abcam

Product datasheet

# Anti-RNA polymerase II CTD repeat YSPTSPS antibody ab52202

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## 概述

| | |
|---|---|
| **产品名称** | Anti-RNA polymerase Ⅱ CTD repeat YSPTSPS抗体 |
| **描述** | 兔多克隆抗体to RNA polymerase Ⅱ CTD repeat YSPTSPS |
| **宿主** | Rabbit |
| **特异性** | ab52202 detects endogenous levels of total RNA polymerase Ⅱ protein. |
| **经测试应用** | **适用于:** WB, IHC-P |
| **种属反应性** | **与反应:** Human, African green monkey |
| **免疫原** | Synthetic peptide corresponding to Human RNA polymerase Ⅱ CTD repeat YSPTSPS aa 1585-1634. Immunogen is in the range of aa 1585 and 1634.<br>Database link: **P24928** |
| **阳性对照** | WB: HepG2, HeLa, Hek293, SW480 cell lysate; COS7 cells treated with EGF (200ng/ml, 30min).<br>IHC-P: Human breast carcinoma tissue. |
| **常规说明** | The Life Science industry has been in the grips of a reproducibility crisis for a number of years. Abcam is leading the way in addressing this with our range of recombinant monoclonal antibodies and knockout edited cell lines for gold-standard validation. Please check that this product meets your needs before purchasing.<br>If you have any questions, special requirements or concerns, please send us an inquiry and/or contact our Support team ahead of purchase. Recommended alternatives for this product can be found below, along with publications, customer reviews and Q&As |

## 性能

| | |
|---|---|
| **形式** | Liquid |
| **存放说明** | Shipped at 4°C. Upon delivery aliquot and store at -20°C. Avoid freeze / thaw cycles. |
| **存储溶液** | pH: 7.40<br>Preservative: 0.02% Sodium azide<br>Constituents: 50% Glycerol (glycerin, glycerine), PBS, 0.87% Sodium chloride |
| **纯度** | Immunogen affinity purified |
| **克隆** | 多克隆 |
| **同种型** | IgG |

## 应用

**The Abpromise guarantee** **Abpromise™承诺保证使用ab52202于以下的经测试应用**

"应用说明"部分 下显示的仅为推荐的起始稀释度;实际最佳的稀释度/浓度应由使用者检定。

| 应用 | Ab评论 | 说明 |
|---|---|---|
| **WB** | (1) | 1/500 - 1/1000. Detects a band of approximately 217 kDa (predicted molecular weight: 217 kDa). |
| **IHC-P** | | Use at an assay dependent concentration. |

## 靶标

**功能** 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 an 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.

**序列相似性** Belongs to the RNA polymerase beta' chain family.

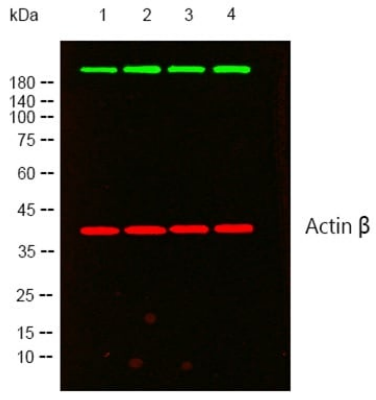
**结构域** The C-terminal domain (CTD) serves as a platform for assembly of factors that regulate transcription initiation, elongation, termination and mRNA processing.

**翻译后修饰** The tandem heptapeptide repeats in the C-terminal domain (CTD) can be highly phosphorylated. The phosphorylation activates Pol II. Phosphorylation occurs mainly at residues 'Ser-2' and 'Ser-5' of the heptapeptide repeat and is mediated, at least, by CDK7 and CDK9. CDK7 phosphorylation of POLR2A associated with DNA promotes transcription initiation by triggering dissociation from DNA. Phosphorylation also takes place at 'Ser-7' of the heptapeptide repeat, which is required for efficient transcription of snRNA genes and processing of the transcripts. The phosphorylation state is believed to result from the balanced action of site-specific CTD kinases and phosphatases, and a 'CTD code' that specifies the position of Pol II within the transcription cycle has been proposed. Dephosphorylated by the protein phosphatase CTDSP1.
Among tandem heptapeptide repeats of the C-terminal domain (CTD) some do not match the Y-S-P-T-S-P-S consensus, the seventh serine residue 'Ser-7' being replaced by a lysine. 'Lys-7' in these non-consensus heptapeptide repeats can be alternatively acetylated, methylated and dimethylated. EP300 is one of the enzyme able to acetylate 'Lys-7'. Acetylation at 'Lys-7' of non-

