SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

EXPLORING THE MOLECULAR AFFINITIES OF MEFENAMIC ACID & CELECOXIB BY USING AUTO-DOCK TOOL

Nitin Bajirao Sapkal[1]*, Seema Pralhad Rathod[2]

[1]*Student of bachelor of pharmacy, Faculty of pharmacy, Dr. Babasaheb Ambedkar Technological University, Lonere, Raigad.*

[2]*Department of pharmaceutical Chemistry, Faculty of pharmaceutical Chemistry, Dr. Babasaheb Ambedkar Technological University, Lonere, Raigad.*

ABSTRACT

Mefenamic acid is a nonsteroidal anti-inflammatory drug (NSAID) known for its analgesic and anti-inflammatory properties. Understanding its interaction with biological targets at the molecular level is crucial for elucidating its therapeutic mechanisms and designing more effective derivatives. Molecular docking, a computational technique, offers insights into the binding modes and affinities of mefenamic acid with target proteins such as cyclooxygenases (COX) and other inflammatory mediators. This review provides an overview of recent advancements in molecular docking studies of mefenamic acid, highlighting its interactions with key residues within the active sites of target proteins. Furthermore, it discusses the implications of these findings for the development of novel mefenamic acid-based therapeutics with enhanced efficacy and reduced side effects.

1.INTRODUCTION TO MEFENAMIC ACID

Mefenamic acid is a nonsteroidal anti-inflammatory drug (NSAID) with analgesic, anti-inflammatory, and antipyretic properties. It belongs to the class of anthranilic acid derivatives and is structurally related to other NSAIDs such as ibuprofen and naproxen. Mefenamic acid was first synthesized in the 1960s and has since been widely used for the treatment of various conditions, including menstrual pain (dysmenorrhea), rheumatoid arthritis, and other inflammatory disorders.

Its mechanism of action involves inhibition of cyclooxygenase (COX) enzymes, particularly COX-1 and COX-2, which are key enzymes involved in the synthesis of prostaglandins from arachidonic acid. Prostaglandins play a crucial role in mediating inflammation, pain, and fever responses. By inhibiting COX enzymes, mefenamic acid suppresses the production of prostaglandins, thereby exerting its anti-inflammatory and analgesic effects.

Mefenamic acid is typically administered orally in the form of tablets or capsules. It is rapidly absorbed from the gastrointestinal tract, with peak plasma concentrations reached within 2-4 hours after administration.

OBJECTIVES

- To investigate the binding interactions of mefenamic acid with key protein targets, including cyclooxygenases (COX-1 and COX-2).
- To elucidate the structural basis of mefenamic acid's pharmacological activity through computational docking studies.
- To identify potential modifications or interactions that could enhance the drug's efficacy or selectivity.

1.1Introduction to Celecoxib

Celecoxib is a nonsteroidal anti-inflammatory drug (NSAID) belonging to the class of selective cyclooxygenase-2 (COX-2) inhibitors. It is widely used for the management of pain, inflammation, and various types of arthritis. Understanding the molecular interactions of celecoxib with its target protein, COX-2, is crucial for elucidating its pharmacological mechanisms and guiding drug design efforts.

Objectives

- To investigate the binding interactions of celecoxib with the active site of COX-2 through molecular docking studies.
- To analyze the binding affinity and energetics of celecoxib binding to COX-2.
- To explore the structural features of the celecoxib-COX-2 complex and identify key interactions contributing to binding specificity.

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

2.BASICS OF MOLECULAR DOCKING

Molecular docking is a widely utilized method for predicting the alignment of small molecule therapeutic compounds with their protein targets, thereby anticipating the affinity and activity of the small molecule. It plays a crucial role in rational drug design. Due to the biological and pharmacological significance of docking studies, substantial efforts have been dedicated to enhancing the algorithms for docking prediction.

Docking is fundamentally a mathematical technique that predicts the optimal orientation of one molecule relative to another when they interact to form a stable complex. Through scoring functions, the strength of the binding affinity between two compounds can be estimated based on their preferred orientation. Here's a breakdown of the basics:

- **Target Molecule:** Usually, the target molecule is a protein receptor, but it can also be DNA, RNA, or other macromolecules.
- **Ligand Molecule:** The ligand is the small molecule (often a potential drug candidate) that is being docked into the target molecule.
- **Scoring Function:** The scoring function typically accounts for factors such as steric hindrance, electrostatic interactions, hydrogen bonding, and hydrophobic interactions.
- **Search Algorithm:** Docking programs employ search algorithms to explore the vast conformational space of possible ligand-receptor orientations. Common search algorithms include genetic algorithms, Monte Carlo simulations, and stochastic searches.
- **Binding Site Prediction:** Before docking, the binding site on the target molecule needs to be identified or predicted. This can be done using experimental methods like X-ray crystallography or NMR spectroscopy, or through computational methods like molecular dynamics simulations or binding site prediction algorithms.
- **Validation:** Docking results are typically validated by comparing them to experimental data or by cross-validation against known ligand-receptor complexes.(1)

2.1Molecular Docking

Molecular docking involves arranging molecules in optimal configurations for interaction with a receptor. It's a process that occurs rapidly within cells as molecules bind together to form stable complexes. (1)

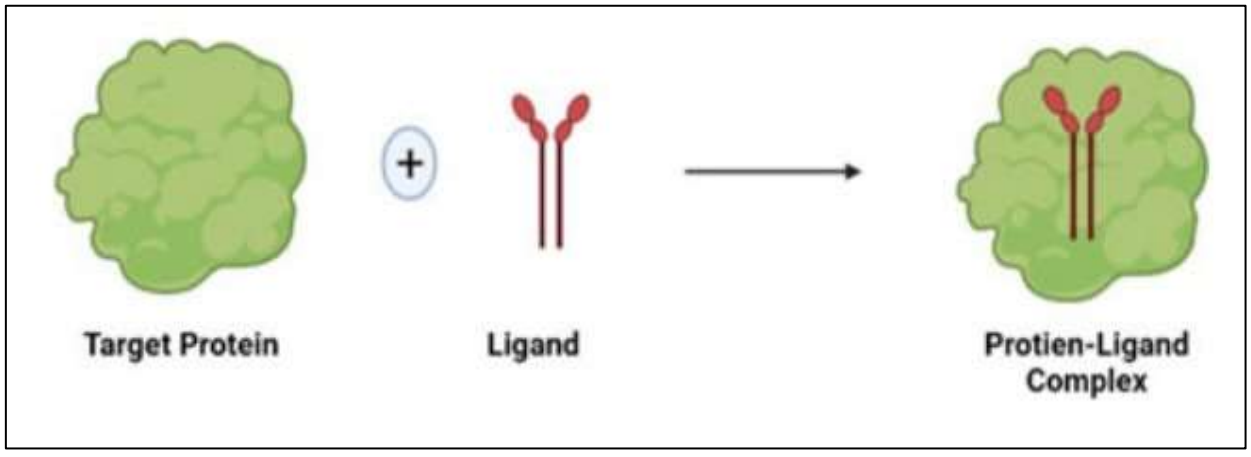

Fig. Molecular Docking

2.2Molecular Modeling

Molecular modeling serves as a versatile tool for generating, describing, and adjusting the configurations and interactions of compounds, including the attributes dependent on their three-dimensional geometries. (1)

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

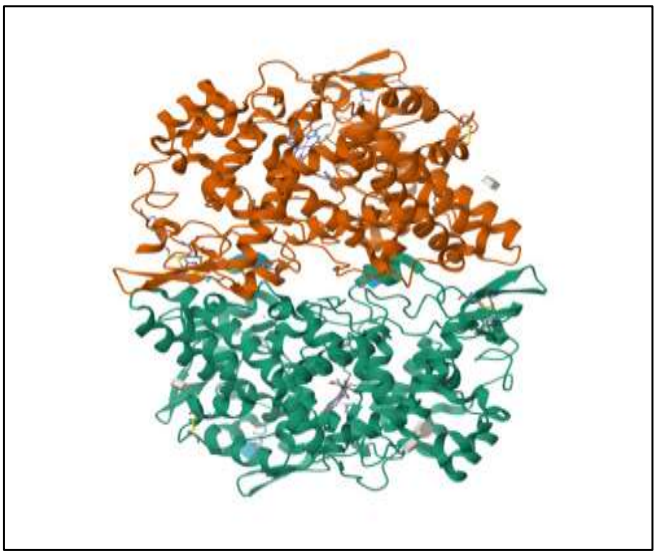

Fig. Molecular Modeling

2.3Types of docking

2.3.1. Rigid docking: Given that the compounds are rigid, our aim is to find an optimal rearrangement of one of the compounds in three-dimensional space to achieve the closest match to the other compound based on a scoring system. The conformation of the ligand can be determined whether it exhibits receptor binding activity or not. (1)

2.3.2. Flexible docking: The ligand and/or the receptor can undergo conformational changes to explore different binding modes and interactions, which can lead to more accurate predictions of ligand-receptor interactions and binding affinities. (1)

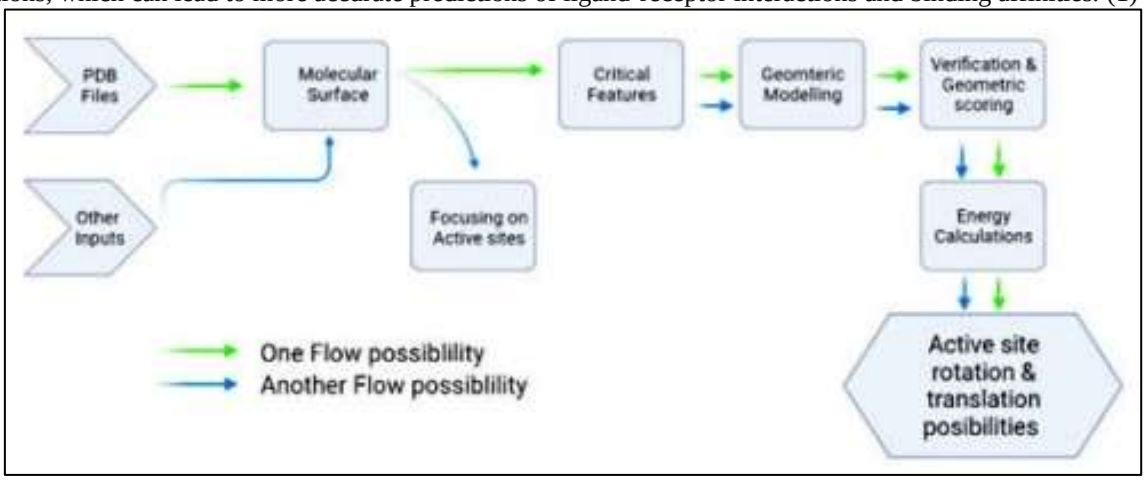

Fig. Rigid & Flexible Docking

2.4Different types of Docking based on Interaction

2.4.1Protein-Ligand Docking:

