Programs:

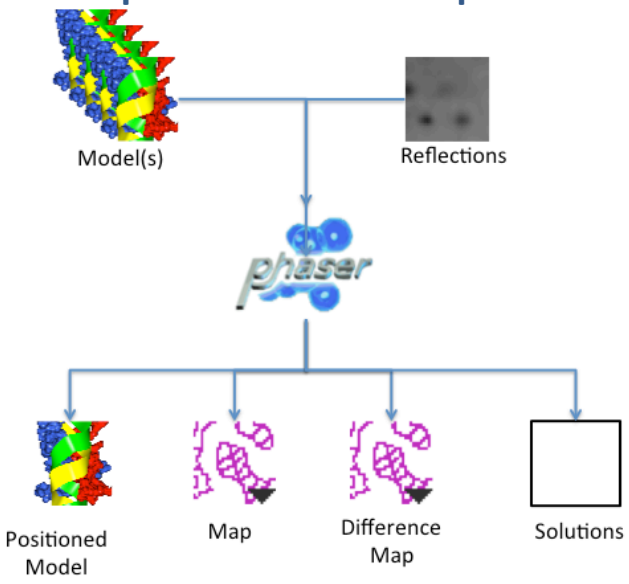
LIDIA, PHASER, ACEDRG, REFMAC, RDKIT, COOT

Scenario

(Accurately) informed that there is "a lot of chod" among the structure ligand complexes in the PDB, you decide to re-solve the structure of everyone's favourite PPI drug target MDM2 in complex with the game-changing tool compound Nutlin 3A.

There is a dodgy 1.6 angstrom structure (4hg7) deposited by a disreputable group….so you plan to use only the deposited reflections for that structure. There is a nice MDM2 structure from another group that you choose for your startpoint (1t4e). You plan to use modern tools to make a start model for Nutlin 3A.

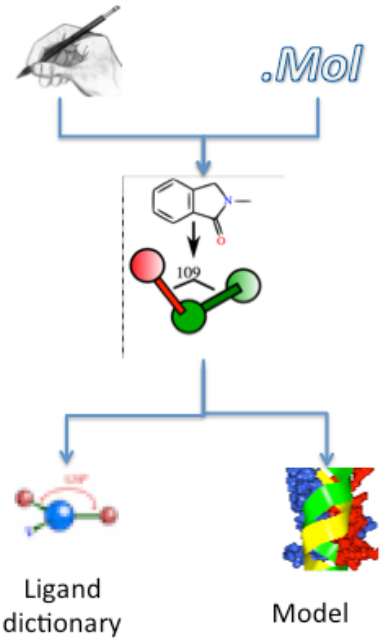
Task 1: Molecular replacement – Molrep or Phaser



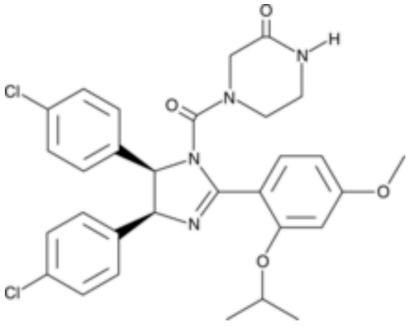
HINT: You can import files (reflections or coordinates) from the PDB directly: in the file browser dialog (accessed by clicking ): a line at the top allows you to provide the accession code.

HINT: Several tasks (e.g. Phaser molecular replacement) allow you to use a "selection" or subset from the coordinates you provide. For molecular replacement, it may be worthwhile specifying to use only one chain of a model you download: they often contain more than one chain. The syntax for specifying subsets is well worth knowing, but to specify chain A, you need only provide the selection string "A/" (quotation marks should not be included).

Task 2: Make your ligand – Make ligand task (LIDIA, ACEDRG, RDKIT)



Hint: The structural formula of Nutlin 3A is:



Hint: Lidia (currently) requires you to click both “Apply” and “Quit” to fire up the coordinate generating stuff

Task 3: Introduce your ligand into the structure (Manual model building: COOT)