“Biophysical proteome, its evolution and relation to cellular phenotype”

Protein sequence encodes complex network of interactions and it is difficult to decipher simple rules in protein science. In spite of this challenge, approximate and semi-empirical rules can be found to describe biophysical properties of different proteins. Using simple models tested against multitude of data, our goal is to unravel such approximate rules to quantitate physicochemical properties of proteins based on sequence and/or structure information. Our next goal is to extend these transferrable laws in a high throughput manner to model the entire collection of proteins inside an organism, called the proteome. The application at the proteome level allows us to bridge the gap between molecular biophysics and cellular phenotype. With this approach we will try to address some questions of broad interest: i) Why are cells so sensitive to temperature? ii) How do thermophilic proteins (derived from organisms that thrive at high temperature) withstand high temperatures compared to their mesophilic (organisms that live at room temperature) counterparts? iii) What is the evolutionary implication of distribution of different rate processes in the proteome and how are they optimized? iv) How do salts slow down cell growth?

References: