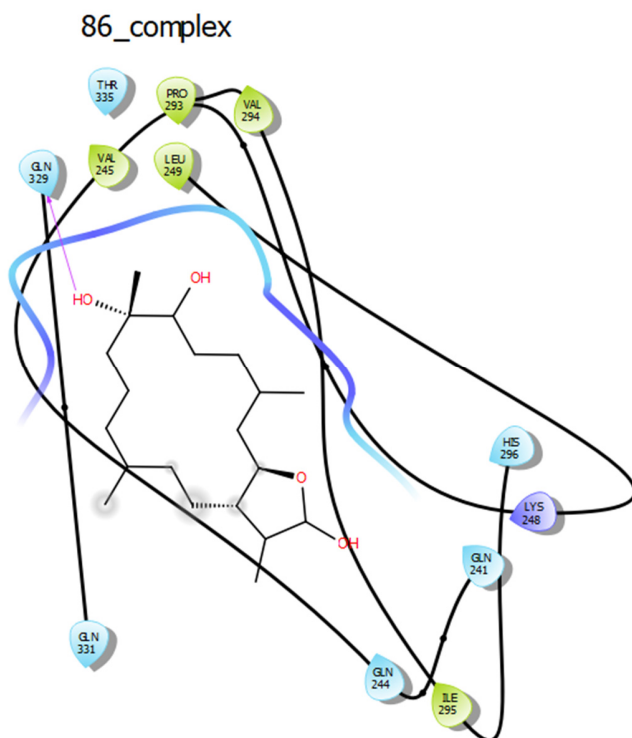
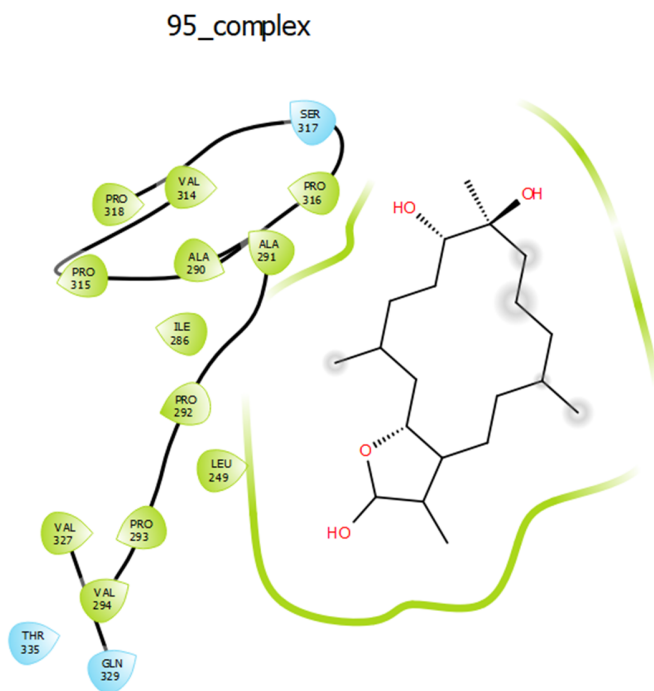


**Figure S1.** Receiver Operator Characteristic (ROC) curve generated after screening active molecules and their decoys against EBOV VP35 protein. The AUC value for the curve was 0.72, indicating the validity of the classification.

A)

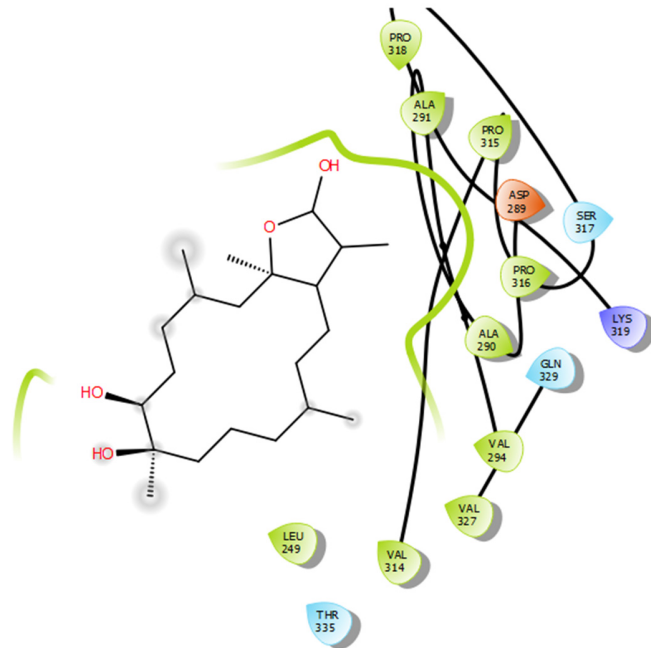


B)



