

TSUBOYAMA LAB.

Beyond the possibilities of biological proteins



Department of Materials and Environmental Science

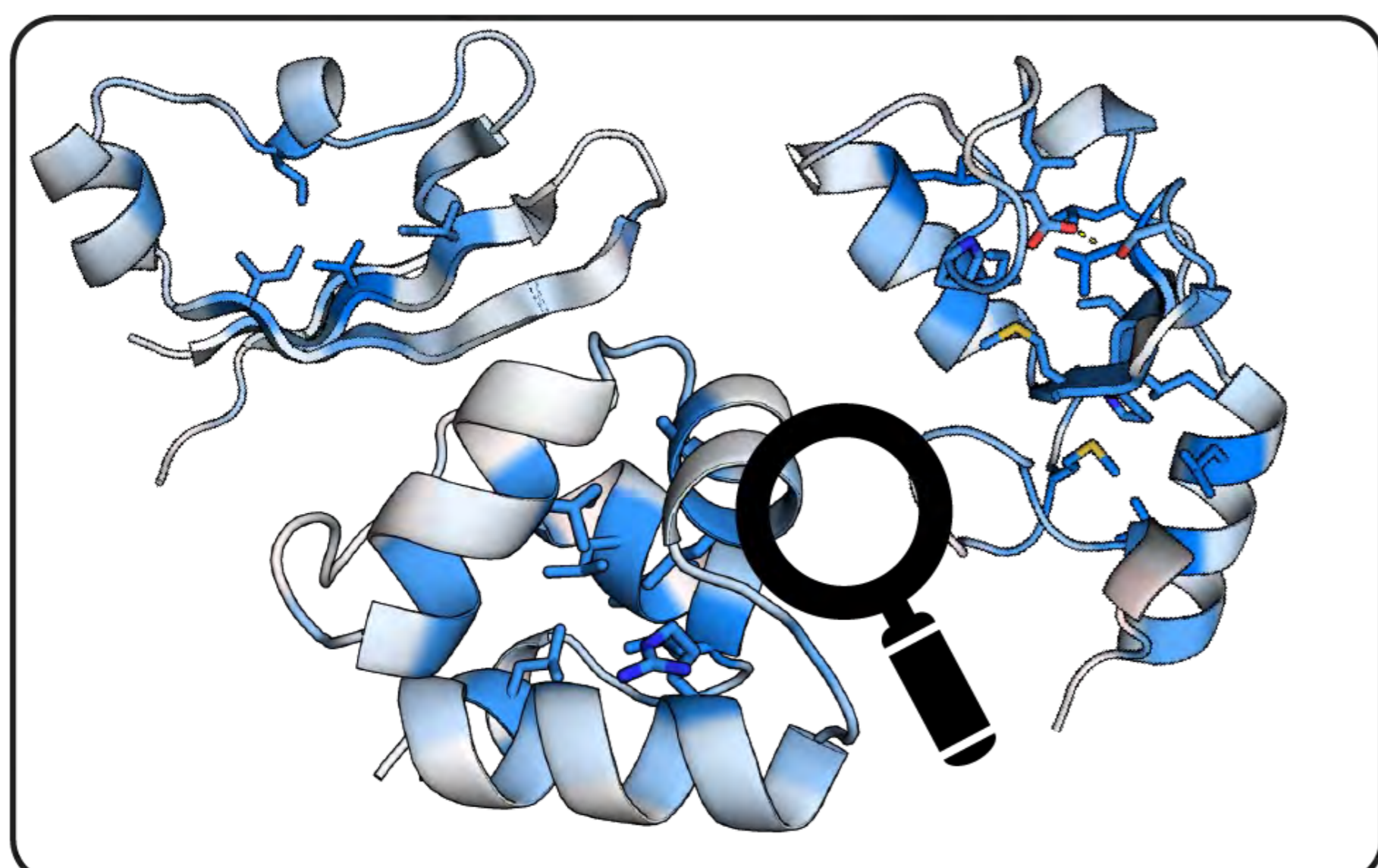
Protein Science
Department of Chemistry and Biotechnology, Graduate School of Engineering

