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](https://www.proteopedia.org/wiki/index.php/pdb-l:Modifying_existing_PDBs) and [pdb-l: Chain order changes: a problem for Proteopedia](https://www.proteopedia.org/wiki/index.php/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](https://www.proteopedia.org/wiki/index.php/Load/Import_Molecule). I have also made a local copy of [hiv-1protease1.pdb](https://www.proteopedia.org/wiki/index.php/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.