

Reduction of Anti-HER2 Resistance in Breast Cancer by Resolving Steric Clashes at the Orthosteric Site of HER2^{T798I} Mutant

Wafa M. Maklouf

M. Sc. Pharmaceutical science

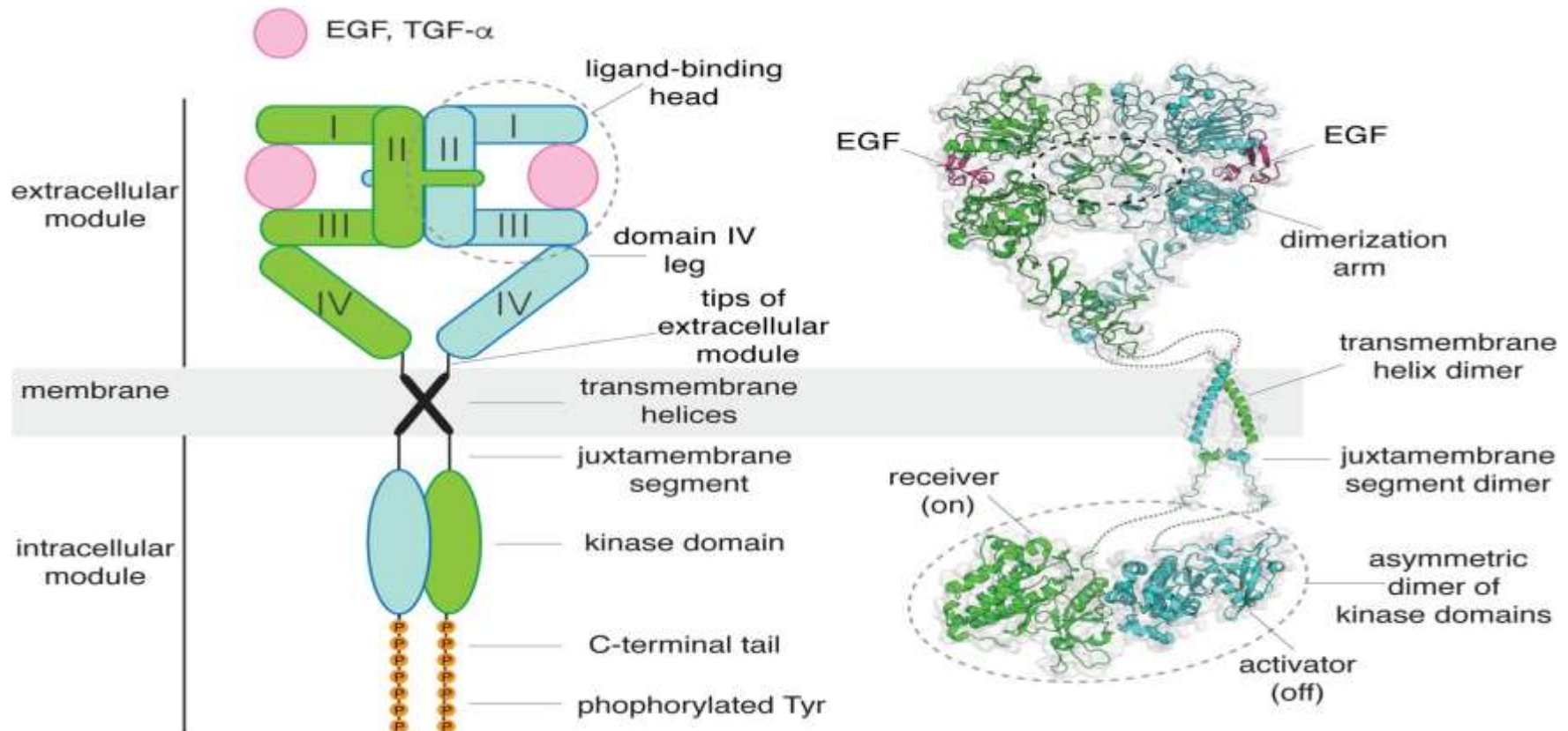
Authors: Dr. Hamed I. Ali , Dr. Radwan Alnajjar

