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Purification of the Holo-Tfiid Complex from *Saccharomyces cerevisiae* for Structural Studies. Raymond Jacobson, Biochemistry & Molecular Biology, Univ. of Texas, MD Anderson Cancer Center, 1515 Holcombe Blvd., Box 117, Houston, TX 77030 USA.

RNA transcription in eukaryotes requires the assembly of an enormous multi-protein complex comprising more than 60 polypeptides. Prior to transcriptional initiation the basal transcription factors TFIIA, TFIIB, TFIID, TFII E, TFII F and TFII H come together at the core promoter to recruit the RNA polymerase II enzyme to the start site of protein coding genes. Together these factors properly position and modulate the RNA polymerase activity. The last decade has seen a dramatic increase in mechanistic and structural information available describing these components culminating in the 3-dimensional structure solution of the RNA Pol II holo complex by the Kornberg group at Stanford. However a number of the important regulatory complexes including TFIID and TFII H have remained less well characterized. Our studies focus on TFIID which is composed of 15 distinct subunits and plays a number of vital roles as a coactivator and as a core promoter selectivity factor. This mega-Dalton complex has remained largely uncharacterized at the structural level due to expression problems resulting from the inherent complexity of this regulatory factor. We will describe our progress in the purification of the holo-TFIID complex from *Saccharomyces* using a TAP (tandem affinity purification) strategy to obtain sufficient material for use in crystallization and the 3-dimensional structure determination of this complex macromolecular assembly.