Supplementary Data

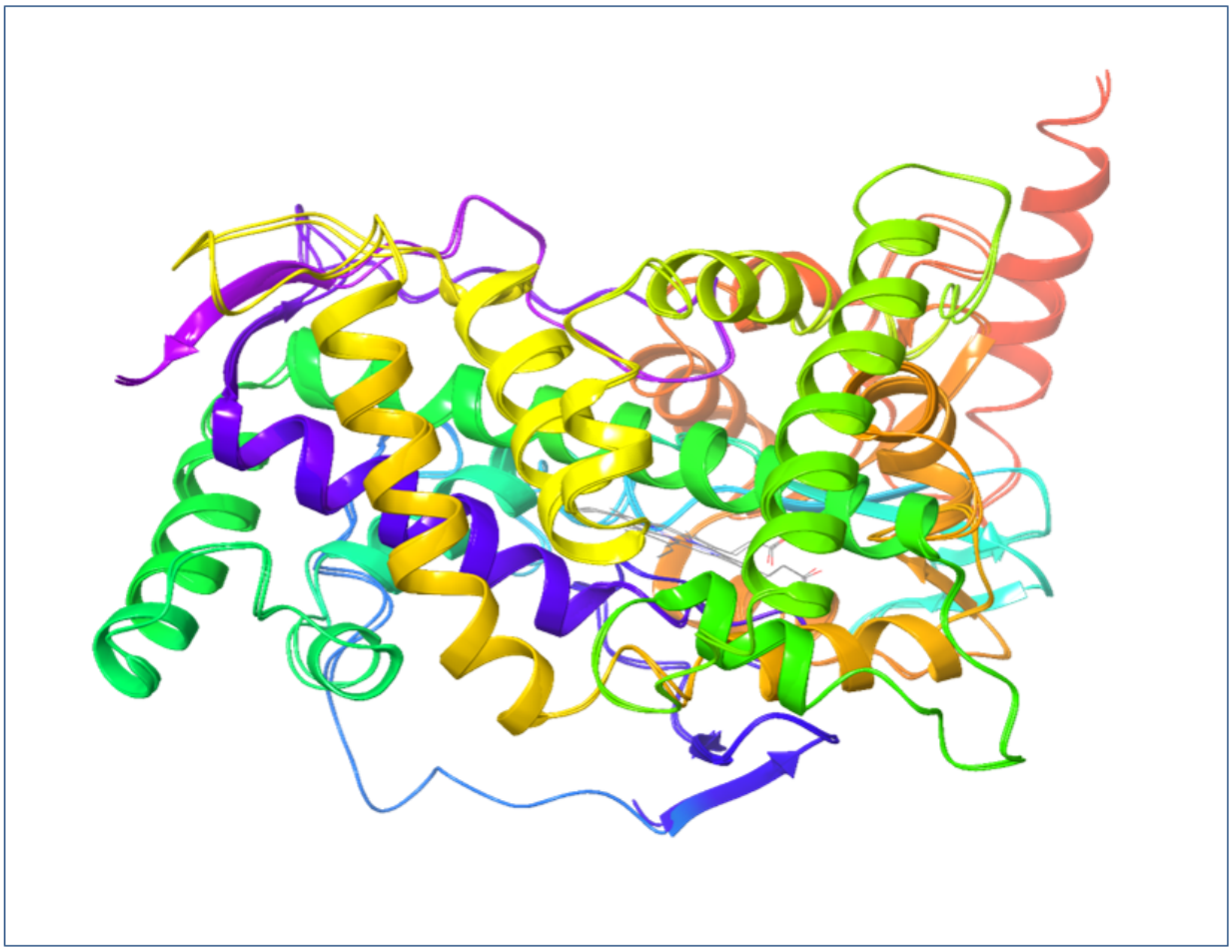
Supplementary material and methods

Homology modelling of *C. auris*

The alignment and sequence analysis showed high homology of *C. auris* protein to *C. albicans* CYP51 crystal structures (PDB: 5V5Z, 5FSA and 5TZ1). The globally conserved residue search identifies *C. albicans* CYP51 crystal structures (PDB: 5V5Z) as a template with 70% identity, 83% positives at alignment score of 2079. ClustalW was used to align the *C. auris* sequence with the template sequence, revealing the matching and mismatched amino acids (**Supplementary Figure 1**). The alignment of protein structure showed low RMSD value of 0.214 Aº **(Supplementary Figure 2)**, while the active site analysis showed 71.7%, 79.25% and 81.13% within 7 Aº identity, similarity, and conservation, respectively (**Supplementary Table 1)**. *C. albicans* CYP51 crystal structures (PDB: 5V5Z) active site amino acids (Ala-62, Gln-66, Leu-87, Ile-304, Cys-470, Phe-475, Tyr-477, Val-487, Gln-479) were mismatched with the *C. auris* constructed model (Val-62, Met-66, Met-87, Val-304, Phe-458, His-463, Cys-465, Ile-466, Gly-467, Tyr-501, Gln-502, Ser-503, Met-504, Val-505 and Thr-506) **(Supplementary Figure 3)**, which are within the 4-6 Aº distance from the co-crystalized ligand of CYP51 enzyme. The homology model of *C. auris* was built using Swiss modeler as shown in (**Supplementary Figure 4)**. The validation of the model was carried out with Ramachandran plot, which showed that most amino acid residues of the modeled protein were clustered in the most favored region (red region) around normal value of phi and psi (**Supplementary Figure 5**).

