

Miniaturization in Structural Biology Pipelines

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High-throughput (HT) structural biology is making significant contributions to our attempts at developing a complete understanding of biological systems. Process pipelines designed using HT approaches have now been implemented to explore protein fold/function space, to accelerate the Structure Based Drug Discovery, to study complete proteomes, and to develop and disseminate methods and technologies for working with integral membrane proteins.

The central theme of the technology development in our laboratory and that of our collaborators has been automation, integration, and miniaturization of processes in High-throughput structural analysis pipeline. These developments have dramatically increased success rates reducing the cost per structure by decreasing time from gene to structure, material usage, and number of personnel needed to accomplish large number of tasks. These factors also shorten feedback loops between processes leading to an almost two-fold decrease in time to arrive at a structure.

New tools for the HT pipeline include development of robust micro-expression protocols, use of NMR micro-probe for rapidly identifying protein targets amenable to further structural studies, use of nanocalorimetry or enthalpy array for biophysical characterization of interactions, and miniaturization, automation of the crystallization experiment, and use of workflow and GRID technologies for use in computational tasks in HT structure determination efforts.

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