Gene Section
Mini Review

HBP1 (HMG-box transcription factor 1)
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Identity

Other names: FLJ16340
HGNC (Hugo): HBP1
Location: 7q22.3
Local order: The HBP1 gene is located between the PRKAR2B gene (left) and the COG5 gene (right).

DNA/RNA

Description
Sequence length 33515; cDNA length 2829; Coding sequence 1545. The gene is comprised of 11 exons; max. exon length 1121, min. exon length 54. Number of SNPs 6.

Transcription
The consensus normal transcript is 2829 nt and the coding sequence is 1545 nt. The consensus normal transcript is produced from 11 exons. The first exon is non-coding. There are 16 different mRNAs produced, including 13 different alternatively spliced variants. Several of these alternatively spliced variants appear to be produced only in tumor cells.

Expression
HBP1 mRNA is expressed in several human organs and tissues: brain; uterus; testis; mixed; uncharacterized tissue; lung; bladder; kidney; heart; lymph node; blood; prostate; trachea; esophagus; cervix; skin; adrenal gland; eye; intestine; vascular; amniotic fluid; mouth; embryonic tissue; spleen; thymus; placenta; connective tissue; liver; mammary gland; muscle; pancreas; stomach; ovary; ascites; ganglia; bone; pharynx; thyroid; adipose tissue; parathyroid; ear; pineal gland; nerve; bone marrow; umbilical cord.

Pseudogene
None known.

Protein

Description
HBP1 encodes a 515 amino acid, 62-kDa, transcriptional repressor. On western blots, HBP1 runs anomalously at 75 kD. HBP1 represses numerous target genes when overexpressed, including N-Myc, cyclin D1 and c-myc. The protein contains two known domains: an HMG box DNA binding domain and a repression domain that contains an ataxin homology domain.

Ensemble Genes

HBP1 Locus on 7q22. Chromosome 7, band q22 is shown at the top of the diagram with the distance on the forward strand marked as indicated. The HBP1 gene is located between the PRKAR2B gene (left) and the COG5 gene (right). Coding exons are shown in bold red, while non-coding are shown with open red boxes. cDNA coding sequence is shown in dark green.
HBP1 Protein Schematic. HBP1 contains two defined domains; an ataxin homology domain (gray) and an HMG box DNA binding domain (red). There are two Rb-interacting motifs (black line) and a p38 MAP kinase-interacting region (yellow). A repression domain (aa200-400) encompasses the Ataxin homology domain.

**Localisation**

HBP1 is predominantly a nuclear protein.

**Function**

**Cell Cycle.** HBP1 was isolated as a cell cycle inhibitor and HMG-box transcriptional repressor. HBP1 binds to Rb and p107 via an LXCXE and IXCXE binding motif as part of HBP1 function in cell cycle regulation. HBP1 expression was uniquely associated with oncogene-mediated senescence in an RB-dependent manner.

**Growth and Differentiation.** Liver-specific expression of HBP1 was shown to inhibit liver regeneration. In addition, ectopic expression of HBP1 regulates differentiation in muscle cells. Similarly, transgenic mice overexpressing HBP1 exhibited altered thymus cellularity and decreased thymocyte development. Finally, HBP1 expression is maintained in the developing testis beyond the onset of spermatogenesis, and the expression of HBP1 in XY germ cells appears to correlate with the onset of mitotic arrest. The repression domain of HBP1 contains an Ataxin homology domain which interacts with the Sin3 corepressor PAH2 domain, thus recruiting HDAC1 to a repression complex.

**Signaling and Transcription.** HBP1 inhibits a number of genes through direct binding to its cognate recognition sequence, including N-myc and p47 phox.

**Homology**

HBP1 contains two recognized homology motifs; an Ataxin homology domain and an HMG box DNA binding domain.

**Mutations**

**Somatic**

In an analysis of 76 breast tumors, 10 HBP1 mutations/variants were identified that were associated with fully invasive breast cancer. Some of these mutants/variants were shown to be the result of genomic mutations.
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**Implicated in**

Breast Cancer

**Disease**
Aberrations in HBP1 are associated with invasive breast cancer. The HBP1 gene is either mutated or reduced in breast cancer. As cited above in the "Somatic Mutation section", HBP1 mutations/variants were associated with fully invasive breast cancer, some of which arose from genomic mutations. In a new analysis, a subset of invasive breast cancer tumors had markedly reduced expression of the HBP1 mRNA.

**Prognosis**
Statistical analysis of a breast cancer patient database predicted that reduced HBP1 mRNA levels were associated with a decreased relapse-free survival and recurrence with distant metastases (Paulson et al., 2007).

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