It involves simulating the interaction between the protein and ligand to predict their optimal spatial arrangement and binding affinity. Protein-ligand docking plays a crucial role in rational drug design by providing insights into the molecular interactions that govern the binding between potential drug candidates and their target proteins. This information can be used to guide the design and optimization of novel therapeutics with improved potency and selectivity.(2)

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

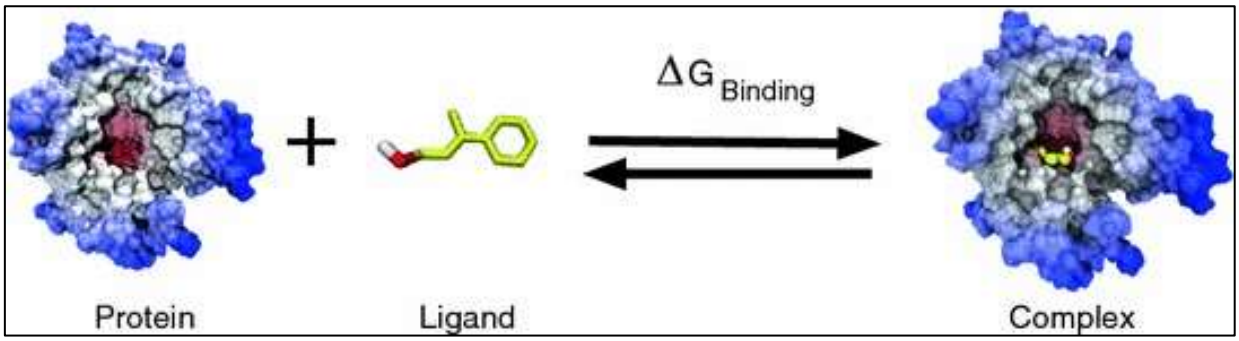

Fig. Protein-Ligand Docking

2.4.2Protein-Protein Docking

In protein-protein docking, the determination of protein complexes involves sequence alignments, structural comparisons, and analysis of multiple protein-protein interactions, considering their specific conformations and docking positions. Also, Protein-protein docking is important for understanding biological processes such as signal transduction, enzymatic reactions, and protein complex formation. (2)

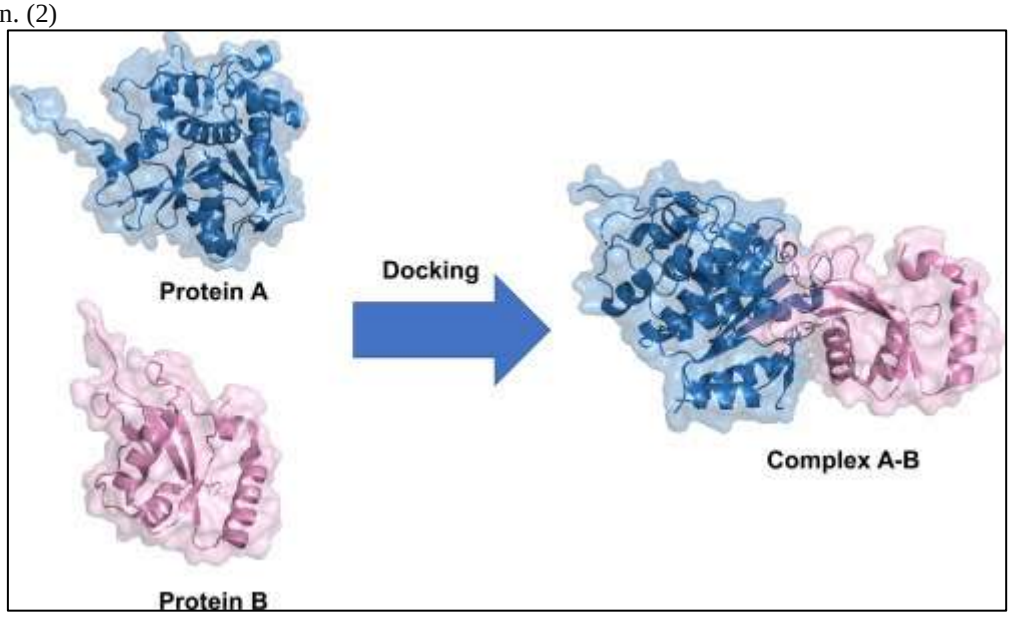

Fig. Protein-Protein Docking

3.Requirements of Molecular Docking:

Tools	Key features
1) Research Collaboratory for Structural Bioinformatics (RCSB)	1. The Research Collaboratory for Structural Bioinformatics Protein Data Bank (RCSB PDB) 2. Information about 3D Dimensional
2) Pubchem	1. Served as a central data repository for the NIH's Molecular Libraries Program (MLP) 2. Mostly high-throughput screening (HTS) data from NIH's MLP and other HTS projects.
3) Pymol	1. To visualize different kinds of molecules such as proteins, compounds, or molecules. 2. Save high-quality images in PNG format.
4) Auto dock Tool 1.5.7	1. 3D molecule visualization, Hydrogen addition, Partial atomic charge assignment, Grid box setup, Results analysis
5) proteins plus	1. They are used in Binding site detection 2D interaction diagrams
6)Discovery Studio Visualizer (BIOVIA)	1. Visualization tool for analyzing protein and modeling data

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

3.1 Auto Docking Tool

This guide will provide an overview of docking procedures utilizing the Auto-Dock suite of software. We'll be utilizing a Graphical User Interface (GUI) known as Auto-Dock Tools (ADT), which simplifies the setup of the docking process for two molecules. ADT facilitates the initiation of external computational tasks within Auto-Dock, and upon completion of the docking simulations, it allows users to interactively examine the results in 3D.

Auto-Dock has been widely used in structure-based drug design, virtual screening, and understanding protein-ligand interactions. It continues to be actively developed and maintained, with newer versions and improvements being released periodically to enhance its capabilities and performance.

3.2 Application of Auto Dock tool:

- Auto-Dock is a molecular modeling simulation software known for its efficacy in protein-ligand docking studies.
- Widely acknowledged in the research community, Auto-Dock stands as one of the most referenced docking software applications.
- The software comprises two main programs: Auto-Grid and Auto-Dock. Auto-Grid primarily calculates relevant energy in a grid, while Auto-Dock handles conformation search and evaluation during docking simulations.
- Auto- Dock facilitates lead optimization by predicting the binding modes and affinities of ligands within the active sites of target proteins. Medicinal chemists use these predictions to design and optimize lead compounds with improved binding properties and pharmacokinetic profiles.

3.3 Ligand preparation steps

1. Utilize a Java applet to create visual representations of your ligands or upload individual ligand files or multiple ligands.
2. Employ Marvin Sketch, a Java-based software offering a wide array of editing features and templates, to draw chemical structures with ease.
3. Upload ligand files in various formats such as MDL MOL, SYBYL MOL2, PDB, HYPERCHEM HIN, or SMILES.
4. Upload multiple ligands in SDF format and customize simulation parameters like desired pH, structure optimization, and partial charge calculations using molecular mechanics or semi-empirical quantum chemical methods.
5. Automatically set up rotatable bonds and atom types, or manually adjust them as needed.
6. Download the provided files in formats like mol, pdb, mol2, and pdbqt. Organize your ligands into folders according to your preferences.

4. MOLECULAR DOCKING FOR MEFENAMIC ACID & CELECOXIB:

Introduction :- Mefenamic acid (Test Drug) is a member of the anthranilic acid derivatives (or fenamate) class of nonsteroidal anti-inflammatory drugs (NSAIDs), and is used to treat mild to moderate pain

Introduction: - Celecoxib (Standard Drug) is a nonsteroidal anti-inflammatory drug (NSAID) belonging to the class of selective cyclooxygenase-2 (COX-2) inhibitors. It is widely used for the management of pain, inflammation, and various types of arthritis.(3)

4.1Receptor and Ligand profile

- **Receptor Name:** The Structure of Mefenamic Acid Bound to Human Cyclooxygenase-2
- **PDB ID:** 5ikr
- **PDB DOI:** https://doi.org/10.2210/pdb5IKR/pdb
- **Classification:** OXIDOREDUCTASE
- **Organism:** Homo sapiens
- **Expression System:** Spodoptera frugiperda

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

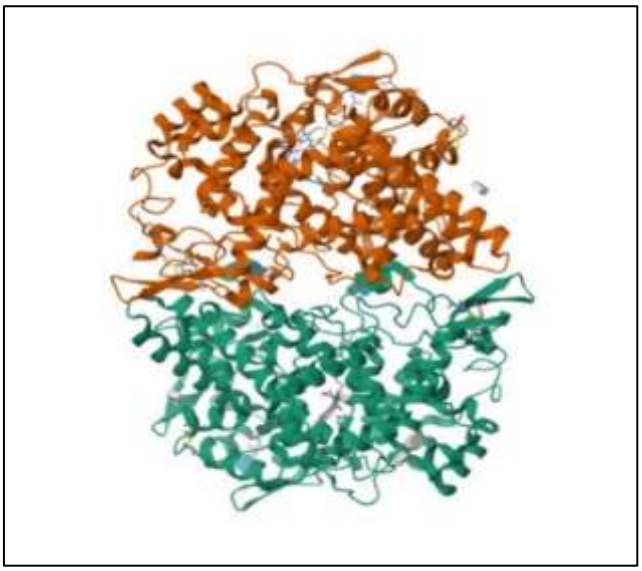

Fig: The Structure of Mefenamic Acid Bound to Human Cyclooxygenase-2

- **Method:** X-RAY DIFFRACTION
- **Resolution:** 2.34 Å
- **R-Value Free:** 0.211
- **R-Value Work:** 0.185(4)

