

# TIA1 Rabbit mAb

Catalog # AP77662

### Specification

# TIA1 Rabbit mAb - Product Information

Application Primary Accession Reactivity Host Clonality Calculated MW WB, IHC-P, IP, ICC <u>P31483</u> Human, Mouse Rabbit Monoclonal Antibody 42963

### TIA1 Rabbit mAb - Additional Information

Gene ID 7072

Other Names TIA1

**Dilution** WB~~1/500-1/1000 IHC-P~~N/A IP~~N/A ICC~~N/A

Format Liquid

### **TIA1** Rabbit mAb - Protein Information

Name TIA1

Function

RNA-binding protein involved in the regulation of alternative pre-RNA splicing and mRNA translation by binding to uridine-rich (U- rich) RNA sequences (PubMed:<a href="http://www.uniprot.org/citations/11106748" target="\_blank">11106748</a>, PubMed:<a href="http://www.uniprot.org/citations/12486009" target="\_blank">12486009</a>, PubMed:<a href="http://www.uniprot.org/citations/17488725" target="\_blank">17488725</a>, PubMed:<a href="http://www.uniprot.org/citations/17488725" target="\_blank">8576255</a>). Binds to U-rich sequences immediately downstream from a 5' splice sites in a uridine-rich small nuclear ribonucleoprotein (U snRNP)-dependent fashion, thereby modulating alternative pre-RNA splicing (PubMed:<a href="http://www.uniprot.org/citations/8576255" target="\_blank">8576255</a>). Preferably binds to the U- rich IAS1 sequence in a U1 snRNP-dependent manner; this binding is optimal if a 5' splice site is adjacent to IAS1 (By similarity). Activates the use of heterologous 5' splice sites; the activation depends on the intron sequence downstream from the 5' splice site, with a preference for a downstream U-rich sequence (PubMed:<a href="http://www.uniprot.org/citations/11106748" target="\_blank">11106748</a>). By



interacting with SNRPC/U1-C, promotes recruitment and binding of spliceosomal U1 snRNP to 5' splice sites followed by U-rich sequences, thereby facilitating atypical 5' splice site recognition by U1 snRNP (PubMed:<a href="http://www.uniprot.org/citations/11106748"">http://www.uniprot.org/citations/11106748</a>

target=" blank">11106748</a>, PubMed:<a href="http://www.uniprot.org/citations/12486009" target=" blank">12486009</a>, PubMed:<a href="http://www.uniprot.org/citations/17488725" target=" blank">17488725</a>). Activates splicing of alternative exons with weak 5' splice sites followed by a U-rich stretch on its own pre-mRNA and on TIAR mRNA (By similarity). Acts as a modulator of alternative splicing for the apoptotic FAS receptor, thereby promoting apoptosis (PubMed:<a href="http://www.uniprot.org/citations/11106748" target=" blank">11106748</a>, PubMed:<a href="http://www.uniprot.org/citations/17488725" target="\_blank">17488725</a>, PubMed:<a href="http://www.uniprot.org/citations/1934064" target=" blank">1934064</a>). Binds to the 5' splice site region of FAS intron 5 to promote accumulation of transcripts that include exon 6 at the expense of transcripts in which exon 6 is skipped, thereby leading to the transcription of a membrane-bound apoptotic FAS receptor, which promotes apoptosis (PubMed:<a href="http://www.uniprot.org/citations/11106748" target=" blank">11106748</a>, PubMed:<a href="http://www.uniprot.org/citations/17488725" target=" blank">17488725</a>, PubMed:<a href="http://www.uniprot.org/citations/1934064" target=" blank">1934064</a>). Binds to a conserved AU-rich cis element in COL2A1 intron 2 and modulates alternative splicing of COL2A1 exon 2 (PubMed:<a href="http://www.uniprot.org/citations/17580305" target=" blank">17580305</a>). Also binds to the equivalent AT-rich element in COL2A1 genomic DNA, and may thereby be involved in the regulation of transcription (PubMed:<a href="http://www.uniprot.org/citations/17580305" target=" blank">17580305</a>). Binds specifically to a polypyrimidine-rich controlling element (PCE) located between the weak 5' splice site and the intronic splicing silencer of CFTR mRNA to promote exon 9 inclusion, thereby antagonizing PTB1 and its role in exon skipping of CFTR exon 9 (PubMed:<a href="http://www.uniprot.org/citations/14966131" target=" blank">14966131</a>). Involved in the repression of mRNA translation by binding to AU-rich elements (AREs) located in mRNA 3' untranslated regions (3' UTRs), including target ARE-bearing mRNAs encoding TNF and PTGS2 (By similarity). Also participates in the cellular response to environmental stress, by acting downstream of the stress-induced phosphorylation of EIF2S1/EIF2A to promote the recruitment of untranslated mRNAs to cytoplasmic stress granules (SGs), leading to stress-induced translational arrest (PubMed:<a href="http://www.uniprot.org/citations/10613902" target=" blank">10613902</a>). Formation and recruitment to SGs is regulated by Zn(2+) (By similarity). Possesses nucleolytic activity against cytotoxic lymphocyte target cells (PubMed: <a href="http://www.uniprot.org/citations/1934064" target=" blank">1934064</a>).

#### **Cellular Location**

Nucleus. Cytoplasm Cytoplasm, Stress granule Note=Accumulates in cytoplasmic stress granules (SG) following cellular damage (PubMed:10613902, PubMed:15371533). Recruitment to SG is induced by Zn(2+) (By similarity). {ECO:0000250|UniProtKB:P52912, ECO:0000269|PubMed:10613902, ECO:0000269|PubMed:15371533}

#### **Tissue Location**

Expressed in heart, small intestine, kidney, liver, lung, skeletal muscle, testes, pancreas, and ovary (at protein level)

#### TIA1 Rabbit mAb - Protocols

Provided below are standard protocols that you may find useful for product applications.

- <u>Western Blot</u>
- <u>Blocking Peptides</u>
- Dot Blot
- Immunohistochemistry
- Immunofluorescence



# • Immunoprecipitation

- Flow Cytomety
- <u>Cell Culture</u>
- TIA1 Rabbit mAb Images

