Shows how to prepare ligand and use AutoDock Wizard. Please note that pdb structure has been changed since I made this video (see, for instance, [pdb-l: Modifying existing PDBs](#) and [pdb-l: Chain order changes: a problem for Proteopedia](#)). Please use PyRx's built-in text editor available under Documents tab (or any other text editor) as described in [Load/Import Molecule](#). I have also made a local copy of [hiv-1protease1.pdb](#) that you can use to follow this screencast.

Shows how to read SDF files, do energy minimization and convert them into PDBQT.