4.2Ligand Profile 1

- **Drug name:** Mefenamic Acid
- **PubChem CID:** 4044
- **Classification:** Anthranilic acid derivative class of NSAIDs (fenamates)
- **Molecular Formula:** C15H15NO2
- **IUPAC Name:** 2-(2,3-dimethylanilino)benzoic acid(3)

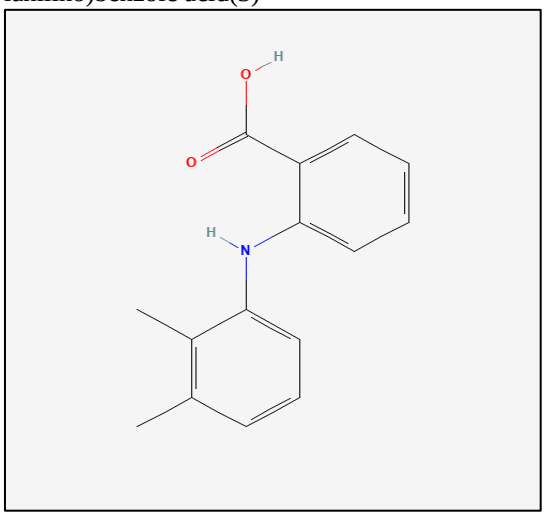

Fig: Structure Of Mefenamic Acid

4.3Ligand profile 2

- **Drug name:** Celecoxib.
- **PubChem CID:** 2662
- **Classification:** Celecoxib is in a class of NSAIDs called COX-2 inhibitors.
- **Molecular Formula:** C17H14F3N3O2S
- **IUPAC Name:** 4-[5-(4-methylphenyl)-3-(trifluoromethyl)pyrazol-1-yl]benzenesulfonamide(3)

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

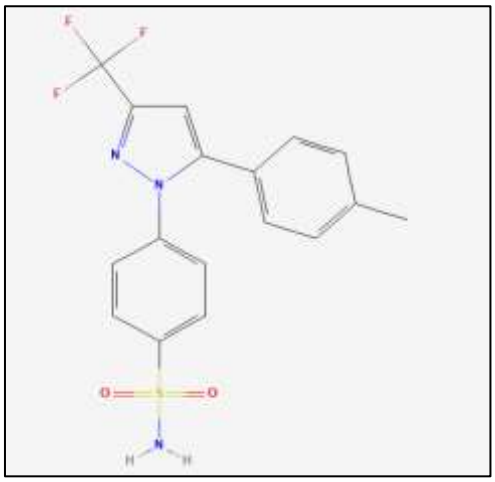

Fig: Structure Of Celecoxib

5.SWISS-ADME Of Mefenamic Acid

Swiss-ADME is a web tool designed for predicting pharmacokinetics and drug-likeness properties of small molecules. It's primarily utilized in drug discovery and development processes to evaluate the absorption, distribution, metabolism, excretion, and toxicity (ADME/Tox) properties of potential drug candidates.

