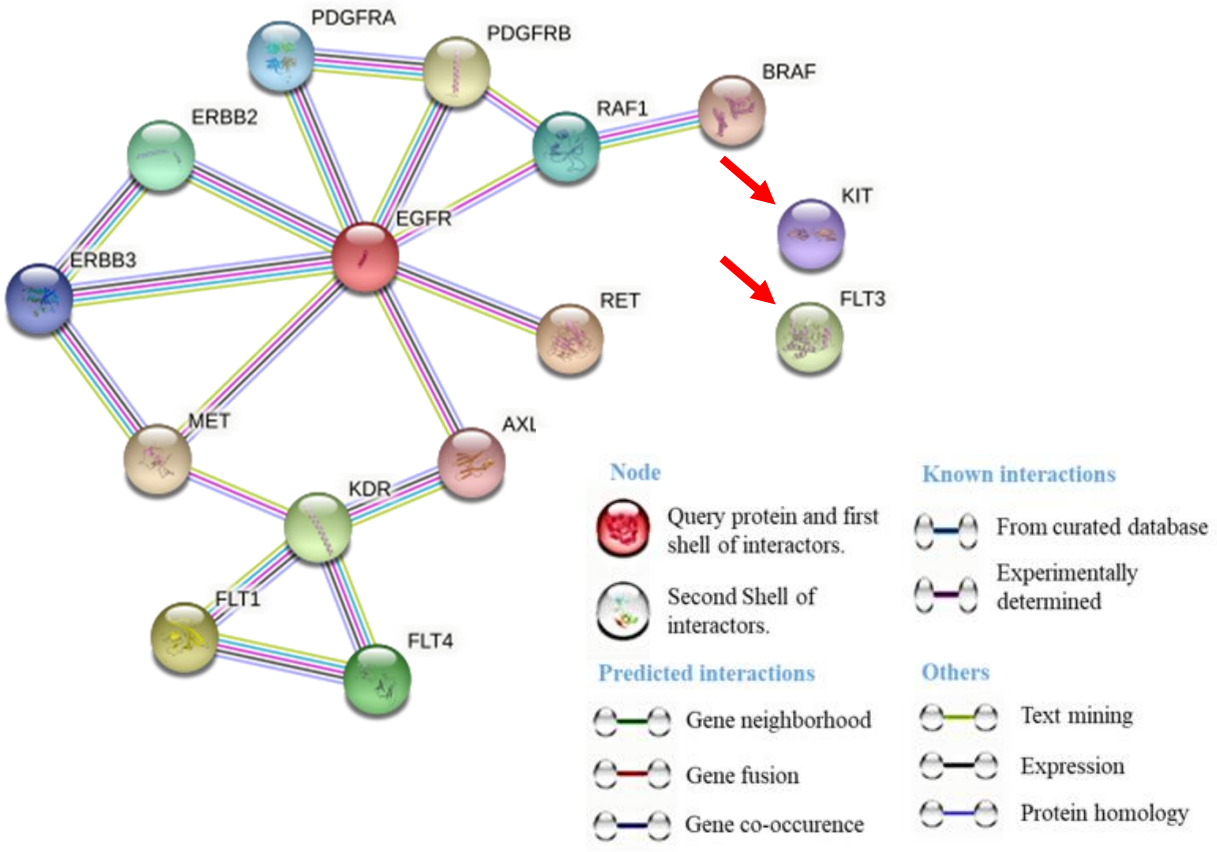
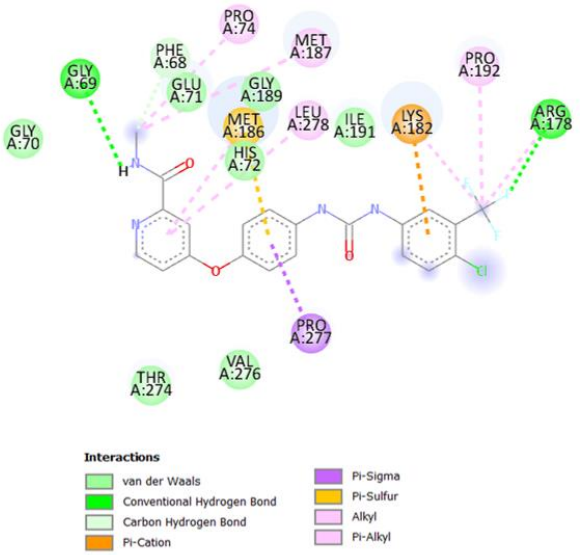


