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POLR1A Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP51762

Product Information

Application	WB
Primary Accession	O95602
Reactivity	Human, Mouse, Rat
Host	Rabbit
Clonality	Polyclonal
Calculated MW	194811

Additional Information

Gene ID	25885
Other Names	DNA-directed RNA polymerase I subunit RPA1, RNA polymerase I subunit A1, A190, DNA-directed RNA polymerase I largest subunit, DNA-directed RNA polymerase I subunit A, RNA polymerase I 194 kDa subunit, RPA194, POLR1A
Dilution	WB~~1:1000
Format	0.01M PBS, pH 7.2, 0.09% (W/V) Sodium azide, Glycerol 50%
Storage	Store at -20 °C.Stable for 12 months from date of receipt

Protein Information

Name	POLR1A {ECO:0000303|PubMed:25913037, ECO:0000312|HGNC:HGNC:17264}
Function	Catalytic core component of RNA polymerase I (Pol I), a DNA- dependent RNA polymerase which synthesizes ribosomal RNA precursors using the four ribonucleoside triphosphates as substrates. Transcribes 47S pre-rRNAs from multicopy rRNA gene clusters, giving rise to 5.8S, 18S and 28S ribosomal RNAs (PubMed:11250903, PubMed:11283244, PubMed:16858408, PubMed:34671025, PubMed:34887565, PubMed:36271492). Pol I-mediated transcription cycle proceeds through transcription initiation, transcription elongation and transcription termination stages. During transcription initiation, Pol I pre-initiation complex (PIC) is recruited by the selectivity factor 1 (SL1/TIF-IB) complex bound to the core promoter that precedes an rDNA repeat unit. The PIC assembly bends the promoter favoring the formation of the transcription bubble and promoter escape. 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. Highly processive, assembles in structures referred to as 'Miller trees' where many elongating Pol I complexes queue and transcribe the same rDNA

	coding regions. At terminator sequences downstream of the rDNA gene, PTRF interacts with Pol I and halts Pol I transcription leading to the release of the RNA transcript and polymerase from the DNA (PubMed:11250903, PubMed:11283244, PubMed:16858408, PubMed:34671025, PubMed:34887565, PubMed:36271492). Forms Pol I active center together with the second largest subunit POLR1B/RPA2. Appends one nucleotide at a time to the 3' end of the nascent RNA, with POLR1A/RPA1 contributing a Mg(2+)-coordinating DxDGD motif, and POLR1B/RPA2 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 the 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. Has proofreading activity: Pauses and backtracks to allow the cleavage of a missincorporated nucleotide via POLR1H/RPA12. High Pol I processivity is associated with decreased transcription fidelity (By similarity) (PubMed:11250903, PubMed:11283244, PubMed:16858408, PubMed:34671025, PubMed:34887565, PubMed:36271492).
Cellular Location	Nucleus, nucleolus. Chromosome {ECO:0000250|UniProtKB:O35134}

Background

DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. Largest and catalytic core component of RNA polymerase I which synthesizes ribosomal RNA precursors. Forms the polymerase active center together with the second largest subunit. A single stranded DNA template strand of the promoter is positioned within the central active site cleft of Pol I. A bridging helix emanates from RPA1 and crosses the cleft near the catalytic site and is thought to promote translocation of Pol I 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 (By similarity).

References

Wang D.,et al.Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
Ota T.,et al.Nat. Genet. 36:40-45(2004).
Mural R.J.,et al.Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
Bechtel S.,et al.BMC Genomics 8:399-399(2007).
Panov K.I.,et al.Mol. Cell. Biol. 26:5436-5448(2006).