DDX5 (DEAD (Asp-Glu-Ala-Asp) box polypeptide 5)

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Identity

Other names: DKFZp434E109, DKFZp686J01190, G17P1, HLR1, HUMP68, p68
HGNC (Hugo): DDX5
Location: 17q23.3

Note
DDX5/p68 RNA helicase is a member of DEAD box RNA helicases. As an example of a cellular RNA helicase, the ATPase and the RNA unwinding activities of p68 RNA helicase were documented with the protein that was purified from human 293 cells (Iggo and Lane, 1989; Ford et al., 1988; Hirling et al., 1989) and recombinant protein expressed in E. coli (Huang and Liu, 2002). The gene is expressed in all dividing cells of different vertebrates (Lane and Hoeffler, 1980; Stevenson et al., 1998). p68 RNA helicase is involved in multiple cellular processes, including gene transcription (Endoh et al., 1999; Rossow and Janknecht, 2003), pre-mRNA processing (Liu, 2002; Yang et al., 2006), pre-rRNA processing (Jalal et al., 2007), pre-miRNA processing (Fukuda et al., 2007), DNA methylation and de-methylation (Jost et al., 1999), and chromatin remodeling (Carter et al., 2010). A number of different post-translational modifications of p68 are reported, including phosphorylations, sumoylation, and ubiquitylation (Causevic et al., 2001; Yang et al., 2005; Jacobs et al., 2007).

DNA/RNA

Note
DDX5/p68 RNA helicase is expressed in dividing cells of different vertebrates. Transcription of p68 RNA helicase gene generates a single mRNA precursor with 13 exons and 12 introns. Alternative splicing produces two mRNA transcripts, 2.3 kb and 4.4 kb (Rössler et al., 2000). The 2.3 kb mRNA transcript codes full length p68, while no translational product from the 4.4 kb mRNA transcript is detected in cellular and tissue extracts (Rössler et al., 2000).

Diagram of pre-mRNA of p68 RNA helicase. The red bars are exons and the blue thin lines are introns.
Domain structure of p68 RNA helicase. Functional sequence motifs are marked.

**Protein**

**Description**
Size of p68: 614 amino acids, 69 kDa.

**Expression**
Expressed in almost all tissue types. Its expression is increased in cancer cells.

**Localisation**
Dominately localized in the cell nucleus. It is also found in the cytoplasm in various physiological conditions. p68 is a nucleocytoplasm shuttling protein (Wang et al., 2009).

**Function**

**Pre-mRNA splicing.** The protein was demonstrated to associate with spliceosome by mass-spectroscopy and an RNA-protein crosslinking analyses (Hartmuth et al., 2002; Liu et al., 1997; Neubauer et al., 1998). p68 is functionally involved in assembly of the spliceosome by mediating the U1 snRNP and the 5'ss interaction (Liu, 2002). p68 RNA helicase is also shown to regulate the splice site selection in the alternative splicing of several growth related genes, such as c-H-ras and tau (Kar et al., 2011; Guil et al., 2003).

**Transcriptional regulation.** The protein is shown to involve in transcriptional regulation by different mechanism of actions dependent on each individual regulated gene and biological processes (Stevenson et al., 1998; Endoh et al., 1999; Yang et al., 2005; Kahlina et al., 2004; Wei and Hu, 2001; Warner et al., 2004). p68 may regulate gene transcription by direct interaction with transcription factors or activators, such as p53, ERAlpha (Endoh et al., 1999; Bates et al., 2005), or by mediating chromatin remodeling, such as modulating chromatin remodeling complex (Carter et al., 2010).

**Epithelial-Mesenchymal-Transition** (EMT), p68 becomes phosphorylated at Y593 upon growth factor stimulation by c-Abl. The tyrosine phosphorylation of p68 mediates growth factor stimulated Epithelial-Mesenchymal-Transition (EMT) (Yang et al., 2006).

**Other functions.** (1) p68 RNA helicase is shown to unwind the human let-7 microRNA precursor duplex. The protein is required for let-7-directed silencing of gene expression (Salzman et al., 2007). p68 is an indispensible part of Drosha complex. Its activity is required for primary miRNA and rRNA processing (Fukuda et al., 2007). (2) It is also demonstrated that the RNA helicases p68/p72 and the noncoding RNA SRA are coregulators of MyoD and skeletal muscle differentiation (Caretti et al., 2006). (3) Phosphorylation of p68 at Thr residues mediates cell apoptosis (Yang et al., 2007).

**Homology**
Yeast DBP2.

**Mutations**

**Note**
Very few mutations of p68 gene were reported. A recent study shows that a S480A mutation in hepatic stellate cells is associated with hepatic fibrosis (Guo et al., 2010).

**Implicated in**

**Colon cancer**

**Note**
p68 expression is significantly increased in colon cancer (Shin et al., 2007). Phosphorylation of p68 at Tyr correlation with colon cancer metastasis (Yang et al., 2006; Yang et al., 2005).
Prognosis
Phosphorylation of p68 at tyrosine can be used as a diagnosis/prognosis marker for cancer.

References
Ford MJ, Anton IA, Lane DP. Nuclear protein with sequence homology to translation initiation factor eIF-4A. Nature. 1988 Apr 21;332(6166):736-8
Igo RD, Lane DP. Nuclear protein p68 is an RNA-dependent ATPase. EMBO J. 1989 Jun 8;14:1827-31


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