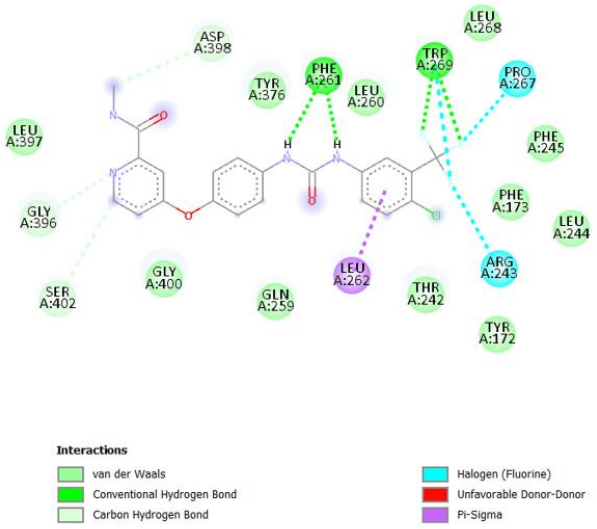
Fig. 7. Prediction of protein–protein interaction using STRING v.11.0. Arrowhead in red, shows no interaction with proteins

(A)

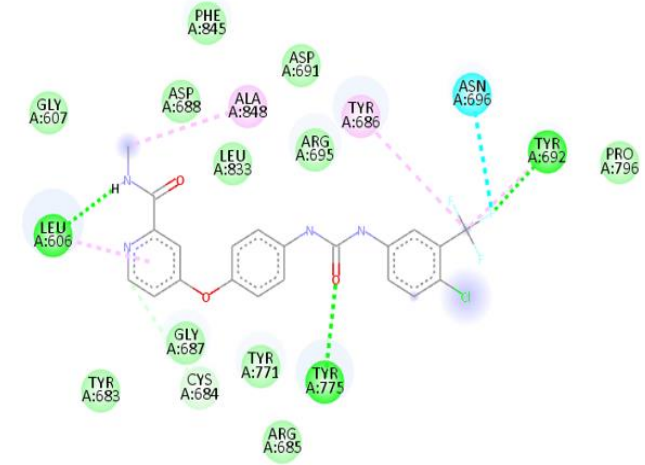
Sorafenib



