CDCS
CENTER FOR DATA AND COMPUTING
IN NATURAL SCIENCES

OPENING SYMPOSIUM 2022

Universität Hamburg
DER FORSCHUNG | DER LEHRE | DER BILDUNG

DESY.

TUHH

Contribution ID: **90** Type: **Poster**

ProteinsPlus: On-The-Fly Structure-Based Design on the Web

The ProteinsPlus web server (https://proteins.plus)[1] offers modelling support for numerous challenges concerning the in-depth investigation of biomolecules. Its unique tools provide easy access to various structure-based analyses for interdisciplinary researchers through an intuitive user interface. Users can perform numerous computational studies for more than 174,000 three-dimensional protein structures from the Protein Data Bank (PDB)[2] and app. 992,000 predicted AlphaFold Protein Structure Database[3] models.
The services include structure quality analyses for X-ray models based on electron density fit and further criteria, structure preparation offering support for: hydrogen atom coordinate assignment, water placement and metal coordination geometry analysis, pocket prediction, druggability assessment, automated and manually adjustable binding site comparison, on-the-fly molecular docking through an automated preprocessing pipeline for ligand and protein preparation, interaction visualization in 2D and 3D and protein-protein interface classification regarding its biological impact. The results are available for download for further analyses and statistical evaluations.
In this contribution, we will present the services of the ProteinsPlus web server in a nutshell with implications on their potential application domains. We discuss several tools which are still in active development: GeoMine[4] for textual, numerical and geometric queries on predicted and ligand-occupied binding sites in the PDB, PoseView[5] for protein-ligand interaction mapping in 2D, and DoGSiteScorer[6] for pocket detection and druggability prediction. Moreover, we will introduce novel services in development which are currently tested for their application to real-life challenges in the field of structure-based design covering the challenges of protein-ligand and protein-protein interface comparisons and the analysis of channels in protein crystals.
References:
[1] Schöning-Stierand, K., Diedrich, K., Fährrolfes, R., Flachsenberg, F., Meyder, A., Nittinger, E., Steinegger, R., and Rarey, M. (2020). ProteinsPlus: interactive analysis of protein-ligand binding interfaces. Nucleic Acids Res 48, W48-W53.
[2] Berman, H.M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T.N., Weissig, H., Shindyalov, I.N., and Bourne, P.E. (2000). The Protein Data Bank. Nucleic Acids Res 28, 235-242.
[3] Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., Tunyasuvunakool, K., Bates, R., Zidek, A., Potapenko, A., et al. (2021). Highly accurate protein structure prediction with AlphaFold. Nature 596, 583-589.
[4] Graef, J., Ehrt, C., Diedrich, K., Poppinga, M., Ritter, N., and Rarey, M. (2022). Searching Geometric Patterns in Protein Binding Sites and Their Application to Data Mining in Protein Kinase Structures. J Med Chem 65, 1384-1395.
[5] Stierand, K., and Rarey, M. (2010). PoseView - molecular interaction patterns at a glance. J Cheminformatics 2, 50.
[6] Volkamer, A., Kuhn, D., Grombacher, T., Rippmann, F., and Rarey, M. (2012). Combining global and local measures for structure-based druggability predictions. J Chem Inf Model 52, 360-372.

Primary authors: Dr SCHÖNING-STIERAND, Katrin (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr FÄHRROLFES, Rainer (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr GRAEF, Joel (Universität

Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr DIEDRICH, Konrad (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr EHMKI, Emanuel (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr FLACHSENBERG, Florian (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr SIEG, Jochen (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr PENNER, Patrick (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr PLETZER-ZELGERT, Jonathan (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Mr POBURSKI, Thorben (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Dr EHRT, Christiane (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design); Prof. RAREY, Matthias (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design)

Presenter: Dr EHRT, Christiane (Universität Hamburg, ZBH - Center for Bioinformatics, Research Group for Computational Molecular Design)

Session Classification: Poster session with buffet

Track Classification: CDL3 (Systems Biology)