Introduction

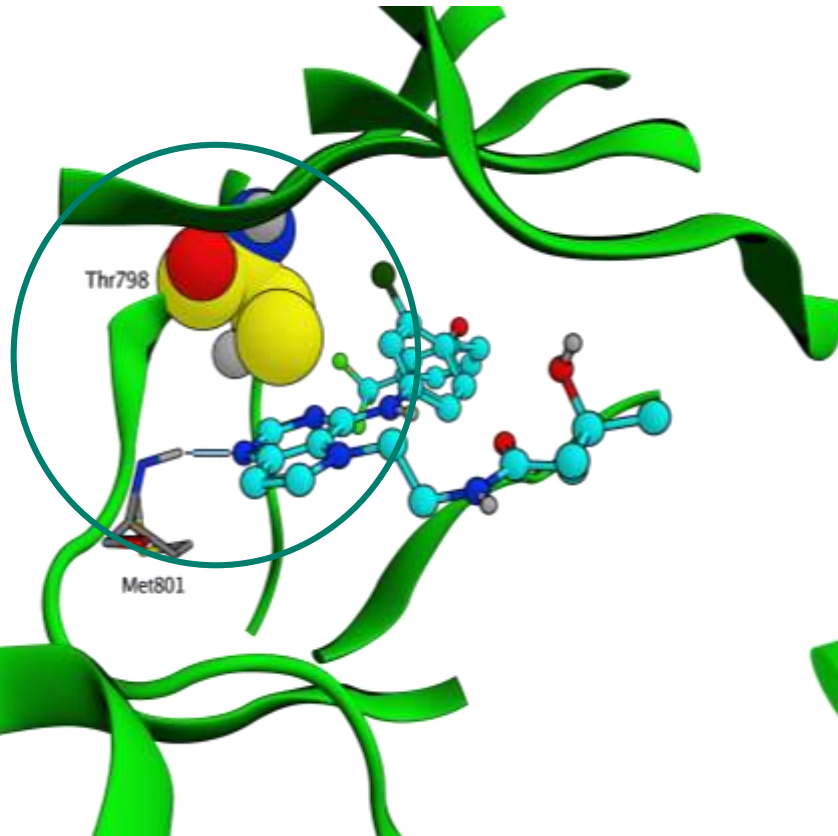
- Breast cancer develops from cells that grow uncontrollably.
- Classified into three subtypes or classes based on the presence or absence of specific proteins in the cancer cells.

Around 70% of BC cases are hormone receptor-positive, meaning they have either the progesterone receptor (PR) or estrogen receptor (ER) protein. Another 15 to 20% are HER2-positive, indicating high levels of the HER2 protein. The remaining 15% of cases are triple-negative, meaning the cancer cells lack all Three target proteins: ER, PR, and HER2.

