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

The ProteinsPlus web server (<https://proteins.plus>) [1] offers modelling support for in-depth investigation of biomolecules. Users can perform computational studies for experimental protein structures from the Protein Data Bank (PDB) [2] and predicted models from the AlphaFold Protein Structure Database [3].

The services include structure quality analyses, structure preparation, geometric analyses, pocket prediction and characterization, binding site comparison, automated molecular docking, 2D interaction visualization, protein-protein interface classification, and mutation analyses.

In this contribution, we will present the ProteinsPlus web server in a nutshell with implications on their potential application domains in structure-based design.

[1] Schöning-Stierand *et al.* (2020). *Nucleic Acids Res* 48, W48-W53.

[2] Berman *et al.* (2000). *Nucleic Acids Res* 28, 235-242.

[3] Jumper *et al.* (2021). *Nature* 596, 583-589.

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1, 2, 3, 4

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