

W0390

Crystal Structure of a 7 Residue Segment of the Yeast Sup35 Prion Protein: Small Crystals, Big Problems. M.R. Sawaya, R. Nelson, M. Balbirnie, A. Madsen, C. Riek, R. Grothe, D. Eisenberg. Howard Hughes Medical Inst. UCLA-DOE Inst. for Genomics and Proteomics, UCLA, Los Angeles, CA 90095.

The crystal structure of a 7 residue peptide from yeast Sup35 prion was recently solved after five years of struggling for accurate and sufficient data. Although well ordered, the crystals are exceedingly small, the largest of these being 50 x 2 x 2 μm . Early efforts at data collection focused on powder methods. It was routinely possible to record diffraction of X-rays to 1.3 \AA on an in-house source; however, the problem of overlapping reflections limited the size of the data set to too few reflections. Molecular replacement methods using structure factors extracted from powder data produced feasible solutions, but could never be refined to an R-factor below 35%. Single crystals were capable of diffracting electrons to ultra high-resolution (0.5 \AA); however dynamic scattering effects limited the usefulness of these data. Finally, it was possible to collect single crystal X-ray diffraction data for the very largest of these microcrystals at the microfocus beamline ID-13 at ESRF. Anomalous scattering from a well ordered zinc ion was sufficient to produce a readily interpretable electron density map using the SAD method of phasing.