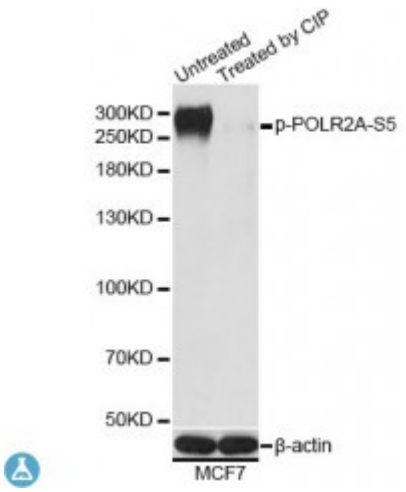
Anti-Phospho-POLR2A-(S5) Antibody



Description	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.

Model	STJ117926
Host	Rabbit
Reactivity	Human, Mouse
Applications	WB
Immunogen	A phospho specific peptide corresponding to residues surrounding S5 of human POLR2A
Gene ID	5430
Gene Symbol	POLR2A
Dilution range	WB 1:500 - 1:2000
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	DNA-directed RNA polymerase II subunit RPB1 RNA polymerase II subunit B1

Molecular Weight	217.176 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	PBS with 0.02% sodium azide, 50% glycerol, pH7.3.
Storage Instruction	Store at -20C. Avoid freeze / thaw cycles.
Database Links	HGNC:9187OMIM:180660Reactome:R-HSA-112382
Alternative Names	DNA-directed RNA polymerase II subunit RPB1 RNA polymerase II subunit B1
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, Regulation of gene expression levels depends on the balance between methylation and acetylation levels of tha CTD-lysines , Initiation or early elongation steps of transcription of growth-factors-induced immediate early genes are regulated by the acetylation status of the CTD 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,
Cellular Localization	Nucleus
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,