SANTA CRUZ BIOTECHNOLOGY, INC.

Pol II (A-10): sc-17798

BACKGROUND

RNA polymerase II (Pol II) is an enzyme that is composed of twelve subunits and is responsible for the transcription of protein-coding genes. Transcription initiation requires Pol II-mediated recruitment of transcription machinery to a target promoter, thereby allowing transcription to begin. The largest subunit of Pol II (referred to as RPB1 or RPB205) is a 1,840 amino acid protein that contains one C_2H_2-type zinc finger and a C-terminal domain comprised of several heptapeptide repeats. Although Pol II function requires the cooperation of all twelve subunits, the largest subunit conveys Pol II catalytic activity and, together with the second largest subunit, forms the active center of the Pol II enzyme. Additionally, the large subunit participates in forming the DNA-binding domain of Pol II, a groove that is necessary for transcription of the DNA template. Without proper function of the large subunit, mRNA synthesis and subsequent transcription elongation cannot occur.

CHROMOSOMAL LOCATION

Genetic locus: POLR2A (human) mapping to 17p13.1; Polr2a (mouse) mapping to 11 B3.

SOURCE

Pol II (A-10) is a mouse monoclonal antibody raised against amino acids 1-224 mapping at the N-terminus of RNA Pol II of human origin.

PRODUCT

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

Pol II (A-10) is available conjugated to agarose (sc-17798 AC), 500 µg/0.25 ml agarose in 1 ml, for IP; to HRP (sc-17798 HRP), 200 µg/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-17798 PE), fluorescein (sc-17798 FITC), Alexa Fluor® 488 (sc-17798 AF488), Alexa Fluor® 546 (sc-17798 AF546), Alexa Fluor® 594 (sc-17798 AF594) or Alexa Fluor® 647 (sc-17798 AF647), 200 µg/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor® 680 (sc-17798 AF680) or Alexa Fluor® 790 (sc-17798 AF790), 200 µg/ml, for Near-Infrared (NIR) WB, IF and FCM.

APPLICATIONS

Pol II (A-10) is recommended for detection of Pol II of mouse, rat and human origin by Western Blotting (starting dilution 1:200, dilution range 1:200-1:2,000), 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) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Suitable for use as control antibody for Pol II siRNA (h): sc-36290, Pol II siRNA (m): sc-36291, Pol II shRNA Plasmid (h): sc-36290-SH, Pol II shRNA Plasmid (m): sc-36291-SH, Pol II shRNA (h) Lentiviral Particles: sc-36290-V and Pol II shRNA (m) Lentiviral Particles: sc-36291-V.

Molecular Weight (predicted) of Pol II: 217 kDa.

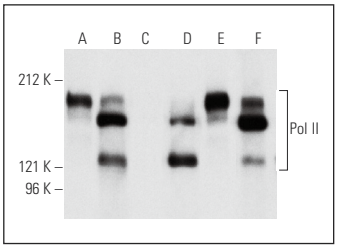
Molecular Weight (observed) of Pol II: 192-253 kDa.

Positive Controls: A-431 nuclear extract: sc-2122, A-673 nuclear extract: sc-2128 or P19 cell lysate: sc-24760.

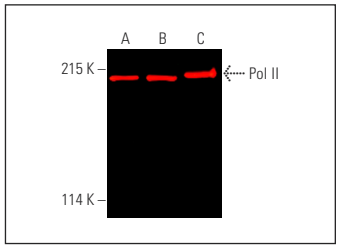
STORAGE

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

DATA



p-Pol II (8A7): sc-13583. Western blot analysis of Pol II phosphorylation in untreated (**A**), heat shocked (**C**) and calyculin-treated (**E**) HeLa cultures. Total Pol II levels were determined in the same respective extracts by using Pol II (A-10): sc-17798 (**B**,**D**,**F**).



Pol II (A-10) Alexa Fluor® 790: sc-17798 AF790. Direct near-infrared western blot analysis of Pol II expression in A-673 (**A**) and A-431 (**B**) nuclear extracts and P19 whole cell lysate (**C**). Blocked with UltraCruz® Blocking Reagent: sc-516214.

SELECT PRODUCT CITATIONS

1. Stolze, I.P., et al. 2004. Genetic analysis of the role of the asparaginyl hydroxylase factor inhibiting hypoxia-inducible hactor (HIF) in regulating HIF transcriptional target genes. J. Biol. Chem. 279: 42719-42725.
2. Li, M., et al. 2011. The SET2-RPB1 interaction domain of human RECQ5 is important for transcription-associated genome stability. Mol. Cell. Biol. 31: 2090-2099.
3. Zhang, X., et al. 2012. Mutations in UVSSA cause UV-sensitive syndrome and destabilize ERCC6 in transcription-coupled DNA repair. Nat. Genet. 44: 593-597.
4. Narita, T., et al. 2015. Regulation of transcription elongation by the XPG-TFIIH complex is implicated in Cockayne syndrome. Mol. Cell. Biol. 35: 3178-3188.
5. Sin, Y., et al. 2016. The C-terminal region and SUMOylation of cockayne syndrome group B protein play critical roles in transcription-coupled nucleotide excision repair. J. Biol. Chem. 291: 1387-1397.
6. Li, B., et al. 2017. Therapeutic rationale to target highly expressed CDK7 conferring poor outcomes in triple-negative breast cancer. Cancer Res. 77: 3834-3845.
7. Li, M., et al. 2018. SUMO2 conjugation of PCNA facilitates chromatin remodeling to resolve transcription-replication conflicts. Nat. Commun. 9: 2706.
8. Kazim, N., et al. 2019. The transcription elongation factor TCEA3 promotes the activity of the myogenic regulatory factors. PLoS ONE 14: e0217680.

RESEARCH USE

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