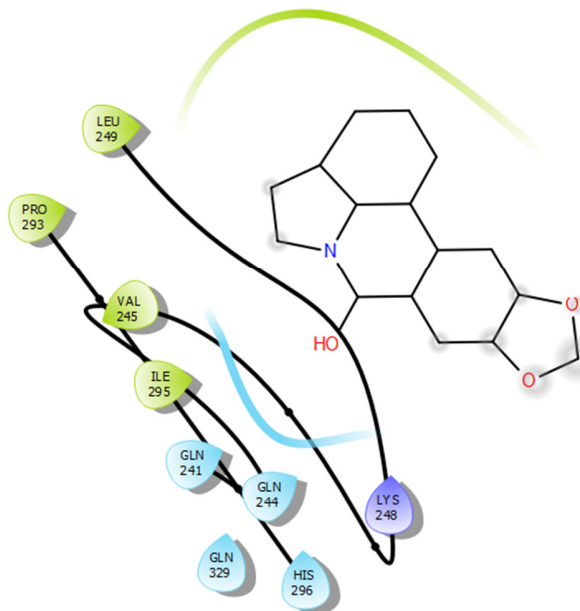
C)

142\_complex



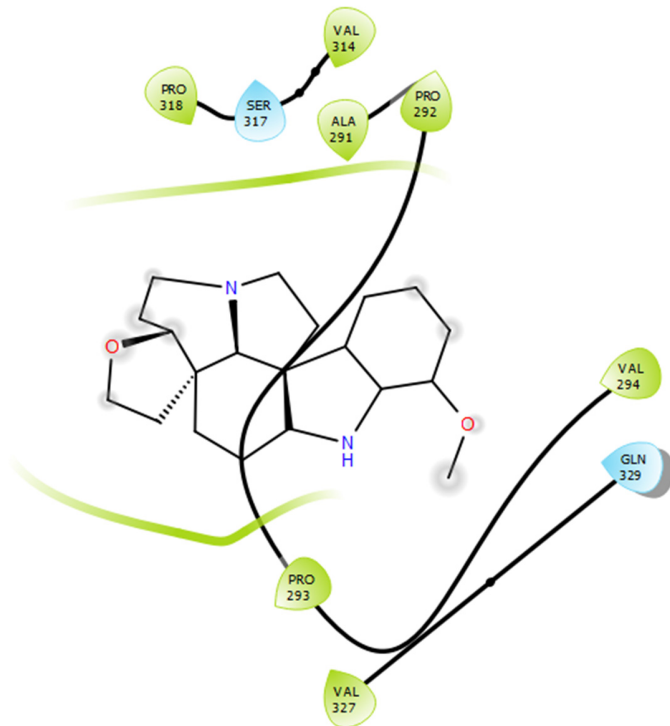
D)

205\_complex



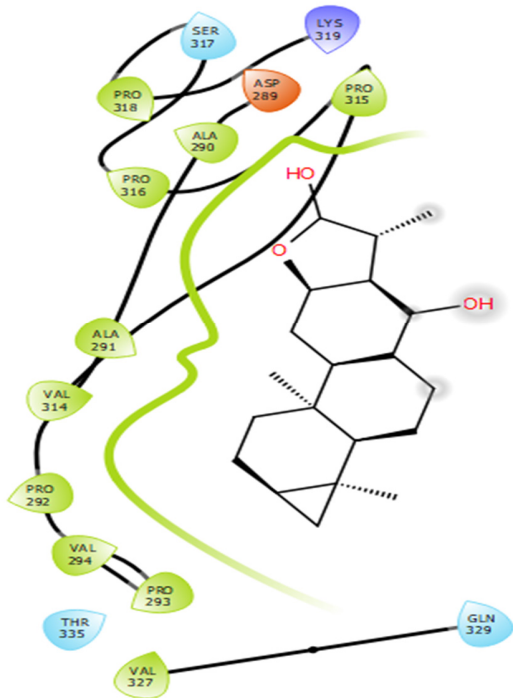
E)

397\_complex



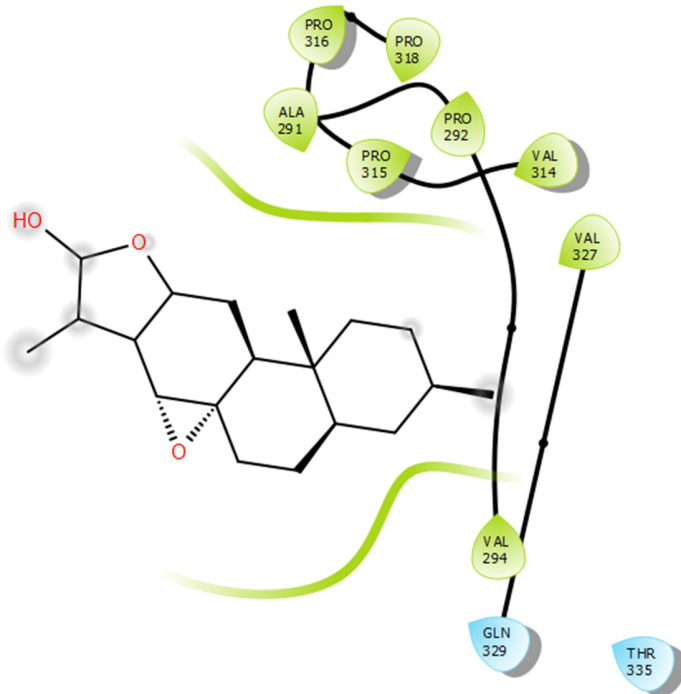
F)

