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**A Simple Method for the Identification of Protein/Ligand Complexes Using Protein Powder Diffraction.** M. Allaire, N. Moiseeva, C. Botez, P. Stephens, National Synchrotron Light Source, Brookhaven National Laboratory, Upton, NY.

The drug discovery process would benefit from the development of a method that could screen a specific protein with a large library of chemicals in order to identify lead compounds and provide structural information on the binding modes of the target. Protein powder diffraction represents an attractive alternative for High-Throughput Screening (HTS) of protein/ligand complexes. The concept is that diffraction of protein powder would differ in comparing an unbound with a ligand-bound protein. In this study we compare the powder diffraction of unbound lysozyme and lysozyme mixed with glucose, N-acetylglucosamine (NAG) and (NAG)<sub>3</sub>. The powder data in the region of Bragg spacing corresponding to 9 and 3Å were collected at the NSLS beamline X3B1. The results indicate that high correlation is obtained between diffraction data of identical samples. The comparison of correlation coefficients for the different lysozyme/ligand complexes with the unbound lysozyme reveals that the presence of glucose does not affect the diffraction pattern but lower correlation is obtained when lysozyme is mixed with NAG and (NAG)<sub>3</sub>. These results are consistent with the known specificity of lysozyme and suggest that this method could be generalized for HTS in drug discovery.