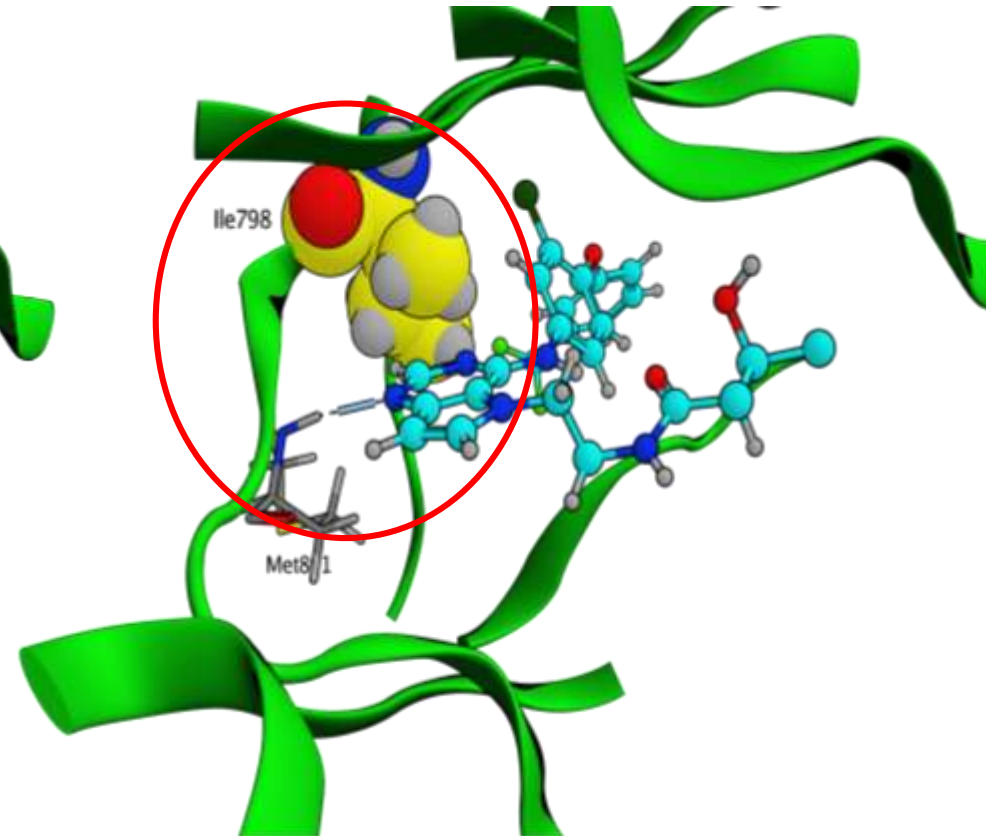
Human Epidermal Growth Factor Receptor 2 (HER2)



Mutated Receptor



Wild HER2 kinase (HER2^{T798})



Mutant HER2 kinase (HER2^{I798})

Aim of the Project

The study aims to reduce anti-HER2 resistance in breast cancer by eliminating steric clashes at the orthosteric site in mutant HER2^{T798I}, flexible lapatinib analogs will be designed to avoid these clashes.

Methods & Material

We use computational methodologies and modeling software by using

- Maestro software to prepare and dock for ligand and protein.
- The next step is monitoring pharmacokinetics by Swiss ADME assign
- And pose ligand by Molecular Dynamics (MD) Simulations.

Methods & Material

1. Prepare and dock for ligand _ protein

High-throughput
virtual screening
(HTVS)

1,474,068
Ligands

Standard-
precision (SP)

1000 Ligands

Extra-precision
(XP) docking

200 Ligands

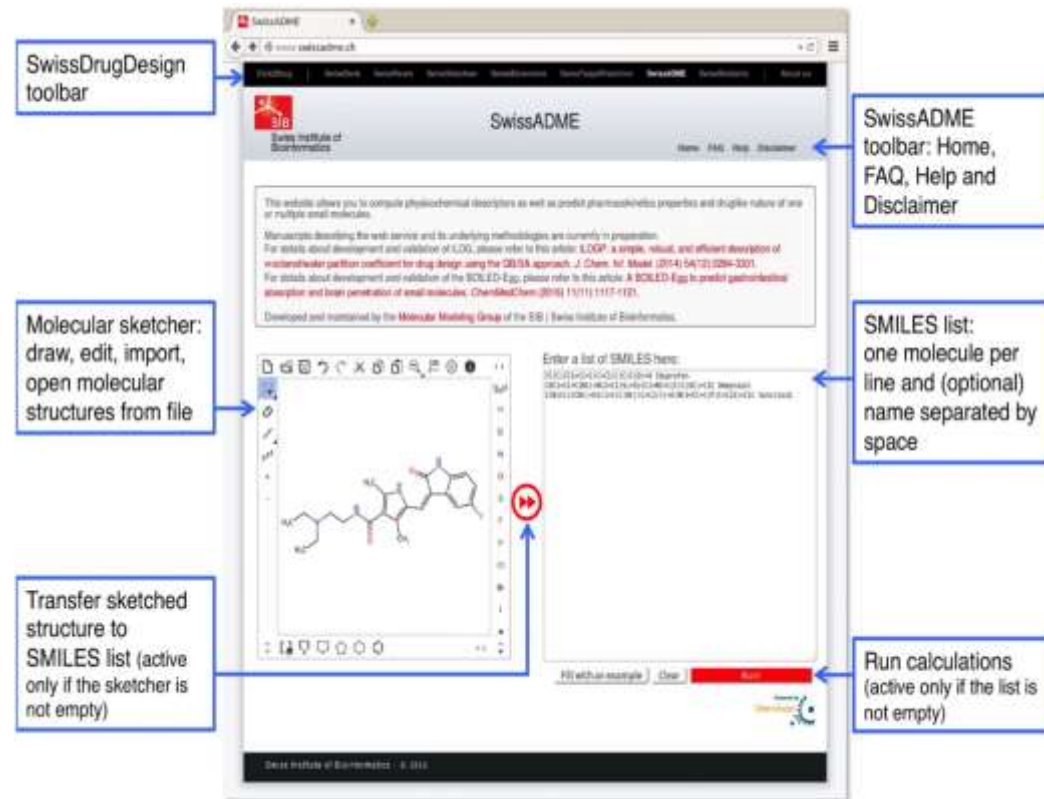
The best
ligands have
the best pose
and a high
docking
score

