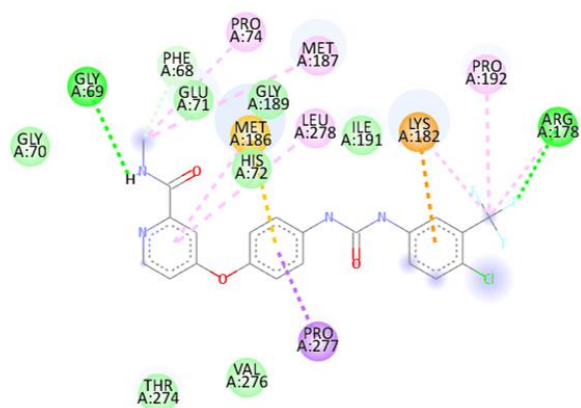


Fig. 7. Prediction of protein–protein interaction using STRING v.11.0. Arrowhead in red, shows no interaction with proteins

(A)

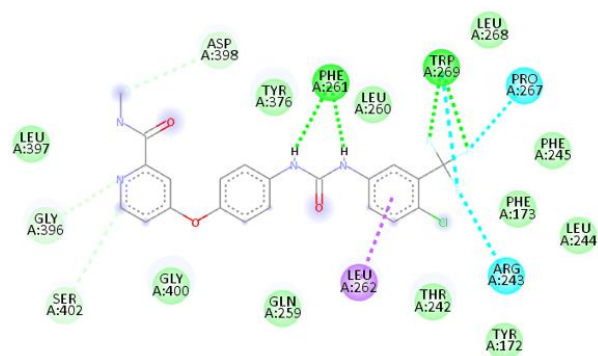
Sorafenib



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Pi-Sigma
- Pi-Sulfur
- Alkyl
- Pi-Alkyl

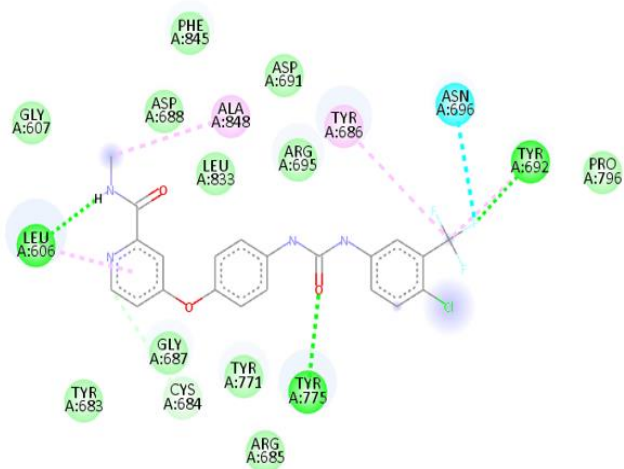
BRAF



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Halogen (Fluorine)
- Unfavorable Donor-Donor
- Pi-Sigma

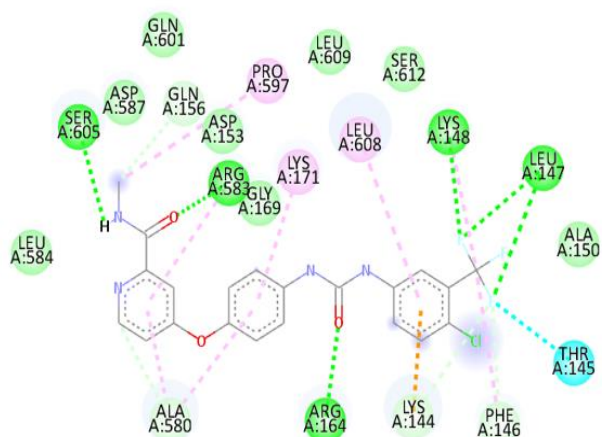
FLT



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Halogen (Fluorine)
- Alkyl
- Pi-Alkyl

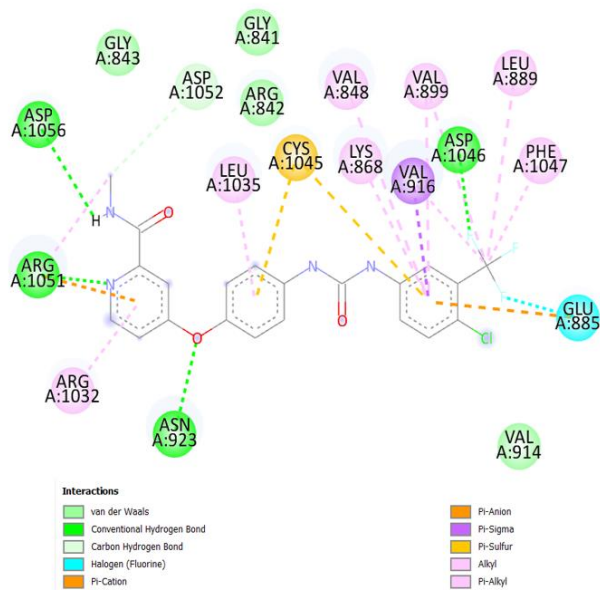
PDGFRB



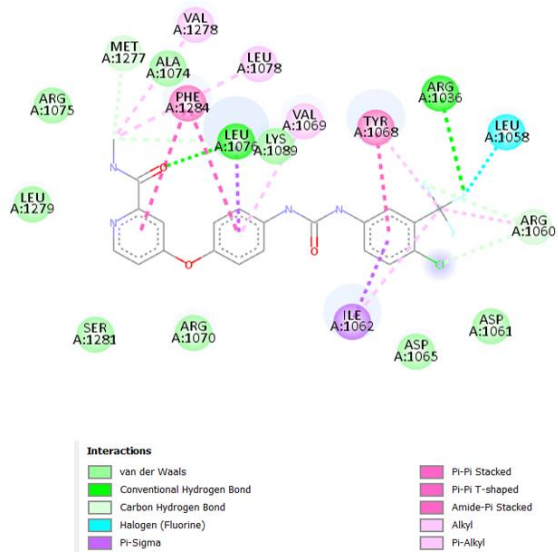
Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Halogen (Fluorine)
- Pi-Cation
- Alkyl
- Pi-Alkyl

