MXI1 (MAX interactor 1)

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Identity
HGNC (Hugo): MXI1
Location: 10q24-25

DNA/RNA
Description
The gene spans approximately 60 kb; 6 exons.

Transcription
2.6 kb mRNA; two transcription initiation sites.

Protein
Description
228 amino acids; 26 kDa; contains a basic region/helix-loop-helix/leucine zipper (B-HLH-LZ) motif that is similar to that found in Myc family.

Expression
Tissue specific; induced during cells terminal differentiation.

Localisation
Nuclear.

Function
Mxil, discovered in 1993, is, with Mad, one of the proteins that can regulate Max, a human protein containing a basic helix-loop-helix leucine zipper (bHLH-zip) that allows the formation of cMyc-Max heterodimers and that activates transcription; Mad and Mxil may be involved in tumour suppression since they can compete with Myc proteins for the interaction with Max; Mxil normally functions to suppress cell growth: experimental induction of the gene resulted in the accumulation of cells in G2-M phase.

Homology
Belongs to the basic helix-loop-helix (bhlh) family of transcription factors.

Mutations
Somatic
Mutations have been described in some sporadic prostate cancers but no germline mutations were found in a study of 38 families with possible predisposition to this disease; a correlation between a polymorphic repeat in the 3’ untranslated region in Mxil mRNA and regulation of its transcription and degradation has been suggested.

Implicated in
Implicated in some sporadic cases of prostate cancer and glioblastoma as a tumour suppressor gene

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