

Assessing molecules from some Indian Medicinal Plants against breast cancer

Devendra Prajapat^{1,2} and *B. Jayaram*^{1,2,3,*}

1– Supercomputing Facility for Bioinformatics & Computational Biology, 2 – Department of Chemistry, 3 – Kusuma School of Biological Sciences, Indian Institute of Technology Delhi, Hauz Khas, New Delhi, India – 110016.

devendra@scfbio-iitd.res.in, bjayaram@chemistry.iitd.ac.in, Ph: 01126591505

Abstract

The cornerstone of breast cancer hormonal therapy is estrogen receptors (ER α and ER β)¹. Estrogen binds to ERs, causing DNA synthesis and cellular proliferation in hormone-responsive breast cancer. About 75% of breast tumours express ER α and may be cured with drugs that inhibit estrogen-mediated signalling. In this work, we propose to use Indian medicinal plants: Neem, Tulsi and Turmeric², to design ER α Inhibitors as these plants have extensively been used in Ayurveda. We prepared a database of 360 molecules from these plants and performed virtual screening using in-house developed [RASPD](#)³. The top 100 molecules from screening were put through molecular docking using in-house developed [ParDock](#)⁴, and finally, the top 10 molecules were assessed with molecular simulations and free energy estimations. The molecules with the favourable free energy of binding are proposed to be tested on ER α (MCF-7) and ER β (MDA-MB-231) cell lines to study their biological activity and cytotoxicity and siRNA silencing analysis to verify the ER α selectivity. This study is expected to add to the success stories of *Sanjeevini*⁵ and revalidate the idea that understanding the magical cures that Indian Medicinal Plants offer at a molecular level will help in disseminating the knowledge and cures to the whole world.

References

1. Bhatnagar S, Soni A, Kaushik S, Rikhi M, Santhoshkumar TR, Jayaram B. Nonsteroidal estrogen receptor isoform-selective biphenyls. *Chem Biol Drug Des.* **2018** Feb;91(2):620-630.
2. http://www.scfbio-iitd.res.in/plants_scfbio/
3. Holderbach, Stefan, et al. "RASPD+: fast protein-ligand binding free energy prediction using simplified physicochemical features." *Frontiers in molecular biosciences*, 7 (2020): 601065.
4. Gupta A et al. ParDOCK: an all-atom energy-based Monte Carlo docking protocol for protein-ligand complexes. *Protein Pept Lett.* **2007**;14(7):632-46.
5. Ankita Singh, Shashank Shekhar, B. Jayaram, "CADD: Some success stories from *Sanjeevini* and the way forward", in *Innovations and Implementations of Computer Aided Drug Discovery Strategies in Rational Drug Design*", Springer Nature, Singapore Pte Ltd. S. K. Singh (ed.), **2020**.