<https://bio-design-eng.iis.u-tokyo.ac.jp/>

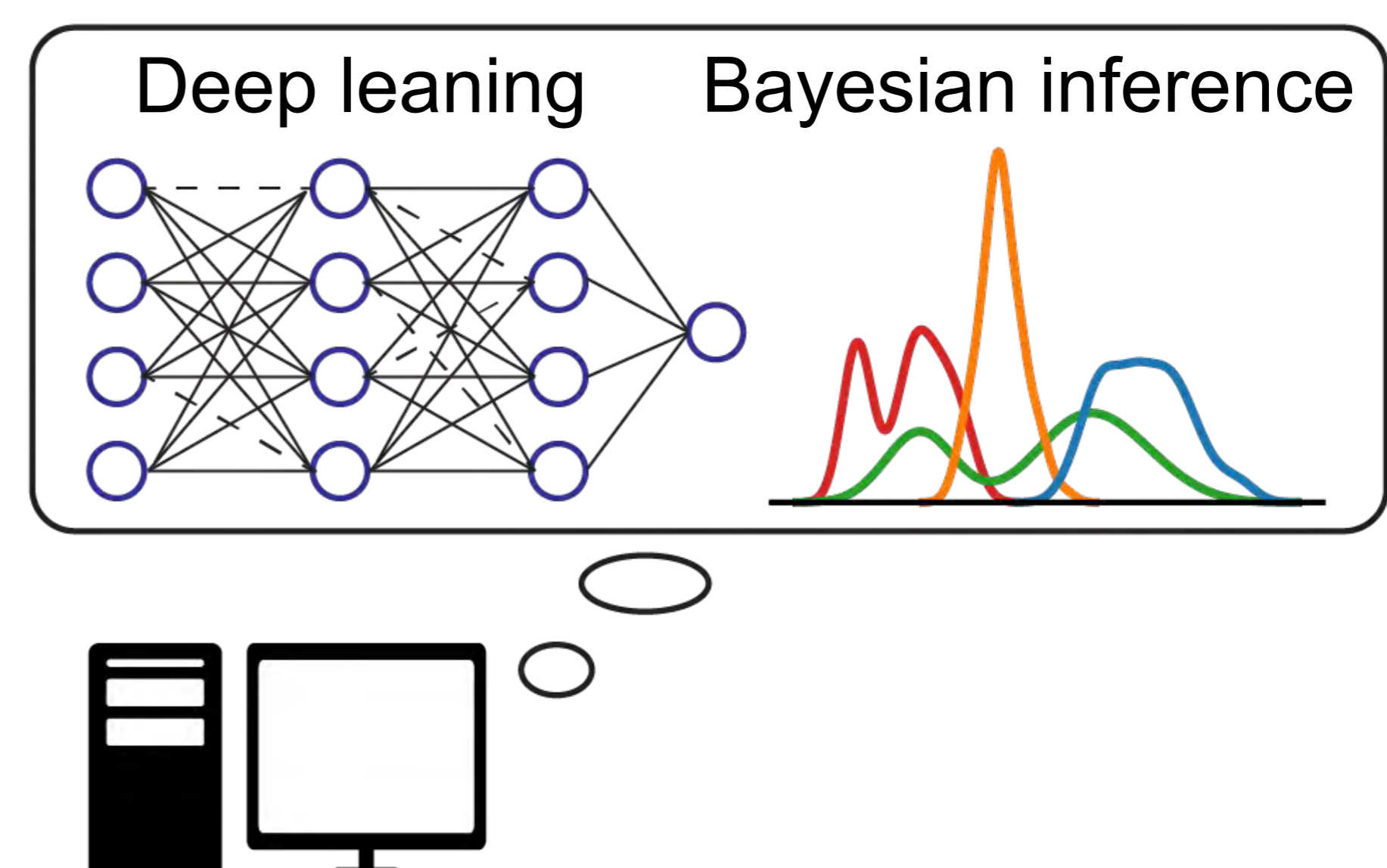
Rational Design of Functional *De Novo* Proteins

Proteins are composed of 20 different amino acids, providing a vast range of functions and a high level of diversity. Because the possible space is too huge, it remains difficult to rationally design *de novo* proteins without a thorough understanding of the fundamental relationships between amino acid sequence, structure, and function. To overcome this challenge, we are combining large-scale measurements with machine learning, including deep learning, to gain a better understanding of the relationships between amino acid sequence, structure, and function. Then, based on this new knowledge, we design *de novo* proteins to verify and re-analyze the new findings. In this way, we repeat such analysis and design to achieve both an understanding of the fundamental laws of proteins and rational design of *de novo* proteins.