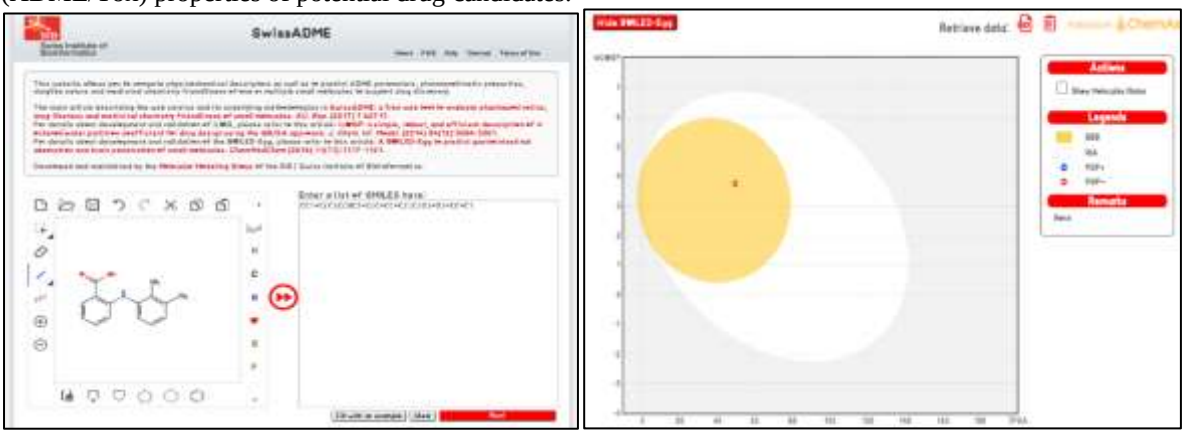

Fig. Boiled Egg of Mefenamic Acid

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

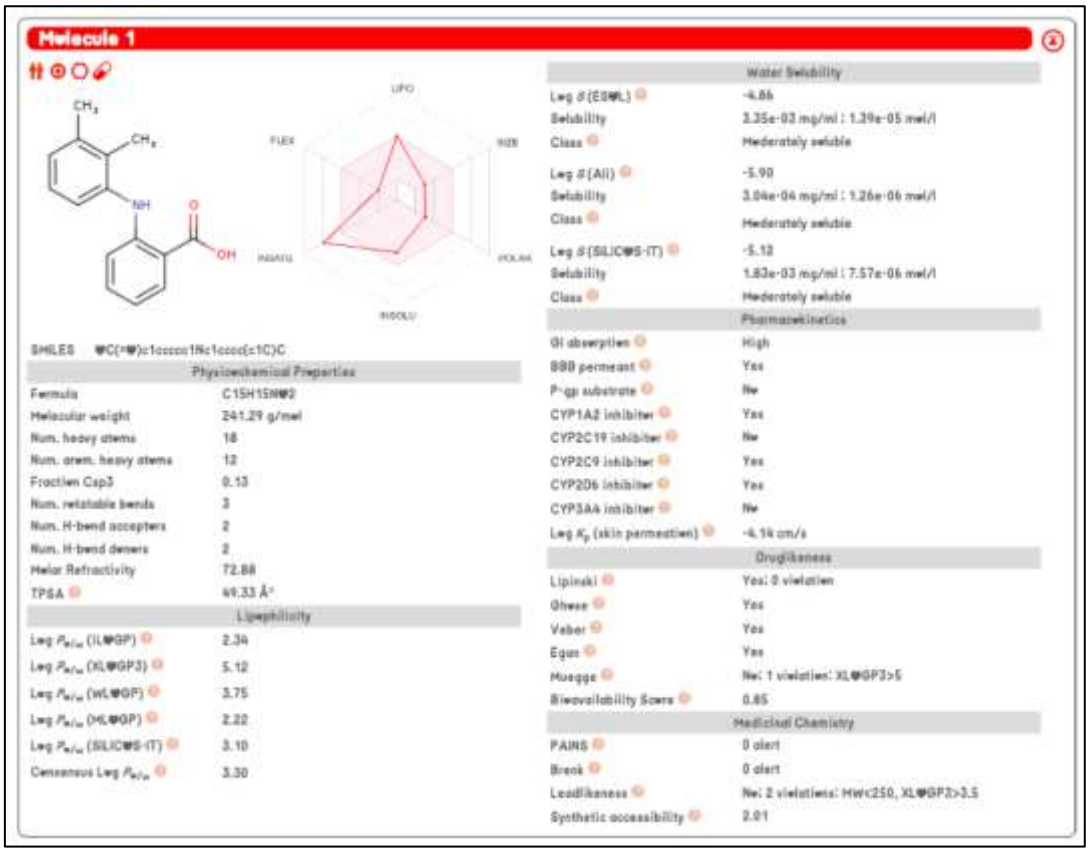

Fig. ADME Study of Mefenamic Acid

5.1SWISS-ADME Of Celecoxib

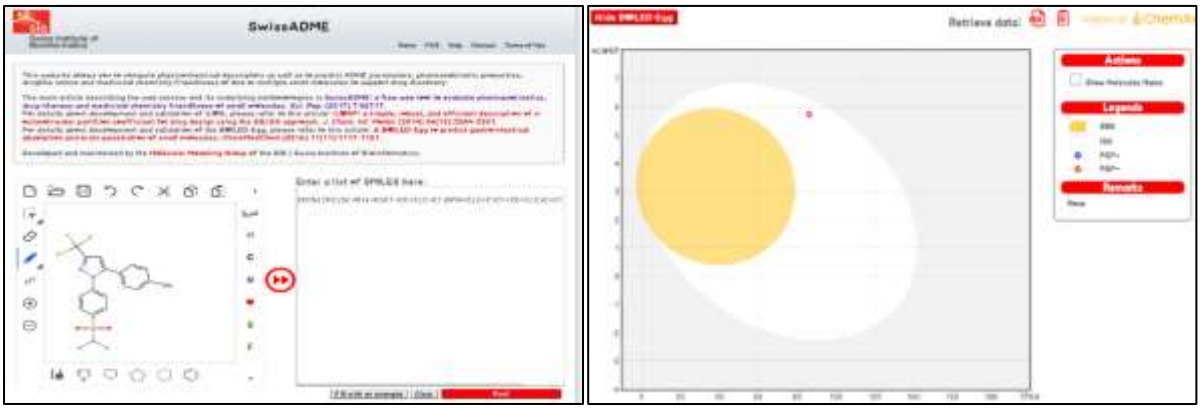

Fig. Boiled Egg of Celecoxib

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

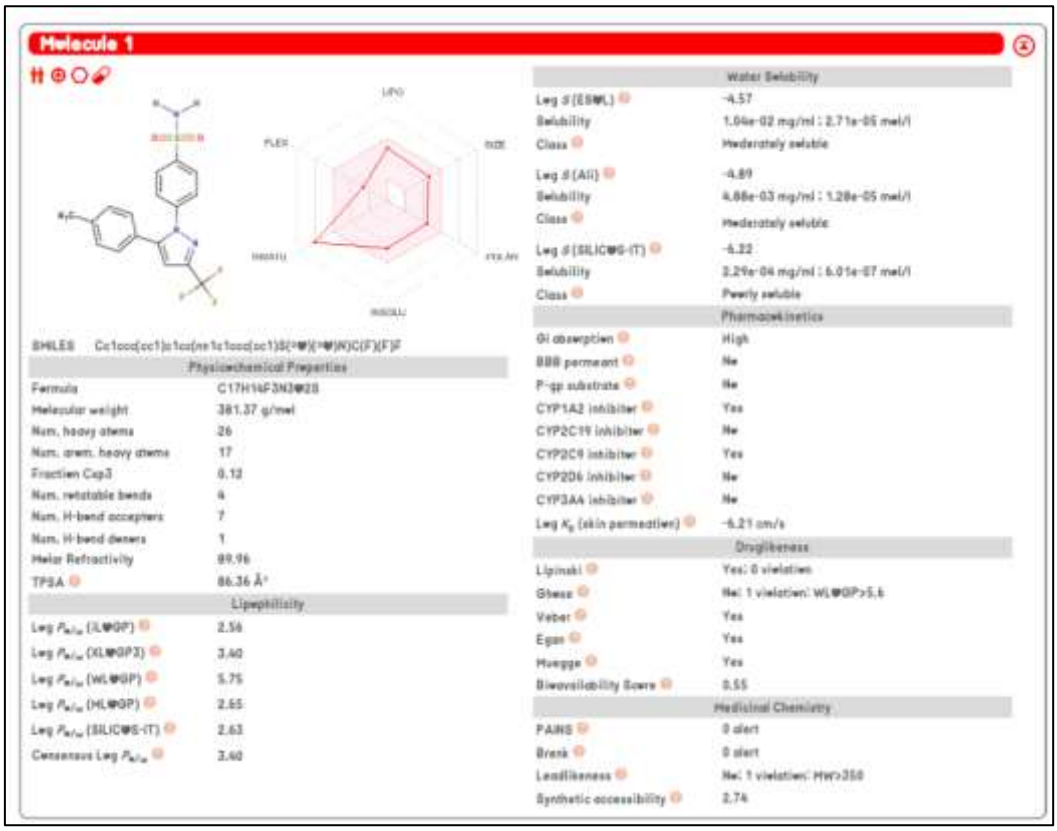

Fig. ADME Study of Celecoxib

5.2Conclusion

Swiss ADME software is a valuable tool in drug discovery and development processes. It offers a range of functionalities related to Absorption, Distribution, Metabolism, and Excretion (ADME) properties of compounds, which are crucial factors in determining the efficacy and safety of potential drug candidates.

6.AUTO-DOCK TOOL

Auto dock Vina is an open-source software tool used for molecular docking. Developed and implemented by Dr. Oleg Trott at the Molecular Graphics Lab, Scripps Research Institute, it offers enhanced accuracy in predicting binding modes compared to Auto dock, based on assessments conducted on the training set used during Auto dock's development.(5)

6.1Target preparation:

The preparation of the receptor is a crucial step. The formation of the receptor-ligand complex is vital for pharmacological activity. In this study, the structure of mefenamic acid bound to human cyclooxygenase-2 was selected from literature survey for investigation. Inhibiting this specific receptor may impede the progression of the disease.

Fig: RCSB Database with PDB ID-5ikr

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

A) Protein preparation

1) Open the PDB format of receptor 5ikr in Auto dock Vina by clicking vina by clicking 'file in subsection read molecule.
2) Go to Edit & Deleting Water molecule, select from string as shown in fig 1:

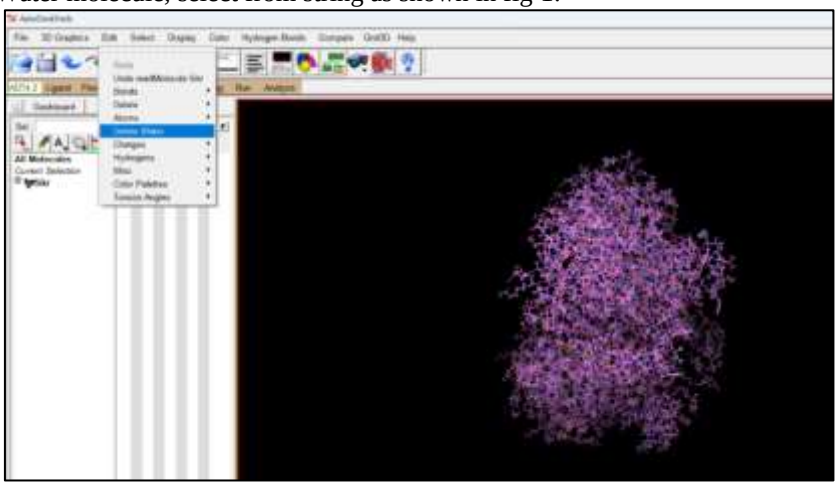

Fig 1: Protein Preparation

3) Then go to select & click on select from string and add Hetatm as show in Fig No:2 & 3

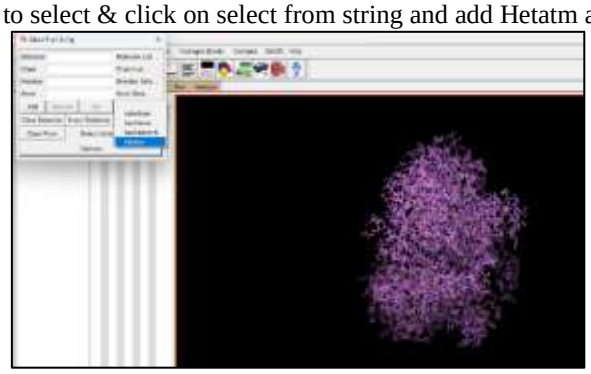

Fig No 2: Select & click select from string

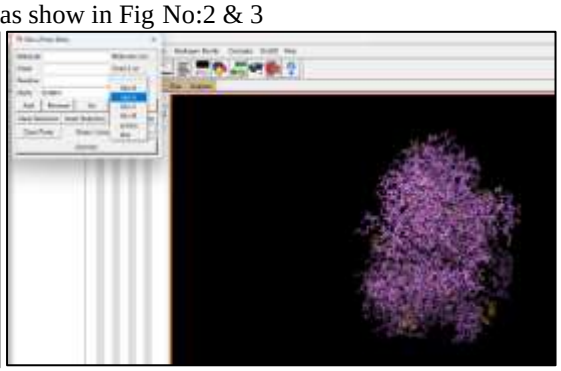

Fig No 3: Add Hetatm

4) Then go to edit and click on Delete Selected Atoms as shown in Fig No:4

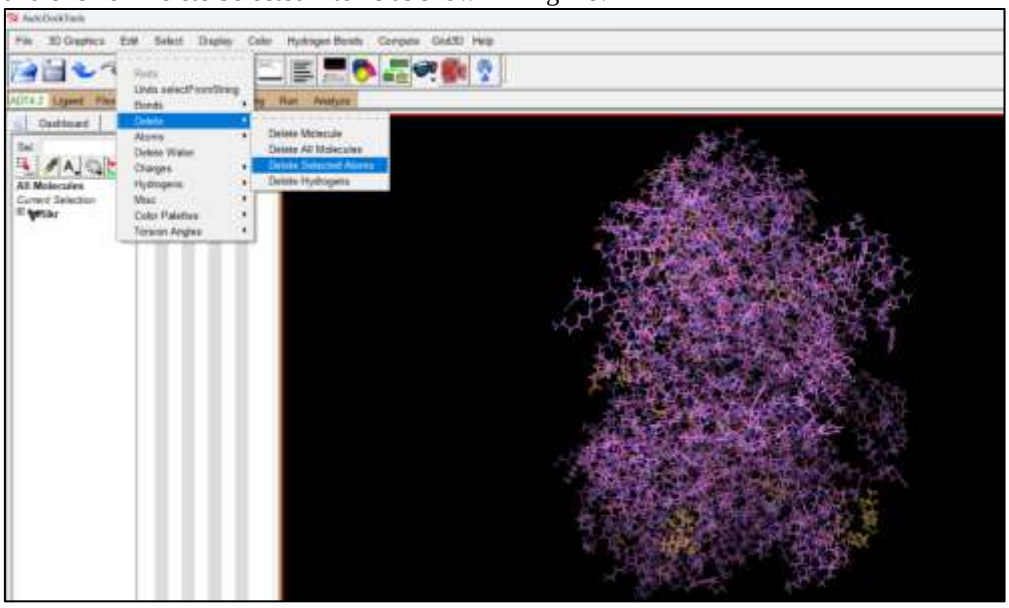

Fig No 4: Delete selected Atom.

