In silico identification of Potential drug compound against N-Terminal Domain of the Androgen Receptor by Virtual screening, Docking, ADME toxicity and MD Simulation for the treatment of Prostate cancer

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Prostate Cancer is a type of cancer affecting the prostate gland. As the prostate gland is directly involved with sexual reproduction, this disease affects semen production and fertility in males. In intial stages of the disease, no symptoms may occure but in later stages it can lead to difficulty in urination, hematuria, pain in the pelvis, pain in back and pain while urinating. Currently no effective treatment is available. Approaches such as combination of surgery, radiation therapy, hormone therapy or chemotherapy are some prefers. N-Terminal Domain (NTD) of the Androgen Receptor (AR) harbors the critical region for transcriptional activity which initiates the cancer development. As reported earlier, the N-Terminal Domain of the Androgen Receptor has already been recognized as a potential site for therapeutic target for the discovery and development of novel anti-cancer drugs. Currently, it has been reported that the experimental 3D structure of the said receptor helps us exclusively to identify potential drug candidate for the treatment of the said disease. In this study, the virtual screening technique was employed to explore the potent inhibitors of 3D structue of the N-Terminal Domain of androgen Receptor from Zinc Database. Total 3444 hits were identified which were further filtered based on drug-like proterties using Lipinski's rule of five, Egan Rule, Muegge Rule, Veber Rule, Ghose Rule. The results showed 44 molecules as leads which were further subjected to Lead Optimization by Docking, ADME and Toxicity study tools. The results identified 06 potential molecules which can be useful as the potential drug candidates for the treatment of Prostate cancer. The number of drug candidates could be further reduced by MD simulation and the results could be validated using In-vitro/In-vivo studies.