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.