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

5) Then go to edit and click on “add hydrogen (polar only) as show in Fig No:5 & 6

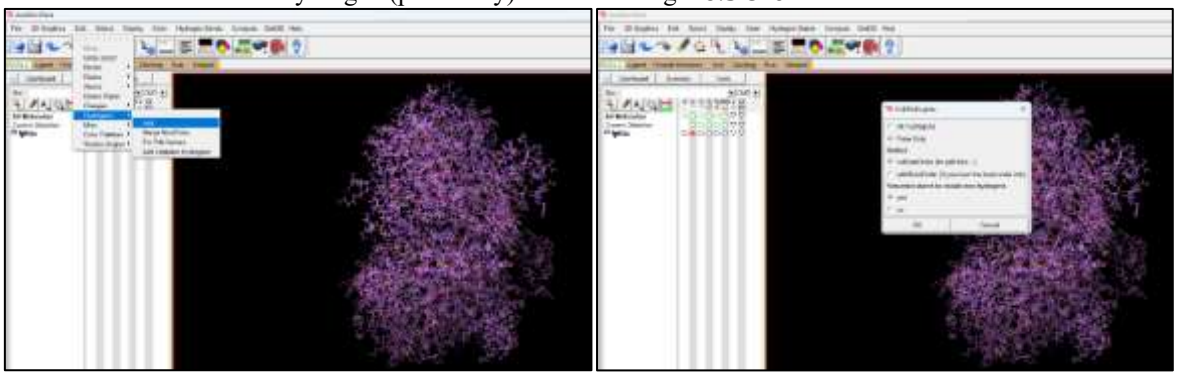

Fig No 5 & 6: Add hydrogen (polar only)

6) Then go to edit and “add kollman charges” as shown in Fig No:7

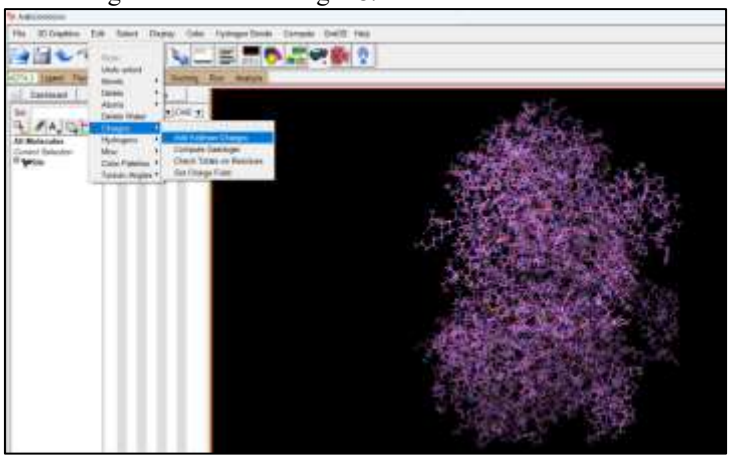

Fig No 7: Add Kollman Charges

7) Then go to edit and click on atoms chose “Assign AD4 type”.as shown in the Fig no:8

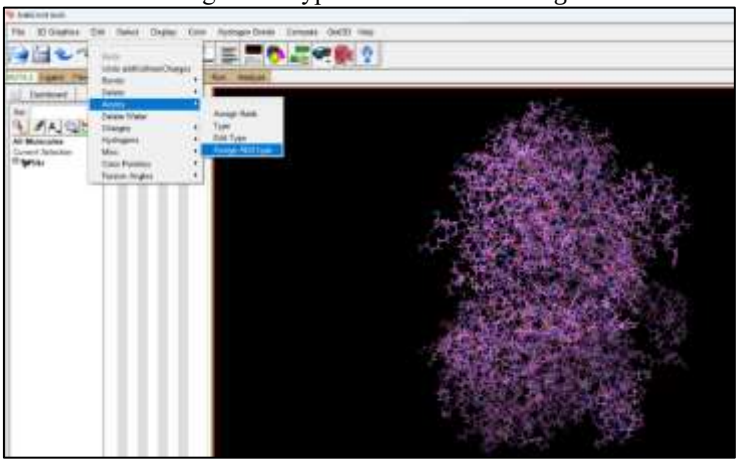

Fig No 8: Assign AD4 type.

8) Then go to the file section and save bottom then select PDBQT format to save & select the END and add molecule, as shown in Fig No:9 & 10

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

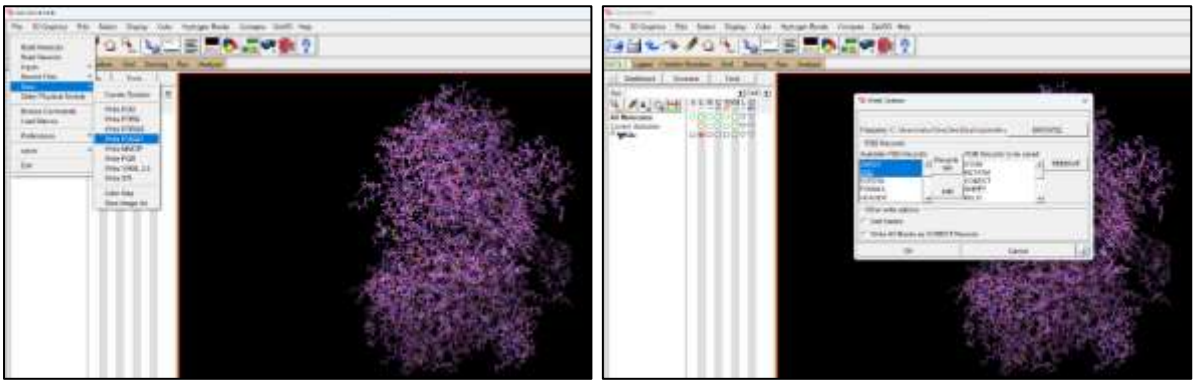

Fig No 9 & 10: Save PDBQT Format

B) ligand preparation

1) click the ligand section then choose input add click on the open option. As shown Fig No:1

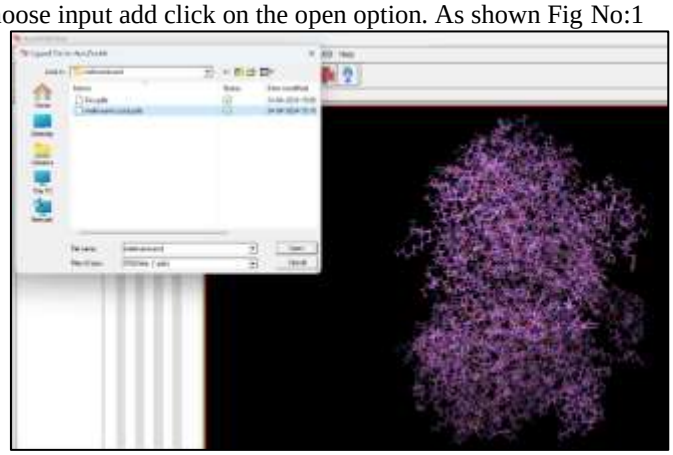

Fig No 1: Click the ligand section then choose input add click.

2) After loading the molecule click the on-torsion tree under the same ligand section and click on **choose root then detect root**.as shown in Fig No.2

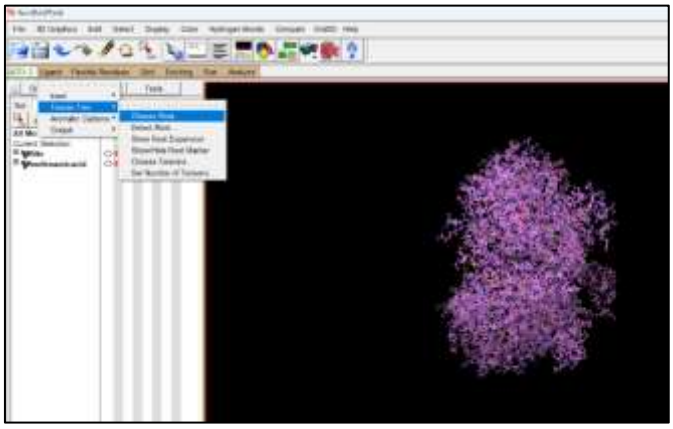

Fig No 2: Choose root then detect root.

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

3) Then go to the output option and save it in PDBQT format. As shown in Fig No.3

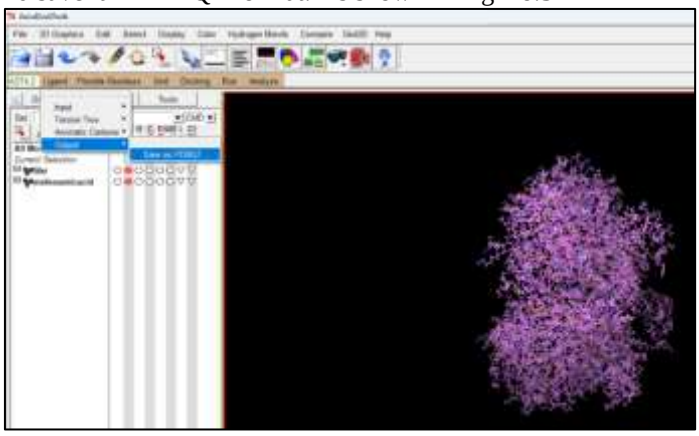

Fig No 3: Save PDBQT

C) Grid generation

1) Open PDBQT of 5ikr receptor which is saved in an earlier step. then the grid and choose and choose a receptor as a macromolecule. Then select the 5ikr receptor molecule and click No for reserve change as shown in Fig No.1 & 2

