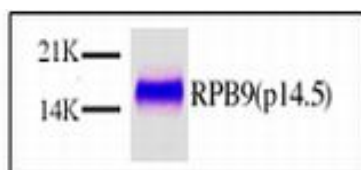


## RNA pol II-hRPB9

RNA Polymerase II, p14.5 subunit

human, recombinant, *E. coli*

Cat. No.	Amount
PR-716	10 µg



For *in vitro* use only  
Quality guaranteed for 12 months  
Store at -80°C

### Avoid freeze / thaw cycles

### Form

Liquid. Supplied in 20 mM Tris-HCl pH 8.0, 100 mM KCl, 0.2 mM EDTA, 1 mM DTT and 20% glycerol.

### Activity

20 ng are sufficient for reconstituted transcription assays and 100 ng are sufficient for a protein-protein interaction assay.

### Purity

> 95% by SDS-PAGE

### Description

hRPB9 is a subunit unique to RNA Polymerase II, although it has sequence homologues in RNA Polymerases I and III. The gene for Rpb9 is not essential for yeast cell viability, but is essential in *Drosophila*. hRPB9 has roles in both transcription initiation and transcription elongation. In the initiation reaction it is necessary for accurate start site selection. In the elongation reaction, RPB9, along with TFIIIS facilitates the conversion of an arrest-competent conformation to a read-through competent conformation. RNA Polymerase II lacking the RPB9 subunit uses alternate transcription initiation sites *in vitro* and *in vivo* and is unable to respond to the transcription elongation factor TFIIIS *in vitro*. A role in the modulation of initiation and elongation is consistent with the localization of RPB9 in the three-dimensional structure of yeast RNA Polymerase II. RPB9 is located at the tip of the so-called "jaws" of the enzyme, which is thought to function by clamping the DNA downstream of the active site. RPB9 comprises two zinc ribbon domains joined by a conserved linker region. The C-terminal zinc ribbon is similar in sequence to that found in TFIIIS.

Recombinant p14.5 is isolated from an *E. coli* strain that carries the coding sequence of human RPB9 under the control of a T7 promoter.

hRPB9 has been applied in *in vitro* transcription assays, *in vitro* elongation assays and protein-protein interaction assays.

Protein is greater than 95% homogeneous and contains no detectable protease, DNase, and RNase activity.

### Selected References:

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- Furter-Graves (1991) SHI, a new yeast gene affecting the spacing between TATA and transcription initiation sites. *Mol. Cell. Biol.* **11**:4121.
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