Analysis
of the
docking
results

Methods & Material

2. Swiss ADME

- The Swiss ADME web tool presented here is freely accessible Pharmacokinetics examining absorption, distribution, metabolism, and excretion.
- Early estimation during discovery reduces pharmacokinetics-related failure in clinical phases.



The screenshot shows the SwissADME web interface. Annotations include:

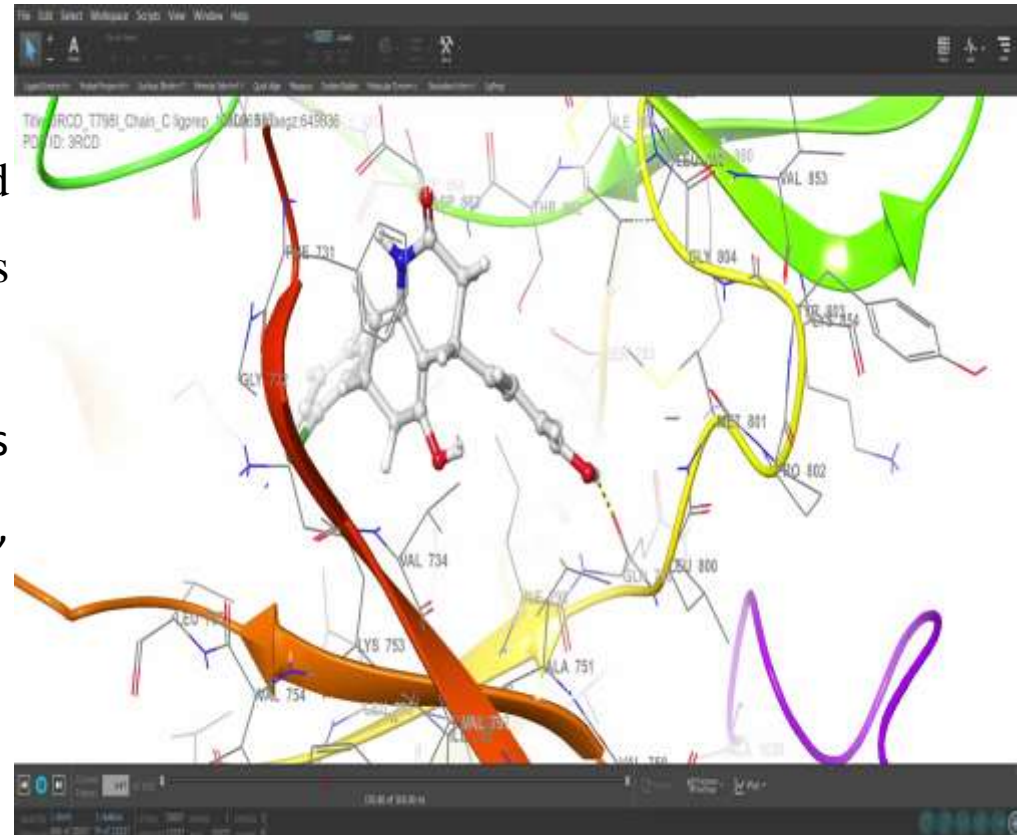
- SwissDrugDesign toolbar**: Points to the top navigation menu.
- SwissADME toolbar: Home, FAQ, Help and Disclaimer**: Points to the top right navigation links.
- Molecular sketcher: draw, edit, import, open molecular structures from file**: Points to the sketcher toolbar on the left.
- Transfer sketched structure to SMILES list (active only if the sketcher is not empty)**: Points to the red double arrow button between the sketcher and the SMILES list.
- SMILES list: one molecule per line and (optional) name separated by space**: Points to the text input area for SMILES strings.
- Run calculations (active only if the list is not empty)**: Points to the red 'Run' button at the bottom right.