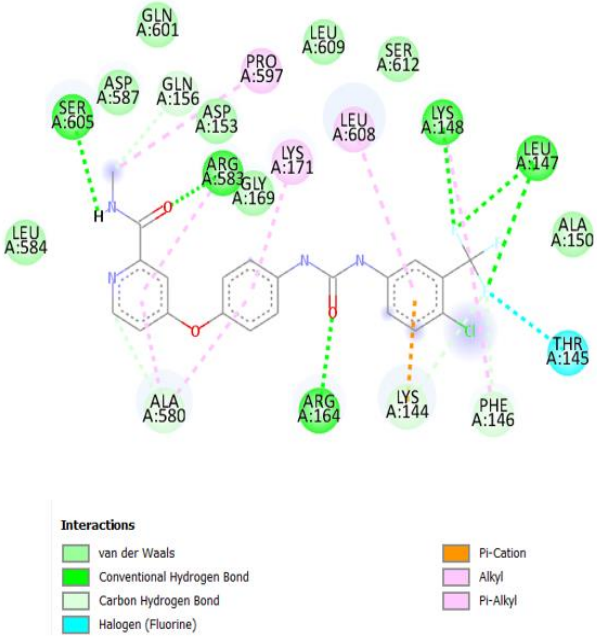
BRAF



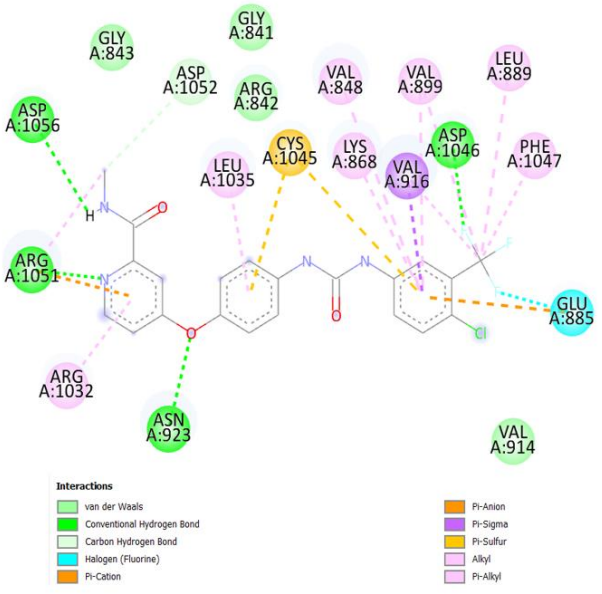
FILT



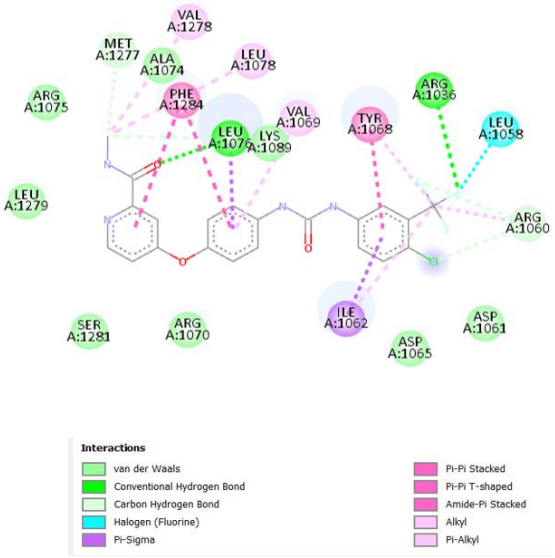
PDGFRB



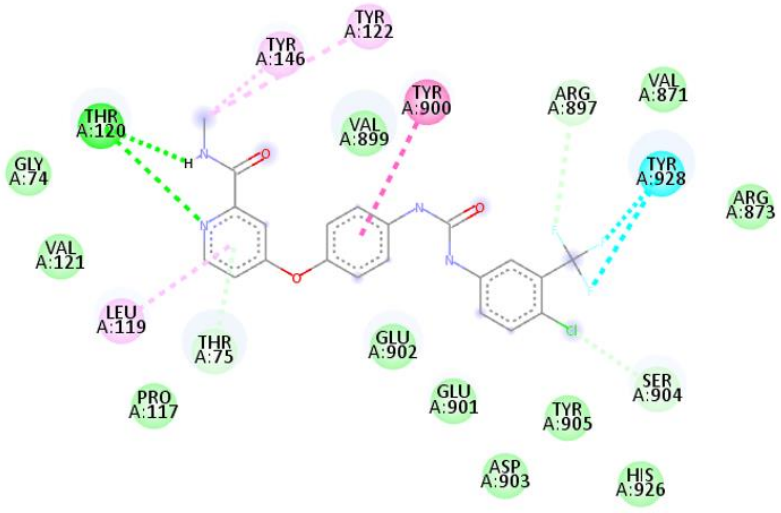
RAF1



VEGFR2



