The prostate cancer-fighting powers of soursop fruit: *in silico* evaluation to give insight into binding affinity of selected bioactive compounds on selected prostate cancer targets.

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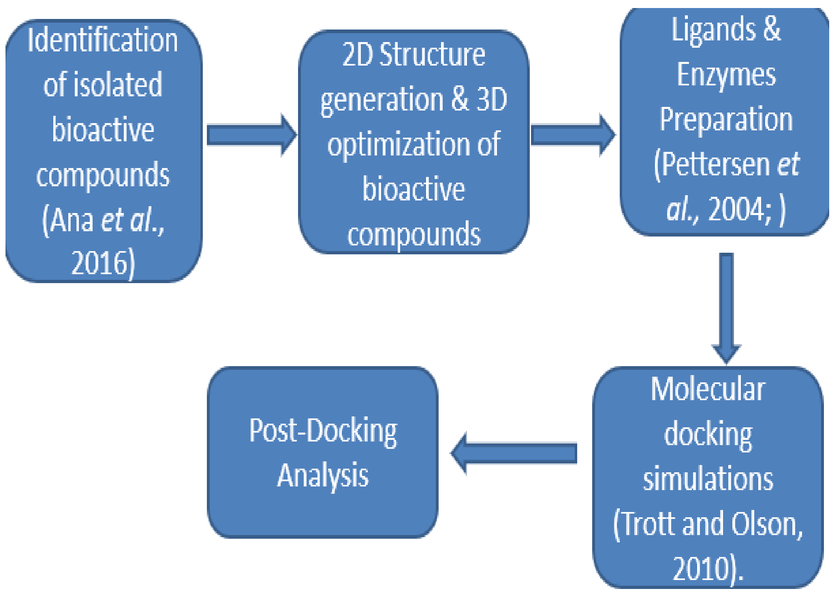
Introduction

Sour sop, (*Annona muricata*) which is indigenous to the tropics belongs to the family Annonaceae. Parts of the plant has been used in traditional medicine to cure several diseases. The physiological, physicochemical and nutritional characteristics of sour sop plant has been reported in several studies, alongside the presence of bioactive compounds in the pulp, seed, columella and peel. (Ana et al., 2016)

Prostate cancer is the most cancer diagnosis in men and is still the third-leading cause of cancer related death in males.

Bioactive compounds isolated from the pulp have demonstrated cytotoxic activity against human prostate cancer cells, as reported by several studies. Amongst which seven were selected for the purpose of this study. This study employed *in silico* method to provide insight into the binding affinity of some bioactive compounds present in soursop pulp as compared to native ligand present in the target enzymes Androgen Receptor (AR) and primary poly (ADP-ribose) polymerase (PARP) with PDB (Protein Data Bank) codes, 2HYD and 7ONS respectively.

Method



Results and Discussion

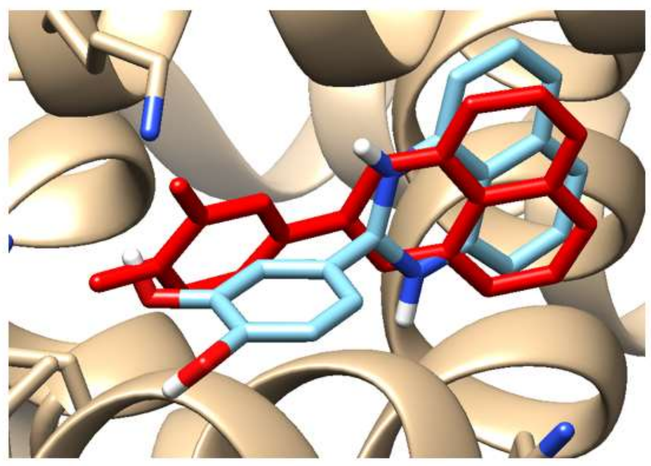


FIG 1:Crystal structure of enzyme complex and re-docked ligand super-imposed on the crystal structu of AR for validation. The redocked ligand is blue

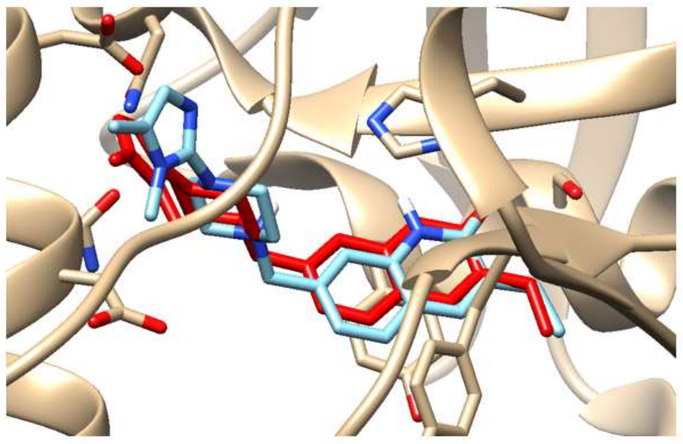


FIG 2 :Crystal structure of enzymes complexes and re-docked ligand super-imposed on the crystal structure for validation PARP1. The redocked ligand is blue.

Table 1: Showing the binding energy result of the co-crystallized ligands; Ligands 1-7 against PARP1 and AR

Ligands	PARP1 [7ONS];(-11.1 kcal/mol)	AR [2YHD] (-6.1) kcal/mol
Lig1	-9.4	-6.1
Lig2	-9.0	-5.6
Lig3	-9.0	-5.4
Lig4	-8.8	-5.5
Lig5	-7.4	-4.0
Lig6	-9.3	-5.7
Lig7	-9.5	-5.4

Conclusions

- Binding free energy analysis revealed that Lig 1,6 and 7 binding to enzymes (2YHD and7ONS) was favorable with high negative ΔG values. This correlated with the favorable contribution of the van der Waals and electrostatic energy.
- Favorable binding also existed between the active site residues of both enzymes 2YHD and 7ONS and the selected ligands which could account for its stabilization and binding affinity.
- We are certain that these outcomes will advance therapeutic interventions towards the treatment of Prostate cancer and the structure-based design of potent anti-cancer.

Acknowledgments

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