

ARG10661 anti-RNA Polymerase II CTD repeat YSPTSPS phospho (Ser5) antibody [CTD 4H8]

Package: 100 µg

Store at: -20°C

Summary

Product Description	Mouse Monoclonal antibody [CTD 4H8] recognizes RNA Polymerase II CTD repeat YSPTSPS phospho (Ser5)
Tested Reactivity	Hu, Ms, Rat, AGMK, Arabi, Ce, Dm, S. cerevisiae, S. pombe
Tested Application	ChIP, ChIP-seq, FACS, ICC/IF, IHC-P, IP, WB
Host	Mouse
Clonality	Monoclonal
Clone	CTD 4H8
Isotype	IgG1
Target Name	RNA Polymerase II CTD repeat YSPTSPS
Species	Human
Immunogen	Synthetic peptide: 10 repeats of YSPTSPS (Phosphorylated on Ser5).
Conjugation	Un-conjugated
Alternate Names	EC 2.7.7.6; RPO2; RPB1; RPOL2; POLRA; DNA-directed RNA polymerase II subunit A; hSRPB1; EC 2.7.7.48; RNA-directed RNA polymerase II subunit RPB1; hRPB220; POLR2; RNA polymerase II subunit B1; DNA-directed RNA polymerase II subunit RPB1; RpIILS; RPBh1; DNA-directed RNA polymerase III largest subunit

Application Instructions

Application table	Application	Dilution
	ChIP	Assay-dependent
	ChIP-seq	Assay-dependent
	FACS	Assay-dependent
	ICC/IF	Assay-dependent
	IHC-P	Assay-dependent
	IP	Assay-dependent
	WB	Assay-dependent
Application Note	* The dilutions indicate recommended starting dilutions and the optimal dilutions or concentrations should be determined by the scientist.	
Positive Control	HeLa cell line.	

Properties

Form	Liquid
Purification	Affinity purification with immunogen.
Buffer	PBS and 0.02% Sodium azide.
Preservative	0.02% Sodium azide
Storage instruction	For continuous use, store undiluted antibody at 2-8°C for up to a week. For long-term storage, aliquot and store at -20°C or below. Storage in frost free freezers is not recommended. Avoid repeated freeze/thaw cycles. Suggest spin the vial prior to opening. The antibody solution should be gently mixed before use.
Note	For laboratory research only, not for drug, diagnostic or other use.

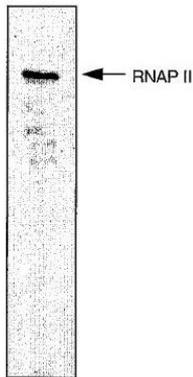
Bioinformation

Database links	GeneID: 20020 Mouse GeneID: 5430 Human Swiss-port # P08775 Mouse Swiss-port # P24928 Human
Gene Symbol	POLR2A
Gene Full Name	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
Background	This gene encodes the largest subunit of RNA polymerase II, the polymerase responsible for synthesizing messenger RNA in eukaryotes. The product of this gene contains a carboxy terminal domain composed of heptapeptide repeats that are essential for polymerase activity. These repeats contain serine and threonine residues that are phosphorylated in actively transcribing RNA polymerase. In addition, this subunit, in combination with several other polymerase subunits, forms the DNA binding domain of the polymerase, a groove in which the DNA template is transcribed into RNA. [provided by RefSeq, Jul 2008]
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 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. [UniProt]
Calculated Mw	217 kDa
PTM	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 trimethylation 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 Ilo) is ubiquitinated on UV damage sites without leading to degradation: ubiquitination is facilitated by KIAA1530/UVSSA and promotes RNA pol Ilo backtracking to allow access to the nucleotide excision repair machinery.

Images



ARG10661 anti-RNA Polymerase II CTD repeat YSPTSPS phospho (Ser5) antibody [CTD 4H8] WB image

Western blot: RNAP II stained with ARG10661 anti-RNA Polymerase II CTD repeat YSPTSPS phospho (Ser5) antibody [CTD 4H8] at 1:1000 dilution.