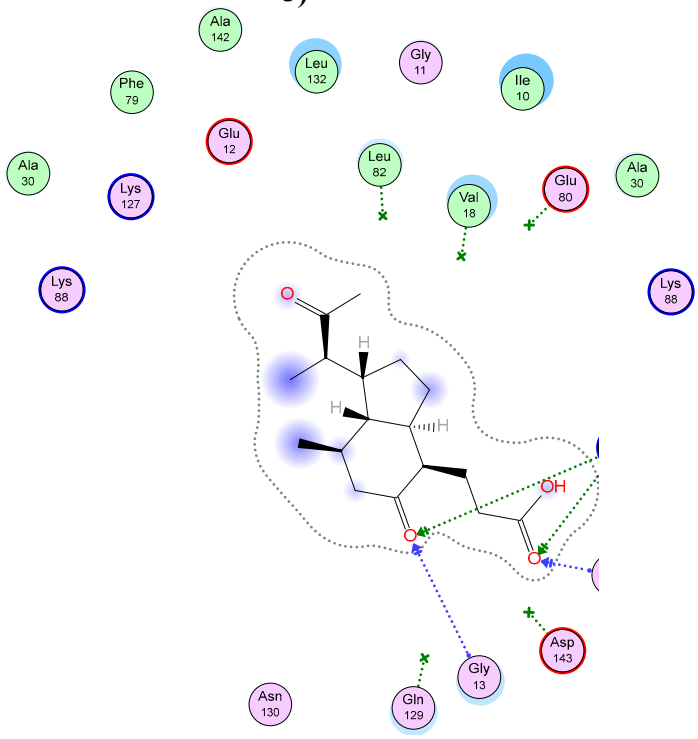
Supporting Information

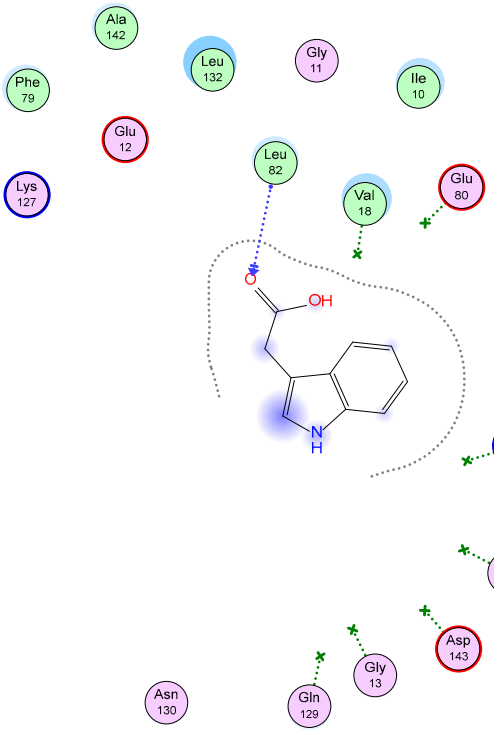
Molecular Docking Simulations

Indene propanoic acid **derivative (Molecule 3)**



Rhodinodohyde **(Molecule 5)**