Large-scale quantification



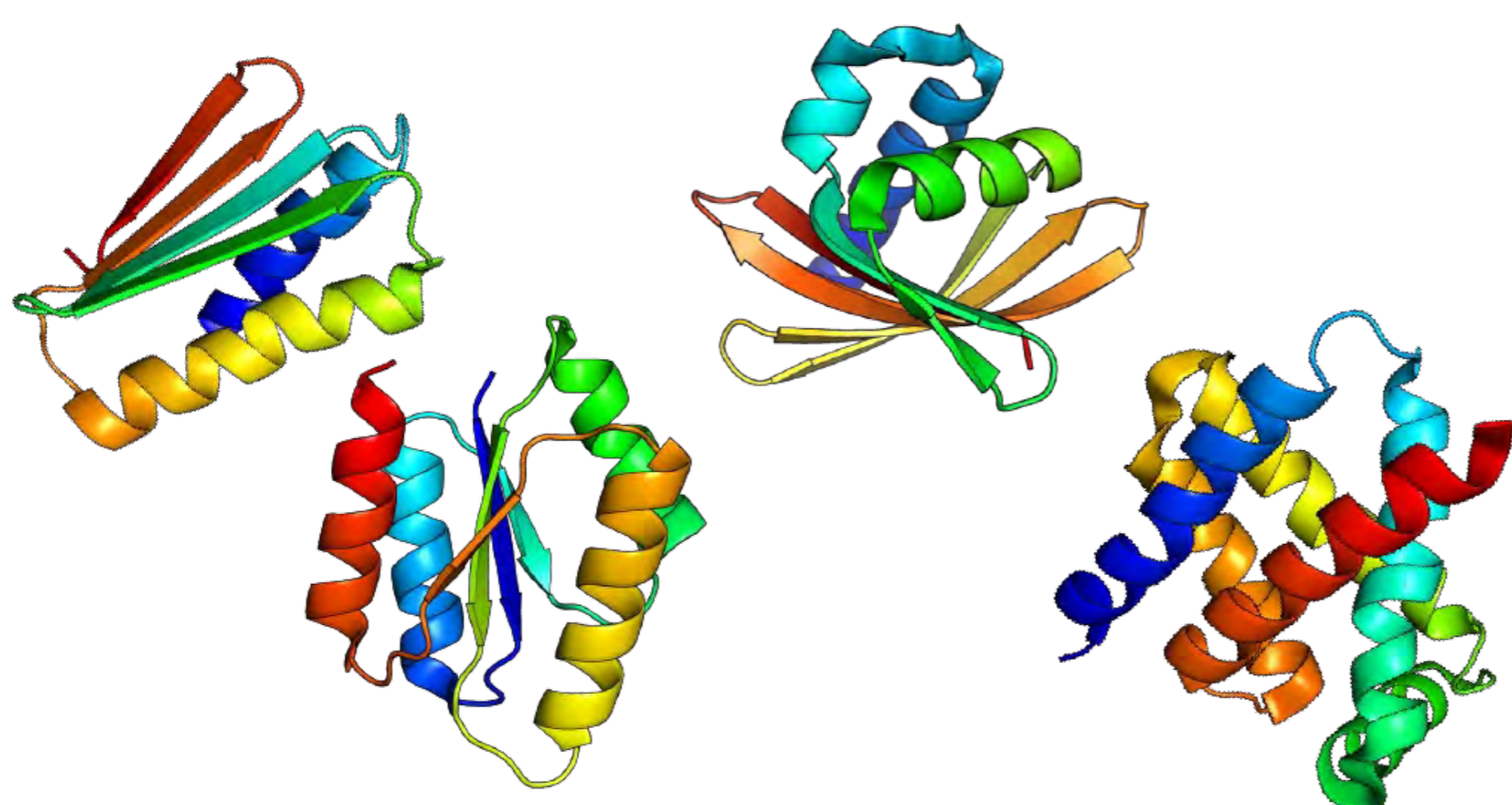
Big data analysis



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Efficient *de novo* protein design



Elucidation of protein basic laws