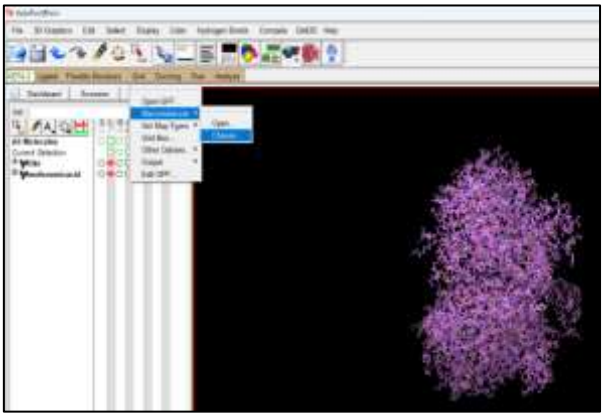

Fig No: 1

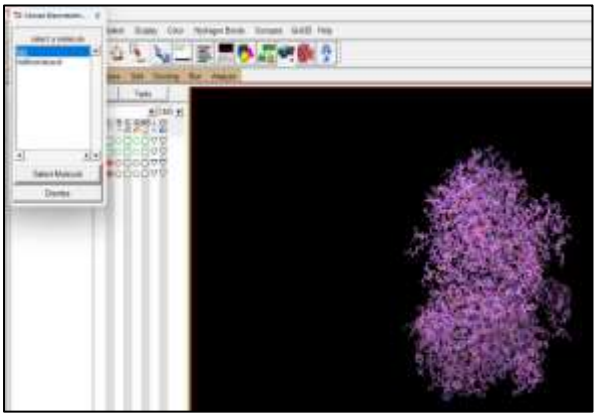

Fig No: 2

2) Then click on Set map types and choose ligand as shown FigNo:3

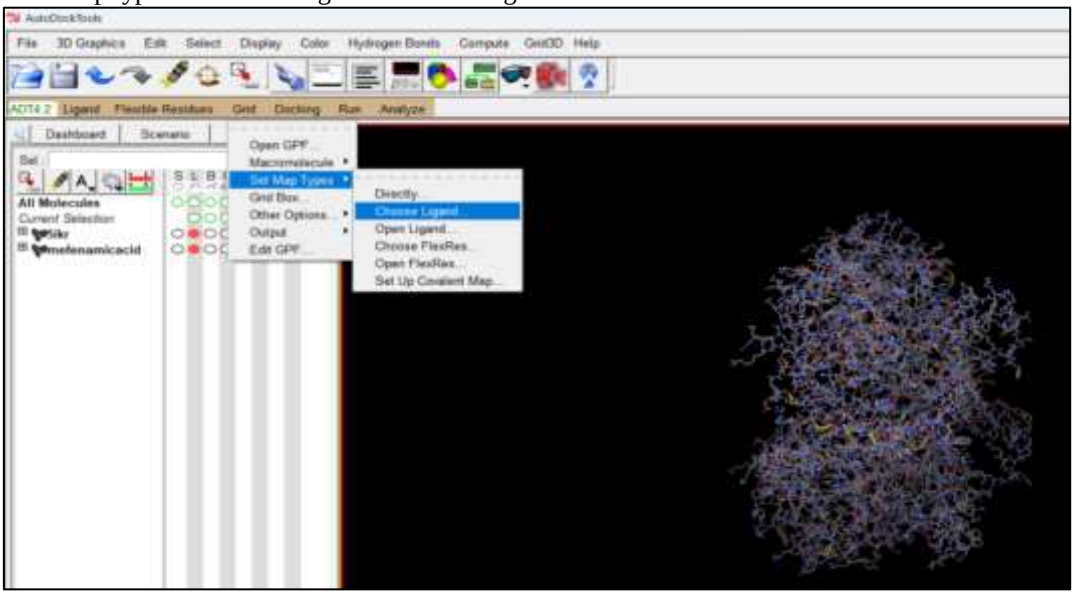

Fig No 3: Set map types and choose ligand.3) Then in the grid section, click on the grid box as shown in Fig No:5

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

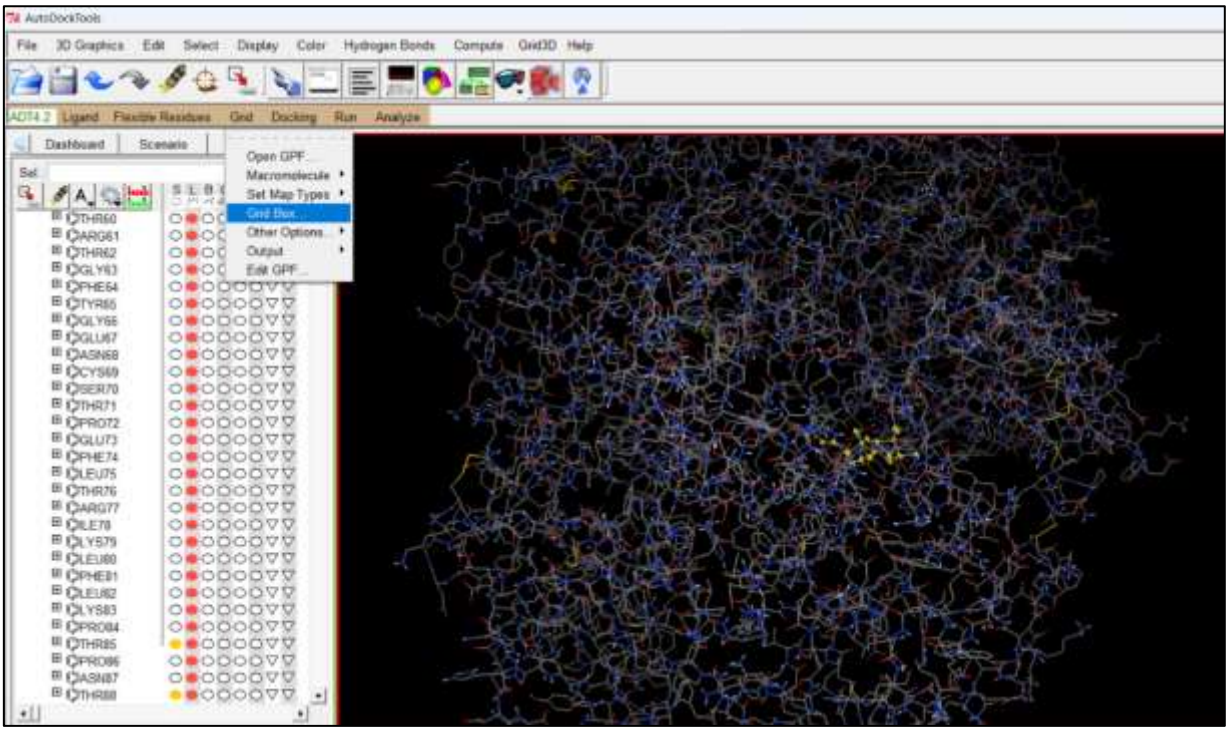

Fig No 5: Grid section

4) Then click on the grid box Adjust the grid box using the grid box coordinates so that the receptor molecule is enclosed within the box then click the button in the grid option and select "output grid dimension file" as shown in Fig No:6

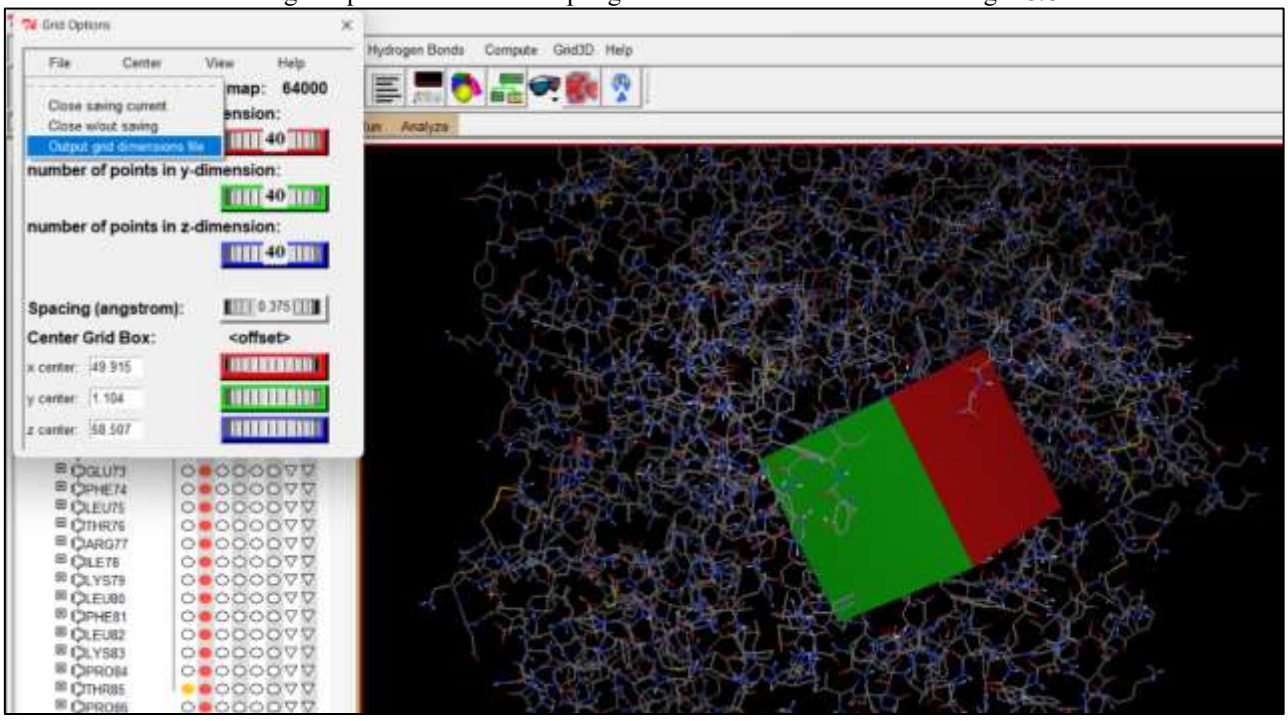

Fig No 6: Output grid dimension file

D) Config file

1) Open a new document file and enter the configuration details of the grid box, receptor name, ligand name, energy range and exhaustiveness as given in picture not as shown in Fig No:1

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

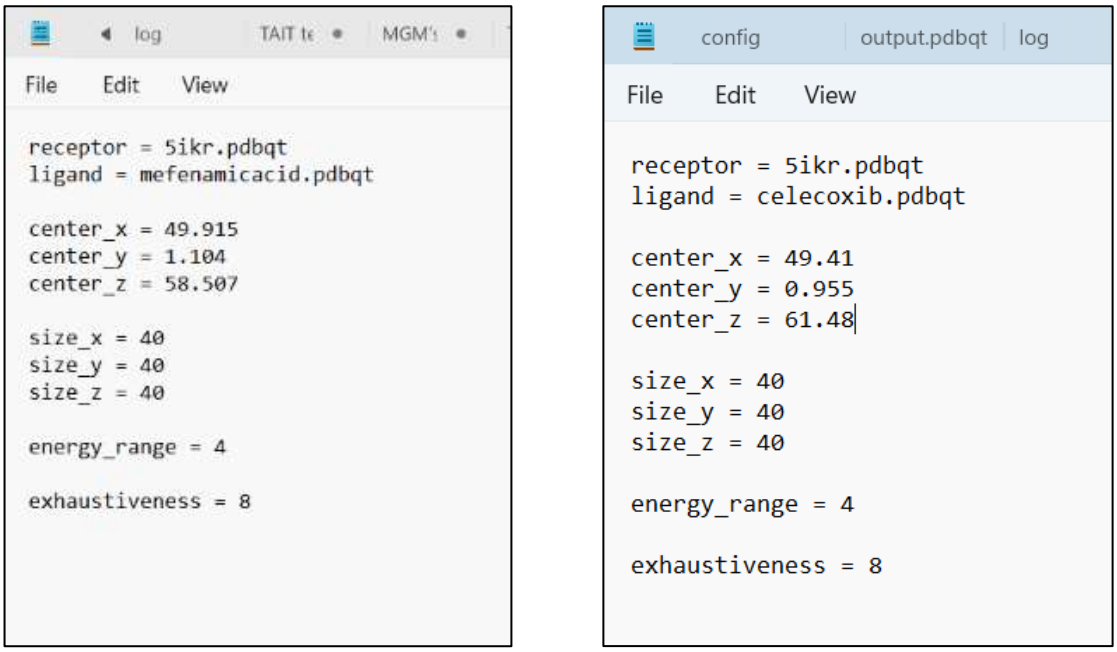

Fig No 1: Config file

E) Command Prompt:

1) Search for command prompt in your laptop or computer.

