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**Structural Genomics of *Caenorhabditis Elegans*: Structures of SDR Family Members and Problems with Prediction of Function.** N. Schormann, J. Symersky, Y. Zhang, E. Karpova, J. Zhou, C.-H. Luan, M. Luo, UAB, CBSE, 1025 18th St. S., Birmingham, AL.

As part of the Structural Genomics Initiative on *Caenorhabditis Elegans* we have solved the structures of a number of proteins belonging to the extensive family of short-chain dehydrogenases/reductases (SDR family). This family consists of tyrosine-dependent oxidoreductases using NAD(P)H as cofactor. Proteins in this family typically show a low sequence homology (20-30% identity) but exhibit (at least for the core domain of about 250 residues) a relatively high structural homology. Although the cofactor (NADH versus NADPH) specificity can be (at least for certain subgroups) reliably assigned based on the amino acid sequence in the cofactor fingerprint region, the biological assembly (dimer versus tetramer) and the substrate specificity are difficult to predict. This even holds after the structure has been solved and refined. We will present several structural examples and discuss the underlying problem.