INSTITUTE for PROTEIN RESEARCH
OSAKA UNIVERSITY

大阪大学蛋白質研究所
第4回 ASPiReセミナー

ポストAlphaFold時代における計算機による生体分子モデリング

Computational biomolecular structure modeling beyond AlphaFold

木原 大亮 先生

パデュー大学 教授

蛋白研 産学国際連携研究室 客員教授

2024年6月14日 (金) 17:00 – 18:30

蛋白質研究所 本館4F セミナー室

AlphaFold is a program which uses deep learning to predict the 3D structure of proteins from their amino acid sequences. As the accuracy of AlphaFold is substantially better than conventional methods, often reaching the error range of experimental methods, it is now frequently used in structural biology and other biological domains. In our lab, we have been extending or repurposing the AlphaFold program in several different directions. In this seminar, we will present some of our ongoing projects involving such applications, including RNA structure prediction and peptide-protein docking.

Contact: koga.nobuyasu.protein@osaka-u.ac.jp