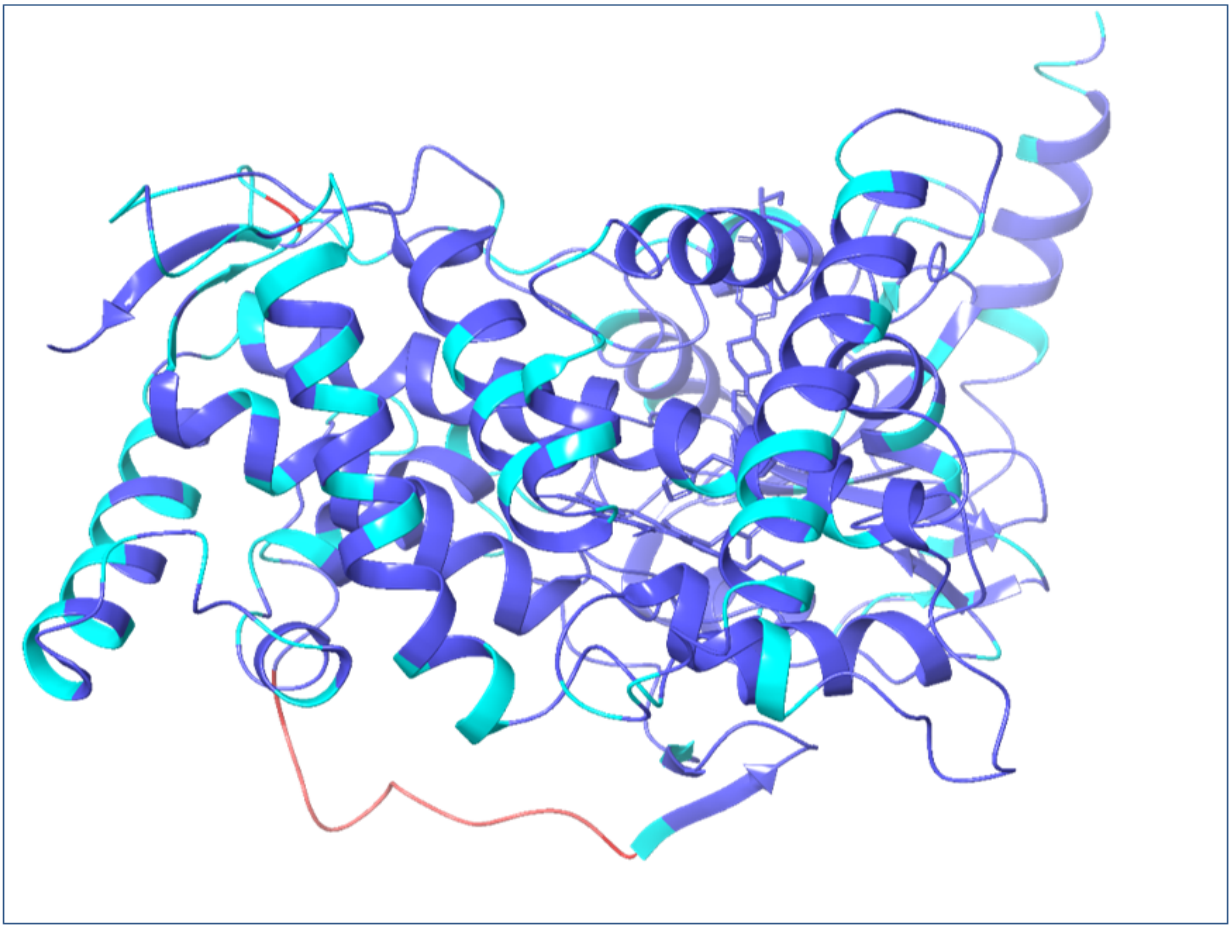
Supplementary Figures

Supplementary Figure 1. Multiple Sequence alignment (MSA) of constructed model of *C. auris* and the template sequence of *C. albicans*.

