

RPA194 (C-1): sc-48385



The Power to Question

BACKGROUND

RNA polymerases transcribe nuclear genes for ribosomal RNA, thus representing ribosomal biogenesis. RNA polymerase I (Pol I) is located in the nucleolus and transcribes class I genes, which code for large ribosomal RNA. Different subunits of the Pol I transcription machinery are targets of various physiological stimuli, which suggests that multiple signaling pathways are involved in carrying out Pol I transcription. RPA40 and RPA16 are subunits of Pol I that associate with each other at an early stage of RNA polymerase I assembly. RPA40 is essential for the function and integrity of the complex and is also an essential subunit of RNA polymerase III (Pol III). RPA40, RPA16 and RPA135 encode the three subunits of RNA polymerase I, respectively. RPA194 is the largest subunit of RNA Pol I and is not a component of Pol II and Pol III.

CHROMOSOMAL LOCATION

Genetic locus: POLR1A (human) mapping to 2p11.2; Polr1a (mouse) mapping to 6 C1.

SOURCE

RPA194 (C-1) is a mouse monoclonal antibody raised against amino acids 1-300 of RPA194 of human origin.

PRODUCT

Each vial contains 200 µg IgG_{2a} kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

RPA194 (C-1) is available conjugated to agarose (sc-48385 AC), 500 µg/0.25 ml agarose in 1 ml, for IP; to HRP (sc-48385 HRP), 200 µg/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-48385 PE), fluorescein (sc-48385 FITC), Alexa Fluor® 488 (sc-48385 AF488), Alexa Fluor® 546 (sc-48385 AF546), Alexa Fluor® 594 (sc-48385 AF594) or Alexa Fluor® 647 (sc-48385 AF647), 200 µg/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor® 680 (sc-48385 AF680) or Alexa Fluor® 790 (sc-48385 AF790), 200 µg/ml, for Near-Infrared (NIR) WB, IF and FCM.

Alexa Fluor® is a trademark of Molecular Probes, Inc., Oregon, USA

APPLICATIONS

RPA194 (C-1) is recommended for detection of RPA194 of mouse, rat and human origin by Western Blotting (starting dilution 1:100, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500), immunohistochemistry (including paraffin-embedded sections) (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Suitable for use as control antibody for RPA194 siRNA (h): sc-38244, RPA194 siRNA (m): sc-38245, RPA194 shRNA Plasmid (h): sc-38244-SH, RPA194 shRNA Plasmid (m): sc-38245-SH, RPA194 shRNA (h) Lentiviral Particles: sc-38244-V and RPA194 shRNA (m) Lentiviral Particles: sc-38245-V.

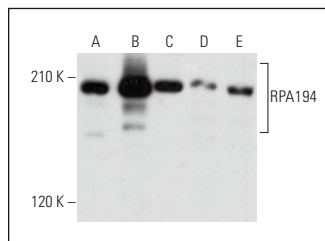
Molecular Weight of RPA194: 194 kDa.

Positive Controls: L8 cell lysate: sc-3807, NIH/3T3 whole cell lysate: sc-2210 or ES-2 cell lysate: sc-24674.

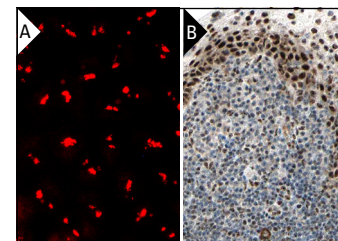
STORAGE

Store at 4° C, ****DO NOT FREEZE****. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

DATA



RPA194 (C-1): sc-48385. Western blot analysis of RPA194 expression in WI-38 (A), ES-2 (B), NIH/3T3 (C), L8 (D) and A-10 (E) whole cell lysates.



RPA194 (C-1): sc-48385. Immunofluorescence staining of methanol-fixed HeLa cells showing nucleolar localization (A). Immunoperoxidase staining of formalin fixed, paraffin-embedded human tonsil tissue showing nuclear staining of surface epithelial and non-follicle cells. Kindly provided by The Swedish Human Protein Atlas (HPA) program (B).

SELECT PRODUCT CITATIONS

- Huang, W.H., et al. 2008. Nucleolar targeting of hepatitis δ antigen abolishes its ability to initiate viral antigenomic RNA replication. *J. Virol.* 82: 692-699.
- Wang, W., et al. 2011. Nucleolar protein Spindlin1 recognizes H3K4 methylation and stimulates the expression of rRNA genes. *EMBO Rep.* 12: 1160-1166.
- Tsai, Y.C., et al. 2012. Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. *Mol. Cell. Proteomics* 11: 60-76.
- Ono, M., et al. 2013. Analysis of human protein replacement cell lines established using snoMEN-PR vector. *PLoS ONE* 8: e62305.
- Ueshima, S., et al. 2014. Upstream binding factor-dependent and pre-rRNA transcription-independent association of pre-rRNA processing factors with rRNA gene. *Biochem. Biophys. Res. Commun.* 443: 22-27.
- Sokka, M., et al. 2015. High levels of TopBP1 induce ATR-dependent shut-down of rRNA transcription and nucleolar segregation. *Nucleic Acids Res.* 43: 4975-4989.
- Huang, S., et al. 2016. DNA replication initiator Cdc6 also regulates ribosomal DNA transcription initiation. *J. Cell Sci.* 129: 1429-1440.
- Xing, Y.H., et al. 2017. SLERT Regulates DDX21 rings associated with Pol I transcription. *Cell* 169: 664-678.e16.
- Daniel, L., et al. 2018. Mechanistic insights in transcription-coupled nucleotide excision repair of ribosomal DNA. *Proc. Natl. Acad. Sci. USA* 115: E6770-E6779.

RESEARCH USE

For research use only, not for use in diagnostic procedures.