Forms the heterodimeric complex core-binding factor (CBF) with CBFB. RUNX members modulate the transcription of their target genes through recognizing the core consensus binding sequence 5'- TGTGGT-3', or very rarely, 5'-TGCGGT-3', within their regulatory regions via their runt domain, while CBFB is a non-DNA-binding regulatory subunit that allosterically enhances the sequence-specific DNA-binding capacity of RUNX. The heterodimers bind to the core site of a number of enhancers and promoters, including murine leukemia virus, polyomavirus enhancer, T-cell receptor enhancers, LCK, IL3 and GM-CSF promoters (Probable). Essential for the development of normal hematopoiesis (PubMed:17431401). Acts synergistically with ELF4 to transactivate the IL-3 promoter and with ELF2 to transactivate the BLK promoter (PubMed:10207087, PubMed:14970218). Inhibits KAT6B-dependent transcriptional activation (By similarity). Involved in lineage commitment of immature T cell precursors. CBF complexes repress ZBTB7B transcription factor during cytotoxic (CD8+) T cell development. They bind to RUNX-binding sequence within the ZBTB7B locus acting as transcriptional silencer and allowing for cytotoxic T cell differentiation. CBF complexes binding to the transcriptional silencer is essential for recruitment of nuclear protein complexes that catalyze epigenetic modifications to establish epigenetic ZBTB7B silencing (By similarity). Controls the anergy and suppressive function of regulatory T-cells (Treg) by associating with FOXP3. Activates the expression of IL2 and IFNG and down-regulates the expression of TNFRSF18, IL2RA and CTLA4, in conventional T-cells (PubMed:17377532). Positively regulates the expression of RORC in T-helper 17 cells (By similarity).

Cellular Location
Nucleus.

Tissue Location
Expressed in all tissues examined except brain and heart. Highest levels in thymus, bone marrow and peripheral blood

Runx1/AML1-ETO polyclonal antibody - Protocols

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

- Western Blot
- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

Runx1/AML1-ETO polyclonal antibody - Images

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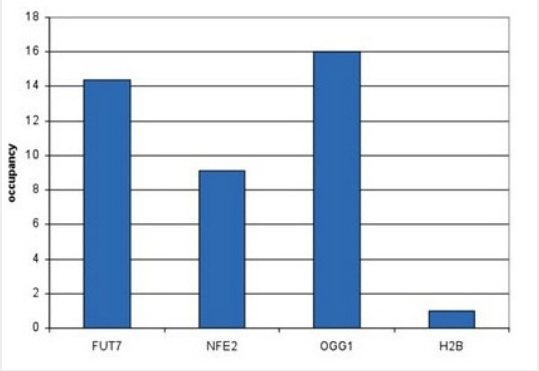
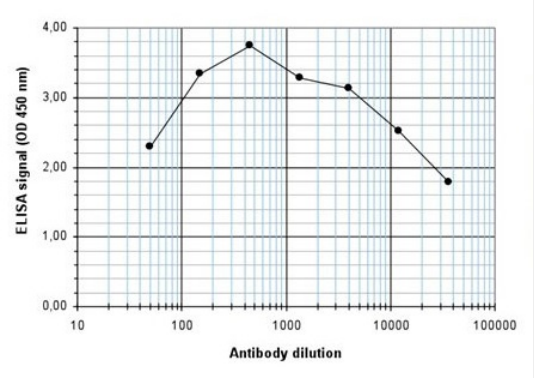


ChIP assays were performed using Kasumi cells and the antibody and optimized PCR primer sets for qPCR. The Fig shows the occupancy, calculated as the ratio + control/background for which the promoter of the H2B gene was used.



To determine the titer, an ELISA was performed using a serial dilution of the antibody. The antigen used was a peptide containing the histone modification of interest. By plotting the absorbance against the antibody dilution the titer of the antibody was estimated to be 1:32,750.

Runx1/AML1-ETO polyclonal antibody - Background

This antibody specifically recognizes the AML1 (RUNX1) - ETO (RUNX1T1) fusion protein that arises due to a translocation between chromosome 8 and 22 (t(8;21)(q22;q22)). This translocation is one of the most frequent karyotypic abnormalities observed in acute myeloid leukemia. It produces a chimerical gene made up of the 5'-region of AML1and the 3'-region of ETO. The chimerical protein is thought to associate with the nuclear corepressor/histone deacetylase complex to block hematopoietic differentiation.