Sanjeevini 2.0 – a complete drug discovery suite

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The Sanjeevini2.0 software package is a cutting-edge, all-encompassing solution that could be utilized for both structure-based as well as ligand-based lead molecule discovery. The suite is made up of five major modules developed in-house, which are active site prediction (AADS[1]), rapid screening of millions of molecules against target proteins (RASPD+[2]), atomic level docking (ParDOCK[3]), scoring and binding affinity prediction (BAPPL+[4]), and reverse screening of target proteins (FishBAIT) to assess bioactivity of input molecules. This pipeline can potentially address challenges currently faced by drug discovery programs across the world in translating a comprehensive understanding of human disease and cutting-edge technology into therapeutic relevant molecules. The pipeline was validated on 120 FDA-approved targets involved in significant life-threatening diseases. A single target protein takes approximately 15–20 minutes for the entire pipeline to complete for predicting a candidate drug molecule. The pipeline was able to successfully re-address the known FDA-approved drugs against the target protein in ~ 90% of cases. As a result, the entire methodology can stimulate and simplify the process without reducing efficiency. This software is freely available to users at http://www.scfbio-iitd.res.in/Sanjeevini/index.php.

References

1. Singh, Tanya, D. Biswas, and B. Jayaram. "AADS-An automated active site identification, docking, and scoring protocol for protein targets based on physicochemical descriptors." Journal of chemical information and modeling 51.10 (2011): 2515-2527.
2. Holderbach, Stefan, et al. "RASPD+: fast protein-ligand binding free energy prediction using simplified physicochemical features." Frontiers in molecular biosciences, 7 (2020): 601065.
3. Gupta, A., et al. "ParDOCK: an all atom energy based Monte Carlo docking protocol for protein-ligand complexes." Protein and peptide letters, 14.7 (2007): 632-646.
4. Soni, Anjali, Ruchika Bhat, and B. Jayaram. "Improving the binding affinity estimations of protein-ligand complexes using machine-learning facilitated force field method." Journal of Computer-Aided Molecular Design 34.8 (2020): 817-830.
5. G. Mukherjee and B. Jayaram. "A rapid identification of hit molecules for target proteins via physico-chemical descriptors." Physical Chemistry Chemical Physics, 15.23 (2013): 9107-9116.
6. Jain, Tarun, and B. Jayaram. "An all atom energy based computational protocol for predicting binding affinities of protein–ligand complexes." FEBS letters 579.29 (2005): 6659-6666.
7. Ruchika Bhat, Rahul Kaushik, Ankita Singh, Debarati DasGupta, Abhilash Jayaraj, Anjali Soni, Ashutosh Shandilya, Vandana Shekhar, Shashank Shekhar, B. Jayaram, " A comprehensive automated computer-aided discovery pipeline from genomes to hit molecules" *Chemical Engineering Science*, **2020**. https://doi.org/10.1016/j.ces.2020.115711