Protein sequence encodes complex network of interactions and it is difficult to decipher simple rules in protein science. This has prompted “one-protein-at-a-time” viewpoint and prevented a holistic approach in the search for universalities. In spite of this challenge, I would argue principles can be found to describe physical properties of different proteins. Using statistical mechanical techniques tested against multitude of data, our goal is to unravel such universal features of proteins. Our next goal is to extend these transferrable laws to make predictions about the proteome, the entire collection of proteins inside a cell. Next, I will show these predictions give us insights to cellular laws, evolutionary tendencies and allow us to address some broad questions of 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 different rate processes in a cell and how are they optimized?