

# Recombinant Rat TTP Protein

**For Research Use Only**

## 1. Basic Product Information

Catalog No.: REP52368

Size: 10ug, 100ug

Protein Name: mRNA decay activator protein ZFP36 (TPA-induced sequence 11) (Tristetraprolin) (Zinc finger protein 36) (Zfp-36)

Synonym: Zfp36, Tis11, Ttp

UniProt ID: P47973

UniProt Link: [www.uniprot.org/uniprotkb/P47973/entry](http://www.uniprot.org/uniprotkb/P47973/entry)

Species Source: Rat

Expression System: HEK293T eukaryotic cell expression system Sequence

Length: 320 AA

Molecular Weight: 34 KD

Protein Tag: C-terminal His6

## 2. Amino Acid Sequence

MDLSAIYESLMSMSHDLSPDHGGTESSGGLWNINSSDSIPSGVTSRLTGRSTSLVEGRSCSWVPPP  
PGFAPLAPRPGPELSPSPTATPTTSSRYKTELCRTYSESGRCRYGAKCQFAHGPGELRQANRH  
PKYKTELCCHKFYLLQGRCPYGSRCHFIHNPTEDLALPGQPHVLRQSISFSGLPGRRTSPPPPGFSGP  
SLSSCSFSPSSPPPPGDLPLSPSAFSAAPGTPVSRRDPTACCPSCRRSTTPSTIWGPLGGLARSP  
SAHSLGSDPDDYASSGSSLGGSDSPVFEAGVFGPPQPPAPPRRLPIFNRISE

## 3. Buffer Composition

Liquid format: PBS-based buffer containing 50% glycerol. Glycerol concentration can be customized upon customer request; please state special requirements when placing your order.

Lyophilized format: Buffer before lyophilization is PBS supplemented with 6% trehalose.

## 4. Storage Conditions

Upon receipt, store the product at -20 °C or -80 °C. Aliquot the product for on-demand use to preserve protein activity and prevent denaturation and inactivation caused by repeated freeze-thaw cycles.

## 5. Product Description

This product is recombinant mRNA decay activator protein ZFP36 (TPA-induced sequence 11) (Tristetraprolin) (Zinc finger protein 36) (Zfp-36) produced using the HEK293T eukaryotic cell expression system. It is suitable for in-vitro functional assays, protein-protein interaction studies, antibody preparation and other biomedical research applications.

**Protein Function:** Zinc-finger RNA-binding protein that destabilizes numerous cytoplasmic AU-rich element (ARE)-containing mRNA transcripts by promoting their poly(A) tail removal or deadenylation, and hence provide a mechanism for attenuating protein synthesis (PubMed:27193233). Acts as an 3'-untranslated region (UTR) ARE mRNA-binding adapter protein to communicate signaling events to the mRNA decay machinery. Recruits deadenylase CNOT7 (and probably the CCR4-NOT complex) via association with CNOT1, and hence promotes ARE-mediated mRNA deadenylation. Also functions by recruiting components of the cytoplasmic RNA decay machinery to the bound ARE-containing mRNAs. Self regulates by destabilizing its own mRNA (By similarity). Binds to 3'-UTR ARE of numerous mRNAs (PubMed:27193233). Also binds to ARE of its own mRNA. Plays a role in anti-inflammatory responses; suppresses tumor necrosis factor (TNF) production by stimulating ARE-mediated TNF mRNA decay and several other inflammatory ARE-containing mRNAs in interferon (IFN)- and/or lipopolysaccharide (LPS)-induced macrophages. Also plays a role in the regulation of dendritic cell maturation at the post-transcriptional level, and hence operates as part of a negative feedback loop to limit the inflammatory response. Promotes ARE-mediated mRNA decay of hypoxia-inducible factor HIF1A mRNA during the response of endothelial cells to hypoxia. Positively regulates early adipogenesis of preadipocytes by promoting ARE-mediated mRNA decay of immediate early genes (IEGs). Negatively regulates hematopoietic/erythroid cell differentiation by promoting ARE-mediated mRNA decay of the transcription factor STAT5B mRNA. Plays a role in maintaining skeletal muscle satellite cell quiescence by promoting ARE-mediated mRNA decay of the myogenic determination factor MYOD1 mRNA. Also associates with and regulates the expression of non-ARE-containing target mRNAs at the post-transcriptional level, such as MHC class I mRNAs. Participates in association with argonaute RISC catalytic components in the ARE-mediated mRNA decay mechanism; assists microRNA (miRNA) targeting ARE-containing mRNAs. May also play a role in the regulation of cytoplasmic mRNA decapping; enhances decapping of ARE-containing RNAs, in vitro. Involved in the delivery of target ARE-mRNAs to processing bodies (PBs). In addition to its cytosolic mRNA-decay function, affects nuclear pre-mRNA processing. Negatively regulates nuclear poly(A)-binding protein PABPN1-stimulated polyadenylation activity on ARE-containing pre-mRNA during LPS-stimulated macrophages. Also involved in the regulation of stress granule (SG) and P-body (PB) formation and fusion. Plays a role in the regulation of keratinocyte proliferation, differentiation and apoptosis. Plays a role as a tumor suppressor by inhibiting cell proliferation in breast cancer cells (By similarity).

**Subcellular Localization:** Nucleus . Cytoplasm . Cytoplasmic granule . Cytoplasm, P-body . Note=Shuttles between nucleus and cytoplasm in a CRM1-dependent manner (PubMed:12054509). Localized predominantly in the cytoplasm in a p38 MAPK- and YWHAB-dependent manner. Colocalizes with SH3KBP1 and MAP3K4 in the cytoplasm. Component of cytoplasmic stress granules (SGs). Localizes to cytoplasmic stress granules upon energy starvation. Localizes in processing bodies (PBs). Excluded from stress granules in a phosphorylation MAPKAPK2-dependent manner. Shuttles in and out of both cytoplasmic P-body and SGs (By similarity).

## 6. Notes

- Avoid repeated freeze-thaw cycles to maintain protein stability and biological activity.
- Please specify special buffer-composition requirements at the time of order placement.



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- For research use only. Not intended for clinical diagnosis, therapeutic use or commercial manufacturing.