2412\_complex



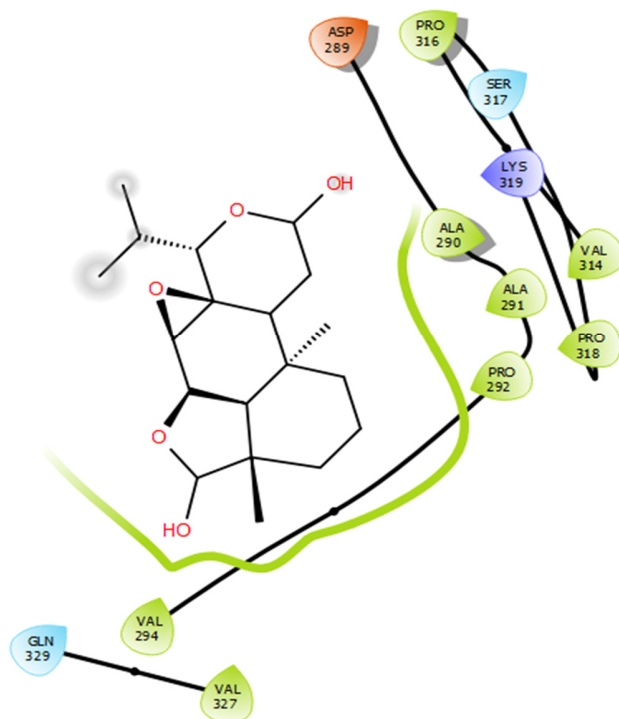
G)

2476\_complex

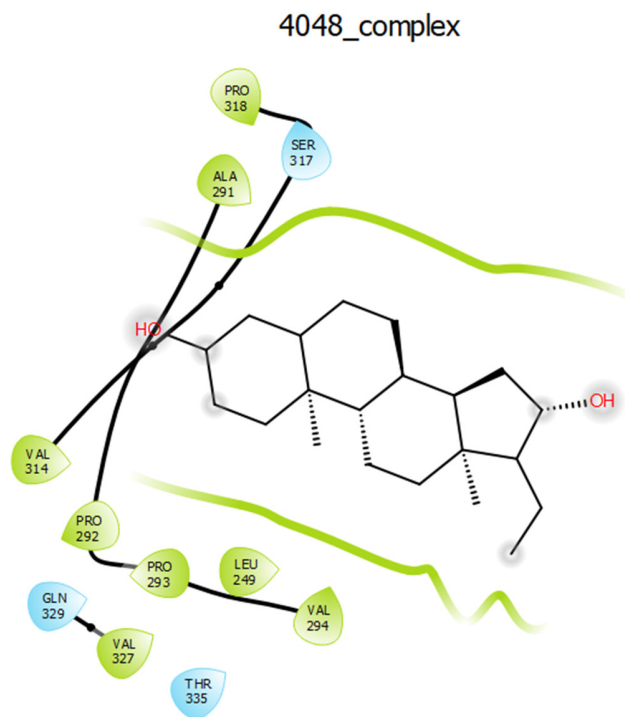


H)

3355\_complex

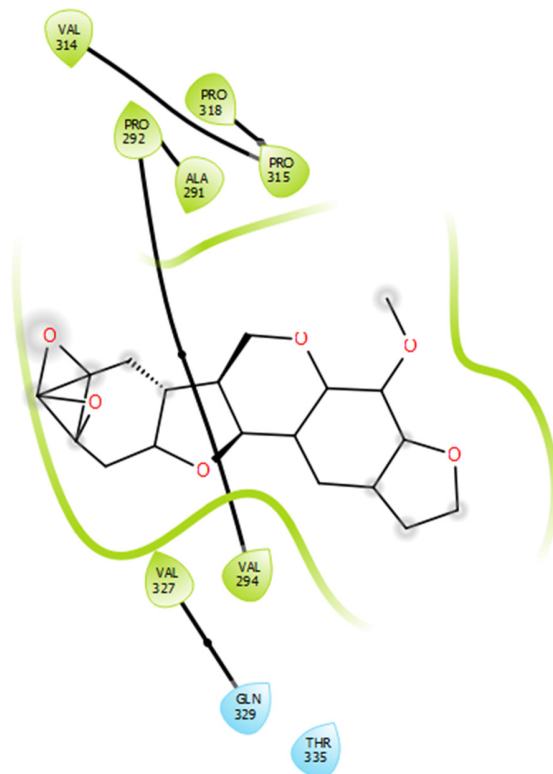


I)



