

W0137

Comparison of Amyloid Fiber Diffraction Data with Structural Computational Models. Janel W. Laidman, Michael R. Sawaya, Todd O. Yeates, Molecular Biology Institute, UCLA, Box 951570 Los Angeles, CA 90095.

Several neurodegenerative diseases like Alzheimer's, Huntington's, Variant Creutzfeldt Jakob disease and others are characterized by a protein conformational change or misfolding event leading to fibrillization of the protein in a form labeled amyloid. Current models for amyloid structure indicate the core of the fiber is composed of beta sheets with strands running perpendicular to the fiber axis. Diagnostic for amyloid is the ability to bind Congo red dye, fibrillar morphology, and a cross-beta diffraction pattern showing a ring at ~ 4.7 angstroms corresponding to beta strand spacing and a ring at ~ 10 angstroms indicative of beta sheet spacing. We report here a compilation of known amyloid fiber diffraction patterns and compare them to current models of amyloid structure and their calculated diffraction patterns. An examination of diffraction patterns calculated from various structural models leads to some non-intuitive observations.