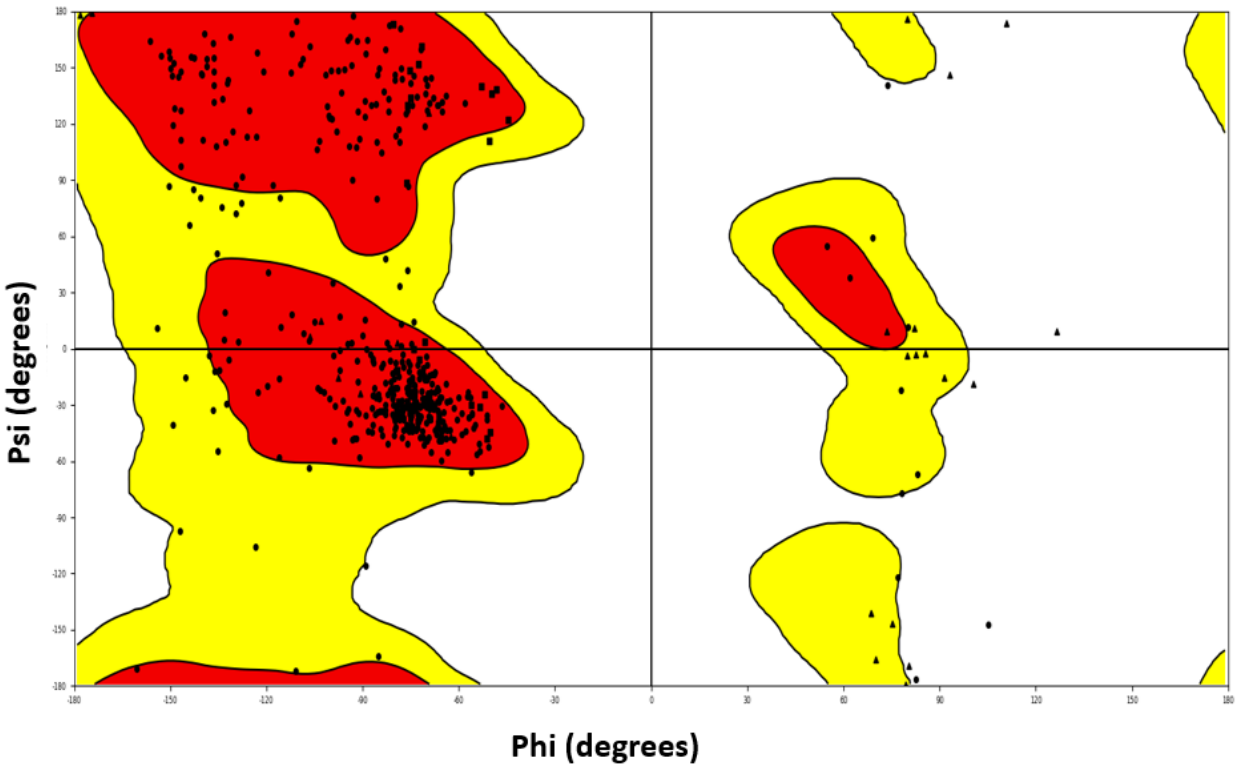


Supplementary Figure 2. Superposition and protein structure alignment with RMSD value 0.214 Aº of the *C. auris* model structure and using *C. albicans* (PDB:5V5Z) template structure. The *C. albicans* (PDB:5V5Z) crystal structure displayed as ribbon schematic color and the model with color blue.

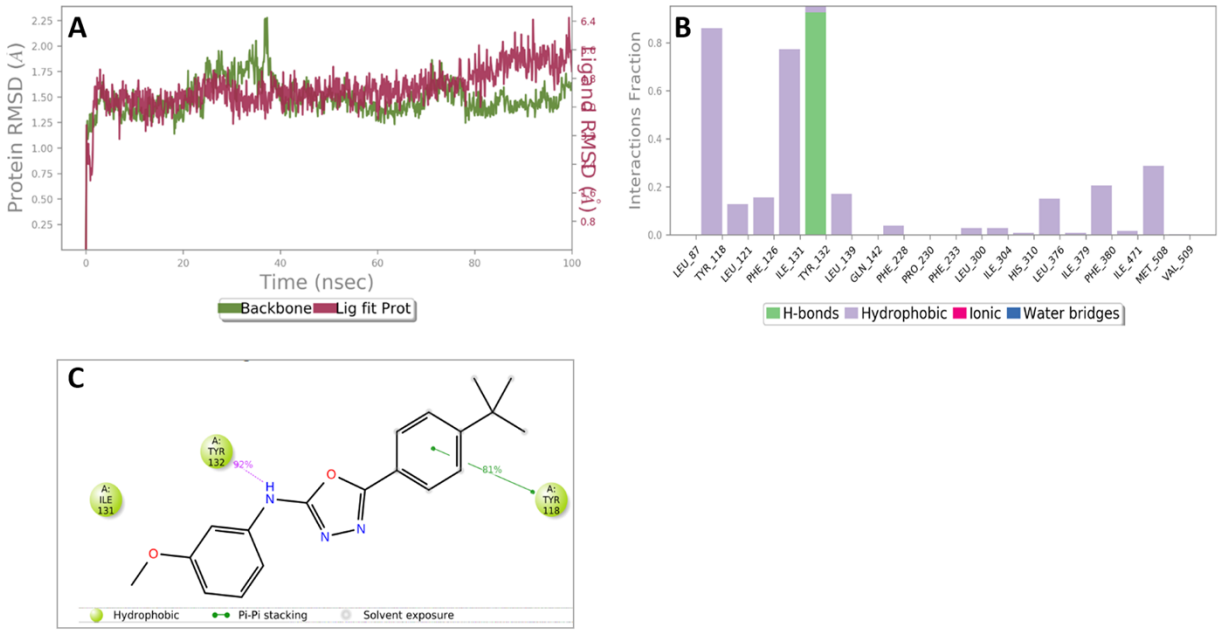
Supplementary Figure 3. Binding site analysis showed the matched and mismatched amino acid residues. The purple, gray color indicates 4, 6 Aº away from the native ligand.



