Datasheet for ABIN2855740

anti-EIF4E2 antibody

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Overview

Quantity:	100 µL
Target:	EIF4E2
Reactivity:	Human
Host:	Rabbit
Clonality:	Polyclonal
Conjugate:	This EIF4E2 antibody is un-conjugated
Application:	Western Blotting (WB), Immunoprecipitation (IP)

Product Details

Immunogen:	Recombinant protein encompassing a sequence within the center region of human EIF4E2. The exact sequence is proprietary.
Isotype:	IgG
Cross-Reactivity:	Human, Mouse
Characteristics:	Rabbit polyclonal antibody to EIF4EL3 (eukaryotic translation initiation factor 4E family member 2) EIF4E2 antibody [N1C3]
Purification:	Purified by antigen-affinity chromatography.
Grade:	KO Validated

Target Details

Target:	EIF4E2

Target Details

Alternative Name:	eukaryotic translation initiation factor 4E family member 2 (EIF4E2 Products)
Background:	Recognizes and binds the 7-methylguanosine-containing mRNA cap during an early step in the initiation of protein synthesis and facilitates ribosome binding by inducing the unwinding of the mRNAs secondary structures.
Molecular Weight:	28 kDa
Gene ID:	9470
UniProt:	O60573
Pathways:	SARS-CoV-2 Protein Interactome

Application Details

Application Notes:	Optimal working dilution should be determined by the investigator.
Comment:	Validation: KO/KD
Restrictions:	For Research Use only

Handling

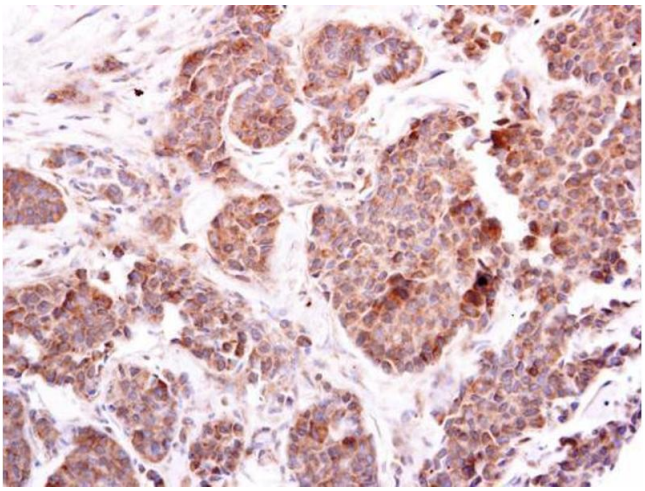
Format:	Liquid
Concentration:	0.27 mg/mL
Buffer:	1XPBS (pH 7), 1 % BSA, 20 % Glycerol, 0.025 % ProClin 300
Preservative:	ProClin
Precaution of Use:	This product contains ProClin: a POISONOUS AND HAZARDOUS SUBSTANCE which should be handled by trained staff only.
Storage:	4 °C,-20 °C
Storage Comment:	Store as concentrated solution. Centrifuge briefly prior to opening vial. For short-term storage (1-2 weeks), store at 4°C. For long-term storage, aliquot and store at -20°C or below. Avoid multiple freeze-thaw cycles.

Publications

Product cited in:	Kitano, Kino, Yamamoto, Takitani, Miyoshi, Ishida, Saito, Arima, Satoh: "Bioinformatics Data Mining Approach Suggests Coexpression of AGTPBP1 with an ALS-linked Gene C9orf72." in:

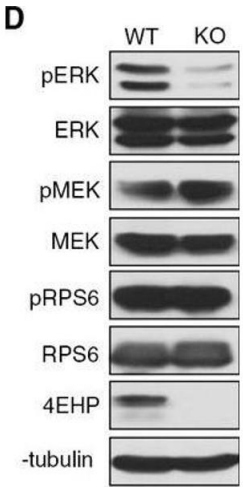
Journal of central nervous system disease, Vol. 7, pp. 15-26, (2015) (PubMed).

Images



Immunohistochemistry

Image 1. IHC-P Image EIF4E2 antibody [N1C3] detects EIF4E2 protein at cytoplasm on human breast carcinoma by immunohistochemical analysis. Sample: Paraffin-embedded human breast carcinoma. EIF4E2 antibody [N1C3] , diluted at 1:500.

