README:

The files included are one Word document explaining our methods and one Excel file that contain our results for each protein target named as NUWAVE\_ProteinTarget.

Each Excel file contains 2 sheets, the first sheet has the Extra Precision (XP) docking results and the second one has the Standard Precision (SP) docking results.

In the Excel files, the compounds are in order of Docking Score, starting with the best compound at the top.

Since we have also built homology models for NSP1 and for the Nucleocapsid protein structure, we have also included the 3D structure of the models that we built and used in a .pdb format.

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