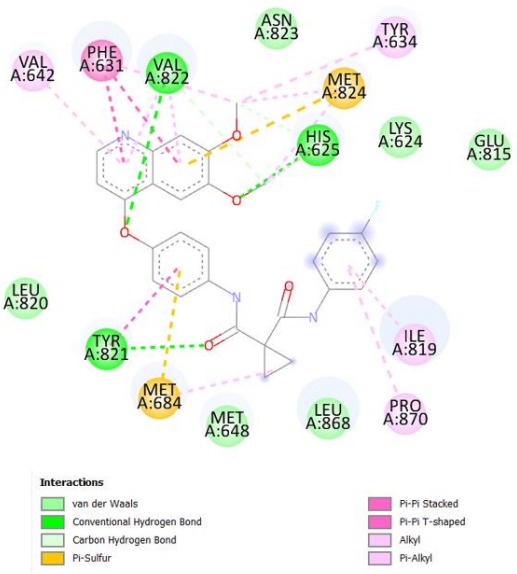
VEGFR3



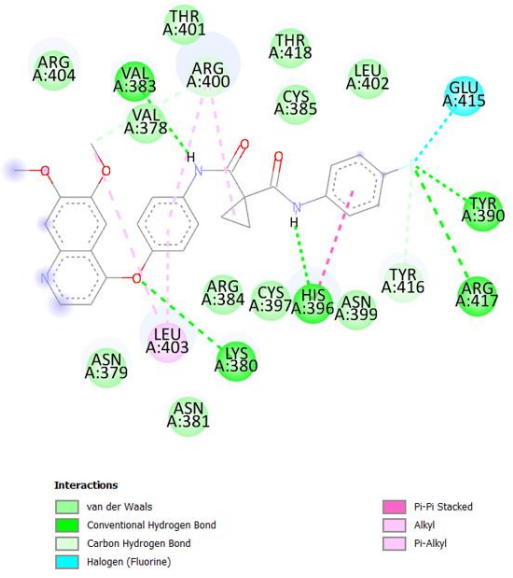
RET

(B)

Cabozantinib s-malate



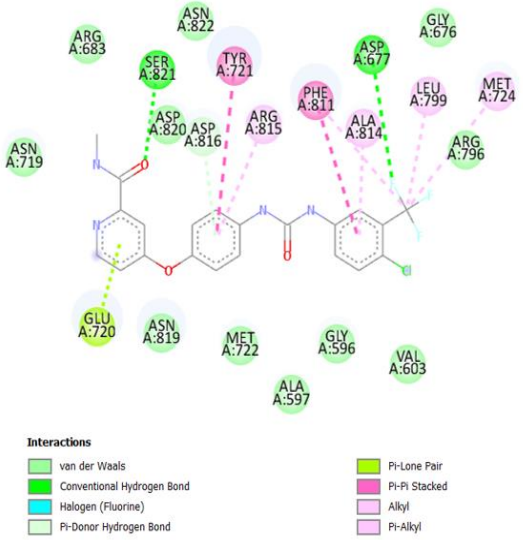
AXL Protein



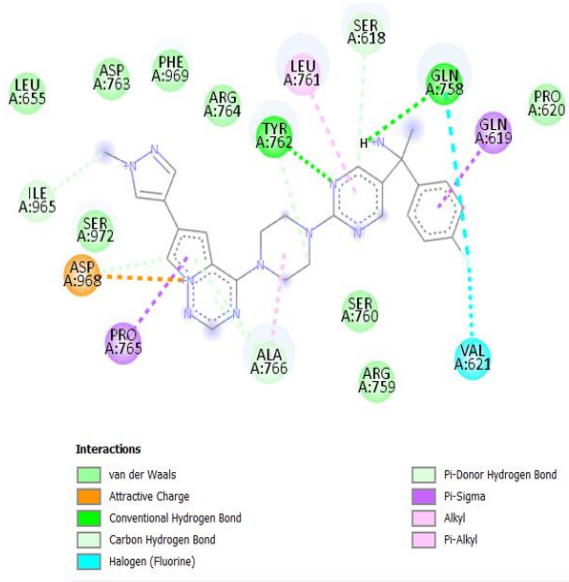
MET Protein

(C)

