RNA 聚合酶 II 抗体

产品货号： mlR6972

英文名称： RNA polymerase II

中文名称： RNA 聚合酶 II 抗体

别　　名： POLR2A; POLR2; DNA directed RNA polymerase II A; DNA-directed RNA polymerase II largest subunit; DNA-directed RNA polymerase II subunit A; RPB1_HUMAN.

研究领域： 细胞生物　免疫学　信号转导　转录调节因子　表观遗传学

抗体来源： Rabbit

克隆类型： Polyclonal

交叉反应： Human, Mouse, Rat, Dog, Pig, Cow, Horse,

产品应用： WB=1:500-2000 ELISA=1:500-1000 IHC-P=1:400-800 IHC-F=1:400-800 IF=1:50-200 （石蜡切片需做抗原修复）

not yet tested in other applications.

optimal dilutions/concentrations should be determined by the end user.

分 子 量： 217kDa

细胞定位： 细胞核

性　　状： Lyophilized or Liquid

浓　　度： 1mg/ml

免 疫 原： KLH conjugated synthetic peptide derived from human Pol II/RNA polymerase II:101-200/1970

亚型： IgG

纯化方法： affinity purified by Protein A

储存液： 0.01M TBS(pH7.4) with 1% BSA, 0.03% Proclin300 and 50% Glycerol.

保存条件： Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

PubMed： PubMed

产品介绍： 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 C2H2-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.

Function:

DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. Largest and catalytic component of RNA polymerase II which synthesizes mRNA precursors and many functional non-coding RNAs. Forms the polymerase active center together with the second largest subunit. Pol II is the central component of the basal RNA polymerase II transcription machinery. It is composed of mobile elements that move relative to each other. RPB1 is part of the core element with the central large cleft, the clamp element that moves to open and close the cleft and the jaws that are thought to grab the incoming DNA template. At the start of transcription, a single stranded DNA template strand of the promoter is positioned within the central active site cleft of Pol II. A bridging helix emanates from RPB1 and crosses the cleft near the catalytic site and is thought to promote translocation of Pol II by acting as a ratchet that moves the RNA-DNA hybrid through the active site by switching from straight to bent conformations at each step of nucleotide addition. During transcription elongation, Pol II moves on the template as the transcript elongates. Elongation is influenced by the phosphorylation status of the C-terminal domain (CTD) of Pol II largest subunit (RPB1), which serves as a platform for assembly of factors that regulate transcription initiation, elongation, termination and mRNA processing. Acts as a RNA-dependent RNA polymerase when associated with small delta antigen of Hepatitis delta virus, acting both as a replicate and transcriptase for the viral RNA circular genome.

Subunit:

Component of the RNA polymerase II (Pol II) complex consisting of 12 subunits. The phosphorylated C-terminal domain interacts with FNBP3 and SYNCRIP. Interacts with SAFB/SAFB1. Interacts with CCNL1 and MYO1C (By similarity). Interacts with CCNL2 and SFRS19. Component of a complex which is at least composed of HTATSF1/Tat-SF1, the P-TEFb complex components CDK9 and CCNT1, RNA polymerase II, SUPT5H, and NCL/nucleolin. Interacts with PAF1. Interacts (via C-terminus) with FTSJD2, CTDSP1 and SCAF8. Interacts via the phosphorylated C-terminal domain with WDR82 and with SETD1A and SETD1B only in the presence of WDR82. Interacts with ATF7IP. When phosphorylated at 'Ser-5', interacts with MEN1; the unphosphorylated form, or phosphorylated at 'Ser-2' does not interact. Interacts with DDX5.

Subcellular Location:

Nucleus.

Post-translational modifications:

Dephosphorylated by the protein phosphatase CTDSP1. [PTM] Ubiquitinated by WWP2 leading to proteasomal degradation (By similarity). [PTM] Methylated at Arg-1810 by CARM1. Methylation occurs only when the CTD is hypophosphorylated, and phosphorylation at Ser-1805 and Ser-1808 prevent methylation (in vitro). It is assumed that methylation occurs prior to phosphorylation and transcription initiation. CTD methylation may facilitate the expression of select RNAs.

Similarity:

Belongs to the RNA polymerase beta' chain family.

SWISS:

P24928

Gene ID:

5430

Important Note:

This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.

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