

Anti-ZFP36L1 Antibody

Catalog # AP51623

Product Information

Application	WB, IHC
Primary Accession	Q07352
Reactivity	Human, Mouse, Rat
Host	Rabbit
Clonality	Polyclonal
Calculated MW	36314

Additional Information

Gene ID	677
Other Names	BERG36; BRF1; ERF1; RNF162B; TIS11B; Zinc finger protein 36, C3H1 type-like 1; Butyrate response factor 1; EGF-response factor 1; ERF-1; Protein TIS11B
Target/Specificity	KLH-conjugated synthetic peptide encompassing a sequence within the center region of human ZFP36L1. The exact sequence is proprietary.
Dilution	WB~~WB (1/500 - 1/1000) IHC~~1:100~500
Format	Liquid in 0.42% Potassium phosphate, 0.87% Sodium chloride, pH 7.3, 30% glycerol, and 0.01% sodium azide.
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:15467755, PubMed:15538381, PubMed:17030608, PubMed:19179481, PubMed:20702587, PubMed:24700863, PubMed:25014217, PubMed:25106868, PubMed:26542173). Acts as a 3'-untranslated region (UTR) ARE mRNA- binding adapter protein to communicate signaling events to the mRNA decay machinery (PubMed:15687258). 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:15687258, PubMed:18326031, PubMed:25106868). 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:[24700863](#)). 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 (VDJ) 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 ARE-mediated 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](#)}

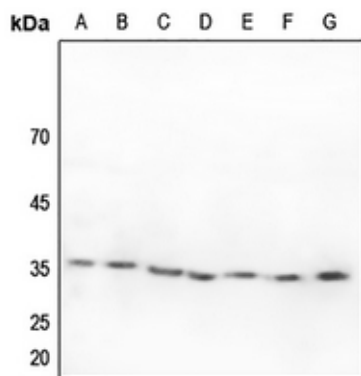
Tissue Location

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](#))

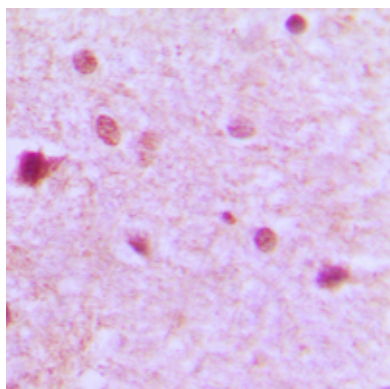
References

- 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).

Images



Western blot analysis of ZFP36L1 expression in HEK293T (A), Hela (B), A549 (C), mouse liver (D), mouse kidney (E), rat liver (F), rat kidney (G) whole cell lysates. (Predicted band size: 36 kD; Observed band size: 36 kD)



Immunohistochemical analysis of ZFP36L1 staining in human brain formalin fixed paraffin embedded tissue section. The section was pre-treated using heat mediated antigen retrieval with sodium citrate buffer (pH 6.0). The section was then incubated with the antibody at room temperature and detected using an HRP conjugated compact polymer system. DAB was used as the chromogen. The section was then counterstained with haematoxylin and mounted with DPX.

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