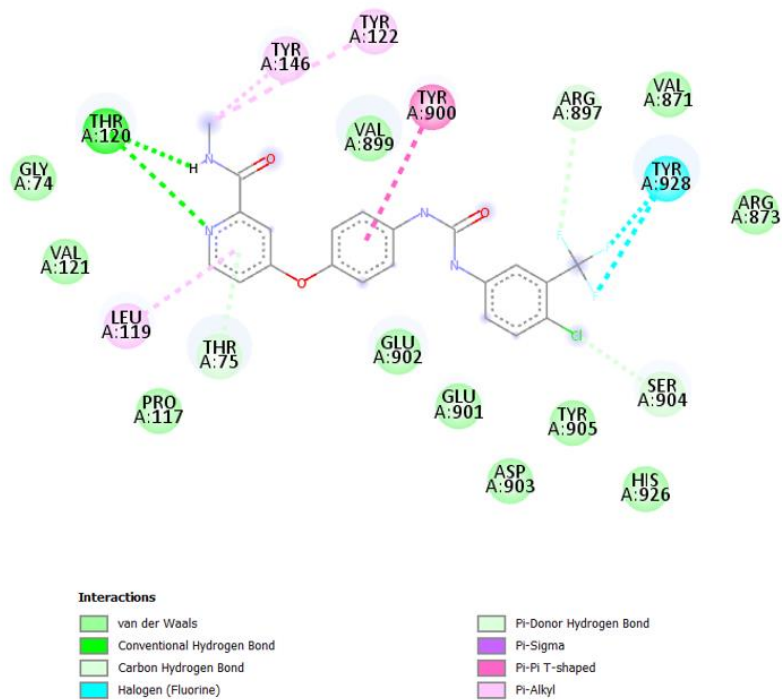
RAF1



VEGFR2



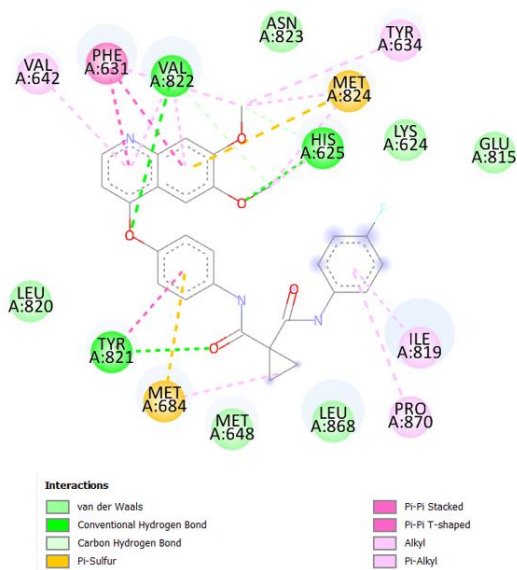
VEGFR3



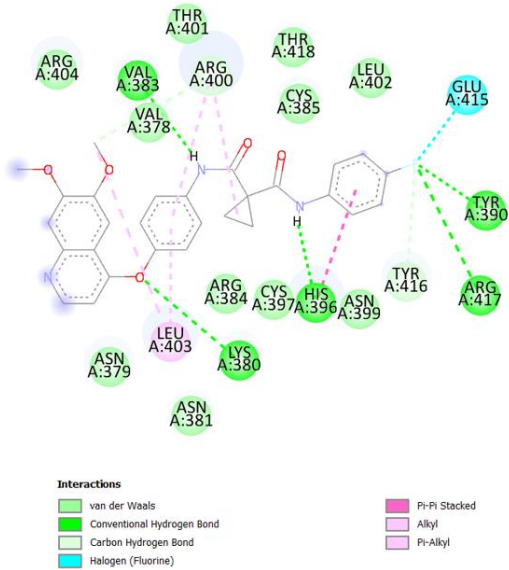
RET

(B)

Cabozantinib s-malate



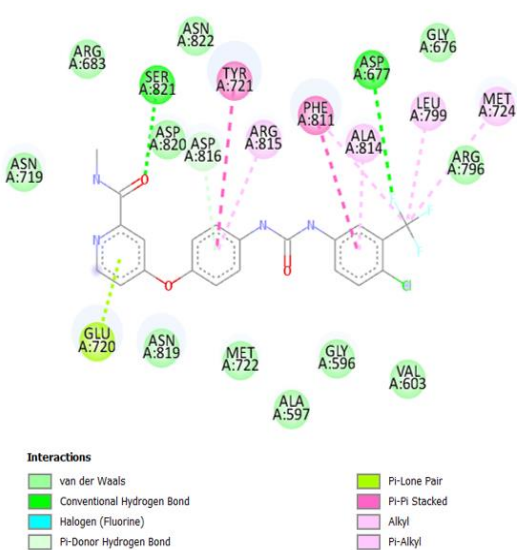
AXL Protein



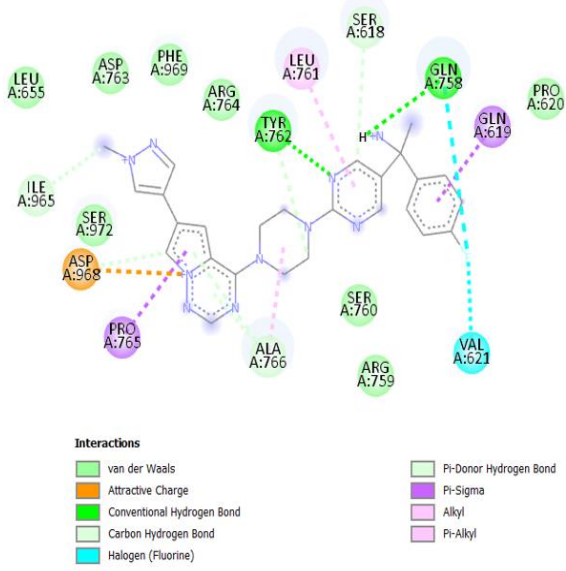
MET Protein

(C)