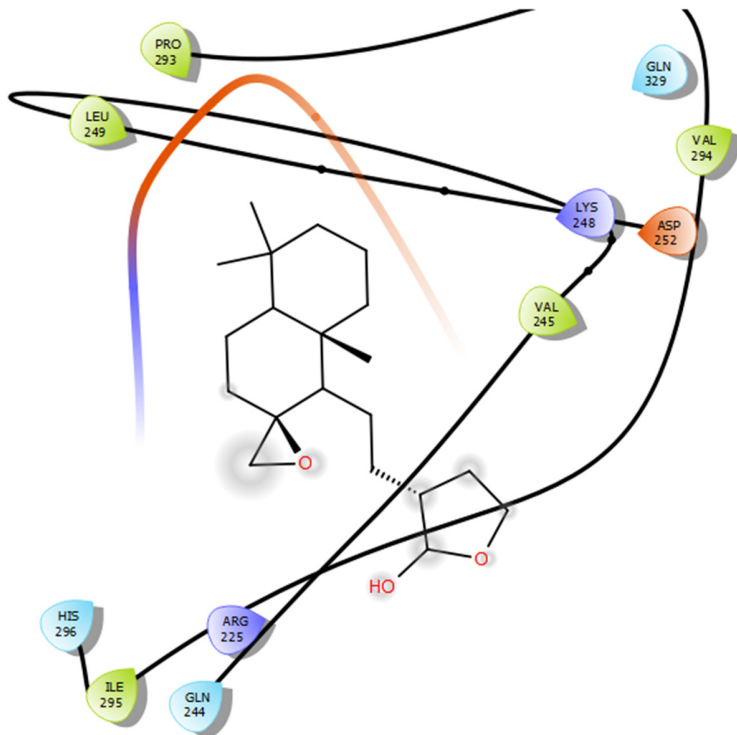
J)

ZINC000014612849\_complex



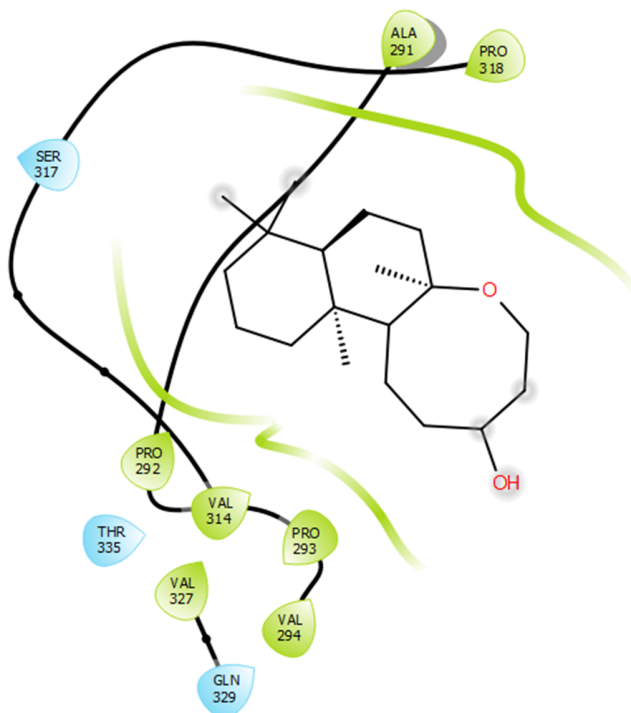
K)

ZINC000033831303\_complex



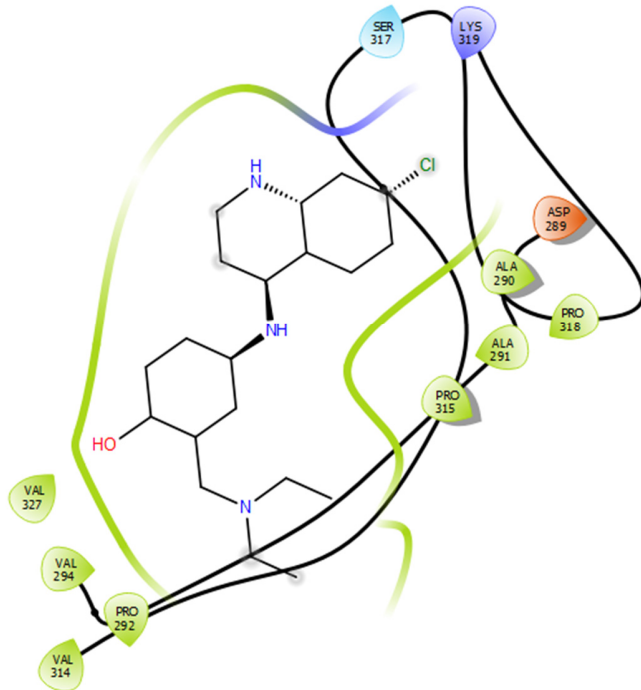
L)

ZINC000095486250\_complex



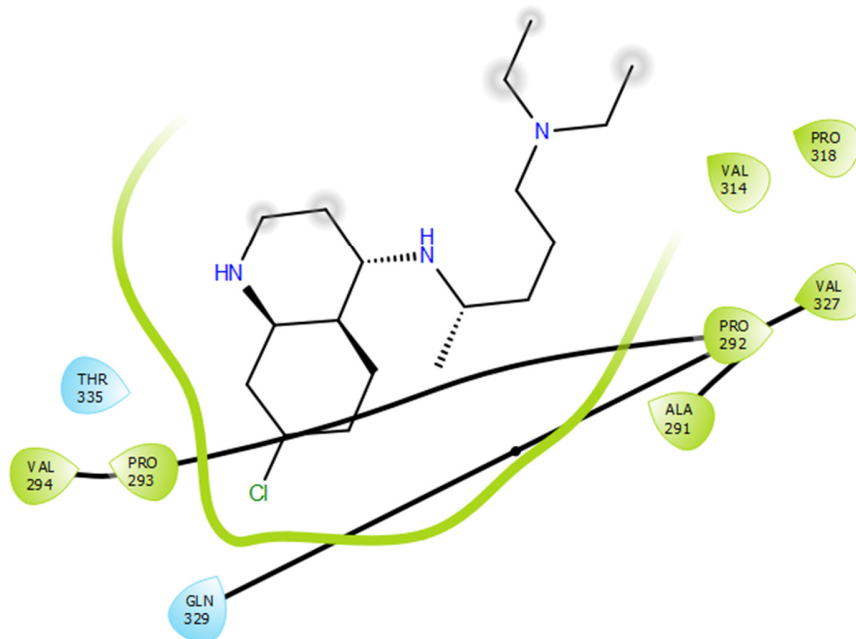
M)