Indole-3-acetic acid **(Molecule 4)**



Mitomycin-K **(Molecule 6)**

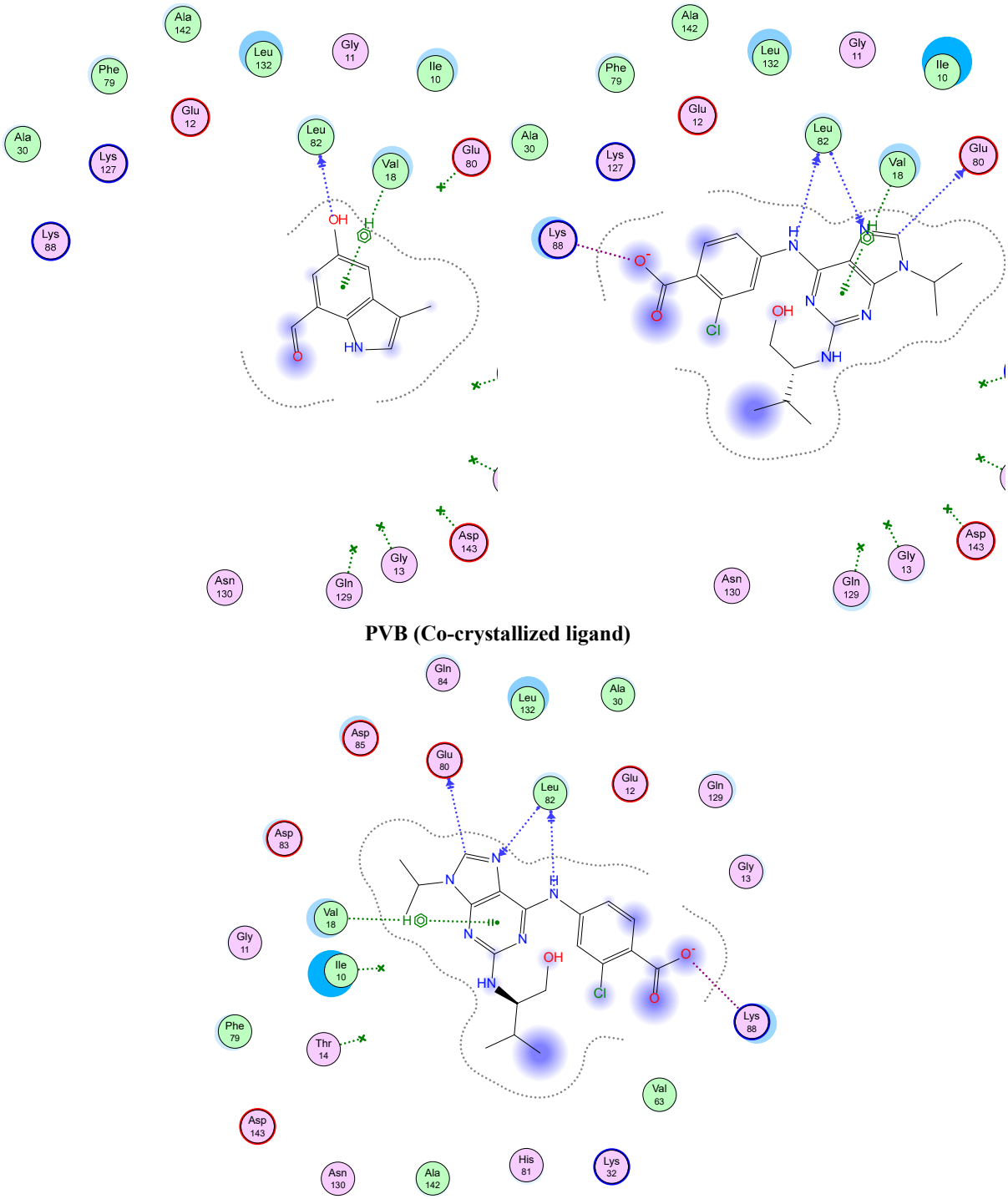
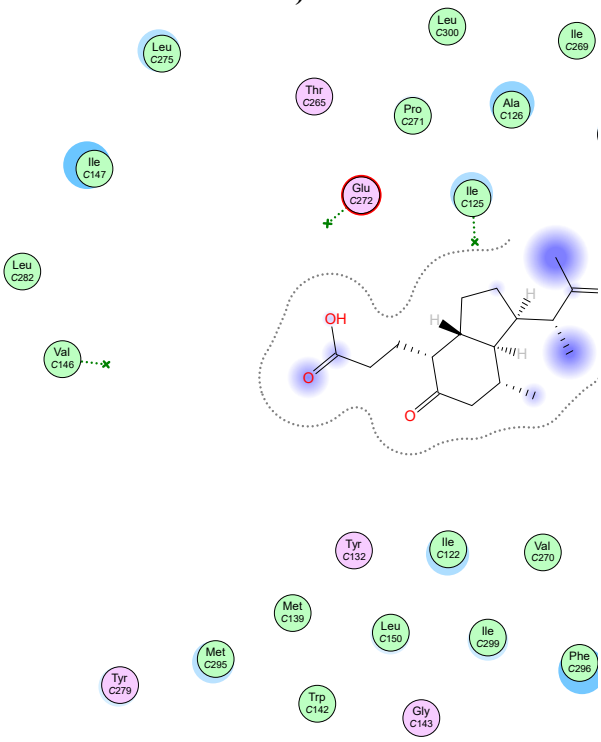
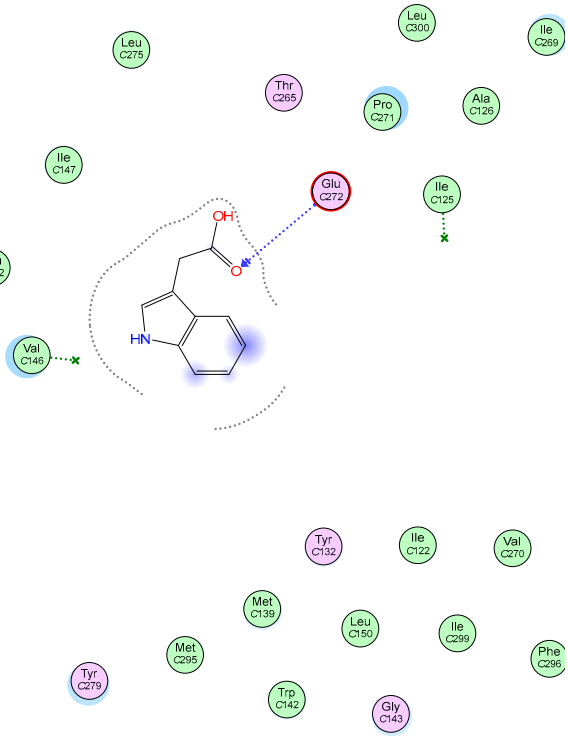


