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Using Structural Genomics Results to Advance Structural Biology in the Academic Laboratory.

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Protein expression and crystallization are two of the primary bottlenecks for X-ray crystallography. During the past five years, structural genomics (SG) consortia have addressed these issues by developing novel technologies for the high-throughput expression and crystallization of hundreds of samples. As a consequence, these groups have also generated considerable amounts of data for every step in the structure determination process. While pipelines on the scale of SG are not feasible for an academic laboratory, many of the strategies and technologies can be successfully adapted for use in single PI laboratories. I will describe how we are adapting the results from SG centers to our own laboratory, and show how they are enabling us to more *rapidly* identify the protein constructs and complexes that are most likely to produce diffraction quality crystals:

- Our use of high-throughput, *affordable* technologies for protein expression screening and production.
- Our use of bioinformatic filters for improved target construct design and optimized crystallization screens for initial crystallization trials.
- Our use of 1D ¹H NMR to identify samples most likely to form diffraction quality crystals since we have shown that only well-folded proteins ultimately produce crystals suitable for structure determination.