

ZFP36L1 Antibody

Purified Rabbit Polyclonal Antibody (Pab) Catalog # AP51623

Product Information

Application WB, IP, IHC-P **Primary Accession** Q07352

Reactivity Human, Mouse, Rat

HostRabbitClonalityPolyclonalCalculated MW36314

Additional Information

Gene ID 677

Other Names Zinc finger protein 36, C3H1 type-like 1, Butyrate response factor 1,

EGF-response factor 1, ERF-1, Protein TIS11B, ZFP36L1, BERG36, BRF1, ERF1,

RNF162B, TIS11B

Target/Specificity KLH-conjugated synthetic peptide encompassing a sequence within the center

region of human ZFP36L1. The exact sequence is proprietary.

Dilution WB~~1:1000 IP~~N/A IHC-P~~N/A

Format 0.01M PBS, pH 7.2, 0.09% (W/V) Sodium azide, Glycerol 50%

Storage Store at -20 °C.Stable for 12 months from date of receipt

Protein Information

Name ZFP36L1 (HGNC:1107)

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:12198173, PubMed:15538381,

PubMed:<u>17030608</u>, PubMed:<u>19179481</u>, PubMed:<u>20702587</u>, PubMed:<u>24700863</u>, PubMed:<u>25014217</u>, PubMed:<u>25106868</u>,

PubMed:<u>26542173</u>). Acts as a 3'-untranslated region (UTR) ARE mRNA- binding adapter protein to communicate signaling events to the mRNA decay machinery (PubMed:<u>15687258</u>). Functions by recruiting the CCR4-NOT deadenylase complex and components of the cytoplasmic RNA decay machinery to the bound ARE-containing mRNAs, and hence promotes ARE-mediated mRNA deadenylation and decay processes (PubMed:<u>15687258</u>, PubMed:<u>18326031</u>, PubMed:<u>25106868</u>). Also induces the degradation of ARE-containing mRNAs even in absence of poly(A) tail (By similarity). Binds to

3'-UTR ARE of numerous mRNAs (PubMed: 12198173, PubMed: 15467755, PubMed:15538381, PubMed:17030608, PubMed:19179481, PubMed:20702587, PubMed:24700863, PubMed:25014217, PubMed: 25106868, PubMed: 26542173). Positively regulates early adipogenesis by promoting ARE-mediated mRNA decay of immediate early genes (IEGs) (By similarity). Promotes ARE- mediated mRNA decay of mineralocorticoid receptor NR3C2 mRNA in response to hypertonic stress (PubMed:<u>24700863</u>). Negatively regulates hematopoietic/erythroid cell differentiation by promoting ARE-mediated mRNA decay of the transcription factor STAT5B mRNA (PubMed: 20702587). Positively regulates monocyte/macrophage cell differentiation by promoting ARE-mediated mRNA decay of the cyclin-dependent kinase CDK6 mRNA (PubMed: 26542173). Promotes degradation of ARE-containing pluripotency-associated mRNAs in embryonic stem cells (ESCs), such as NANOG, through a fibroblast growth factor (FGF)-induced MAPK-dependent signaling pathway, and hence attenuates ESC self-renewal and positively regulates mesendoderm differentiation (By similarity). May play a role in mediating pro-apoptotic effects in malignant B-cells by promoting ARE-mediated mRNA decay of BCL2 mRNA (PubMed:25014217). In association with ZFP36L2 maintains quiescence on developing B lymphocytes by promoting ARE-mediated decay of several mRNAs encoding cell cycle regulators that help B cells progress through the cell cycle, and hence ensuring accurate variable-diversity-joining (VDI) recombination and functional immune cell formation (By similarity). Together with ZFP36L2 is also necessary for thymocyte development and prevention of T-cell acute lymphoblastic leukemia (T-ALL) transformation by promoting AREmediated mRNA decay of the oncogenic transcription factor NOTCH1 mRNA (By similarity). Participates in the delivery of target ARE-mRNAs to processing bodies (PBs) (PubMed: 17369404). In addition to its cytosolic mRNA-decay function, plays a role in the regulation of nuclear mRNA 3'- end processing; modulates mRNA 3'-end maturation efficiency of the DLL4 mRNA through binding with an ARE embedded in a weak noncanonical polyadenylation (poly(A)) signal in endothelial cells (PubMed:21832157). Also involved in the regulation of stress granule (SG) and P-body (PB) formation and fusion (PubMed: 15967811). Plays a role in vasculogenesis and endocardial development (By similarity). Plays a role in the regulation of keratinocyte proliferation, differentiation and apoptosis (PubMed:27182009). Plays a role in myoblast cell differentiation (By similarity).

Cellular Location

Nucleus. Cytoplasm. Cytoplasmic granule. Cytoplasm, P-body Note=Shuttles between the nucleus and the cytoplasm in a XPO1/CRM1- dependent manner (By similarity). Component of cytoplasmic stress granules (PubMed:15967811). Localizes in processing bodies (PBs) (PubMed:17369404). {ECO:0000250 | UniProtKB:P23950, ECO:0000269 | PubMed:15967811, ECO:0000269 | PubMed:17369404}

Tissue Location

Expressed mainly in the basal epidermal layer, weakly in the suprabasal epidermal layers (PubMed:27182009). Expressed in epidermal keratinocytes (at protein level) (PubMed:27182009) Expressed in osteoblasts (PubMed:15465005)

Background

Probable regulatory protein involved in regulating the response to growth factors.

References

Barnard R.C., et al. Nucleic Acids Res. 21:3580-3580(1993). Bustin S.A., et al. DNA Cell Biol. 13:449-459(1994).

Ning Z.Q.,et al.Eur. J. Immunol. 26:2356-2363(1996). Kalnine N.,et al.Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases. Rigbolt K.T.,et al.Sci. Signal. 4:RS3-RS3(2011).

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