Figure S1. Presumptive mode of interaction of molecules **3**, **4**, **5**, **6**, and **PVB** within active site of *P. falciparum* kinase (PDB ID: 1V0P)

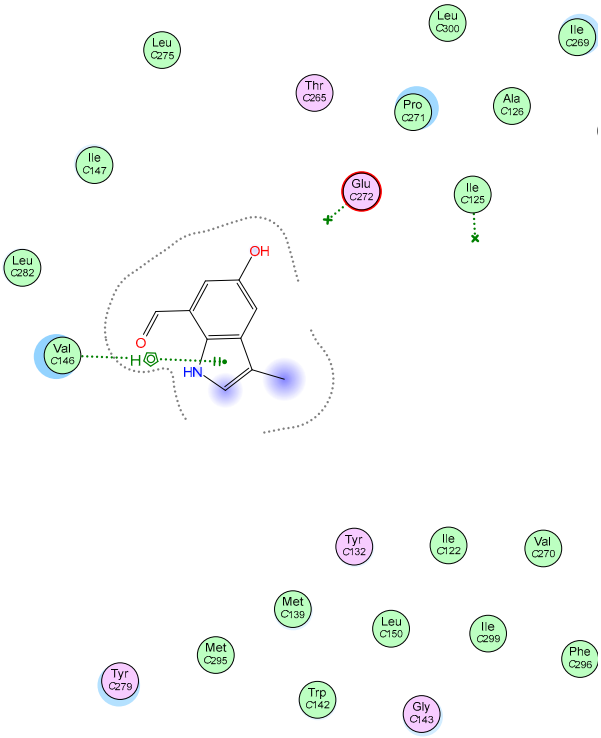
Indene propanoic acid derivative **(Molecule 3)**



