Phospho-Rpb1 CTD (Ser2) (YD11546) Rabbit mAb

货号: AYD14121

产品信息

反应	Human, Mouse, Rat, Saccharomyces cerevisiae
宿主	Rabbit
克隆性	Monoclonal
预测反应	
应用	WB IHC ICC/IF FC IP
推荐浓度	
理论分子量	217kDa/192kDa
实测分子量	
形式	Liquid
保存条件	Store at -20℃. Avoid freeze / thaw cycles. Buffer: PBS with 0.75% BSA,50% glycerol,pH7.3.
偶联物	Unconjugated
阳性对照	
细胞定位	Nucleus, Cytoplasm, Chromosome
纯化	

抗原信息

抗原信息	

靶点信息

研究背景	Catalytic core component of RNA polymerase II (Pol II), a DNA-dependent RNA polymerase which synthesizes mRNA precursors and many functional non-coding RNAs using the four ribonucleoside triphosphates as substrates (By similarity) (PubMed:23748380, PubMed:27193682, PubMed:30190596, PubMed:9852112). Pol II-mediated transcription cycle proceeds through transcription initiation, transcription elongation and transcription termination stages. During transcription initiation, Pol II pre-initiation complex (PIC) is recruited to DNA promoters, with focused-type promoters containing either the initiator (Inr) element, or the TATA-box found in cell-type specific genes and dispersed-type promoters that often contain hypomethylated CpG islands usually found in housekeeping genes. Once the polymerase has escaped from the promoter it enters the elongation phase during which RNA is actively polymerized, based on complementarity with the template DNA strand. Transcription termination involves the release of the RNA transcript and polymerase from the DNA (By similarity) (PubMed:23748380, PubMed:27193682, PubMed:28108474, PubMed:30190596, PubMed:9852112). Forms Pol II active center together with the second largest subunit POLR2B/RPB2. Appends one nucleotide at a time to the 3' end of the nascent RNA, with POLR2A/RPB1 most likely contributing a Mg(2+)-coordinating DxDGD motif, and POLR2B/RPB2 participating in the coordination of a second Mg(2+) ion and providing lysine residues believed to facilitate Watson-Crick base pairing between the incoming nucleotide and template base. Typically, Mg(2+) ions direct a 5' nucleoside triphosphate to form a phosphodiester bond with the 3' hydroxyl of the preceding nucleotide of the nascent RNA, with the elimination of pyrophosphate. The reversible pyrophosphorolysis can occur at high pyrophosphate concentrations (By similarity) (PubMed:30190596, PubMed:8381534, PubMed:9852112). Can proofread the nascent RNA transcript by means of a 3' -> 5' exonuclease activity. If a ribonucleotide is mis-incorporated, backtracks along the template DNA and cleaves the phosphodiester bond releasing the mis-incorporated 5'-ribonucleotide (By similarity) (PubMed:8381534). Through its unique C-terminal domain (CTD, 52 heptapeptide tandem repeats) serves as a platform for assembly of factors that regulate transcription initiation, elongation and termination. CTD phosphorylation on Ser-5 mediates Pol II promoter escape, whereas phosphorylation on Ser-2 is required for Pol II pause release during transcription elongation and further pre-mRNA processing. Additionally, the regulation of gene expression levels depends on the balance between methylation and acetylation levels of the CTD-lysines. Initiation or early elongation steps of transcription of growth-factor-induced immediate early genes are regulated by the acetylation status of the CTD. Methylation and dimethylation have a repressive effect on target genes expression. Cooperates with mRNA splicing machinery in co-transcriptional 5'-end capping and co-transcriptional splicing of pre-mRNA (By similarity) (PubMed:24207025, PubMed:26124092) 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. During a transcription cycle, Pol II, general transcription factors and the Mediator complex assemble as the preinitiation complex (PIC) at the promoter. 11-15 base pairs of DNA surrounding the transcription start site are melted and the single-stranded DNA template strand of the promoter is positioned deeply within the central active site cleft of Pol II to form the open complex. After synthesis of about 30 bases of RNA, Pol II releases its contacts with the core promoter and the rest of the transcription machinery (promoter clearance) and enters the stage of transcription elongation in which it moves on the template as the transcript elongates. Pol II appears to oscillate between inactive and active conformations at each step of nucleotide addition. 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. Pol II is composed of mobile elements that move relative to each other. The core element with the central large cleft comprises RPB3, RBP10, RPB11, RPB12 and regions of RPB1 and RPB2 forming the active center. The clamp element (portions of RPB1, RPB2 and RPB3) is connected to the core through a set of flexible switches and moves to open and close the cleft. 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. In elongating Pol II, the lid loop (RPB1) appears to act as a wedge to drive apart the DNA and RNA strands at the upstream end of the transcription bubble and guide the RNA strand toward the RNA exit groove located near the base of the largely unstructured CTD domain of RPB1. The rudder loop (RPB1) interacts with single-stranded DNA after separation from the RNA strand, likely preventing reassociation with the exiting RNA. The cleft is surrounded by jaws: an upper jaw formed by portions of RBP1, RPB2 and RPB9, and a lower jaw, formed by RPB5 and portions of RBP1. The jaws are thought to grab the incoming DNA template, mainly by RPB5 direct contacts to DNA
基因**ID**	5430
基因名	POLR2A, RPO21
Swiss	P24928, P04050
别名	Phospho-Rpb1 CTD (Ser2) (YD11546)

产品验证

实验步骤

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