# **Using ChIP-nexus to decipher the architecture of transcription factor complexes**

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Transcription factors are key regulators of gene expression. They often form complexes with transcriptional coactivators and/or corepressors. Moreover, individual genes are often regulated by multiple such complexes. Chromatin immunoprecipitation followed by next generation sequencing (ChIP-seq) is a popular method for mapping transcription factor binding sites in a genome-wide manner. However, ChIP-seq typically lacks the resolution required for accurate determination of the exact positioning of regulatory proteins on DNA. This, in turn, limits our ability to determine the relationships between different regulators acting on common target genes. Therefore, methods such as ChIP-exo or ChIP-nexus have been developed to increase the spacial resolution of the genome-wide ChIP assay by employing DNA digestion of regions not protected by DNA-bound proteins. We have used ChIP-nexus to describe the transcription factor network regulating lipid metabolism genes in the fission yeast *Schizosaccharomyces pombe*. We will present a complete workflow for ChIP-nexus data acquisition, processing and analysis, together with the key biological conclusions.