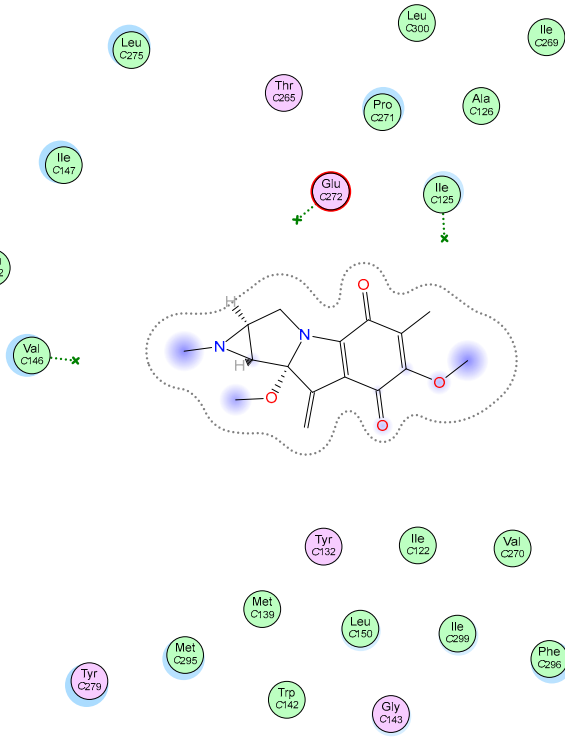
Indole-3-acetic acid **(Molecule 4)**



Rhodinodohyde **(Molecule 5)**



Mitomycin-K **(Molecule 6)**



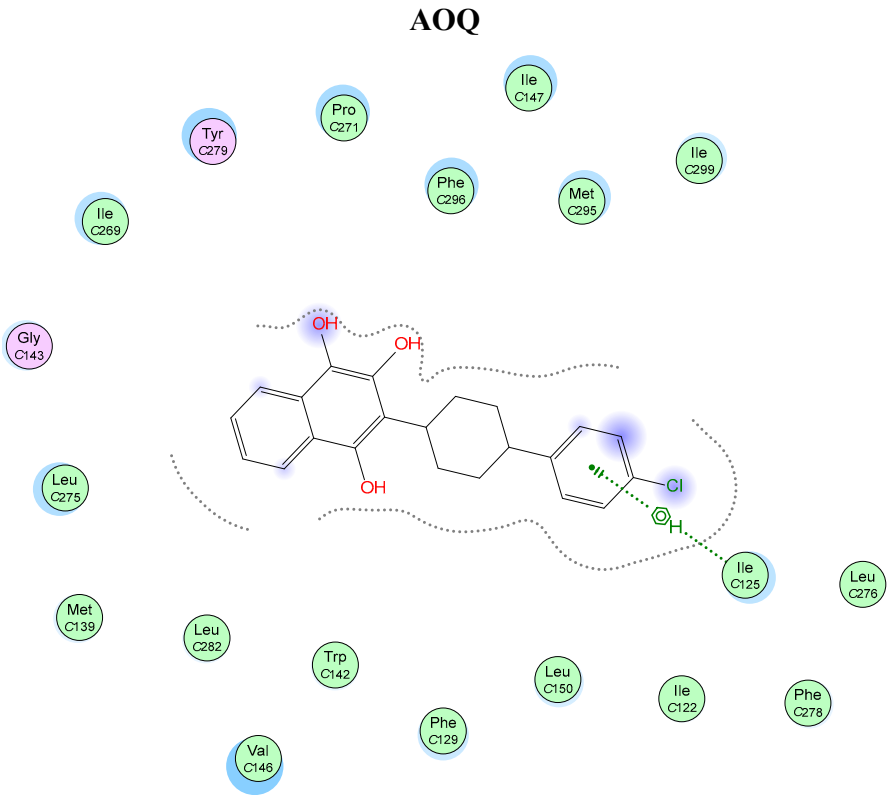
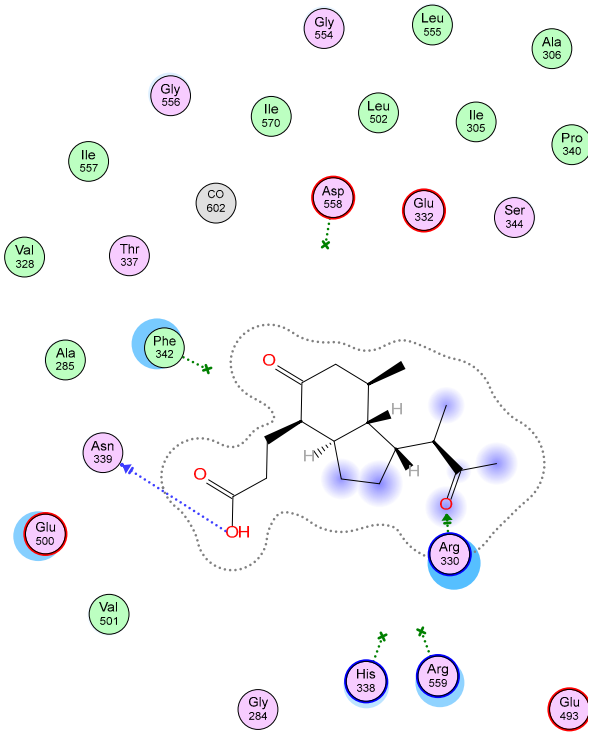
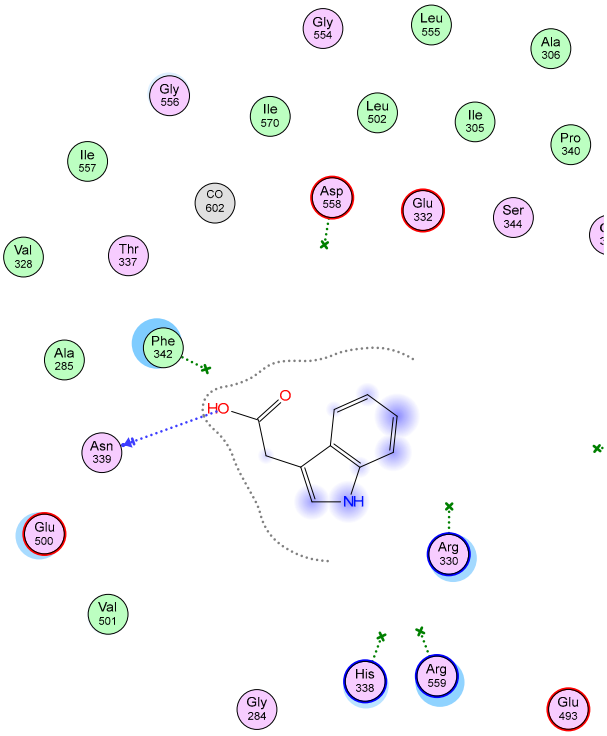


