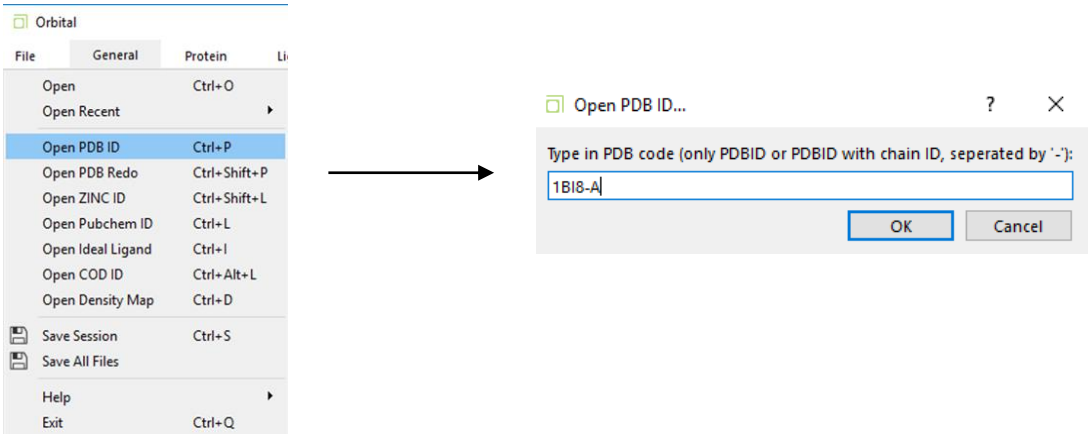
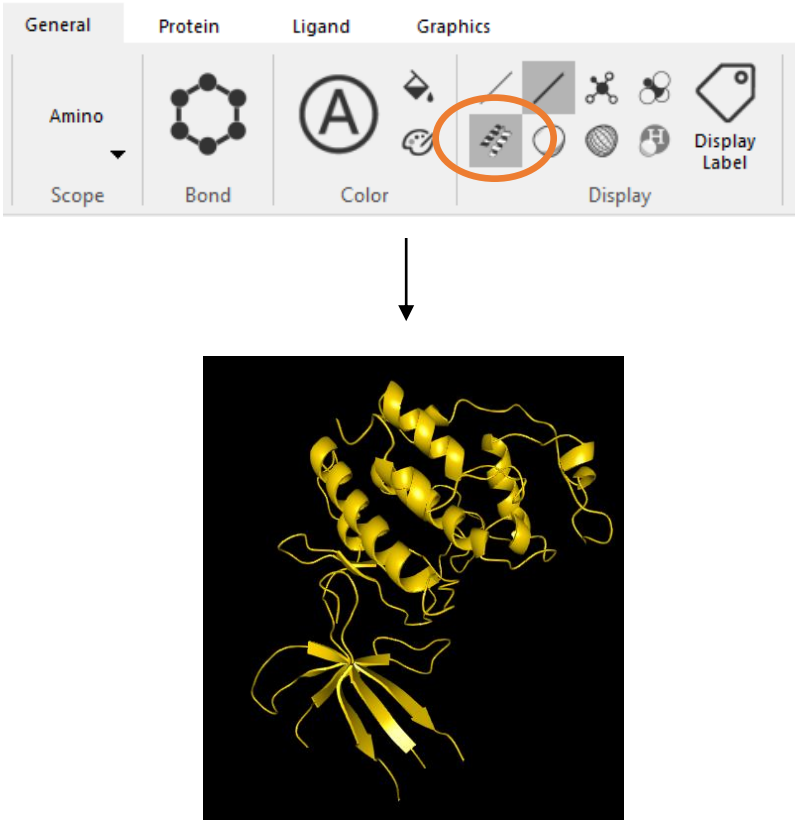
## Ensemble docking of Palbociclib using all similar structures starting from apo CDK structure

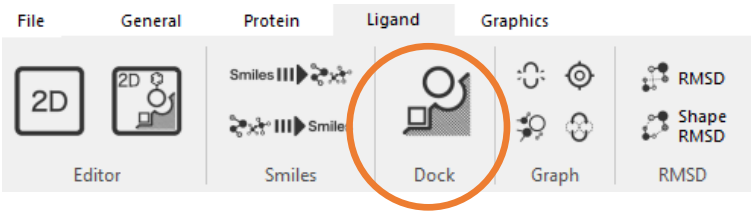
1. **Open** Orbital from the desktop. In the **File** dropdown menu, select **Open PDB ID** (Ctrl+P).
2. In the Open PDB ID popup window, enter the PDB ID **1BI8-A** and select OK in order to open the Crystal structure of the CDK6-P19$^{INK4D}$ inhibitor complex.