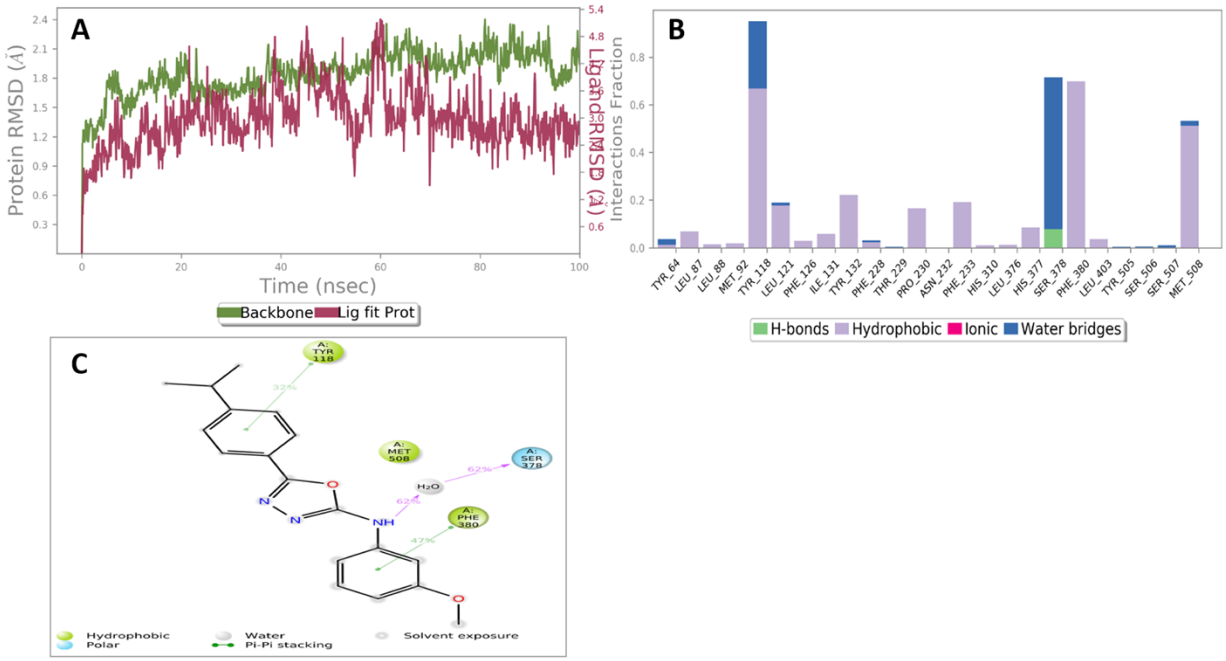
Supplementary Figure 4. Generated model of *C. auris* sequence using *C. albicans* as template**.**



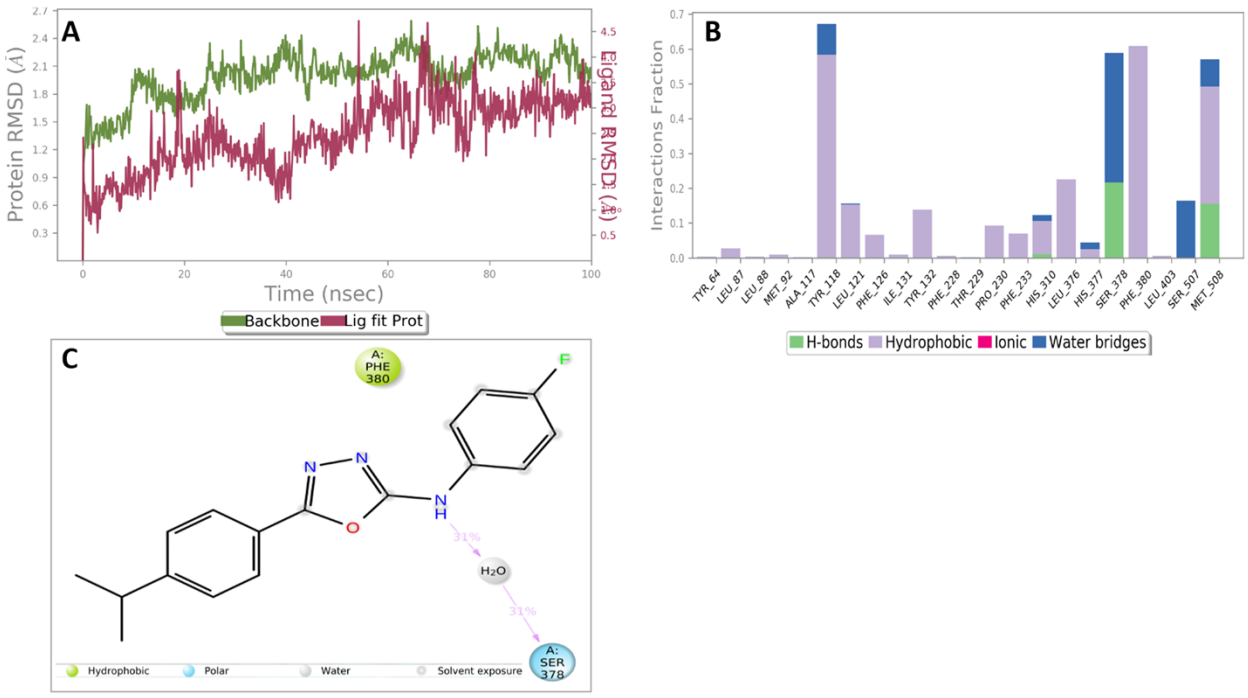
Supplementary Figure 5. Ramachandran plot of *C. auris* modeled protein shows red as most favored regions red, yellow as allowed regions and white as disallowed regions.