Figure S2. Presumptive mode of interaction of molecules **3**, **4**, 5, 6, and **AOQ** within active site of *P. falciparum* mitochondrial cytochrome bc1 complex (PDB ID: 4PD4).

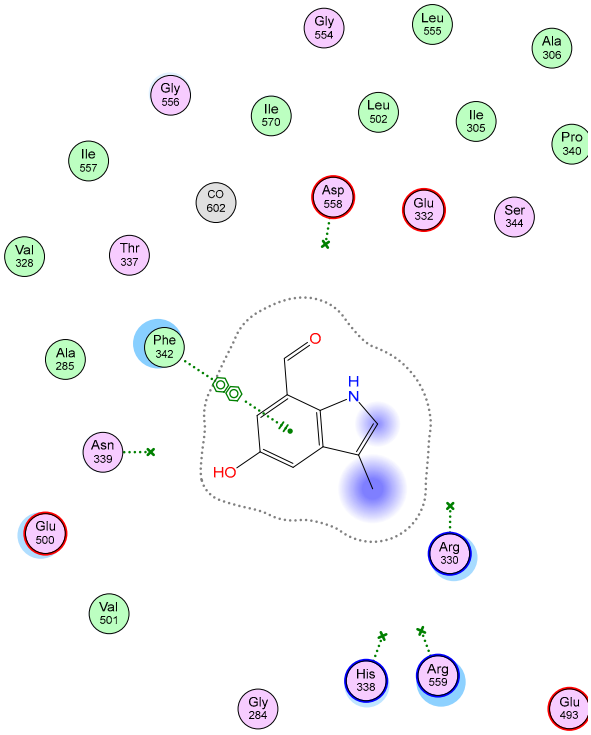
Indene propanoic acid derivative **(Molecule 3)**