Amodiaquine\_complex



N)

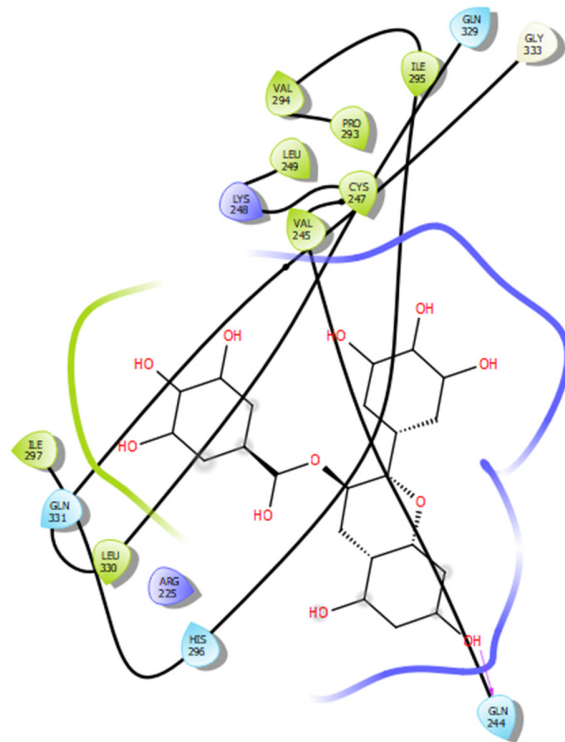
Chloroquine\_complex





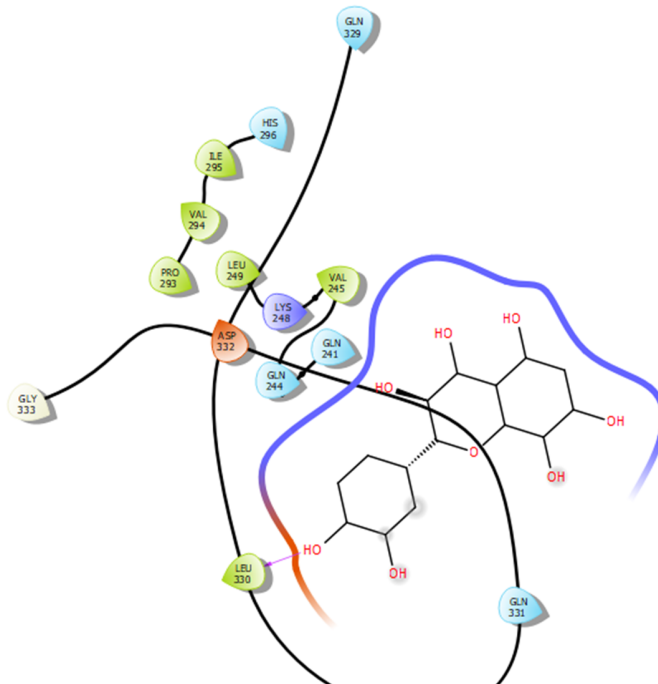
O)