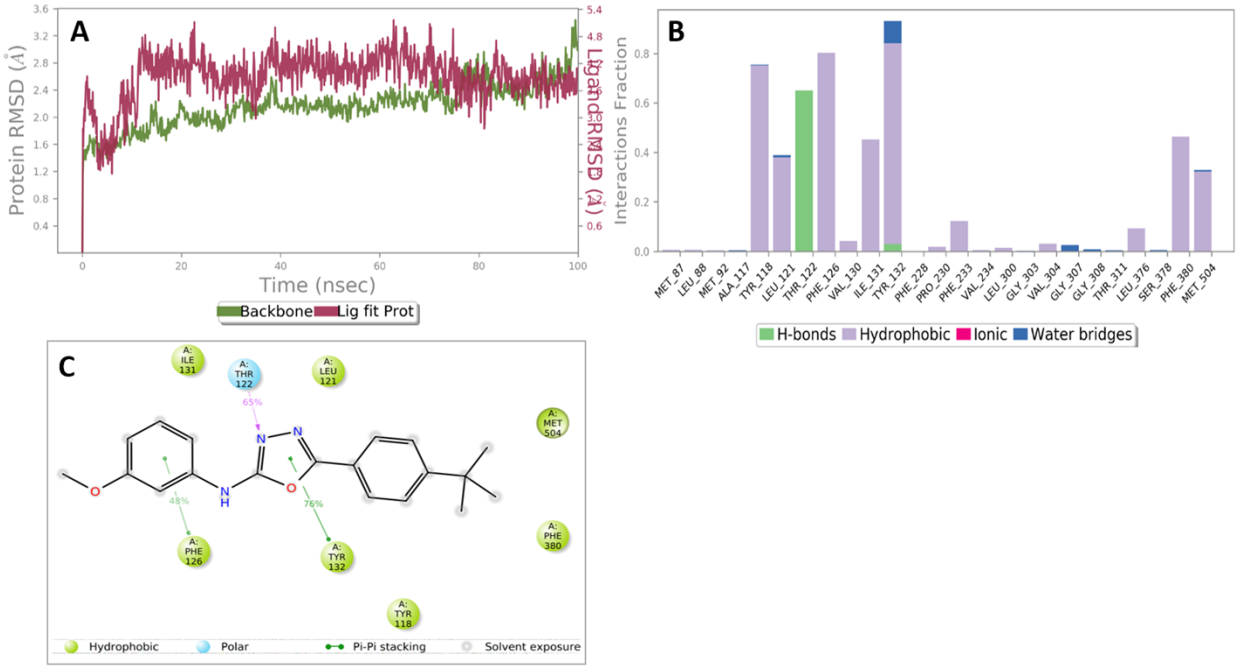
Supplementary Figure 6. (A) The root means standard deviation (RMSD) plot of **UOSO 10** with *C. albicans* CYP51 (PDB: 5V5Z). **(B)** Ligand **UOSO 10** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 10** with *C. albicans* CYP51.



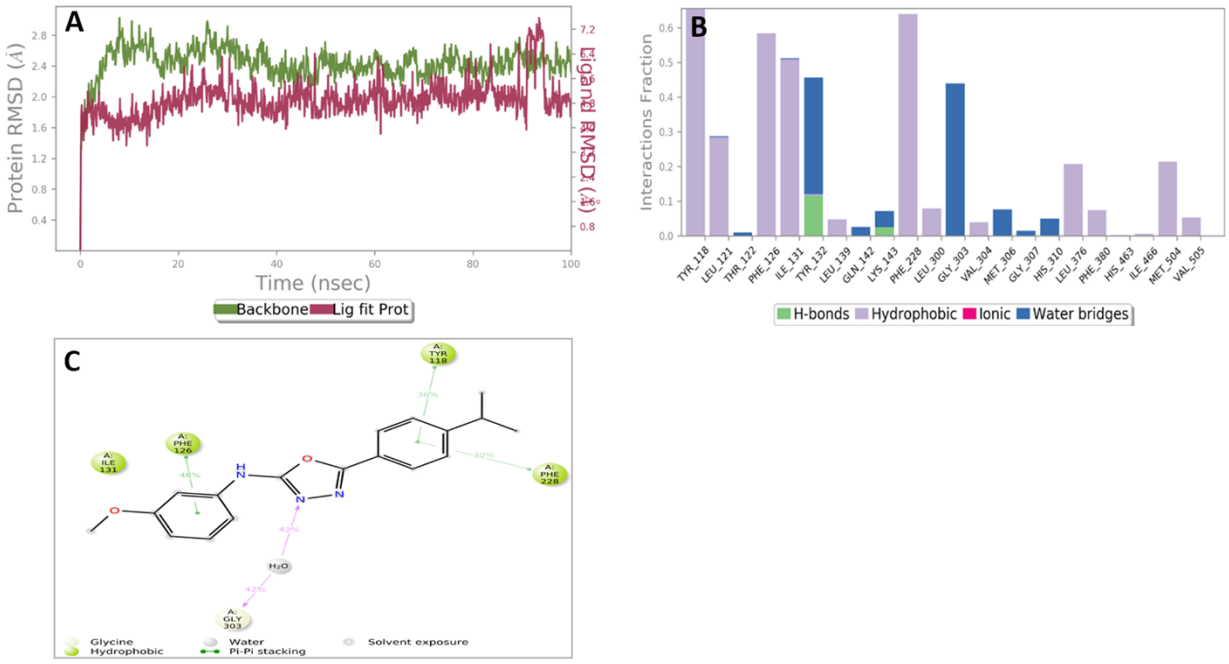
Supplementary Figure 7. (A) The root means standard deviation (RMSD) plot of **UOSO 12** with *C. albicans* CYP51 (PDB: 5V5Z). **(B)** Ligand **UOSO 12** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 12** with *C. albicans* CYP51.



