

**W0548**

**Conformational Variability in Eukaryotic Transcription Complexes Revealed by Cryo-Electron Microscopy Studies.** Grob, P.<sup>1</sup>, Kostek, S.<sup>1</sup>, DeCarlo, S.<sup>1,3</sup>, Tjian, R.<sup>1,3</sup>, Penczek, P.<sup>4</sup>, Nogales, E.<sup>1,2,3</sup>, <sup>1</sup>Molecular and Cell Biology Dept., Univ. of California, Berkeley, CA 94720, <sup>2</sup>Physical Biosciences Div., Lawrence Berkeley National Laboratory, Berkeley, CA 94720, <sup>3</sup>Howard Hughes Medical Inst., Molecular and Cell Biology Dept., Univ. of California, Berkeley, CA 94720, <sup>4</sup>The Univ. of Texas – Houston Medical School, Dept. of Biochemistry and Molecular Biology, 6431 Fannin, MSB 6.218, Houston, TX 77030.

The multi-subunit transcription factor TFIID and RNA Polymerase II are essential elements of the transcription machinery in eukaryotes. We adopted the cryo-electron microscopy and single particle approach to obtain 3D reconstructions of the endogenous human complexes in solution. Additionally we obtained the associated 3D variance maps as well as covariance information. The localization and the amplitude of the variations have given us a novel insight into the dynamics of these complex molecular machines. For human TFIID this strategy has shown that several domains of the complex moved in a concerted manner that reshaped the putative DNA-binding cavities. In human RNA Polymerase II we have identified a more complex set of variable regions that can be interpreted based on the crystallographic structures available for the yeast enzyme.