

Relations among transcription, pre-mRNA processing and chromatin modifications are only partially understood. The human protein SNW1/SKIP belongs to factors which couple these processes. The protein plays role in pre-mRNA splicing and transcription on the level of both initiation and elongation. According to the hypothesis of K. Jones laboratory, it physically and functionally interacts with positive transcription elongation factor b during transcription elongation and influences methylation of histone H3 on lysine 4, a modification characteristic for active transcription (Bres et al., *Genes Dev.* 19:1211-26, 2005, Bres et al., *Mol Cell.* 36:75-87, 2009). The yeast ortholog of SNW1/SKIP, Prp45, was until now reported only in connection with splicing regulation. However, unpublished results from our Laboratory and others showed that it is employed in transcription elongation as well. The aim of the diploma project was to search for the relations between Prp45 and the factors regulating transcription. It was confirmed that the mutation *prp45(1 169)* results in the delay of PHO5 and PHO84 expression during transcriptional induction. Next, we discovered new genetic interactions between PRP45 and several genes encoding the effectors of chromatin modifications. How Prp45 influences the expression of PHO5 and PHO84 was tested in *prp45(1 169)* mutated strains bearing the simultaneous deletion of a selected effector gene (BUR2, PAF1, RAD6, or SET1). It was discovered that the function of Prp45 during the expression of these genes is connected to Rad6 and Set1, which supports its role in transcription regulation. Finally, we provided new data on the influence of selected effectors on PHO5 repression under non-inducing conditions.