PSNGOM010

Comparative in-silico analysis of the toxicity profile and binding affinity of curcumin and dasatinib to lyn protein

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Background

Lyn kinase's discovery as a catalyst for aggressive behaviour in triple-negative breast cancer (TNBC) continues to be a major concern for both researchers and those living with breast cancer. Several biological processes relies on protein-ligand interactions. It is therefore vital to assess a ligand's binding affinity for it's transmembrane receptor as this reveals the effectiveness of the ligand. Molecular docking has emerged a key technique in drug development due to it's relatively low cost implication and it's apparent ease of use. Medicinal plants have been considered the corner stone of health maintenance and care worldwide.

Aim

To comparatively evaluate the binding affinity and toxicity profile of curcumin and dasatinib to lyn protein

Methods

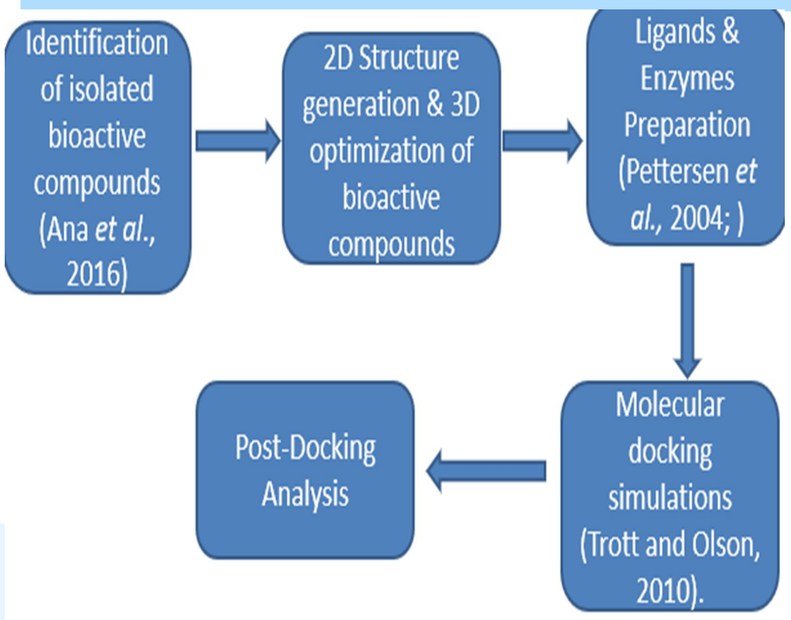
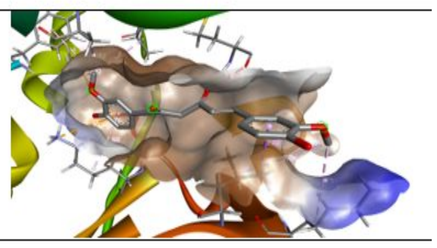
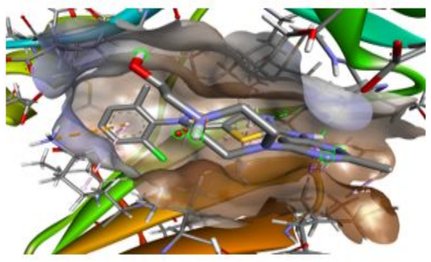


FIG 1 : Flow chart summarizing method used in the study

This study, employed molecular docking techniques as well as in silico methods of toxicity testing to comparatively study the binding affinity as well as toxicity of curcumin as compared to the native ligand (dasatinib) respectively.

Results

TABLE 1: Showing the binding affinity and ligand interaction with receptor

CHEMICAL COMPOUND	BINDING AFFINITY (kcal/mol)	LIGAND INTERACTION WITH RECEPTOR
Curcumin	-7.8	
Dasatinib	-9.8	

