Rabbit Rpb1 CTD Polyclonal Antibody | anti-Rpb1 antibody

Phospho-Rpb1 CTD (Tyr145) Antibody

CATALOG #	HOST	REACTIVITY	APPLICATIONS
AAA328426	**Rabbit**	**Human, Mouse, RatPredicted: Pig, Bovine, Horse, Sheep, Dog, Xenopus**	**ELISA, Immunohistochemistry, Western Blot**

PRODUCT SYNONYMS

Rpb1 CTD; Polyclonal Antibody; Phospho-Rpb1 CTD (Tyr145) Antibody; DNA directed RNA polymerase II subunit RPB1; hRPB220; hsRPB1; POLR2; POLR2A; POLRA; polymerase (RNA) II (DNA directed) polypeptide A; 220kDa; RNA polymerase II subunit 1; RNA polymerase II subunit B1; RP02; RPB220; RPBh1; RpIILS; RPO21; RPOL2; SUA8; anti-Rpb1 antibody

PRODUCT SPECIFICATIONS

Host	Rabbit
Reactivity	Human, Mouse, Rat Predicted: Pig, Bovine, Horse, Sheep, Dog, Xenopus
Clonality	Polyclonal
Isotype	IgG
Specificity	Phospho-Rpb1 CTD (Tyr145) Antibody detects endogenous levels of Rpb1 CTD only when phosphorylated at Tyr145.
Purity/Purification	Purified rabbit serum by affinity purification via sequential chromatography on phospho- and non-phospho-peptide affinity columns.
Form/Format	Liquid; Phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Concentration	1mg/ml (varies by lot)
Sequence Length	1970
Applicable Applications for anti-Rpb1 antibody	ELISA (Peptide ELISA), IHC (Immunohistochemistry), WB (Western Blot)
Immunogen	A synthesized peptide derived from human Rpb1 CTD around the phosphorylation site of Tyr145.
Subcellular Location	Nucleus
Preparation and Storage	Store at -20 degree C. Stable for 12 months from date of receipt.

IMAGES

WB (Western Blot)
Western blot analysis of Phospho-Rpb1 CTD (Tyr145) in lysates of COS7 EGF 200ng/ml 30', using Phospho-Rpb1 CTD (Tyr145) Antibody.

IHC (Immunohistochemisry)
At 1/100 staining human kidney tissue sections by IHC-P. The tissue was formaldehyde fixed and a heat mediated antigen retrieval step in citrate buffer was performed. The tissue was then blocked and incubated with the antibody for 1.5 hours at 22 degree C. An HRP conjugated goat anti-rabbit antibody was used as the secondary

IHC (Immunohiostchemistry)

At 1/100 staining rat heart tissue sections by IHC-P. The tissue was formaldehyde fixed and a heat mediated antigen retrieval step in citrate buffer was performed. The tissue was then blocked and incubated with the antibody for 1.5 hours at 22 degree C. An HRP conjugated goat anti-rabbit antibody was used as the secondary

IHC (Immunohistochemistry)

At 1/100 staining mouse liver tissue sections by IHC-P. The tissue was formaldehyde fixed and a heat mediated antigen retrieval step in citrate buffer was performed. The tissue was then blocked and incubated with the antibody for 1.5 hours at 22 degree C. An HRP conjugated goat anti-rabbit antibody was used as the secondary

ADDITIONAL INFORMATION

Related Product Information for anti-Rpb1 antibody

Description: 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. Regulation of gene expression levels depends on the balance between methylation and acetylation levels of tha CTD-lysines (By similarity). Initiation or early elongation steps of transcription of growth-factors-induced immediate early genes are regulated by the acetylation status of the CTD (PubMed:24207025). Methylation and dimethylation have a repressive effect on target genes expression (By similarity).

Post Translational Modifications: 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. Regulates 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, dimethylated and trimethylated. Methylation occurs in the earliest transcription stages and precedes or is concomitant to 'Ser-5' and 'Ser-7' phosphorylation. Dimethylation and trimehtylation at 'Lys-7' of non-consensus heptapeptide repeats are exclusively associated with phosphorylated CTD. Ubiquitinated by WWP2 leading to proteasomal degradation (By similarity). Following UV treatment, the elongating form of RNA polymerase II (RNA pol IIo) is ubiquitinated on 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.

Subunit Structure: Component of the RNA polymerase II (Pol II) complex consisting of 12 subunits. 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. The large PER complex involved in the repression of transcriptional termination is composed of at least PER2, CDK9, DDX5, DHX9, NCBP1 and POLR2A (active). Interacts (via the C-terminal domain (CTD)) with U2AF2; recruits PRPF19 and the Prp19 complex to the pre-mRNA and may couple transcription to pre-mRNA splicing. Interacts (via the C-terminal domain (CTD)) with SMN1/SMN2; recruits SMN1/SMN2 to RNA Pol II elongation complexes. Interacts via the phosphorylated C-terminal domain with WDR82 and with SETD1A and SETD1B only in the presence of WDR82. When phosphorylated at 'Ser-5', interacts with MEN1; the unphosphorylated form, or phosphorylated at 'Ser-2' does not interact. When phosphorylated at 'Ser-2', interacts with SUPT6H (via SH2 domain). Interacts with RECQL5 and TCEA1; binding of RECQL5 prevents TCEA1 binding. The phosphorylated C-terminal domain interacts with FNBP3 and SYNCRIP. Interacts with ATF7IP. Interacts with DDX5. Interacts with WWP2. Interacts with SETX. Interacts (phosphorylated) with PIH1D1. Interacts (via the C-terminal domain (CTD)) with TDRD3. Interacts with PRMT5. Interacts with XRN2. Interacts with SAFB/SAFB1. Interacts with CCNL1. Interacts with CCNL2, MYO1C, PAF1 and SFRS19. Interacts (via C-terminus) with CMTR1, CTDSP1 and SCAF8. Interacts (via the C-terminal domain (CTD)) with CCNT2 (PubMed:15563843).

Similarity: The C-terminal domain (CTD) serves as a platform for assembly of factors that regulate transcription initiation, elongation, termination and mRNA processing. Belongs to the RNA polymerase beta' chain family.

NCBI AND UNIPROT INFORMATION

NCBI GI #	4505939
NCBI GeneID	5430
NCBI Accession #	NP_000928.1
NCBI GenBank Nucleotide #	NP_000928.1
UniProt Accession #	P24928
Molecular Weight	Observed: 270 kDa Predicted: 218 kDa
NCBI Official Full Name	DNA-directed RNA polymerase II subunit RPB1
NCBI Official Synonym Full Names	RNA polymerase II subunit A
NCBI Official Symbol	POLR2A
NCBI Official Synonym Symbols	RPB1; RPO2; POLR2; POLRA; RPBh1; RPOL2; RpIILS; hsRPB1; hRPB220
NCBI Protein Information	DNA-directed RNA polymerase II subunit RPB1
UniProt Protein Name	DNA-directed RNA polymerase II subunit RPB1
UniProt Gene Name	**POLR2A**
UniProt Synonym Gene Names	POLR2; RNA polymerase II subunit B1
UniProt Entry Name	RPB1_HUMAN

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

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Online datasheet: https://stage.aaabiotech.com/polyclonal/rpb1-ctd-antibody-peptide-elisa-immunohistochemistry-western-blot-elisa/328426