1. Acquire pdb from database, make resfiles, submit first minimization job and convert pdb numbers to rosetta numbering (**resfile\_find\_neighbors.py**). The minimization job command line is in **submit\_minimize.py**
2. Then submit backrub and repack/mutate jobs in a separate directory (**submit\_backrub\_wt.py**)
3. Then submit final minimization step on all 200 structures (wt\_repacked ensemble and mutant ensemble). The job command line is in **submit\_final\_min.py**
4. Then separate monomer from partner (**find\_partners\_wt.py**)
5. Final rescoring of complex, monomer and partrner pdbs (**submit\_final\_natro.py**)
6. Compute DDG using **find\_ddg\_af\_wt.py**