EGCG\_complex

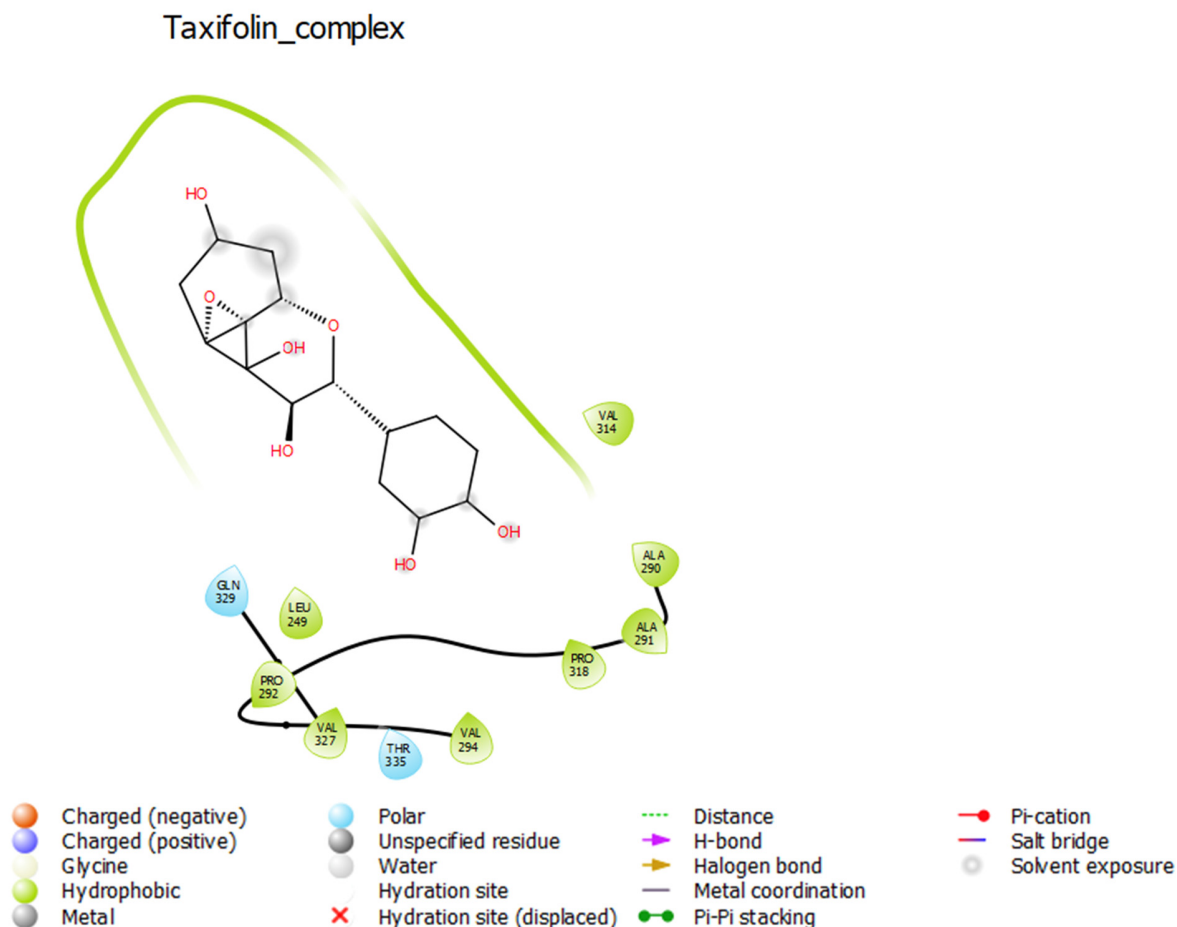


P)

Gossypetin\_complex



Q)



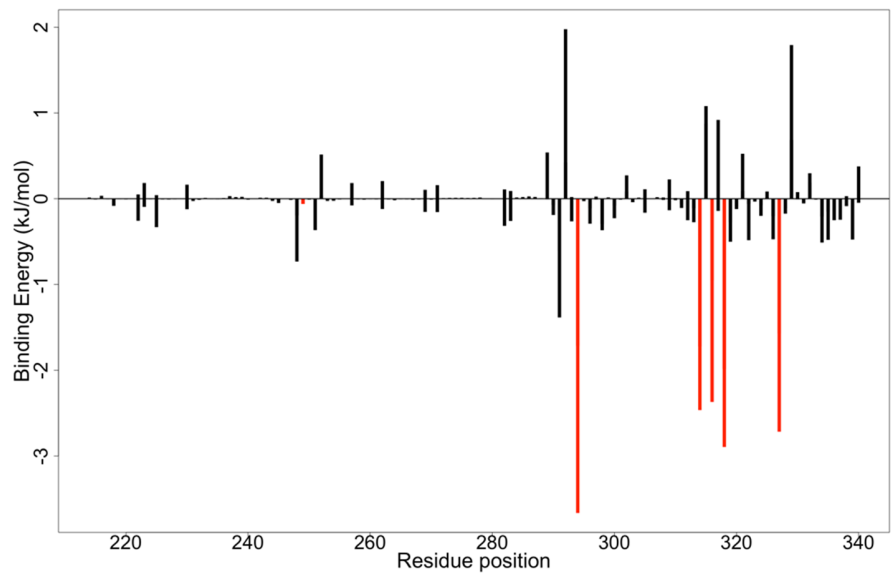
**Figure S2.** 2D diagrams of VP35-ligand complexes showing the hydrogen and hydrophobic interactions with the amino acid residues involved. The hydrogen bond with Gln329 is colored purple. The 2D protein-ligand interaction profile of EBOV VP35 in complex with (A) NANPDB86, (B) NANPDB95, (C) NANPDB142, (D) NANPDB205, (E) NANPDB397, (F) NANPDB2412, (G) NANPDB2476, (H) NANPDB3355, (I) NANPDB4048, (J) ZINC000014612849, (K) ZINC000033831303, (L) ZINC000095486250, (M) Amodiaquine, (N) Chloroquine, (O) EGCG, (P) Gossypetin, and (Q) Taxifolin.