consensus heptapeptide repeats is associated with 'Ser-2' phosphorylation and active transcription. It may regulate initiation or early elongation steps of transcription specially for inducible genes.
Methylated at Arg-1810 prior to transcription initiation when the CTD is hypophosphorylated, phosphorylation at Ser-1805 and Ser-1808 preventing this methylation. Symmetrically or asymmetrically dimethylated at Arg-1810 by PRMT5 and CARM1 respectively. Symmetric or asymmetric dimethylation modulates interactions with CTD-binding proteins like SMN1/SMN2 and TDRD3. SMN1/SMN2 interacts preferentially with the symmetrically dimethylated form while TDRD3 interacts with the asymmetric form. Through the recruitment of SMN1/SMN2, symmetric dimethylation is required for resolving RNA-DNA hybrids created by RNA polymerase II, that form R-loop in transcription terminal regions, an important step in proper transcription termination. CTD dimethylation may also facilitate the expression of select RNAs. Among tandem heptapeptide repeats of the C-terminal domain (CTD) some do not match the Y-S-P-T-S-P-S consensus, the seventh serine residue 'Ser-7' being replaced by a lysine. 'Lys-7' in these non-consensus heptapeptide repeats can be alternatively acetylated, methylated and dimethylated. Methylation occurs in the earliest transcription stages and precedes or is concomitant to 'Ser-5' and 'Ser-7' phosphorylation.
Ubiquitinated by WWP2 leading to proteasomal degradation (By similarity). Following UV treatment, the elongating form of RNA polymerase II (RNA pol IIo) is ubiquitinated UV damage sites without leading to degradation: ubiquitination is facilitated by KIAA1530/UVSSA and promotes RNA pol IIo backtracking to allow access to the nucleotide excision repair machinery.

**细胞定位** Nucleus.

## 图片




Western blot - Anti-RNA polymerase II CTD repeat YSPTSPS antibody (ab52202)

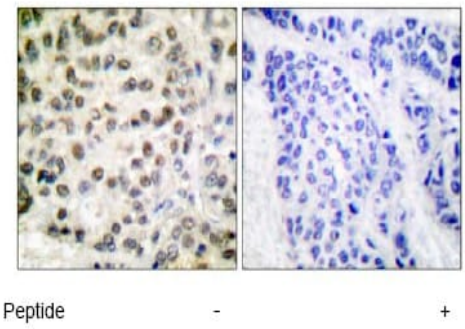
**Lanes 1-3 :** Anti-RNA polymerase II CTD repeat YSPTSPS antibody (ab52202) at 1/1000 dilution
**Lane 4 :** Anti-Swr1 antibody (**ab5202**) at 1/1000 dilution

**Lane 1 :** HepG2 cell lysate
**Lane 2 :** HeLa cell lysate
**Lane 3 :** Hek293 cell lysate
**Lane 4 :** SW480 cell lysate

Lysates/proteins at 20 µg per lane.

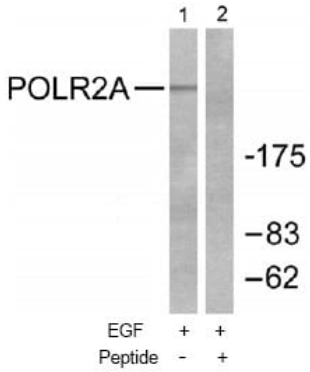
**Secondary**
**All lanes :** Goat Anti-Rabbit IgG (H+L) HRP at 1/10000 dilution

**Predicted band size:** 217 kDa




Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) - Anti-RNA polymerase II CTD repeat YSPTSPS antibody (ab52202)

Immunohistochemical analysis of RNA polymerase II expression in paraffin embedded human breast carcinoma tissue using ab52202 at 1/500.
Left: sample without immunising peptide.
Right: sample with immunising peptide (negative control).




Western blot - Anti-RNA polymerase II CTD repeat YSPTSPS antibody (ab52202)

**All lanes :** Anti-RNA polymerase II CTD repeat YSPTSPS antibody (ab52202) at 1/500 dilution

**Lane 1 :** COS7 cells treated
with EGF (200ng/ml, 30min), without immunising peptide
**Lane 2 :** COS7 cells treated
with EGF (200ng/ml, 30min), with immunising peptide

**Predicted band size:** 217 kDa
**Observed band size:** 217 kDa



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