2) Then enter, followed by 'cd' Paste the folder location in which all require are present them press enter as shown in Fig No:1

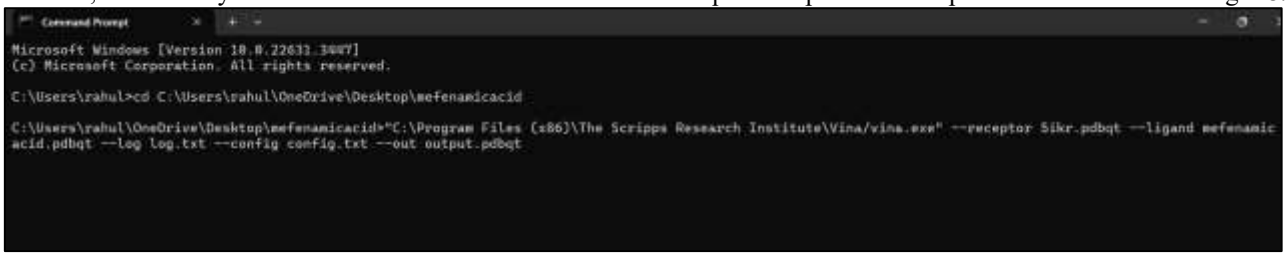

Fig no 1: Command prompt

3) Then run docking vina copy address "vina search-receptor 5ikr.pdbqt –ligand mefenamicacid.pdbqt – config config.txt-log log .txt-out output.pdbqt as shown in Fig No:2

Fig no 2: Run docking vina copy address "vina search-receptor.

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

4) After that it will take some time and give us the result of docking as shown in Fig:3 & 4

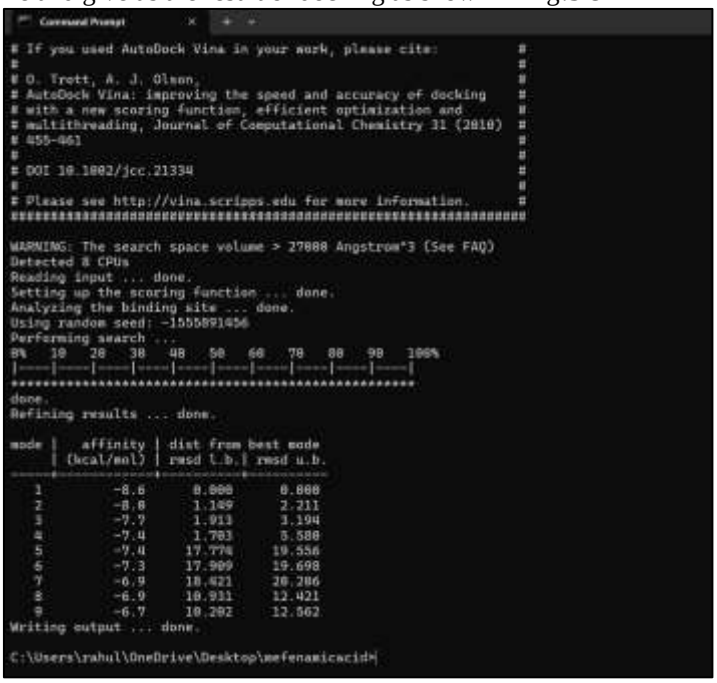

Fig No:3 Docking result of Mefenamic Acid

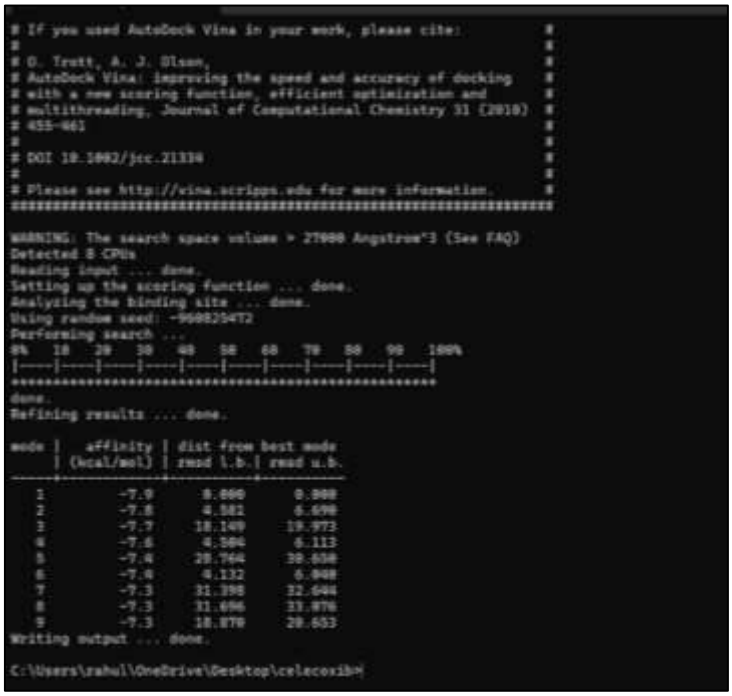

Fig No:4 Docking result of Celecoxib

5) Then Output file of the result will automatically save in the command folder, which can be read by using notepad.

7.VISUALIZATION OF DOCKING RESULT

To visualize the docking results, we use "Discovery Studio BIOVIA". The terminal shown in the figure. To proceed: [6]

1.Open the output file obtained from the docking process by clicking on the file section.

2.Delete all poses except the best pose, which will be labeled as 1 in all cases. Fig:1

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

Fig No:1 Terminal of Discovery Studio of Biovia

3.Now go to the file section and open 5ikr receptor PDBQT file in new terminal of biovia software. From this terminal copy receptor & paste it in ligand terminal. As shown in Fig No:2

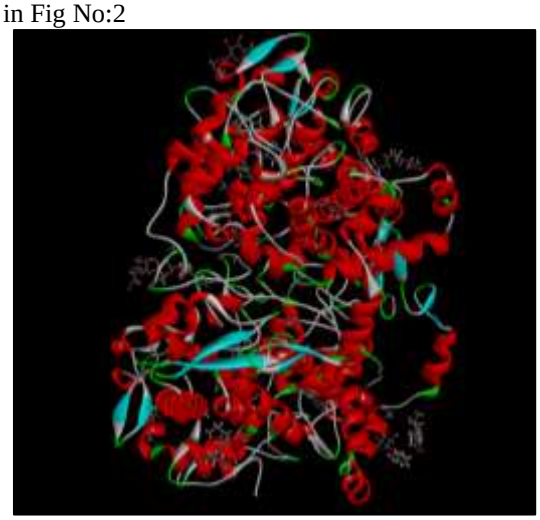

Fig No:2 Complex of ligand with receptor with suitable pose

4.After defining receptor & ligand from the complex, then click on "ligand receptor complex"

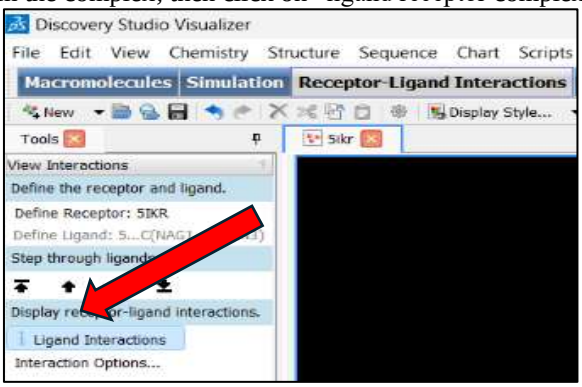

Fig No:3 Ligand interaction option

5.In Show 'receptor ligand interaction in 3d diagram, click on show, 3D Diagram'. Where you will get an image of amino acids attached to ligand in 3D format. As shown in Fig No:4

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

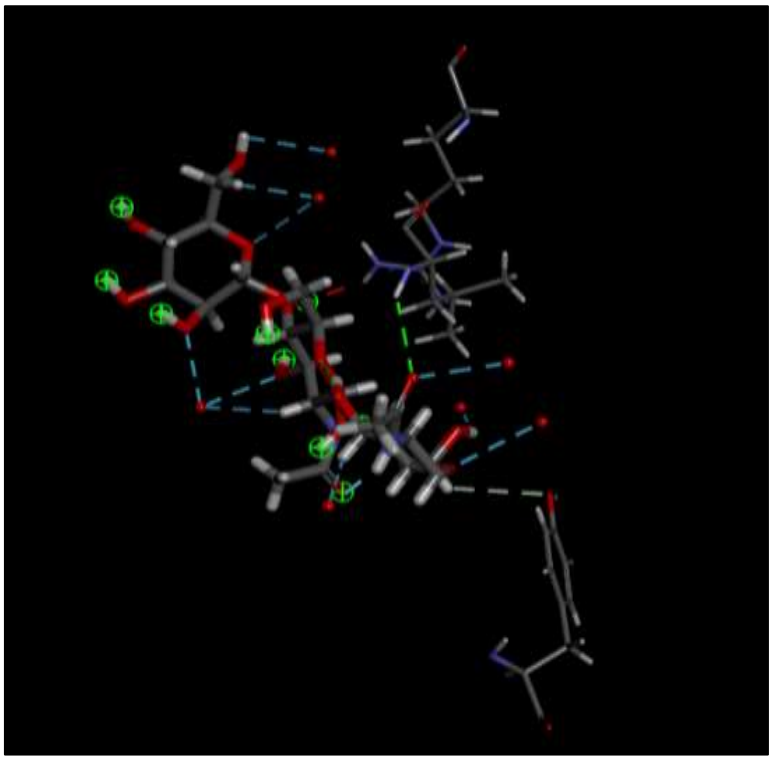

Fig No:4 3D Structure of Ligand (Mefenamic Acid)