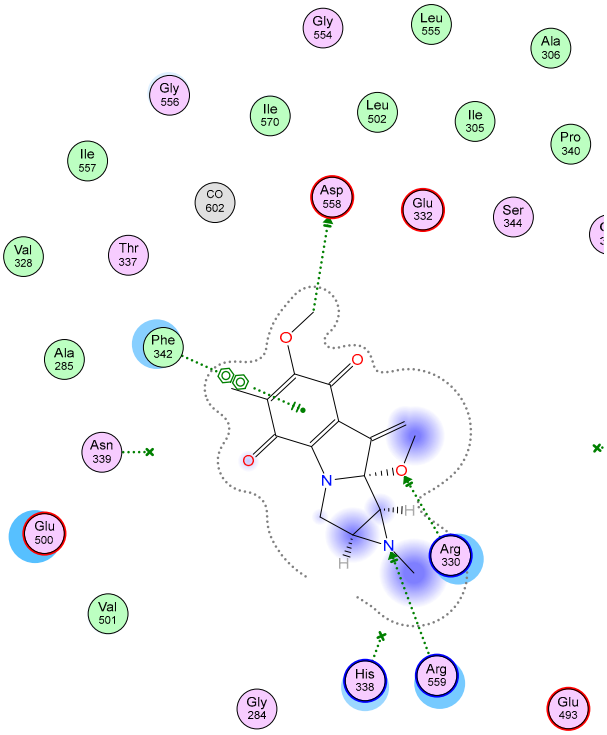
Indole-3-acetic acid **(Molecule 4)**



Rhodinodohyde **(Molecule 5)**



Mitomycin-K **(Molecule 6)**



9X0

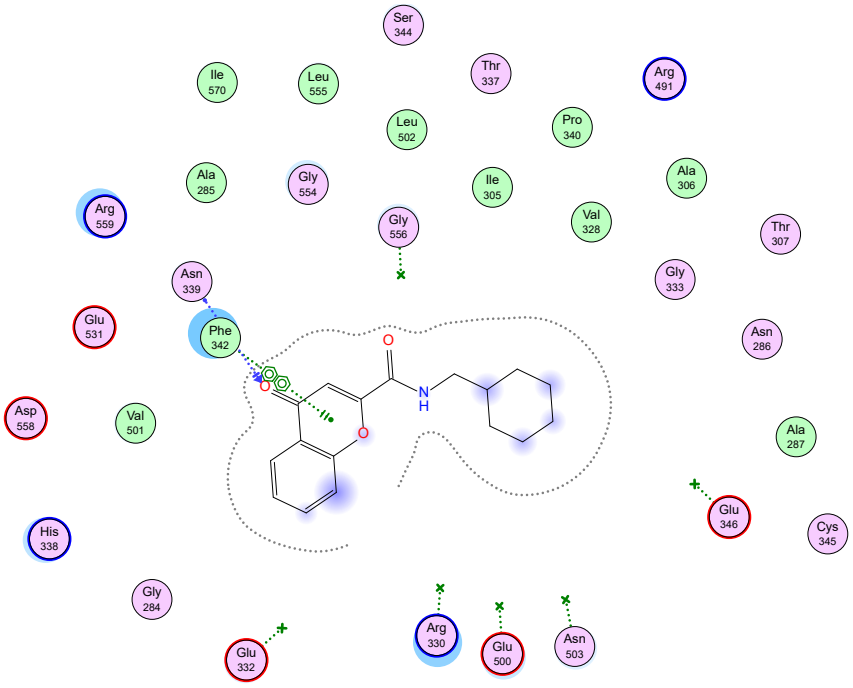


Figure S3. Presumptive mode of interaction of molecules **3**, **4**, **5**, **6**, and **9X0** within active site of *P. falciparum* lysyl-tRNA synthetase (PfKRS1; PDB ID: 6AGT)