

# Recombinant Human TTP Protein

**For Research Use Only**

## 1. Basic Product Information

Catalog No.: REP51028

Size: 10ug, 100ug

Protein Name: mRNA decay activator protein ZFP36 (G0/G1 switch regulatory protein 24) (Growth factor-inducible nuclear protein NUP475) (Tristetraprolin) (Zinc finger protein 36) (Zfp-36)

Synonym: ZFP36, G0S24, NUP475, RNF162A, TIS11A, TTP

UniProt ID: P26651

UniProt Link: [www.uniprot.org/uniprotkb/P26651/entry](http://www.uniprot.org/uniprotkb/P26651/entry)

Species Source: Human

Expression System: HEK293T eukaryotic cell expression system Sequence

Length: 326 AA

Molecular Weight: 34 KD

Protein Tag: C-terminal His6

## 2. Amino Acid Sequence

MDLTAIYESLLSLSPDVPVPSDHGGTESSPGWGSSGPWSLSPSDSSPSGVTSRLPGRSTSLVEGRS  
CGWVPPPPGFAPLAPRLGPELSPSPTSPTATSTTPSRYKTELCRTFSESGRCRYGAKCQFAHGLGE  
LRQANRHPKYKTELCHKFYLLQGRCPYGSRCHFIHNPSEDLAAPGHPPVLRQSI SFSGLP SGRRRTSP  
PPPGLAGPSLSSSSSFSPSSSPPPPGDLPLSPSAFSAAPGTPLARRDPTPVCCPSCRRATPISVWGPL  
GGLVRTPSVQSLGSDPDEYASSGSSLGGSDSPVFEAGVFAPPQPVAAPRRLPIFNRI SVSE

## 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 (G0/G1 switch regulatory protein 24) (Growth factor-inducible nuclear protein NUP475) (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 several 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:10330172, PubMed:10751406, PubMed:11279239, PubMed:12115244, PubMed:12748283, PubMed:15187101, PubMed:15634918, PubMed:16702957, PubMed:17030620, PubMed:20221403, PubMed:20702587, PubMed:21775632, PubMed:23644599, PubMed:25815583, PubMed:27193233, PubMed:31439631, PubMed:9703499). Acts as an 3'-untranslated region (UTR) ARE mRNA-binding adapter protein to communicate signaling events to the mRNA decay machinery (PubMed:15687258, PubMed:23644599). Recruits deadenylase CNOT7 (and probably the CCR4-NOT complex) via association with CNOT1, and hence promotes ARE-mediated mRNA deadenylation (PubMed:23644599). Functions also by recruiting components of the cytoplasmic RNA decay machinery to the bound ARE-containing mRNAs (PubMed:11719186, PubMed:12748283, PubMed:15687258, PubMed:16364915). Self regulates by destabilizing its own mRNA (PubMed:15187101). Binds to 3'-UTR ARE of numerous mRNAs and of its own mRNA (PubMed:10330172, PubMed:10751406, PubMed:12115244, PubMed:15187101, PubMed:15634918, PubMed:16702957, PubMed:17030620, PubMed:19188452, PubMed:20221403, PubMed:20702587, PubMed:21775632, PubMed:25815583). Plays a role in anti-inflammatory responses; suppresses tumor necrosis factor (TNF)-alpha production by stimulating ARE-mediated TNF mRNA decay and several other inflammatory ARE-containing mRNAs in interferon (IFN)- and/or lipopolysaccharide (LPS)-induced macrophages (By similarity). 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 (PubMed:18367721). Promotes ARE-mediated mRNA decay of hypoxia-inducible factor HIF1A mRNA during the response of endothelial cells to hypoxia (PubMed:21775632). Positively regulates early adipogenesis of preadipocytes by promoting ARE-mediated mRNA decay of immediate early genes (IEGs) (By similarity). Negatively regulates hematopoietic/erythroid cell differentiation by promoting ARE-mediated mRNA decay of the transcription factor STAT5B mRNA (PubMed:20702587). Plays a role in maintaining skeletal muscle satellite cell quiescence by promoting ARE-mediated mRNA decay of the myogenic determination factor MYOD1 mRNA (By similarity). Associates also with and regulates the expression of non-ARE-containing target mRNAs at the post-transcriptional level, such as MHC class I mRNAs (PubMed:18367721). Participates in association with argonaute RISC catalytic components in the ARE-mediated mRNA decay mechanism; assists microRNA (miRNA) targeting ARE-containing mRNAs (PubMed:15766526). May also play a role in the regulation of cytoplasmic mRNA decapping; enhances decapping of ARE-containing RNAs, in vitro (PubMed:16364915). Involved in the delivery of target ARE-mRNAs to processing bodies (PBs) (PubMed:17369404). In addition to its cytosolic mRNA-decay function, affects nuclear pre-mRNA processing (By similarity). Negatively regulates nuclear poly(A)-binding protein PABPN1-stimulated polyadenylation activity on ARE-containing pre-mRNA during LPS-stimulated macrophages (By similarity). Also involved in the regulation of stress granule (SG) and P-body (PB) formation and fusion (By similarity). Plays a role in the regulation of keratinocyte proliferation, differentiation and apoptosis (PubMed:27182009). Plays a role as a tumor suppressor by inhibiting cell proliferation in breast cancer cells (PubMed:26926077).; (Microbial infection) Negatively regulates HTLV-1 TAX-dependent transactivation of viral long terminal repeat (LTR) promoter.

Subcellular Localization: Nucleus . Cytoplasm . Cytoplasmic granule . Cytoplasm, P-body . Note=Shuttles between nucleus and cytoplasm in a CRM1-dependent manner (By similarity). Localized predominantly in the cytoplasm in a p38 MAPK- and YWHAB-dependent manner (By similarity). Colocalizes with SH3KBP1 and MAP3K4 in the cytoplasm (PubMed:20221403). Component of cytoplasmic stress granules (SGs) (By similarity). Localizes to cytoplasmic stress granules upon energy starvation (PubMed:15014438). Localizes in processing bodies (PBs) (PubMed:17369404). Excluded from stress granules in a phosphorylation MAPKAPK2-dependent manner (By similarity). Shuttles in and out of both cytoplasmic P-body and SGs (By similarity).; Nucleus . Cytoplasm . Note=(Microbial infection) Colocalizes with HTLV-1 TAX in the nucleus and the cytoplasm in a region surrounding the nucleus.

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