Virtual Screening on HIV-1 Reverse Transcriptase Inhibitors

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Abstract

Acquired Immunodeficiency Syndrome (AIDS) epidemic has affected human lives in both developed and developing countries equally. The causative agent for this dreaded disease is a virus called HIV (Human Immunodeficiency Virus). The enzyme reverse transcriptase (RT) plays an important role in its activity. High-throughput screening (HTS) has been advantageous over traditional methods of screening in terms of time and money. HTS uses a brute-force approach to collect a large amount of experimental data – usually observations about how some biological entity reacts to exposure to various chemical compounds, in a relatively less time interval. The inhibitors in RT were explored using flexible docking involving computational approaches and were ranked by the calculated affinity. During the course of present study, a diversity set of 1990 molecules (NCI diversity database) were screened using UCSF DOCK 5.0. Fifteen molecules were found to have docked in the NNRTIs pocket with very low energies. The ligand-protein model produced a way to evaluate the activity of interested inhibitors. These compounds can act as potential lead compounds. The active compounds found are polycyclic (aromatic as well as aliphatic) and nitrogen heterocyclic. Each molecule gave a good number of conformations showing the flexible behavior of the ligand. The total energy of receptor-ligand complexes in best fit mode has also been calculated.