3. Under the **General** tab select the **Cartoon** setting in the **Display** panel and deselect the **Sticks** icon in order show the protein in its cartoon structure.

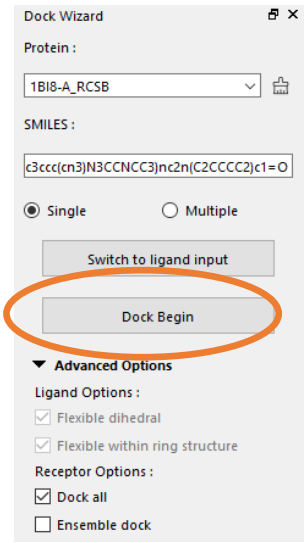


4. Next, select the **Ligand** tab and open the **dock wizard**

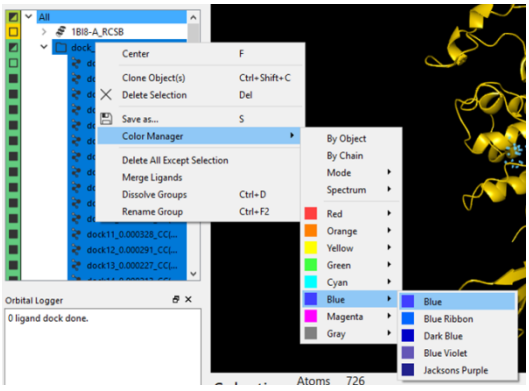



5. In the dock wizard, select **Switch to SMILES input.** Next, copy and paste the SMILES value for the ligand **LQQ** from the ligand summary on the RCSB PDB web page in the the Ligand Input in the Dock Wizard. (SMILES input: CC(=O)c1c(C)c2cnc(Nc3ccc(cn3)N3CCNCC3)nc2n(C2CCCC2)c1=O http://www.rcsb.org/pdb/ligand/ligandsummary.do?handler=biologyChemistry&hetId=LQQ)

6. Under **Advanced Options** check the dock all box and select **Dock Begin**.

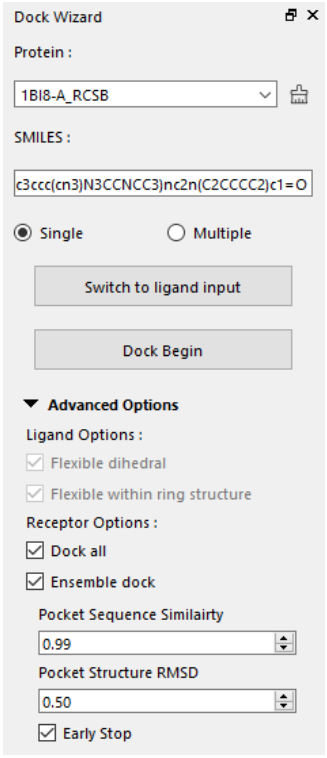


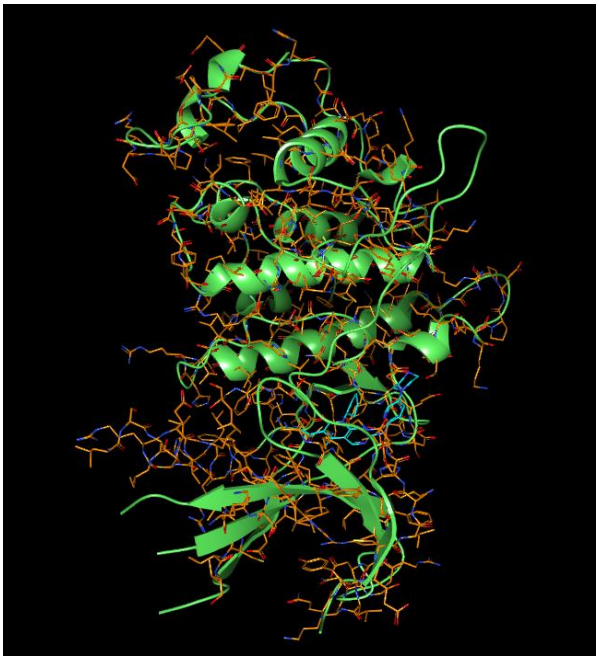

7. After the calculation is complete, select all docked conformations in the **Object Manager**, right click and change the color of the ligands to blue under **Color Manager.**

