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From Images to Co-crystal Structures in a Single Automated Process. J.Badger¹, P.Collins¹, R.Rosenfeld¹, B.Smith¹, R.Athay², D.E.McRee¹, (1) ActiveSight, 4045 Sorrento Valley Blvd., San Diego CA 92121 USA and (2) Rigaku Americas Corporation, 491 S. Orem Blvd., Orem, UT 84058, USA.

A major focus for protein crystallography in the commercial sector is the rapid determination of large numbers of protein:ligand structures for lead compound optimization. X-ray crystallography now also contributes directly to lead discovery through fragment screening methodologies and our experience with the ActiveSight fragment library (http://www.active-sight.com/products_screening.htm) is that fragment-based screening projects typically requires the examination of 100-200 electron density maps.

To assist the protein crystallographer analyze these volumes of data we have recently extended our previous automated structure determination application (<http://mi.active-sight.com/MIAutoStructure.html>) to include image data processing and various options for ligand placement. Neither the image data processing step (d*TREK v97 or MOSFLM) nor the structure determination steps (CCP4/MOLREP and CCP4/REFMAC5) managed by this application occupy more than a few minutes on a modern laptop computer. For this reason the structure solution GUIs and underlying Python script system are designed to conveniently support the processing of *multiple* related data sets within a single job and maintain convenient logs of the structure solution tasks. Amongst the outputs from this application is a session file for convenient loading of models and maps into the MIFit software. The MIFit program allows for the independent but simultaneous display of models and maps from multiple data sets.

We have used this software to analyze many hundreds of data sets across several fragment screening projects.