

Gene Section

Mini Review

WRAP53 (WD repeat containing, antisense to TP53)

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Identity

Other names: FLJ10385; TCAB1; WDR79

HGNC (Hugo): WRAP53

Location: 17p13.1

DNA/RNA

Description

The WRAP53 gene encompasses 16 kb of DNA; 13 exons (three non-coding alternative start exons: exon 1alpha, 1beta and 1gamma. Exon 1alpha directly overlaps the first exon of TP53 in an antisense fashion by up to 227 base pairs (bp), depending on transcription start site (TSS) usage. Exon 1gamma of WRAP53 is located in the first intron of TP53 overlapping the previously identified transcript Hp53int1 in an antisense fashion.

Transcription

At least 17 splice variants. 1.9 kb mRNA; 1647 bp open reading frame.

Regulatory antisense RNA

Expression: widely expressed at low levels.

Localisation: cytoplasm and nucleus.

Function: regulates p53 mRNA levels by interacting with the 5'UTR of p53 mRNA.

Homology: conserved in mouse.

Diseases implication currently not analysed.

Pseudogene

Not known.

Protein

Description

548 amino acids; 75 kDa protein; contains from N-term to C-term, a proline-rich region (aa 8-57), a WD40 domain, 5 repeats (160-441), and a glycine-rich region (533-545).

Expression

Widely expressed, overexpressed in cancer.

Localisation

Cytoplasm and nucleus (enriched in Cajal bodies).

Function

Essential for Cajal body formation and maintenance. Targets the SMN complex, scaRNAs and telomerase enzyme (via TERC) to Cajal bodies. Inhibition of WRAP53 triggers mitochondrial-dependent apoptosis specifically in cancer cells.

Homology

Highly-conserved in mammals, the WD40 domain is conserved from human to fly.

Mutations

Note

Single nucleotide polymorphisms (SNPs) in women with breast cancer (see below).

Germinal

Not reported.

Somatic

Not reported.

Implicated in**Breast and ovarian cancer****Note**

Single nucleotide polymorphisms (SNPs) in WRAP53 were found to be overrepresented in women with breast cancer, in particular estrogen receptor negative breast cancer. The same SNPs were also associated with aggressive ovarian cancer. The SNPs are located in the coding region of WRAP53 and results in the amino acid change R68G.

Spinal muscular atrophy (SMA)**Note**

WRAP53 targets the SMN complex to Cajal Bodies. WRAP53 and SMN association is disrupted in SMA patients suggesting a role of WRAP53 in SMA pathogenesis.

Disease

Spinal muscular atrophy (SMA) is a common neurodegenerative disorder caused by reduced levels of SMN due to mutations or deletions of the SMN1 gene. SMA is the leading genetic cause of infant mortality worldwide, affecting approximately 1 in 6000 infants.

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