Structure-based inference of molecular functions of proteins of unknown function from Berkeley Structural Genomics Center

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Advances in sequence genomics have resulted in an accumulation of a huge number of protein sequences 1derived from genome sequences. However, the functions of a large portion of them cannot be inferred based on the current methods of sequence homology detection to proteins of known functions. Three-dimensional structure can have an important impact in providing inference of molecular function (physical and chemical function) of a protein of unknown function. Structural genomics centers worldwide have been determining many 3-D structures of the proteins of unknown functions, and possible molecular functions of them have been inferred based on their structures. Combined with bioinformatics and enzymatic assay tools, the successful acceleration of the process of protein structure determination through high throughput pipelines enables the rapid functional annotation of a large fraction of hypothetical proteins. We present a brief summary of the process we used at the Berkeley Structural Genomics Center to infer molecular functions of proteins of unknown function.