MIXL1 (Mix1 homeobox-like 1 (Xenopus laevis))

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Identity

Other names: MGC138179, MILD1, MIX, MIXL
HGNC (Hugo): MIXL1
Location: 1q42.12
Local order: MIXL1 is flanked on its 3’ end by Lin9. This proximity is evolutionarily conserved.

DNA/RNA

Description

MIXL1 is 2131 bps long and consists of two exons of length 393 bp and 306 bp, and one intron (Guo et al., 2002; Sahr et al., 2002).

Transcription

MIXL1 is transcribed to a full-length 699 bp mRNA. There are no known splice variants.

Pseudogene

There are no known pseudogenes for MIXL1.
**Protein**

**Description**

MIXL1 is a paired type homeobox protein which has 232 amino acids, and a molecular weight of 27 kDa. The protein contains three identified domains: a proline-rich domain, a paired-type homeobox, and a C-terminal acidic domain. While MIXL1 does have an expected weight of 27 kDa, it will migrate on a Western Blot at 36 kDa (Guo et al., 2002). MIXL1 is phosphorylated in the amino-terminal region at Tyr20 (Guo et al., 2006).

**Expression**

MIXL1 expression is restricted to embryonic mesendoderm precursors and adult hematopoietic stem cells and progenitors.

**Localization**

MIXL1 expression is predominantly nuclear.

**Function**

MIXL1 is paired-type homeobox transcription factor, and as such preferentially binds to the DNA sequence TAAT. MIXL1 homologs preferentially bind as dimers to 11 bp palindromic sequences consisting of two TAAT segments and a three nucleotide spacer (Wilson et al., 1993). MIXL1 expression is required for both mesendoderm development and hematopoiesis. The MIXL1 homologs are necessary intermediate factors to the BMP4 (bone morphogenetic protein 4)-mediated mesendoderm formation, as dominant negative mutants block this pathway (Mead et al., 1996). Development into mesoderm and endoderm cell layers is dependant on the expression collaborating factors. MIXL1 expression is required for the early stages of hematopoiesis and is normally expressed in all early hematopoietic precursor types (Guo et al., 2002).

**Homology**

MIXL1 is a member of the Mix/Bix family of transcription factors, of which it is the only member identified in humans. It is also a member of the larger grouping of paired type homeoboxes, a family of genes which share sequence similarity in the homeobox domain with paired box family (PAX). MIXL1 shares 41% sequence similarity to its chicken homolog, and 69% to its mouse homolog. Its homeodomain is highly conserved across species, sharing identity of 66% to that of Xenopus Mix1, 79% to that of chicken Mix1, and 94% to that of mouse Mix1.

**Implicated in**

**Hodgkin's lymphoma**

**Disease**

MIXL1 is aberrantly expressed in patient samples derived from Hodgkin's lymphoma, along with the following Hodgkin cell lines: L-1236, L-428, HD-MyZ, HD-LM2, MDA-E, MDA-V, KM-H2, and Daudi (Drakos et al., 2007).

**T-cell NHL lymphoma**

**Disease**

MIXL1 is aberrantly expressed in patient samples derived from High Grade T-cell non-Hodgkin's lymphoma, along with the following T-cell NHL established lines: Karpas 299, MAC2A, SR-786, and Peer (Drakos et al., 2007; Guo et al., 2002).

**B-cell NHL lymphoma**

**Disease**

MIXL1 is aberrantly expressed in patient samples derived from High Grade B-cell non-Hodgkin's lymphoma, along with the following B-cell NHL established lines: SKI-DLBL, DB, DOHH1, IM-9, IM-10.
Mino, Sp-53, Z-138, and CJ (Drakos et al., 2007; Guo et al., 2002).

**Acute myeloid leukemia**

**Disease**

Retroviral transduction of Mixl1 into mouse bone marrow resulted in transplantable acute myeloid leukemia in all lethally irradiated recipient mice after a latency period (Glaser et al., 2006).

The following established AML cell lines aberrantly express MIXL1: U937, KG1, and ML3 (Guo et al., 2002).

**Chronic myeloid leukemia**

**Disease**

MIXL1 is aberrantly expressed in the K562 established cell line (Guo et al., 2002).

**T-cell leukemia**

**Disease**

The Mixl1 promoter in mouse was identified as a site of viral insertion, using the Moloney murine leukemia virus, which collaborates with loss of p27 in induction of lymphomagenesis (Hwang et al., 2002).

MIXL1 is aberrantly expressed in the following T-cell leukemia established lines: Jurkat, SKW-3, and CEM (Drakos et al., 2007; Guo et al., 2002).

**B-cell leukemia**

**Disease**

MIXL1 is aberrantly expressed in the following B-cell leukemia established lines: NALM6, REH-1 (Drakos et al., 2007; Guo et al., 2002).

**References**


This article should be referenced as such: