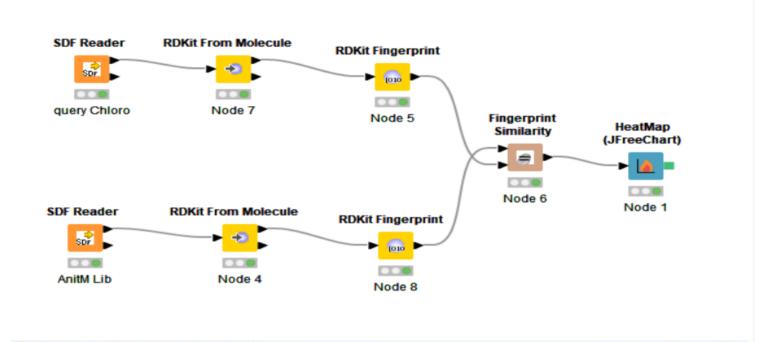
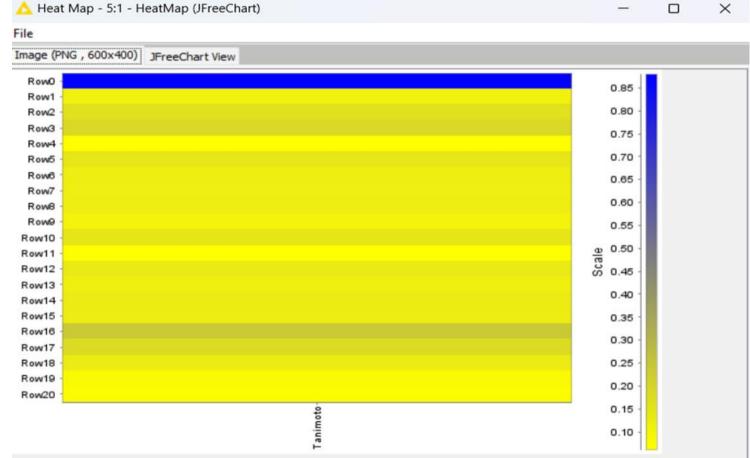
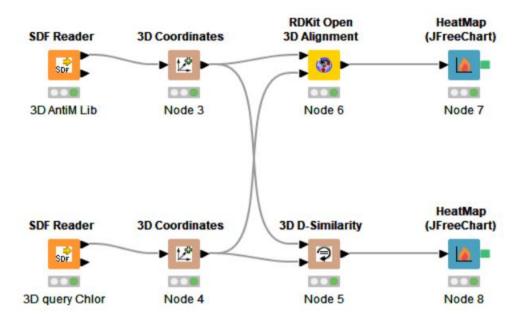
# Result

### 2D workflow and Heatmap

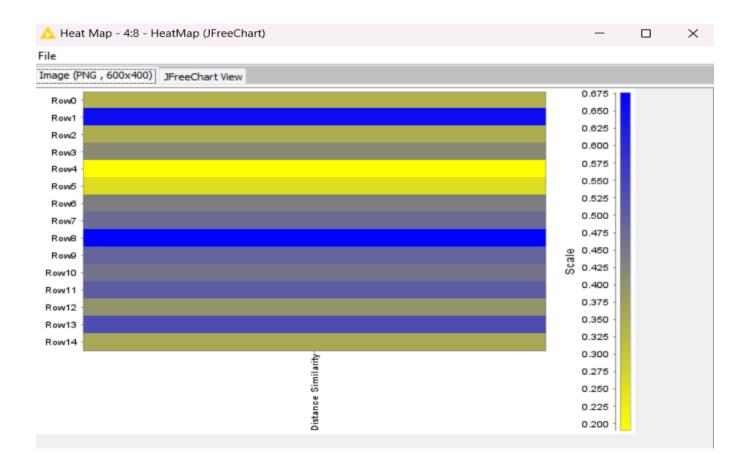




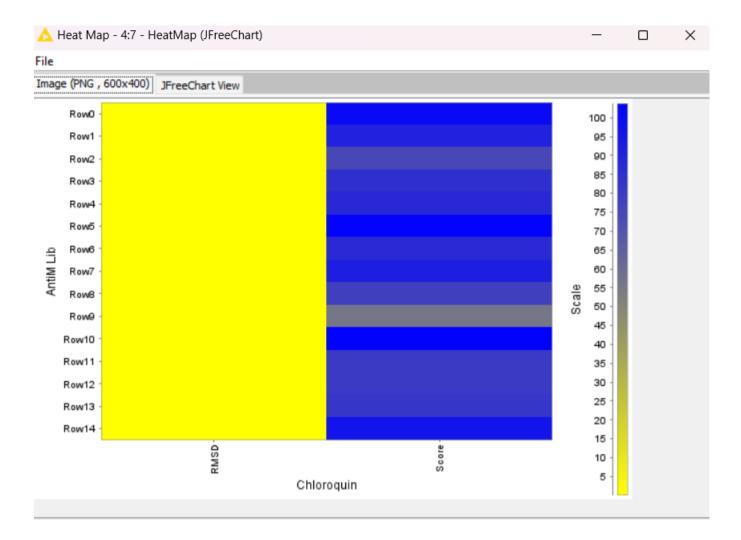
### 3D Workflow (Using CDK and RDkit Packages)



### Heatmap (3D similarity using CDK Package)



## Heatmap (3D alignment Using RDkit package)



1.

### **Molecular Docking**

Protein Name: Adenosine deaminase (plasmodial vivax)

Protein ID – 3EWC PDB DOI: https://doi.org/10.2210/pdb3ewc/pdb

Ligand Name	Ligand ID	Energy value	Dock Image
2-N-(3-chlorophenyl)- 4-N-(furan-2- ylmethyl)quinazoline- 2,4-diamine	1285085	-8.2	A:152  A:152  A:153  A:167  A:165  A:165  A:195  A:166  Interactions  Conventional Hydrogen Bond  Pi-Sulfur  Pi-Sulfur

N,N-diethyl-5-pyridin- 4- yliminobenzo[a]pheno xazin-9-amine	44226912	-8.4	ASN A:318  A:318  A:318  A:312  Cys A:34  TYR A:30  Interactions  Conventional Hydrogen Bond Carbon Hydrogen Bond Carbon Hydrogen Bond P-Alloi
1-(3,4-dichlorophenyl)-8-methyl-N-[2-(methylamino)ethyl]-9H-pyrido[3,4-b]indole-3-carboxamide	156869265	-7.5	Interactions  P-Ponor Hydrogen Bond  P-P F1 Stacked  P-P IT-shaped