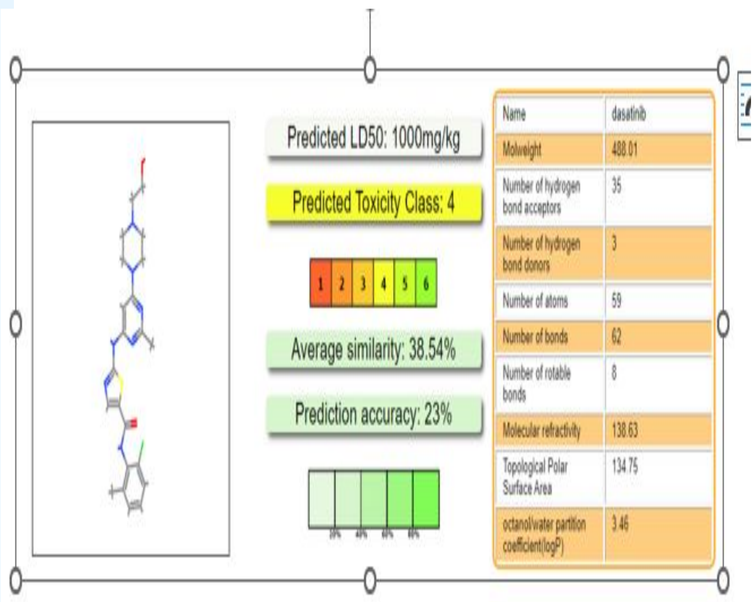


FIG 2 : Toxicity profile of dasatinib

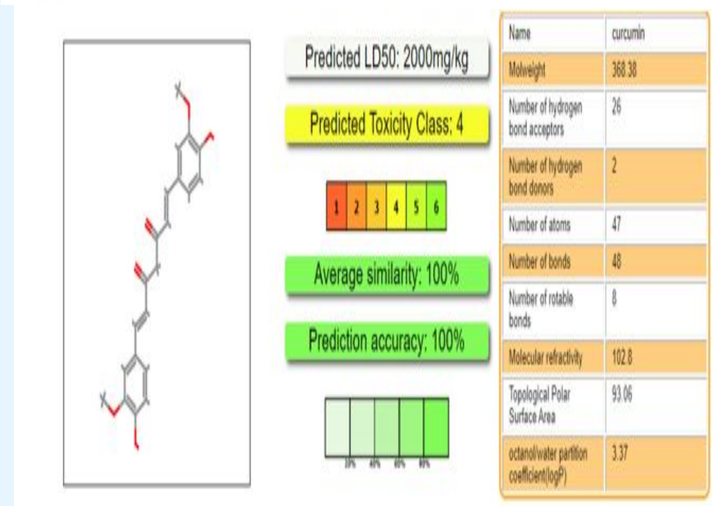


FIG 3: Toxicity profile of curcumin

More Results

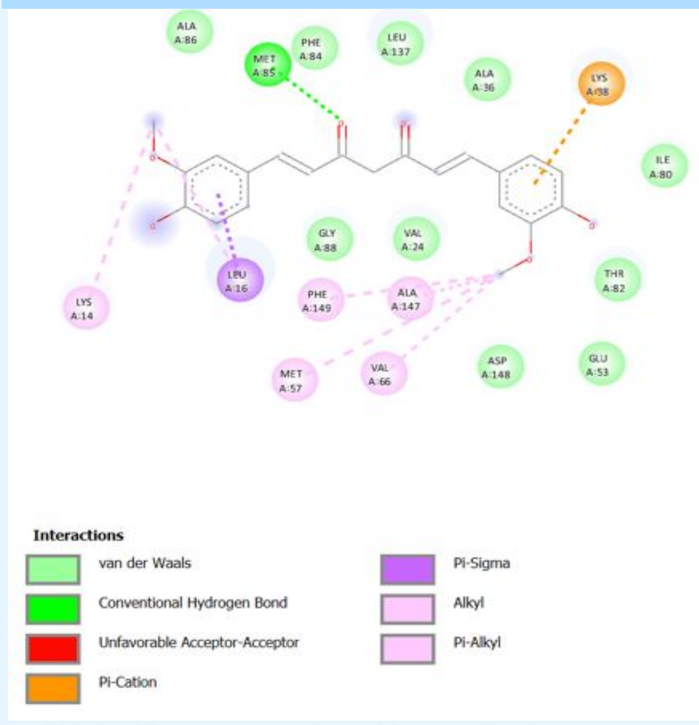


FIG 4: 2D representation of interaction between curcumin and residues on the target

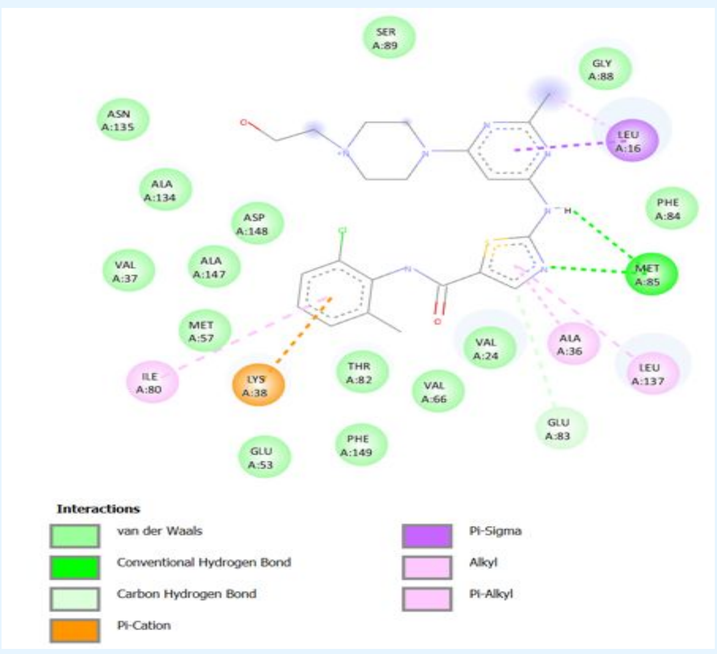


FIG 5: 2D representation of interaction between dasatinib and residues on the target

Conclusions

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Binding free energy analysis revealed that the binding of curcumin to Lyn enzyme was favorable with high negative ΔG values comparable to that of dasatinib. This correlated with the favorable contribution of the van der Waals and electrostatic energy. Favorable binding also existed between the active site residues of curcumin and Lyn which could account for its stabilization and binding affinity.
The toxicity profile revealed that curcumin was less toxic than dasatinib, though they both fall under class 4.
Results obtained from this study revealed the anticancer potential of curcumin: this could make it easier to create bioactive molecules using structure-based drug design and ultimately cure triple-negative breast cancer.

•References

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