Avapritinib



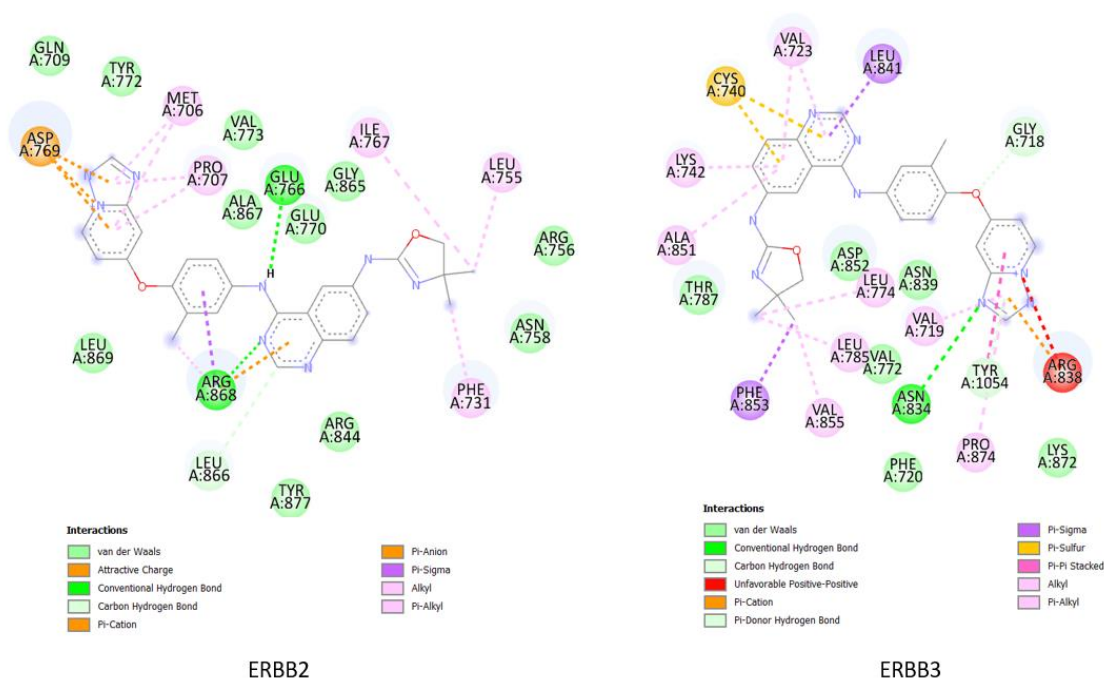
KIT Protein



PDGFRA Protein

(D)

Tukysa/ Tucatinib



(E)

Motesanib diphosphate

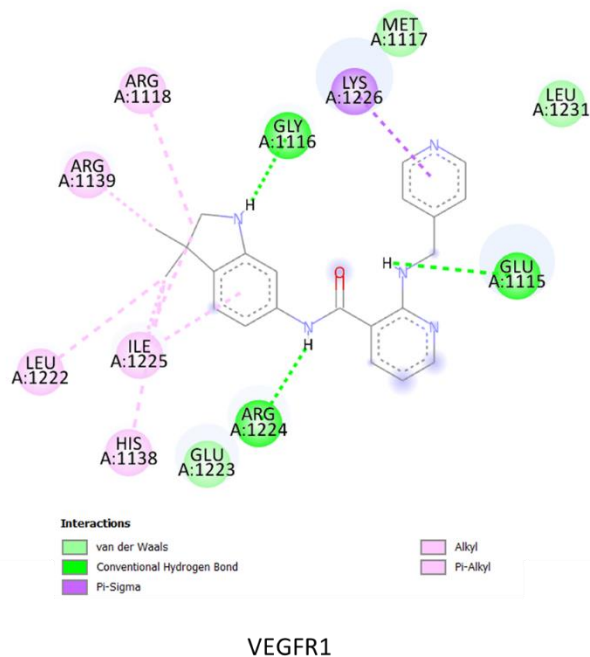


Fig. 8 (A) 2D molecular interactions of docked complex (Sorafenib+BRAF, FILT, PDGFRB, RAF1, VEGFR2, VEGFR3, and RET), with hydrogen bonds and hydrophobic bonds. (B) 2D interactions of docked complex (Cabozantinib s-malate-AXL, and MET), with hydrogen bonds and hydrophobic bonds. (C) 2D interactions of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