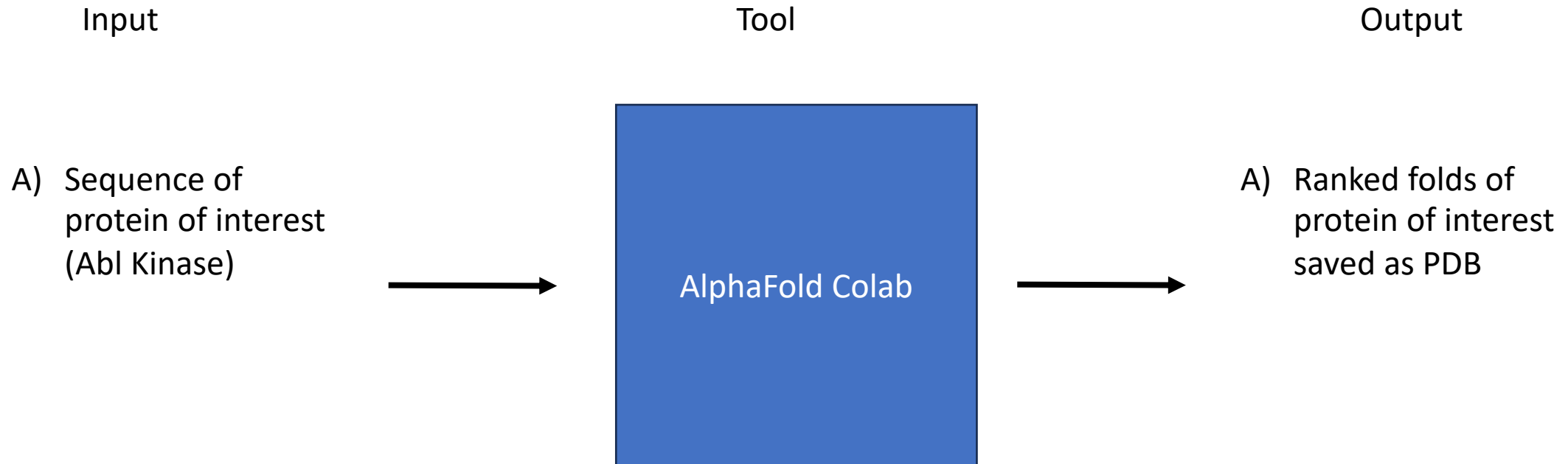


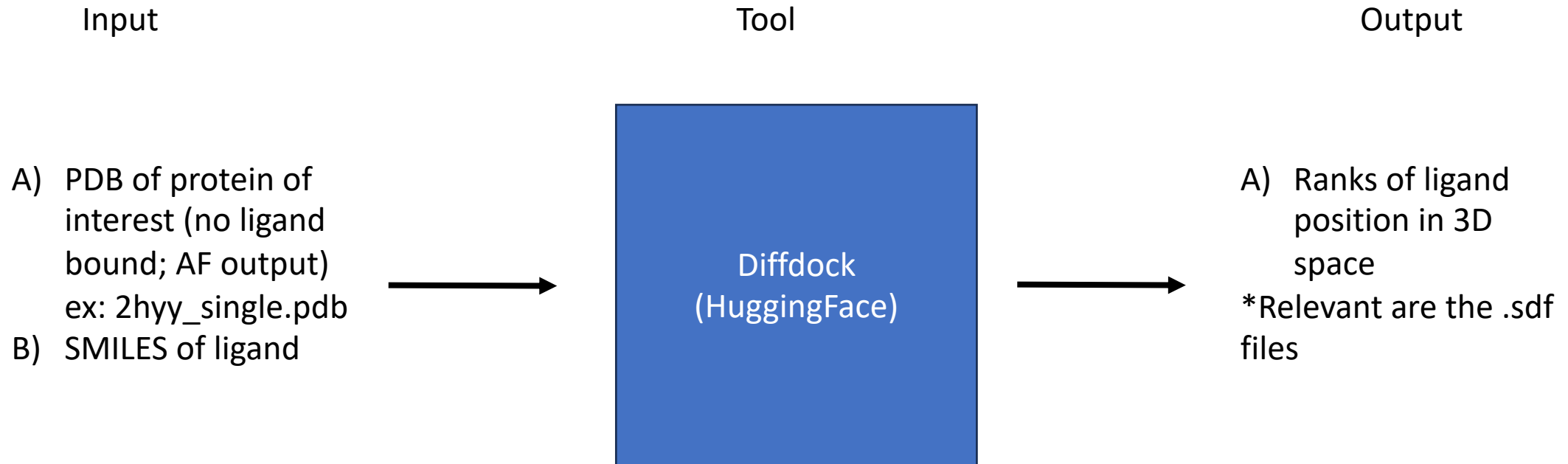
Procedure for Assessment II

2023.11.20

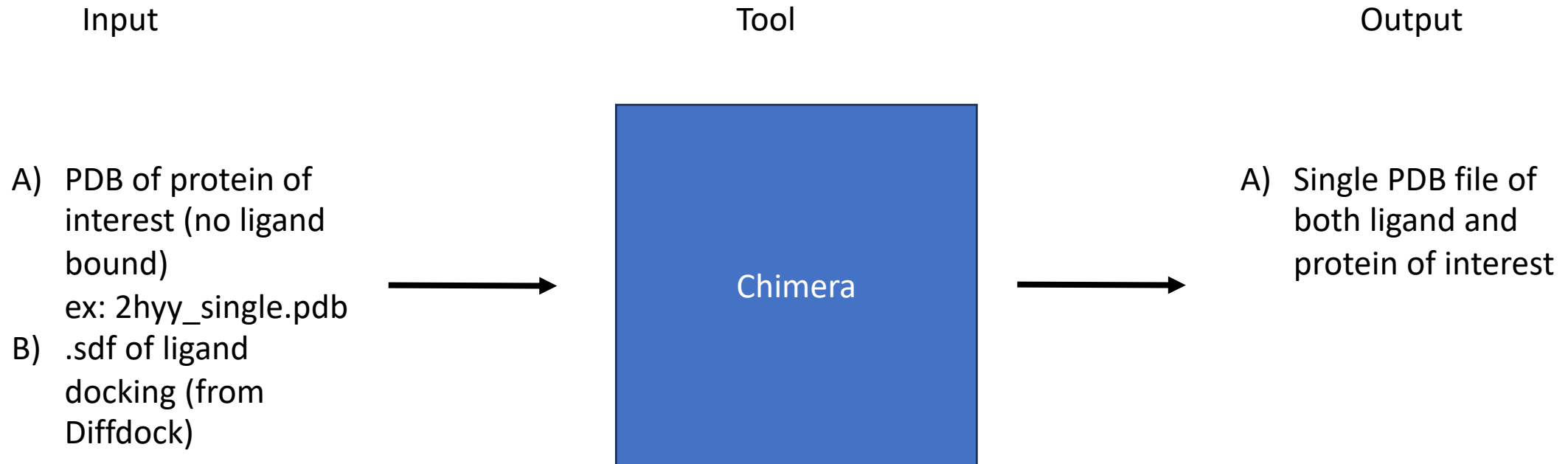
Step 0. (Pre-Work related) Fold your protein with AlphaFold



Step 1. Docking your Ligand



Step 2. Saving diffdock/PDB files to a PDB



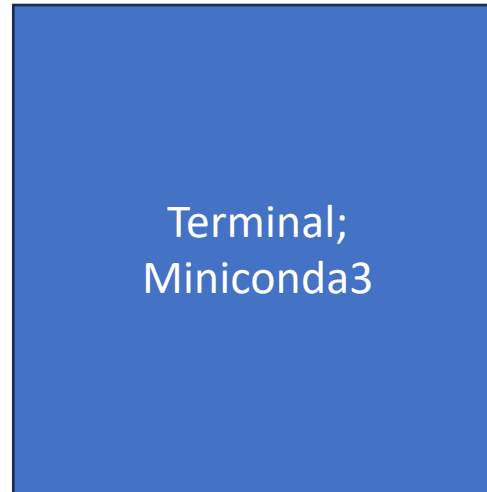
Step 3. Combining PDB docking as a readable input for LigPlot

Input

Tool

Output

- A) PDB from Step 2.
- B) `process_ligand_protein.py`



- A) Combined single PDB file of both protein of interest and ligand position

Step 4. Visualizing in LigPlot+

