

**EIF4A3 Antibody (C-term)**  
**Affinity Purified Rabbit Polyclonal Antibody (Pab)**  
**Catalog # AP19330B**

**Specification**

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**EIF4A3 Antibody (C-term) - Product Information**

Application	WB,E
Primary Accession	<a href="#">P38919</a>
Other Accession	<a href="#">Q3B8Q2</a> , <a href="#">A6M931</a> , <a href="#">Q91VC3</a> , <a href="#">Q4R3O1</a> , <a href="#">Q7ZVA6</a> , <a href="#">Q5ZM36</a> , <a href="#">Q2NL22</a> , <a href="#">O42226</a> , <a href="#">Q5U526</a> , <a href="#">NP_055555.1</a>
Reactivity	Human
Predicted	Xenopus, Bovine, Chicken, Zebrafish, Monkey, Mouse, Pig, Rat
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit IgG
Calculated MW	46871
Antigen Region	297-325

**EIF4A3 Antibody (C-term) - Additional Information**

**Gene ID** 9775

**Other Names**

Eukaryotic initiation factor 4A-III, eIF-4A-III, eIF4A-III, ATP-dependent RNA helicase DDX48, ATP-dependent RNA helicase eIF4A-3, DEAD box protein 48, Eukaryotic initiation factor 4A-like NUK-34, Eukaryotic translation initiation factor 4A isoform 3, Nuclear matrix protein 265, NMP 265, hNMP 265, Eukaryotic initiation factor 4A-III, N-terminally processed, EIF4A3, DDX48, KIAA0111

**Target/Specificity**

This EIF4A3 antibody is generated from rabbits immunized with a KLH conjugated synthetic peptide between 297-325 amino acids from the C-terminal region of human EIF4A3.

**Dilution**

WB~~1:1000

**Format**

Purified polyclonal antibody supplied in PBS with 0.09% (W/V) sodium azide. This antibody is purified through a protein A column, followed by peptide affinity purification.

**Storage**

Maintain refrigerated at 2-8°C for up to 2 weeks. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.

**Precautions**

EIF4A3 Antibody (C-term) is for research use only and not for use in diagnostic or therapeutic procedures.

## EIF4A3 Antibody (C-term) - Protein Information

**Name** EIF4A3

**Synonyms** DDX48, KIAA0111

**Function** ATP-dependent RNA helicase (PubMed:[16170325](#)). Involved in pre-mRNA splicing as component of the spliceosome (PubMed:[11991638](#), PubMed:[22961380](#), PubMed:[28076346](#), PubMed:[28502770](#), PubMed:[29301961](#)). Core component of the splicing-dependent multiprotein exon junction complex (EJC) deposited at splice junctions on mRNAs (PubMed:[16170325](#), PubMed:[16209946](#), PubMed:[16314458](#), PubMed:[16923391](#), PubMed:[16931718](#), PubMed:[19033377](#), PubMed:[20479275](#)). The EJC is a dynamic structure consisting of core proteins and several peripheral nuclear and cytoplasmic associated factors that join the complex only transiently either during EJC assembly or during subsequent mRNA metabolism. The EJC marks the position of the exon-exon junction in the mature mRNA for the gene expression machinery and the core components remain bound to spliced mRNAs throughout all stages of mRNA metabolism thereby influencing downstream processes including nuclear mRNA export, subcellular mRNA localization, translation efficiency and nonsense-mediated mRNA decay (NMD). Its RNA-dependent ATPase and RNA-helicase activities are induced by CASC3, but abolished in presence of the MAGOH-RBM8A heterodimer, thereby trapping the ATP-bound EJC core onto spliced mRNA in a stable conformation. The inhibition of ATPase activity by the MAGOH-RBM8A heterodimer increases the RNA-binding affinity of the EJC. Involved in translational enhancement of spliced mRNAs after formation of the 80S ribosome complex. Binds spliced mRNA in sequence-independent manner, 20-24 nucleotides upstream of mRNA exon-exon junctions. Shows higher affinity for single-stranded RNA in an ATP-bound core EJC complex than after the ATP is hydrolyzed. Involved in the splicing modulation of BCL2L1/Bcl-X (and probably other apoptotic genes); specifically inhibits formation of proapoptotic isoforms such as Bcl-X(S); the function is different from the established EJC assembly (PubMed:[22203037](#)). Involved in craniofacial development (PubMed:[24360810](#)).

### Cellular Location

Nucleus. Nucleus speckle. Cytoplasm {ECO:0000250|UniProtKB:Q3B8Q2}.

Note=Nucleocytoplasmic shuttling protein. Travels to the cytoplasm as part of the exon junction complex (EJC) bound to mRNA. Detected in dendritic layer as well as the nuclear and cytoplasmic (somatic) compartments of neurons. Colocalizes with STAU1 and FMR1 in dendrites (By similarity) {ECO:0000250|UniProtKB:Q3B8Q2}

### Tissue Location

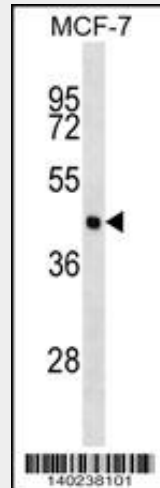
Ubiquitously expressed.

## EIF4A3 Antibody (C-term) - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

## EIF4A3 Antibody (C-term) - Images



EIF4A3 Antibody (C-term)(Cat. #AP19330b) western blot analysis in MCF-7 cell line lysates (35ug/lane). This demonstrates the EIF4A3 antibody detected the EIF4A3 protein (arrow).

#### **EIF4A3 Antibody (C-term) - Background**

This gene encodes a member of the DEAD box protein family. DEAD box proteins, characterized by the conserved motif Asp-Glu-Ala-Asp (DEAD), are putative RNA helicases. They are implicated in a number of cellular processes involving alteration of RNA secondary structure, such as translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly. Based on their distribution patterns, some members of this family are believed to be involved in embryogenesis, spermatogenesis, and cellular growth and division. The protein encoded by this gene is a nuclear matrix protein. Its amino acid sequence is highly similar to the amino acid sequences of the translation initiation factors eIF4A1 and eIF4A2, two other members of the DEAD box protein family.

#### **EIF4A3 Antibody (C-term) - References**

- Koroleva, O.A., et al. *Plant Cell* 21(5):1592-1606(2009)
- Karam, R., et al. *Oncogene* 27(30):4255-4260(2008)
- Ma, X.M., et al. *Cell* 133(2):303-313(2008)
- Giorgi, C., et al. *Cell* 130(1):179-191(2007)
- Zhang, Z., et al. *Proc. Natl. Acad. Sci. U.S.A.* 104(28):11574-11579(2007)