Methods & Material

3. Molecular dynamics analysis

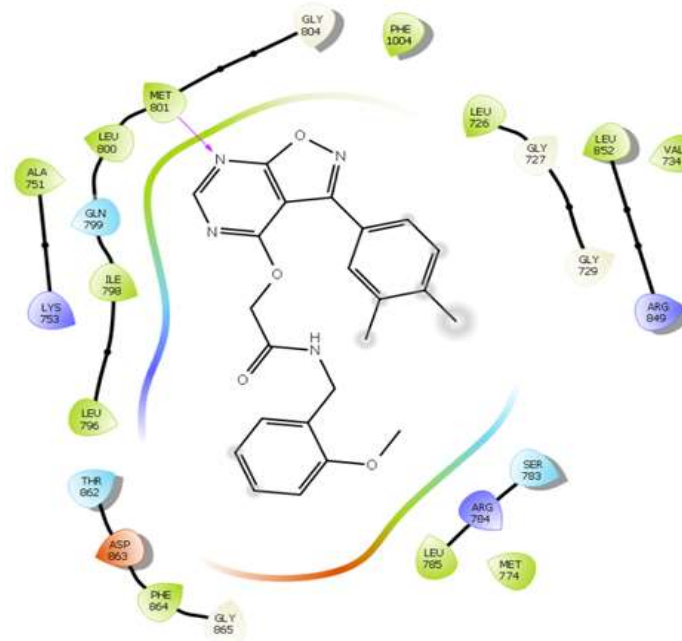
Molecular dynamics simulation is a method used to determine how atoms and molecules move over a certain time.

The timeline depicts protein interactions with ligands, including H-bonds, hydrophobic, ionic, and water bridges.



Results and discussion

1. Docking analysis: Compound have docking higher than Lapatinib.



Compound (C):856174

Docking score: -9.921

Results and discussion

2. Swiss ADME analysis

A. Physicochemical Properties

Compound	MW Daltons (Da)	TPSA Å	Rotatable bonds	HBA	HBD	ESOL Class	CLog P
856174 (C)	418.45	99.37	8	7	1	Moderately soluble	3.29

B. Pharmacokinetics Properties:

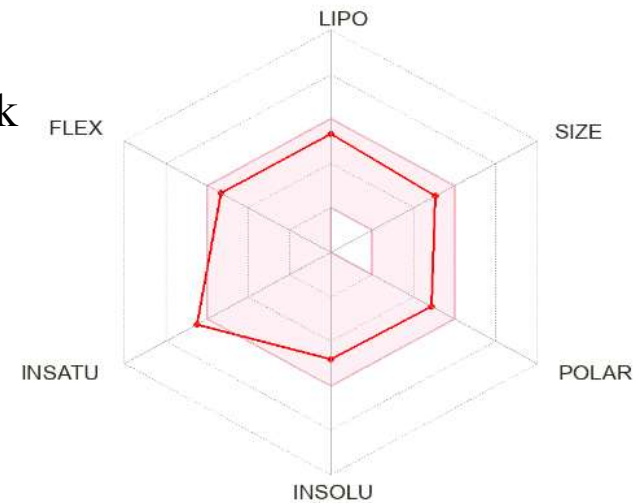
Compound	Predicted LD50: mg/kg	Predicted Toxicity Class	Hepato- toxicity	GI absorption	BBB permeant
856174 (C)	10000mg/kg	6	Inactive	High	No

Results and discussion

C. Bioavailability

Bioavailability radars for the most active compound: **C** The pink area represents the optimal range for each property:

- lipophilicity (LIPO) (XLOGP3 between -0.7 and $+5.0$)
- Molecular mass (SIZE) (between 150 and $500 \text{ g}\cdot\text{mol}^{-1}$)
- polarity (POLAR) (TPSA between 20 and 130 \AA^2)
- Solubility (INSOLU) ($\log S$ not higher than 6)
- Saturation (INSATU) (fraction of carbons in the sp^3 hybridization not less than 0.25)
- Flexibility (FLEX) (no more than nine rotatable bonds).



(C):856174

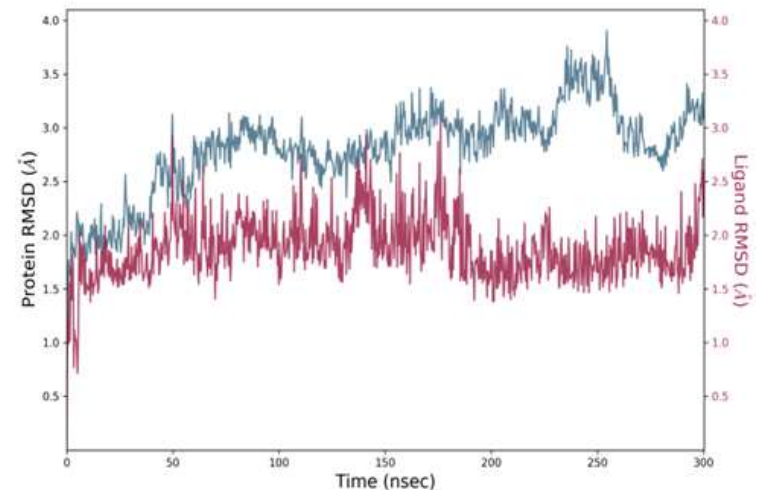
Ideal Drug likeness

Results and discussion

3. Molecular dynamics analysis

Shows the C α protein backbone starts stable but at 235.5 ns of trajectory has significant fluctuations ranging between 3.4–3.6 Å indicating no large conformational changes to the protein.

(Lig)fit on the protein plot the protease complex's overall RMSD plot compound(C)856174, which displays ripples between 1.5-3 Å, indicates that the ligand is stably attached to the binding site of the protease and has not dispersed away from it

