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Recent Developments in the *BnP* Package for Automated Protein Structure Determination. W. Furey¹, L. Pasupulati¹, S. A. Potter², H. Xu², R. Miller^{2,3}, & C. M. Weeks², ¹VA Med. Center, Pittsburgh PA & Dept. Pharmacol., U. Pittsburgh, ²Hauptman-Woodward Inst., Buffalo NY, ³Center for Comp. Res., SUNY at Buffalo.

BnP is a user friendly, graphical user interface driven program package for either the automated or semi-manual determination of protein structures from x-ray data. *BnP* incorporates the *SnB* direct methods program for heavy atom/anomalous scatterer substructure determination, and the PHASES package programs for heavy atom refinement, protein phasing, density modification, and skeletonization. *BnP* also creates data and scripts for external programs required for automated chain tracing, graphical visualization, and refinement. In auto mode *BnP* will use default parameters and procedures throughout the entire structure determination process starting with the observed x-ray data, to generate electron density maps suitable for model building. With a couple of additional button clicks external programs for automated chain tracing or chain tracing/refinement can then be launched. Recent developments simplifying user input, MAD scattering factor selection, speeding up the algorithms, and improvements in the auto chain tracing/refinement options will be presented along with detailed results from a large number of structures. This work was supported by NIH grant EB002057.