Improving Data Quality – without having to grow new Crystals <u>Anita Coetzee</u>^a, Bram Schierbeek^a, Gregor Witte^b, Ute Curth^b, Dietmar J. Manstein^b, Roman Fedorov^b, ^a Bruker AXS B.V. Delft, The Netherlands. ^b Institute for Biophysical Chemistry, Hanover Medical School, Hanover, Germany. E-mail: anita.coetzee@bruker-axs.nl

In order to obtain the best possible results for structure solution and refinement, it is imperative to collect the best quality data from a given crystal. This generally means measuring the highest possible resolution data. With recent advances in microfocus X-ray sources, such as the MicroStar, more brilliant sources are available to evaluate very small crystals in-house. Combining these sources with the latest developments in graded multilayer optics can result in excellent data being measured at home on samples that were previously only tractable at the synchrotron. Using a kappa-goniostat in combination with sophisticated data collection strategy software can ensure that a complete dataset is measured up to the diffraction limit of the crystal. The combination of high resolution, completeness and redundancy can improve the data quality significantly. In this study we will show examples of how data quality can be improved. It was possible to trace more residues in a dimeric single-stranded DNA binding protein, by collecting a dataset using the strategy program COSMO [1] in combination with the 4-circle goniometer on the X8 Proteum.

[1] COSMO, Data collection strategy program, Bruker AXS Keywords: data collection, protein crystallography, detectors