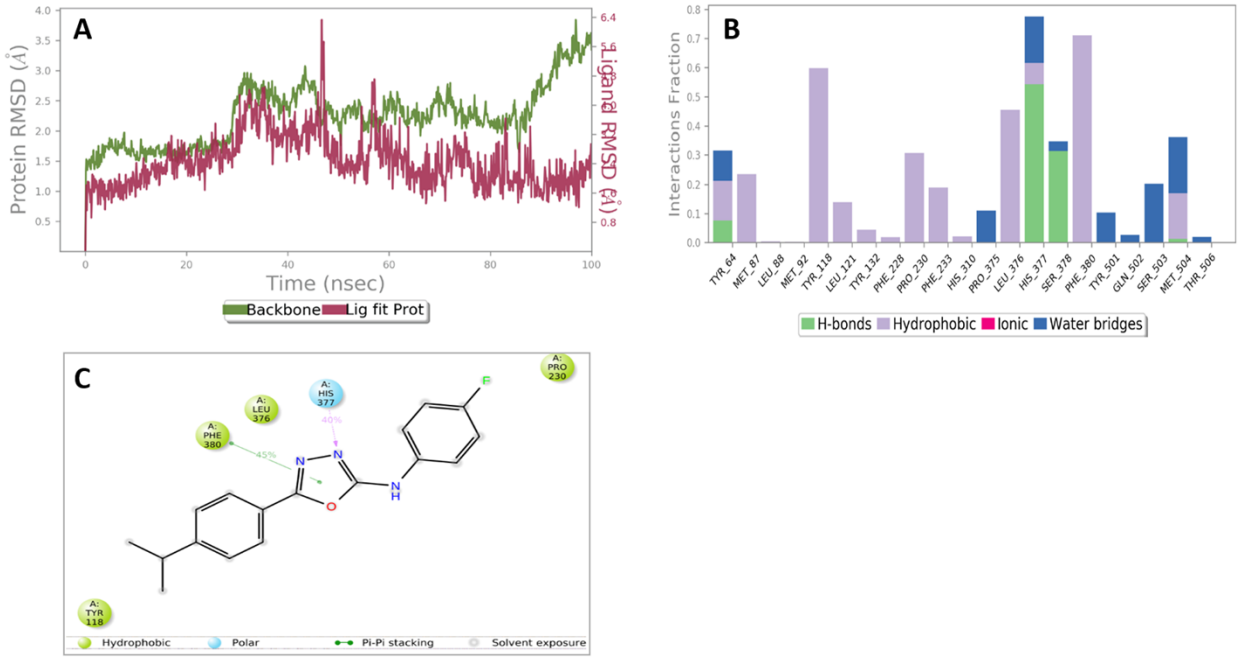
Supplementary Figure 8. (A) The root means standard deviation (RMSD) plot of **UOSO 14** with *C. albicans* CYP51 (PDB: 5V5Z). **(B)** Ligand **UOSO 14** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 14** with C. albicans CYP51.