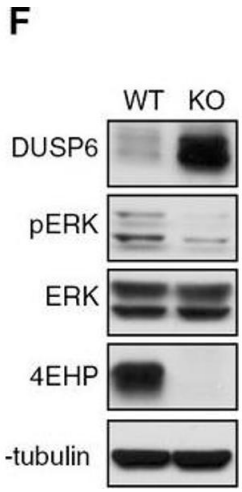


Western Blotting

Image 2. Depletion of 4EHP expression affects cell proliferation, survival, and ERK1/2 phosphorylation.(A) Cell proliferation assay. WT and 4EHP-KO MEFs were seeded in 6-well plates and trypsinized after the indicated time points and cell numbers determined using a hematocytometer. Data are mean ± SD (n = 3). (B) Cell proliferation assay. U251 cells with stable expression of shCTR (control), sh4EHP#1, and sh4EHP#2 were seeded in 6-well plates. Cells were trypsinized after the indicated time points and cell numbers determined using a hematocytometer. Data are mean ± SD (n = 3). (C) Quantitation of cell death by FACS assay, Sub-G population was considered as 'Dead' and G0/1, S and G2/M population was combined as 'Live'. Data are mean ± SD (n = 3). (D) WB for the indicated proteins in the WT and 4EHP-KO MEFs. (E) Polysome profiling/RT-PCR, RNA was extracted from each fraction (collected as described in Figure 2-figure supplement 1J), subjected to electrophoresis on agarose gel and visualized, using Ethidium Bromide (EtBr) staining. RT-PCR analyses of total RNA in each fraction was carried out with primers

specific for Dusp6 and Gapdh mRNAs. (F) WB on the indicated proteins in WT and 4EHP-KO MEFs. (G) WB for the indicated proteins in the WT and 4EHP-KO MEFs, expressing a v5-tagged GFP (GFP-v5) or v5-tagged 4EHP (4EHP-v5).Cell proliferation and translational regulation of DUSP6 expression is affected by 4EHP depletion.(A) WB for the indicated proteins in the WT and 4EHP-KO MEFs. (B) Cell proliferation was assessed using Sulforhodamine B (SRB) assay . Data are mean ± SD (n = 3). (C) Top, Representative cell cycle profiles of the WT and 4EHP-KO MEFs stained with Propidium Iodide and analyzed by FACS. Bottom, quantitation of cell cycle profiles. Data are mean ± SD (n = 3). (D) WB for the indicated proteins in control and stable 4EHP-knockdown U251 cells. (E) WB for the indicated proteins in the control and stable 4EHP-knockdown U87 cells. (F) Cell proliferation assay, U87 cells with stable expression of shCTR, sh4EHP#1, and sh4EHP#2 were seeded in 6-well plates. Cells were trypsinized after the indicated time points and cell numbers determined using a hematocytometer. Data are mean ± SD (n = 3). (G) FACS assay. Representative cell cycle profiles of shCTR, sh4EHP#1, and sh4EHP#2 U251 cells stained with Propidium Iodide and analyzed by FACS. (H) WB for the indicated proteins in the control and stable 4EHP-knockdown U251 cells. (I) WB for the indicated proteins in the control and stable Dusp6-knockdown U251 cells. (J) Polysome profiling, cytoplasmic extract from WT and 4EHP-KO MEFs was fractioned by centrifugation on a 10-50 % sucrose gradient. Fourteen fractions were collected while 254 nm absorbance was recorded. (K) WB for the indicated proteins in control (shCTR) and 4EHP-knockdown (sh4EHP) U251 cells. (L) WB for the indicated proteins in the control and stable 4EHP-knockdown U251 cells. (M) RT-qPCR analysis of Dusp6 mRNA in shCTR and sh4EHP U251 cells. Values are normalized to β-actin. Data are mean ± SD

(n = 3). (N) RNA stability assay of Dusp6 mRNA in shCTR and sh4EHP U251 cells. The amount of RNA at different time points was determined by RT-qPCR. Values are normalized to 28S rRNA. Data are mean ± SD (n = 3). - figure provided by CiteAb. Source: PMID30902983



Western Blotting

Image 3. Depletion of 4EHP expression affects cell proliferation, survival, and ERK1/2 phosphorylation.(A) Cell proliferation assay. WT and 4EHP-KO MEFs were seeded in 6-well plates and trypsinized after the indicated time points and cell numbers determined using a hematocytometer. Data are mean ± SD (n = 3). (B) Cell proliferation assay. U251 cells with stable expression of shCTR (control), sh4EHP#1, and sh4EHP#2 were seeded in 6-well plates. Cells were trypsinized after the indicated time points and cell numbers determined using a hematocytometer. Data are mean ± SD (n = 3). (C) Quantitation of cell death by FACS assay, Sub-G population was considered as 'Dead' and G0/1, S and G2/M population was combined as 'Live'. Data are mean ± SD (n = 3). (D) WB for the indicated proteins in the WT and 4EHP-KO MEFs. (E) Polysome profiling/RT-PCR, RNA was extracted from each fraction (collected as described in Figure 2-figure supplement 1J), subjected to electrophoresis on agarose gel and visualized, using Ethidium Bromide (EtBr) staining. RT-PCR analyses of total RNA in each fraction was carried out with primers specific for Dusp6 and Gapdh mRNAs. (F) WB on the indicated proteins in WT and 4EHP-KO MEFs. (G) WB for the indicated proteins in the WT and 4EHP-KO MEFs, expressing a v5-tagged GFP (GFP-v5) or v5-tagged 4EHP (4EHP-v5).Cell proliferation and translational regulation of DUSP6 expression is affected by 4EHP depletion.(A) WB for the indicated proteins in the WT and 4EHP-KO MEFs. (B) Cell proliferation was assessed using Sulforhodamine B

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