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# Gene Section

## Short Communication

# THRAP3 (thyroid hormone receptor associated protein 3)

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## Identity

**Other names:** TRAP150

**HGNC (Hugo):** THRAP3

**Location:** 1p34.3

**Local order:** See NCBI and Ensembl.

## DNA/RNA

### Description

The THRAP3 gene contains 12 exons with the size of 80942 bases.

### Transcription

This gene has 4 transcripts (according to Ensembl).

### Pseudogene

3 pseudogene are found (Review record(s) in Gene).

## Protein

### Description

TRAP150 contains an arginine/serine (RS)-rich sequence in the N-terminal region, while its C-terminal region has 48% overall identity with BCLAF1, a cell death-promoting transcriptional repressor bcl2-associated factor (Ito et al., 1999; Kasof et al., 1999). Notably, BCLAF1 also contains an RS domain in the N-terminus.

Based on the high similarity between TRAP150 and BCLAF1, these two proteins constitute a gene family. Within the BCLAF1 homologous domain of TRAP150, a segment of ~90 amino acids shares 30% similarity with MLN51, which is a core component of the exon junction complex (Macchi et al., 2003).

Biochemical identification of proteins with phosphorylated residues has revealed that TRAP150 is likely phosphorylated protein (Beausoleil et al., 2004; Beausoleil et al., 2006; Olsen et al., 2006; Matsuoka et al.,2007; Molina et al., 2007).

### Expression

Ubiquitous.

### Localisation

TRAP150 is primarily localized in the nucleoplasm and accumulated in some punctuate foci, albeit excluded from the nucleoli.

The speckled structures of TRAP150 are colocalized with the splicing factor SC35. Using the heterokaryon assay, TRAP150 was demonstrated to be a nuclear-restricted protein, while it is associated with the mRNA export receptor TAP (Lee et al., 2010).

The mouse TRAP150, like its human homolog, was also detected in nuclear speckles, especially, under transcription-inhibition conditions (Sutherland et al., 2001).

### Function

**Transcription**

TRAP150 was initially identified as a subunit of the TRAP (thyroid hormone receptor associated protein)/Mediator complex (Ito et al., 1999). Moreover, it was also detected in a group of proteins that were associated with the tail of histone H3 and H4 (Choi et al., 2007; Heo et al., 2007). However, whether TRAP150 participates in the transcription regulation is poorly documented.

**Splicing**

TRAP150 contains an RS domain and is associated with several precursor mRNA (pre-mRNA) splicing factors (Li et al., 2003; Lee et al., 2010).

Moreover, TRAP150 was also reported to interact with the domains that provide links between transcription and splicing, such as the WW domains of pinin and the

FF domains of CA150 (Smith et al., 2004; Ingham et al., 2005).
Therefore TRAP150 has been proposed to function in coupling of transcription and pre-mRNA processing (Auboeuf et al., 2005).
This possibility was supported by independent biochemical analyses of mRNA ribonucleoprotein (mRNP) complexes. Firstly, TRAP150 was identified as a component of mRNPs; its association with mRNAs was splicing- and cap-binding complex (CBC)-independent (Merz et al., 2007).
Moreover, TRAP150 was detected in the spliceosomal complex B, which is a fully assembled splicing complex prior to the catalytic step of splicing (Bessonov et al., 2008; Wahl et al., 2009). Finally, experimental evidence showed that overexpression of TRAP150 activated the splicing of a reporter pre-mRNA, while knockdown of TRAP150 impaired the splicing (Lee et al., 2010), indicating the role of TRAP150 in facilitating pre-mRNA splicing.

**Other pre-mRNA processing events**

TRAP150 and its analog BCLAF1 are associated with SNIP1 (Smad nuclear interacting protein 1), pinin and SkIP (Ski-interacting protein) to form the SNIP1/SkIP-associated RNA processing (SNARP) complex. The SNARP regulates the expression level of cyclin D1 probably by recruiting U2AF65 to its pre-mRNA (Bracken et al., 2008; Witzel et al., 2010).
To date, whether TRAP150 is directly involved in alternative pre-mRNA splicing still remains to be investigated. However, TRAP150 may modulate splicing through protein-protein interactions. In resting T cells, TRAP150 binds to phosphorylated PTB-associated splicing factor (PSF), which results in steric hindrance of the RNA recognition motifs of PSF. Upon T cell activation, de-phosphorylated PSF is dissociated from TRAP150 and therfore could regulate the alternative splicing of CD45 transcripts (Heyd et al., 2010).
In addition to splicing, TRAP150 may participate in mRNA degradation. When tethered to a reporter precursor mRNA, TRAP150 could promote the degradation of the spliced mRNA, which occurs in a translation-independent manner and in the nucleus (Lee et al., 2010).

### *Homology*

Homologous genes of TRAP150 are found in chimpanzee, dog, cow, mouse, rat, chicken and zebrafish (homologs of the THRAP3 gene).

## Implicated in

**Note**

See t(1;17)(p34;p13) in aneurysmal bone cyst.

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