LESSONS FROM DATA-DRIVEN STABILIZATION OF INDUSTRIAL ENZYMES

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The use of high through-put screening methods has the power to generate vast amounts of information on the link between protein structure and function. With the advancements in affordability and throughput of these technologies, it is increasingly possible to perform data-driven development of enzymes for biotechnological applications. Nowhere is this effort more linked to classical structure-based energy calculation models and our understanding of proteins than when we engineer the stability of proteins. It is now possible to obtain residue-specific information on the effect of all possible single amino acid substitutions on the stability of a protein, thus directly providing statistics and possible answers to some classical ideas on the energy distribution in protein structures.

In the present talk, I will discuss the results from recent protein stability engineering projects in relation to long-standing hypotheses in protein engineering, and attempt to provide an outlook for the use of structure-based energy calculation methods in protein engineering.