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Abstract:

RNA polymerase II (RNAPII) is regulated by multiple modifications to the C-terminal domain (CTD) of the largest subunit, Rpb1. This study has focused on the relationship between hyperphosphorylation of the CTD and RNAPII turnover and proteolytic degradation as well as post-translational modifications of the globular core of RNAPII. Following tandem affinity purification, western blot analysis showed that MG132 treated RTR1 ERG6 deletion yeast cells have accumulation of total RNAPII and in particular, the hyperphosphorylated form of the protein complex. In addition, proteomic studies using MuDPIT have revealed increased interaction between proteins of the ubiquitin-proteasome degradation system in the mutant MG132 treated yeast cells as well as potential ubiquitin and phosphorylation sites in RNAPII subunits, Rpb6 and Rpb1, respectively. A novel Rpb1 phosphorylation site, T1471-P, is located in the linker region between the CTD and globular domain of Rpb1 and will be the focus of future studies to determine biological significance of this post-translational modification.

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