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Tristetraprolin/ZFP36 Rabbit pAb

Catalog # AP97827

Product Information

Application	IHC-P, IHC-F, IF, E
Primary Accession	P26651
Other Accession	P26651
Predicted	Rat, Human, Mouse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	34003
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human Tristetraprolin
Epitope Specificity	101-200/319
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Contains 2 C3H1-type zinc fingers.
SUBUNIT	Interacts (via C-terminus) with CNOT1.
Post-translational modifications	Phosphorylation by MAPKAPK2 increases its stability and binding to 14-3-3 proteins, leading to reduce its ARE affinity leading to inhibition of degradation of ARE-containing transcripts. Phosphorylated upon mitogen stimulation.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	ZFP36 (ZFP36 Ring Finger Protein) is a Protein Coding gene. Among its related pathways are Spinal Cord Injury and ErbB1 downstream signaling. GO annotations related to this gene include poly(A) RNA binding and enzyme binding. An important paralog of this gene is ZFP36L2.

Additional Information

Gene ID	7538
Other Names	G0S24; GOS24; NUP475; RNF162A; TIS11; TTP; zfp-36; TTP_HUMAN; ZFP36; G0/G1 switch regulatory protein 24; Growth factor-inducible nuclear protein NUP475; Tristetraprolin; Zinc finger protein 36 (Zfp-36); TIS11A; TTP_RAT; TPA-induced sequence 11; ZFP36 zinc finger CCCH-type; ZFP36 ring finger protein; zinc finger protein 36, C3H type, homolog (mouse)
Dilution	IHC-P=1:100-500,IHC-F=1:100-500,ICC/IF=1:100-500,IF=1:100-500,ELISA=1:5000-10000
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name ZFP36 (HGNC:12862)

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).

Cellular Location	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) {ECO:0000250|UniProtKB:P22893, ECO:0000269|PubMed:15014438, ECO:0000269|PubMed:17369404, ECO:0000269|PubMed:20221403}
Tissue Location	Expressed in both basal and suprabasal epidermal layers (PubMed:27182009). Expressed in epidermal keratinocytes (PubMed:27182009). Expressed strongly in mature dendritic cells (PubMed:18367721). Expressed in immature dendritic cells (at protein level) (PubMed:18367721).

Please note: All products are 'FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES'.