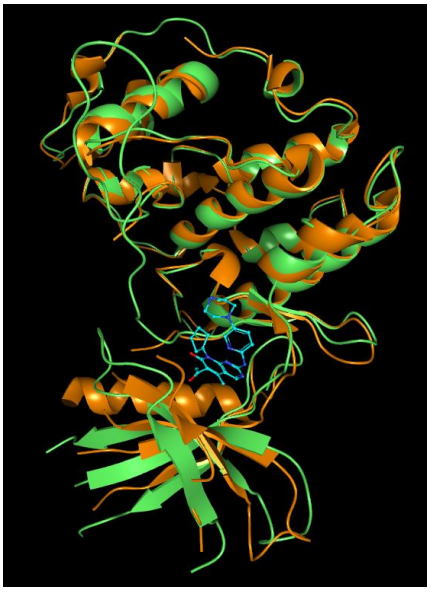


8. Use the scroll button on the mouse to select the first calculated ligand in the **Object Manager**. This action will center the ligand in the viewport.

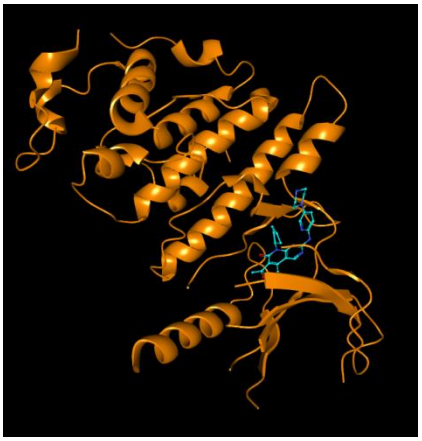
9. Under the Docking Wizard in **Advanced Settings**, select the Ensemble dock button and in **Pocket Sequence Similarity** input a value of 0.99. Hide the all currently selected ligands before pressing **Dock Begin.**



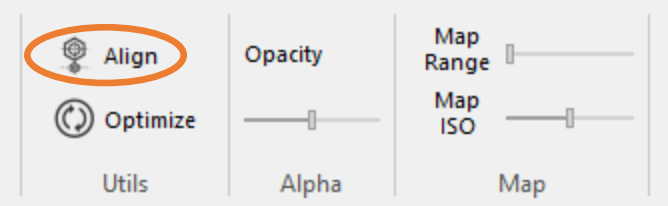


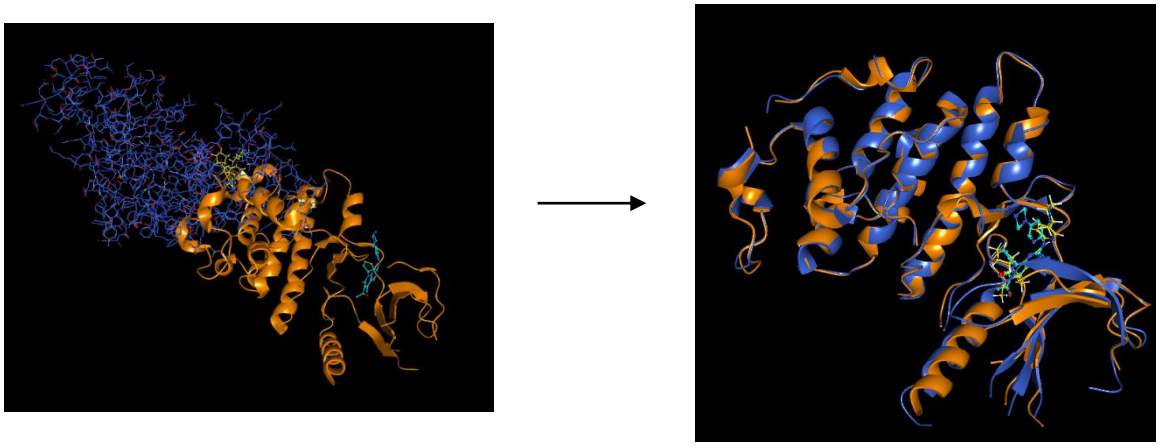
10. Next, in the object manager delete all docked ligands except for the first output (shown in blue). In addition, hide all **sticks** and show **cartoon** in the display panel as before. Next, hide the original protein (in green) by checking the box next to the name in the **object manager.**



11. Open the **File** menu and select **Open PDB ID** (Ctrl+P) to open the protein **5L2I** as shown in step 1.

12. First, select the protein that is moving in the **object manager,** second, select the reference protein and then click **Align** in the General tab in order to finish the structure alignment.



13. Select both ligands with the middle scroll button using the **Object Manager** in order to zoom in on the selection. From here, RMSD can be calculated as shown in previous tutorials. (RMSD = 2.05 Angstroms).