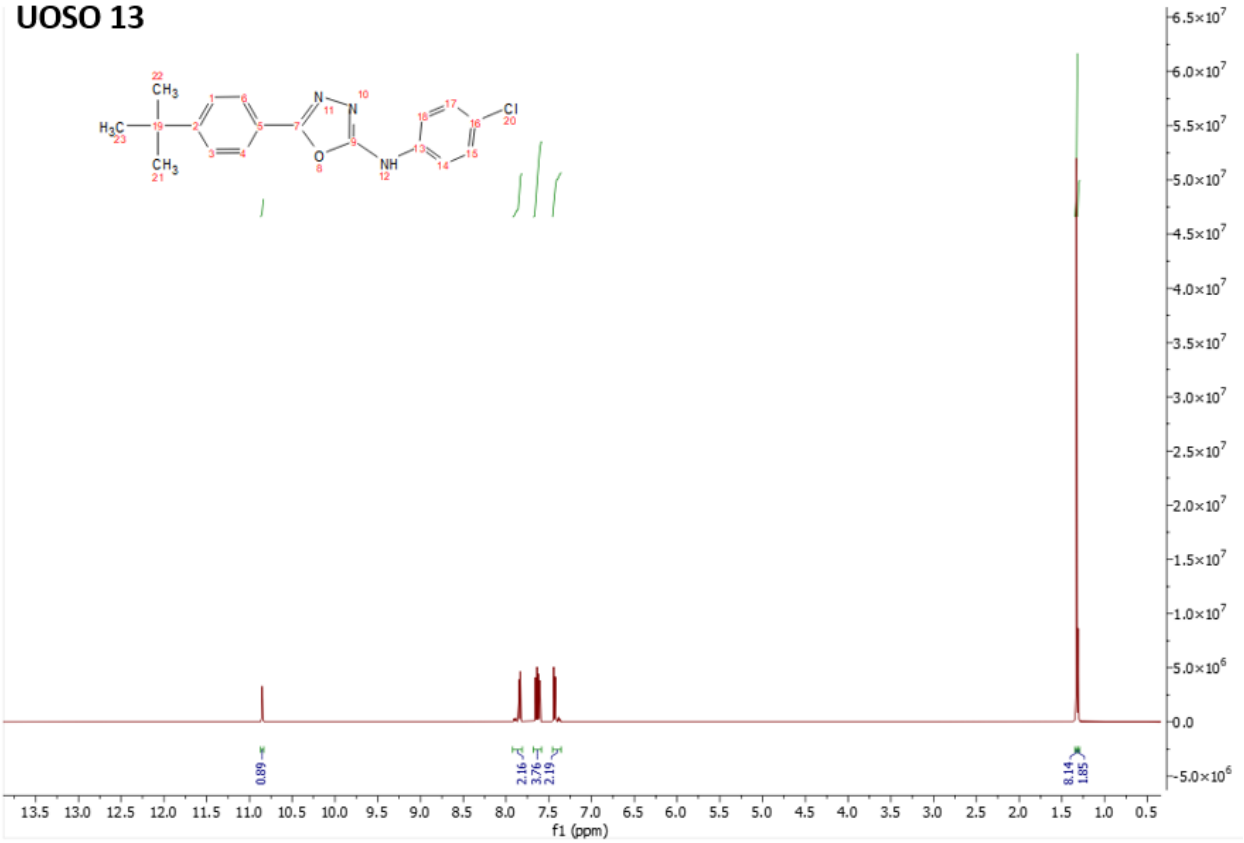
Supplementary Figure 9. (A) The root means standard deviation (RMSD) plot of **UOSO 10** with *C. auris* CYP51 model. **(B)** Ligand **UOSO 10** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 10** with *C. auris* CYP51.



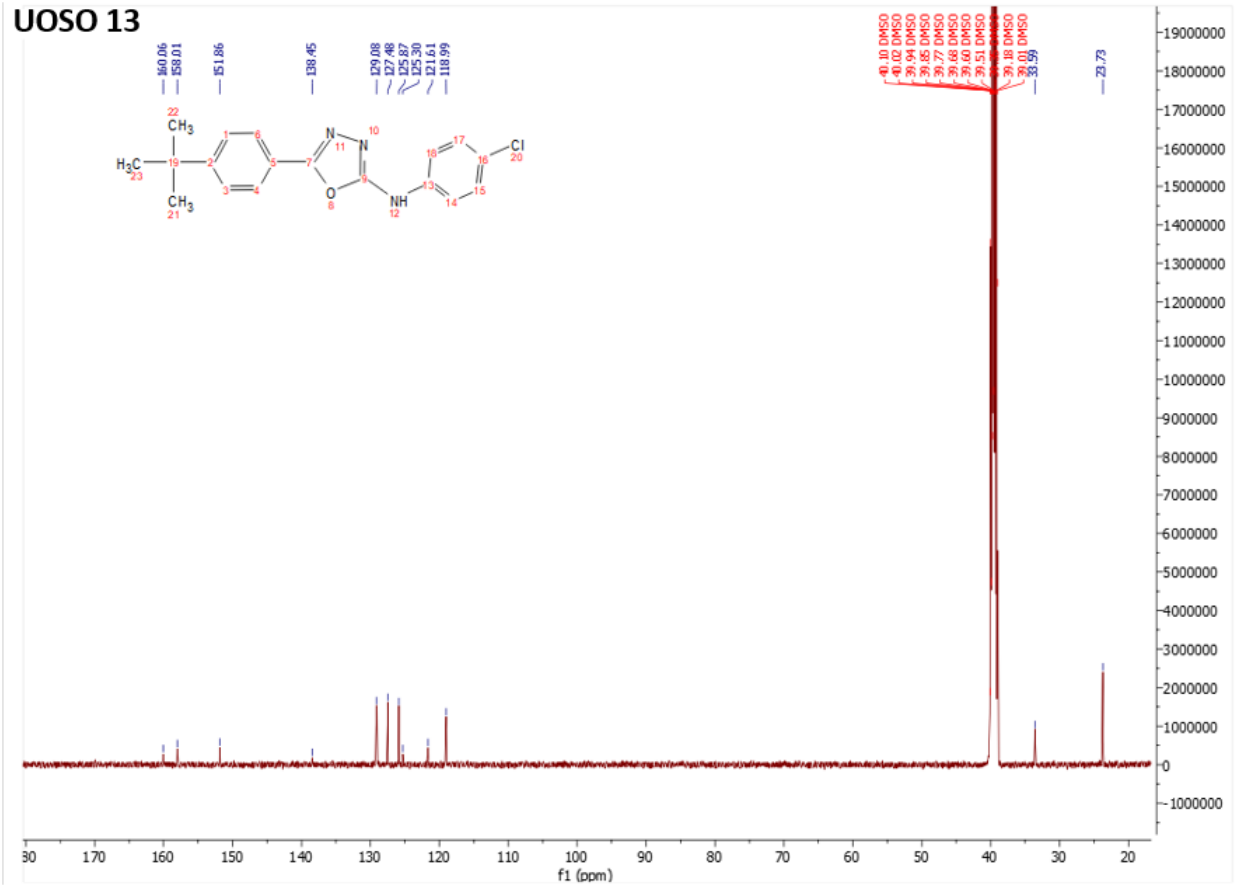
Supplementary Figure 10. (A) The root means standard deviation (RMSD) plot of **UOSO 12** with *C. auris* CYP51 model. **(B)** Ligand **UOSO 12** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 12** with *C. auris* CYP51.



