There is a new article in J. Chem. Inf. Model. that talks about ParaDockS. This is the only other docking program, besides AutoDock 4 and Vina, that is open source. Congradulations to ParaDockS team for making such a great product available!

This means that PyRx can some day use ParaDockS and vise versa, so here I'll summirize main features of ParaDockS. First, it's using particle-swarm optimizer, similar to PSO@Autodock. Unlike, AutoDock 4, which uses force field-derived (AMBER) objective function, ParaDockS is using knowledge-based potentials. I look forward for the new developments in this area.