Avapritinib

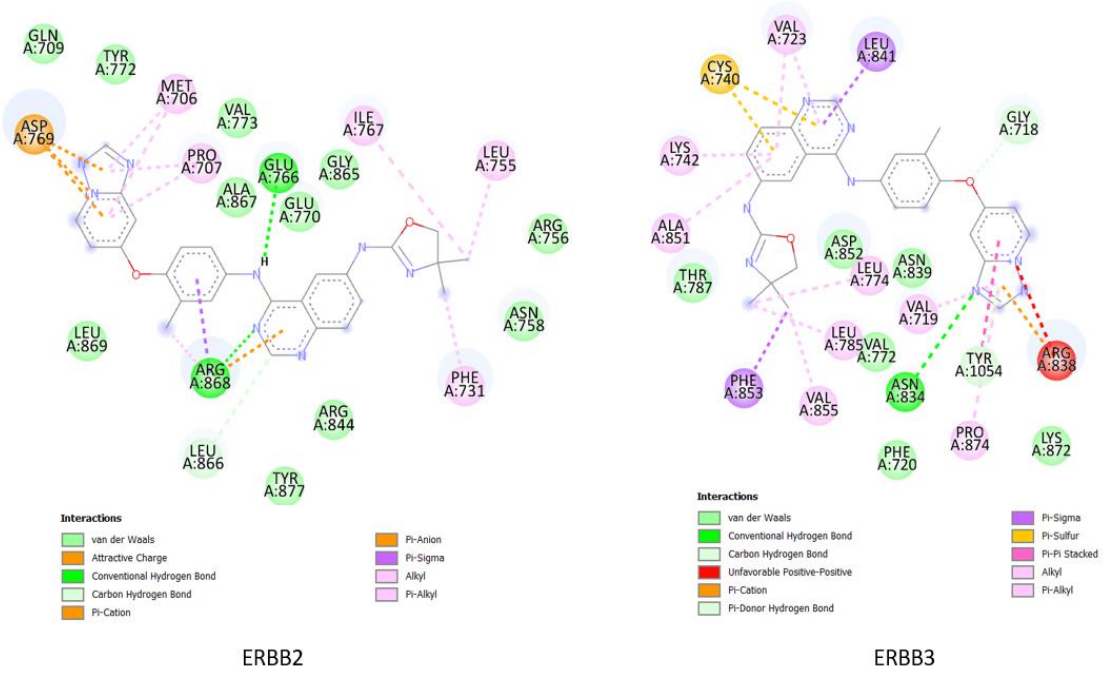


KIT Protein



PDGFRA Protein

(D) Tukysa/ Tucatinib



(E) Motesanib diphosphate

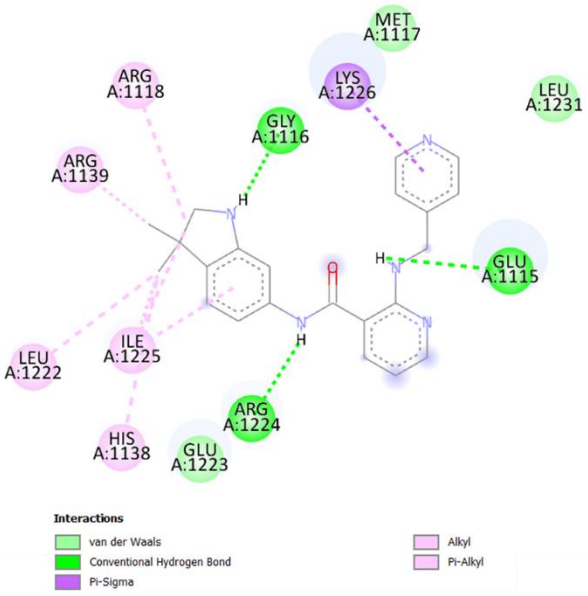


Fig. 8 (A) 2D molecular interactions of docked complex (Sorafenib+BRAF, FILT, PDGFRB, RAF1, VEGFR2, VEGFR3, and RET), with hydrogen bonds and hydrophobic bonds. **(B)** 2D interactions of docked complex (Cabozantinib s-malate-AXL, and MET), with hydrogen bonds and hydrophobic bonds. **(C)** 2D interactions of docked complex (Avapritinib-KIT, PDGFRA),

with hydrogen bonds hydrophobic bonds. **(D)** 2D interactions of docked complex (Tukysa/ Tucatinib-ERBB2, and ERBB3), with hydrogen bonds hydrophobic bonds. **(E)** 2D interactions of docked complex (Motesanib diphosphate + VEGFR2), with hydrogen bonds hydrophobic bonds