The structural basis for recruitment of the Paf1 complex to chromatin

Abstract Eukaryotic gene expression utilizes the activity of RNA polymerase II (Pol II) to transcribe from a chromatin template in which DNA is wrapped around octamers of histone proteins. Chromatin serves to limit access to the DNA, which is just one method the cell uses to regulate transcription, allowing the cell to quickly and precisely respond to environmental stimuli. Gene expression is also regulated by a host of accessory factors which are brought to the transcription complex at different stages of the transcription cycle. Our work has focused on the mechanisms by which the Paf1 complex transcription elongation complex (Paf1C) assists transcription. Paf1C is a five protein complex with multiple regulatory roles including the maintenance of histone modifications and the recruitment of chromatin remodelers and RNA processing factors. Previous results have demonstrated that three Paf1C subunits, Rtf1, Cdc73, and Leo1, contribute to chromatin recruitment. Our analysis, including a combination of biochemical, biophysical, genetic, and structural data, support a bivalent mechanism for Paf1C chromatin recruitment.