**Table S1.** ADME prediction results of 12 compounds and 5 known inhibitors for Cytochrome P450 (CYP) inhibition.

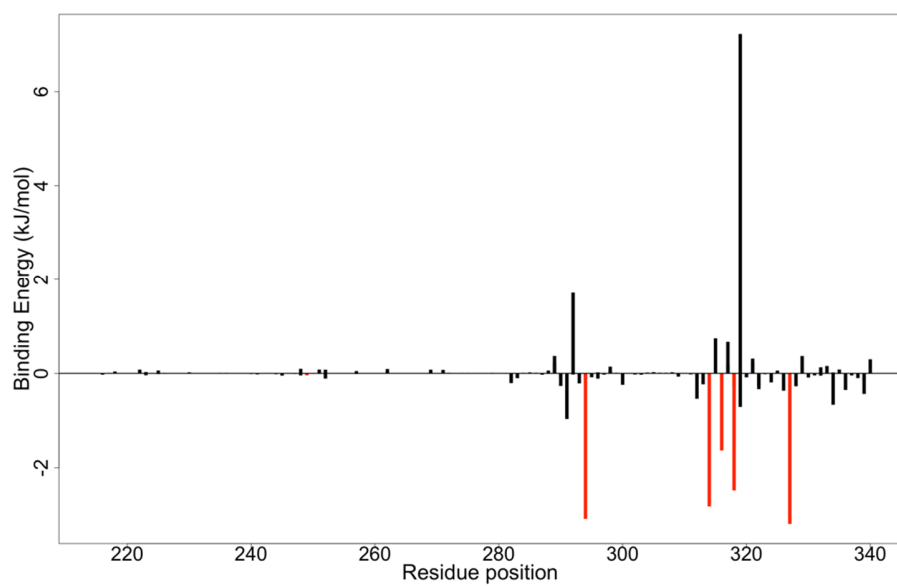
Drug ID/Drug name	CYP1A2	CYP2C19	CYP2C9	CYP2D6	CYP3A4
NANPDB86	No	No	No	No	Yes
NANPDB95	No	No	No	No	No
NANPDB142	No	No	Yes	No	Yes
NANPDB205	No	No	No	No	No

NANPDB397	No	No	No	Yes	Yes
NANPDB2412	No	No	Yes	No	No
NANPDB2476	No	No	Yes	No	No
NANPDB3355	No	No	No	No	No
NANPDB4048	No	Yes	Yes	No	No
Amodiaquine	Yes	Yes	No	Yes	Yes
Chloroquine	Yes	No	No	Yes	Yes
EGCG	No	No	No	No	No
Gossypetin	Yes	No	No	Yes	Yes
Taxifolin	No	No	No	No	No