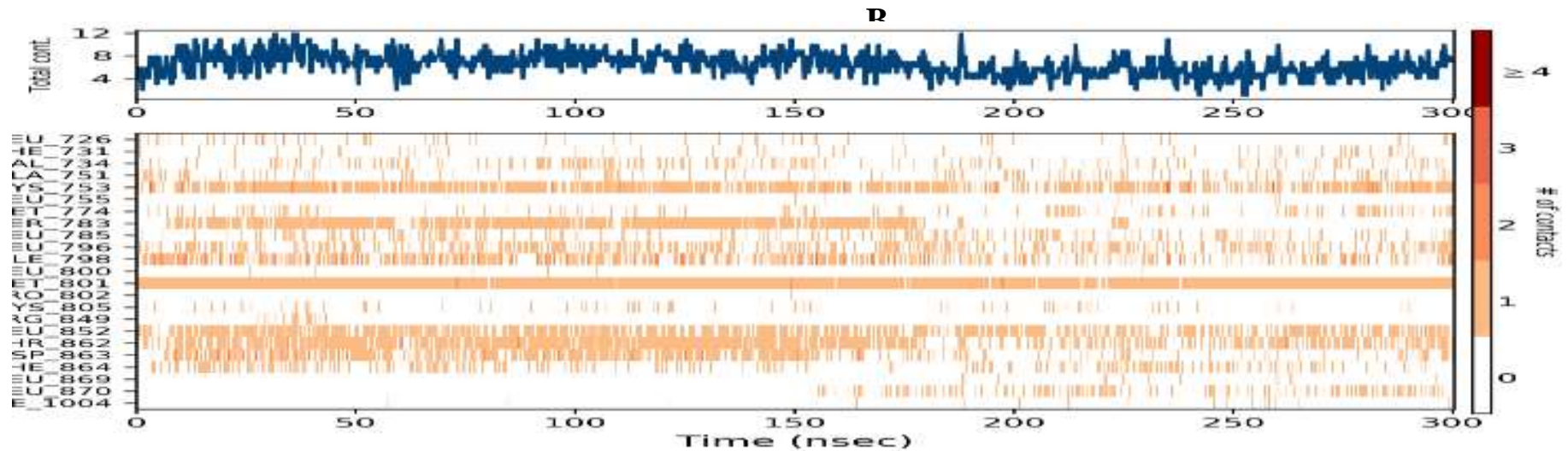


Compound(C):
856174

Results and discussion

Protein-ligand contacts analysis for 3RCD-compound 856174

A



. **Figure.** shows longer continued contact with MET801.

Conclusions and future scope:

The study screened compounds for anti-her2 resistance in breast cancer, with showing best docking scores.

Compound (C)856174, with a docking score of -9.92 kcal/mol, formed H-bonds with receptor residues and showed moderate solubility, low hepatotoxicity, and high GI absorption.

Further studies will be conducted through:

- a) Kinase profiling against HER2 protein kinase.
- b) In vitro and in vivo screening of **Compound (C)856174** to validate its activity.

References :

- ✓ Anand, U., Dey, A., Chandel, A.K.S., Sanyal, R., Mishra, A., Pandey, D.K., De Falco, V., Upadhyay, A., Kandimalla, R., Chaudhary, A. and Dhanjal, J.K., 2023. Cancer chemotherapy and beyond: Current status, drug candidates, associated risks and progress in targeted therapeutics. *Genes & Diseases*, 10(4), pp.1367-1401. <https://doi.org/10.1016/j.gendis.2022.02.007>.
- ✓ Brown, J.S., Amend, S.R., Austin, R.H., Gatenby, R.A., Hammarlund, E.U. and Pienta, K.J., 2023. Updating the definition of cancer. *Molecular Cancer Research*, 21(11), pp.1142-1147. <https://doi.org/10.1158/1541-7786.MCR-23-0411>.
- ✓ Li, S.G. and Li, L., 2013. Targeted therapy in HER2-positive breast cancer. *Biomedical reports*, 1(4), pp.499-505. <https://doi.org/10.3892/br.2013.95>.
- ✓ Daina, A. and Zoete, V., 2016. A boiled-egg to predict gastrointestinal absorption and brain penetration of small molecules. *ChemMedChem*, 11(11), pp.1117-1121. <https://doi.org/https://doi.org/10.1002/cmdc.201600182>..
- ✓ Cerutti, D.S., Rice, J.E., Swope, W.C. and Case, D.A., 2013. Derivation of fixed partial charges for amino acids accommodating a specific water model and implicit polarization. *The Journal of Physical Chemistry B*, 117(8), pp.2328-2338. <https://doi.org/10.1021/jp311851r>.
- ✓ Doak, B.C., Over, B., Giordanetto, F. and Kihlberg, J., 2014. Oral druggable space beyond the rule of 5: insights from drugs and clinical candidates. *Chemistry & biology*, 21(9), pp.1115-1142. <https://doi.org/https://doi.org/10.1016/j.chembiol.2014.08.013>.
- ✓ Lu, C. et al. (2010) 'Structural Evidence for Loose Linkage between Ligand Binding and Kinase Activation in the Epidermal Growth Factor Receptor', *Molecular and Cellular Biology*, 30(22), pp. 5432–5443. doi: 10.1128/MCB.00742-10.

Thank you