## **Structural Proteomics : a Rich Source of Purified Proteins**

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Structural proteomics efforts generate 2-3 times more purified proteins than structures. We have developed general enzymatic assays to screen individually purified proteins for enzymatic activity. The assays have relaxed substrate specificity and are intended to identify sub-subclasses of enzymes (phosphatase, phosphodiesterase, esterase, protease, dehydrogenase, and oxidase) to which the unknown protein belongs. Further biochemical characterization of proteins is facilitated by the application of secondary screens with natural substrates (substrate profiling). We demonstrated the feasibility and merits of this approach for hydrolases and oxidoreductases, two very broad and important classes of enzymes and identified over 40 new enzymes (phosphatases, phosphodiesterases, esterases). The screens were also applied to quickly characterize the large family of unknown proteins in *E. coli*, the haloacid dehalogenase (HAD)-like hydrolases.

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