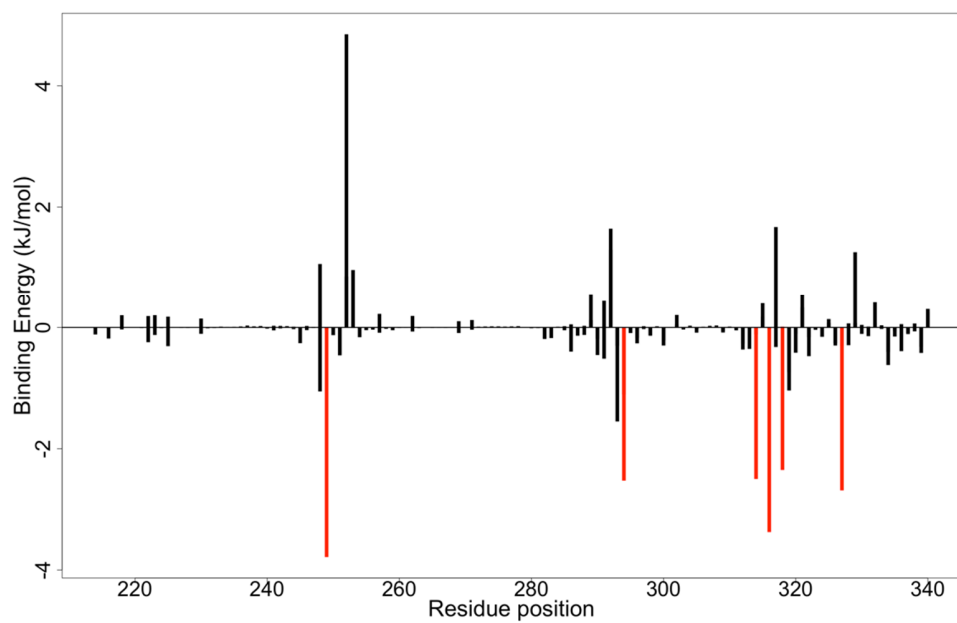
**A)**



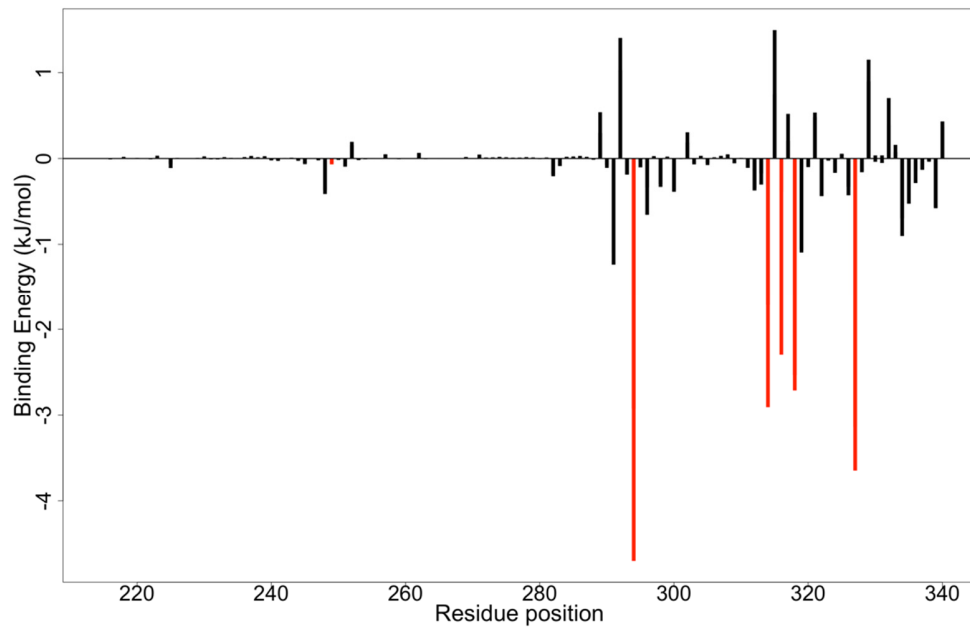
**B)**



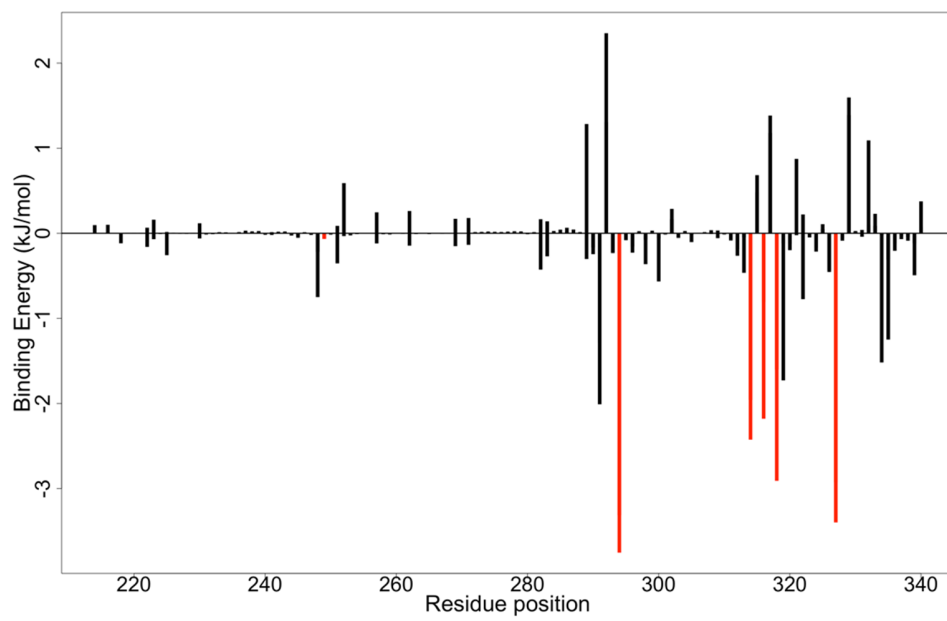
C)



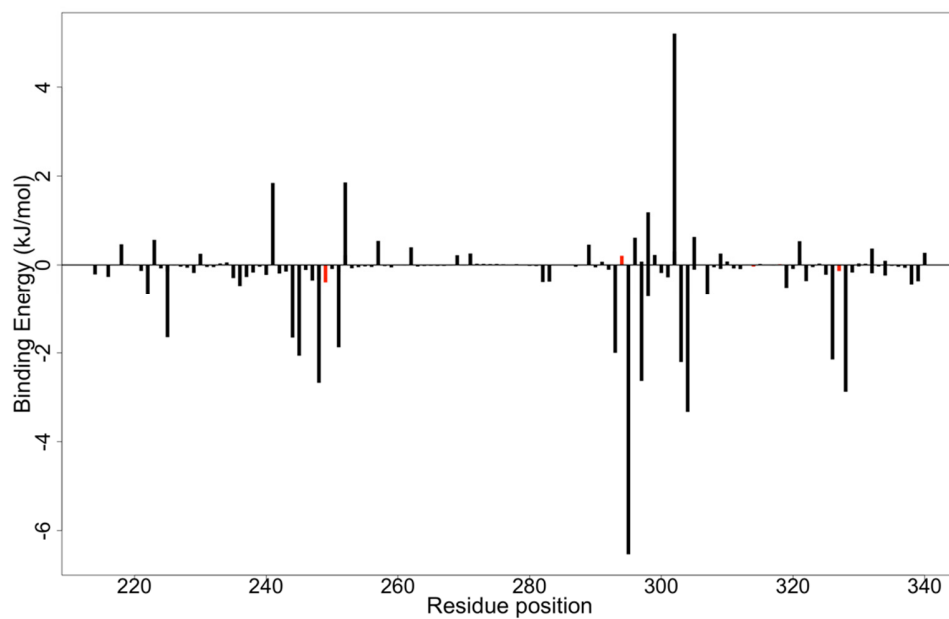
**D)**



**E)**



**F)**



**Figure S3.** Molecular mechanics Poisson-Boltzmann surface area (MM-PBSA) plot of binding free energy contribution per residue of the VP35-ligand complexes: A) NANPDB2412, B) NANPDB2476, C) NANPDB4048, D) ZINC000095486250, E) Amodiaquine, and F) EGCG. Fluctuations by predicted critical residues are shown in red.