\section{Methodology}

At the core of investigating prediction of protease binding affinity to HIV-1 is the Rosetta software. This software is integrated at the University of Copenhagen. In fact, a pipeline has been set up for running $\Delta\Delta G$ calculations. This pipeline is heavily utilized and slightly modified to fit the scope of this paper. \\

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--Explain the pipeline: mutfiles, pdb, alignemnet, relaxation, ddG calculations etc.--

\section{Results}

--Histograms--

--Heatmaps--

--predicted ddG vs. ?log? drug fold--