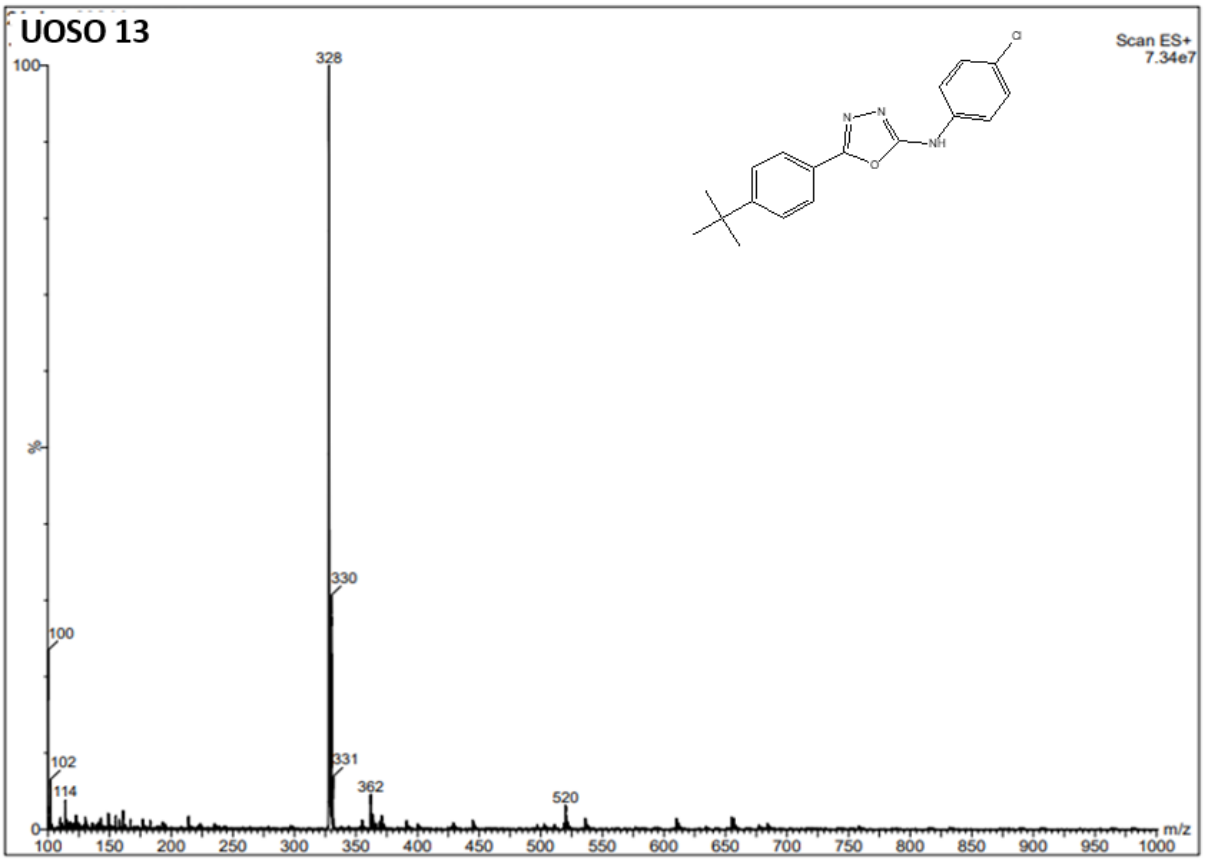
Supplementary Figure 11. (A) The root means standard deviation (RMSD) plot of **UOSO 14** with *C. auris* CYP51 model. **(B)** Ligand **UOSO 14** contacts with active site residues during MD simulation. **(C)** Schematic interaction diagram of **UOSO 14** with *C. auris* CYP51.



Supplementary Figure 12. [1]HNMR of **UOSO 13**.



Supplementary Figure 13. ^{13}CNMR of **UOSO 13.**



Supplementary Figure 14. Mass spectra of **UOSO 13.**

Supplementary Table 1. Binding site analysis.

Distance (Ã…)	ID %	SIM %	CON %
3	82.61	86.96	86.96
4	75.86	82.76	86.21
5	72.97	81.08	83.78
6	71.7	79.25	81.13
7	71.21	77.27	80.3