6.In Show receptor ligand interaction in 2D Diagram, click on show 2D diagram. Where you will get an image of amino acids attached to ligand in 2D format. As shown in Fig No:5

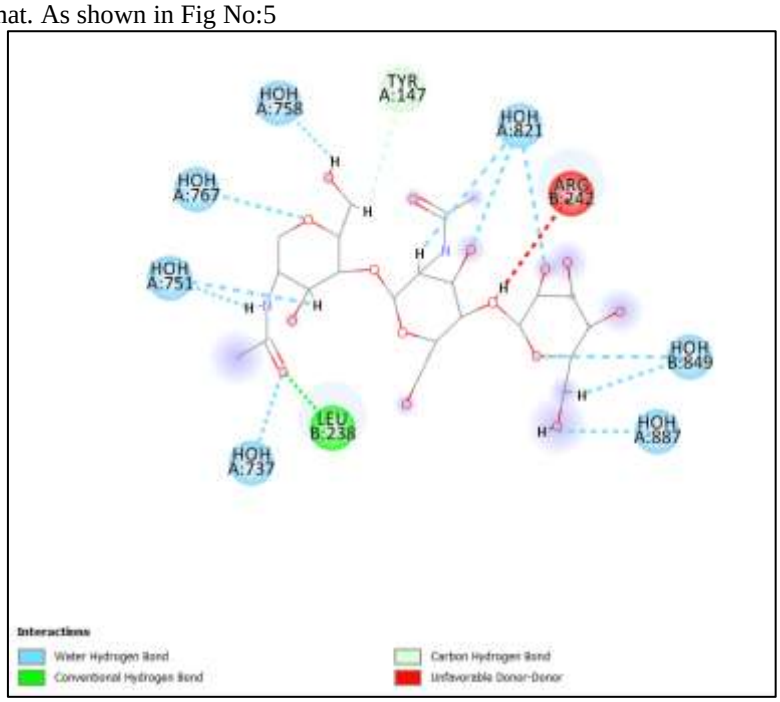

Fig No:5 2D Structure of Ligand (Mefenamic Acid)

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

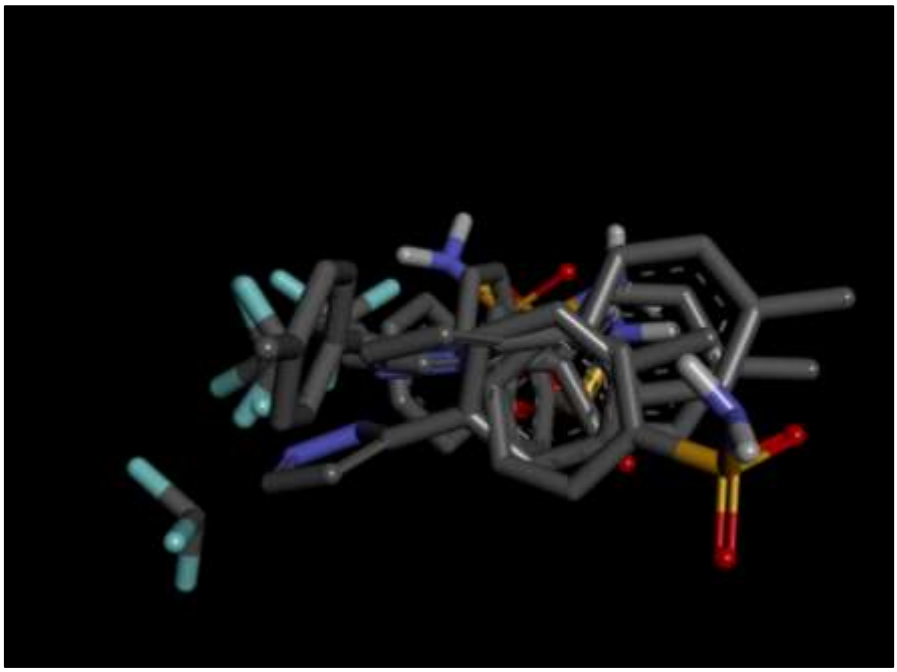

Fig No:6 2D Structure of Ligand (Celecoxib)

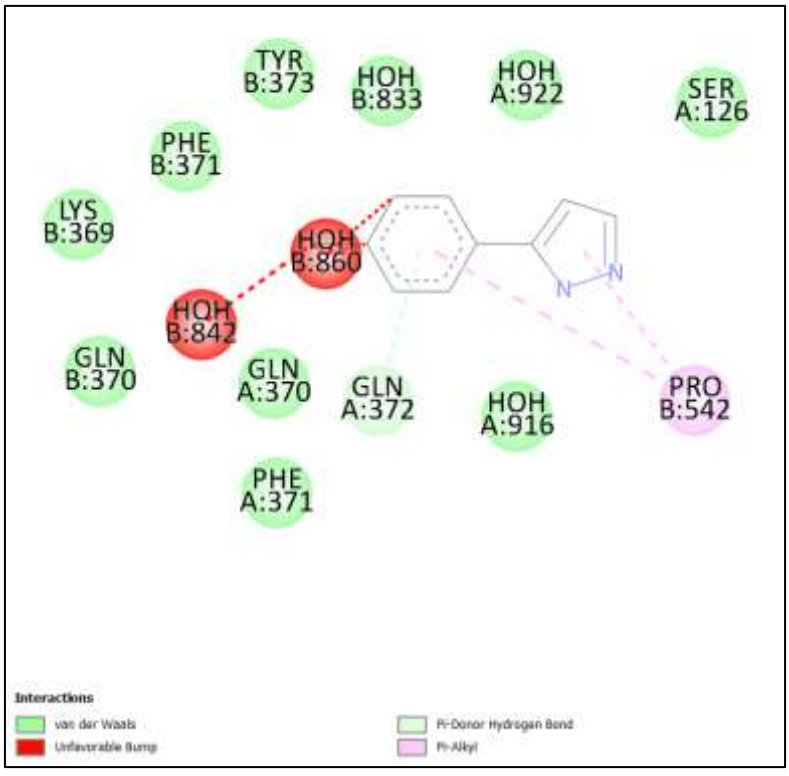

Fig No:7 2D Structure of Ligand (Celecoxib)

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

Result Analysis by: BIOVIA Discovery Studio:

Result Analysis	Visualization Software	Protein	Ligand	Docking Score	Amino acid residue
Auto Dock 1.5.7	**BIOVIA Discovery Studio Visualizer**	**5ikr**	**Mefenamic Acid**	**-8.6**	HOH A:737 HOH A:751 HOH A:758 HOH A:767 HOH A:821 HOH A:887 HOH B:849 TYR A:147 ARG B:242 LEU B:238
Auto Dock 1.5.7	**BIOVIA Discovery Studio Visualizer**	**5ikr**	**Celecoxib**	**-7.9**	HOH A:916 HOH A:922 HOH B:833 HOH B:842 HOH B:860 GLN A:370 GLN A:372 GLN B:370 PHE A:371 PHE B:371 TYR B:373 SER A:126 LYS B:369 PRO B:542

Result Docking

Docking Result of Mefenamic Acid & Celecoxib

The result of test drug Mefenamic acid and Standard drug Celecoxib and their target microorganism, PDB ID: 5ikr binding energy and standard drug like a Celecoxib for comparative study have been summarized as below table by auto-dock vina tool.

Sr.no	Target Name	Organism name	PDB ID	Binding energy of Test drug	Binding energy of Standard drug
1	**Cyclooxygenase (COX-1 & COX-2)**	**Homo Sapiens**	**5ikr**	**-8.6**	**-7.9**
2	**Membrane Permeability Inhibitors**	**Escherichia coli**	**2rdd**	**-6.9**	**6.8 (Ampicillin)**

DISCUSSION

Molecular docking of test drug mefenamic acid and standard drug celecoxib and target name is cyclooxygenase (cox1 & cox2) are binding energy of test drug is -8.6 & standard drug is -7.9 & provide valuable insights into their interactions with target proteins, aiding in the understanding of their pharmacological properties and potential applications in drug discovery.

Mefenamic acid and celecoxib are both nonsteroidal anti-inflammatory drugs (NSAIDs) commonly used to alleviate pain and inflammation. Their primary targets include cyclooxygenase enzymes, particularly COX-1 and COX-2, which are involved in the synthesis of prostaglandins.

CONCLUSION

In summary, molecular docking offers a valuable approach to elucidate the potential interactions of mefenamic acid and celecoxib with target proteins. This method provides insights into their mechanisms of action and potential therapeutic applications, contributing to our understanding of their pharmacological properties.

SJIF Impact Factor (2024): 8.675| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 9 | Issue: 6 | June 2024 - Peer Reviewed Journal

REFERENCE

1. *Raval K, Ganatra T. Basics, types and applications of molecular docking: A review.2022;7(1):12-1*
2. *A textbook of computer aided drug design by Dr. Dev Bukhsh Singh.*
3. *PubChem (nih.gov)*
4. *RCSB PDB: Homepage*
5. *mgltools (scripps.edu)*
6. *Free Download: BIOVIA Discovery Studio Visualizer - Dassault Systèmes (3ds.com)*
7. *Jignasa K. Savjania, Suja Mulamkattilb, Bhavesh Variyaa, Snehal Patela Molecular docking, synthesis and biological screening of mefenamic acid derivatives as anti-inflammatory agents.*
8. *GABA MONIKA et al: AN OVERVIEW ON MOLECULAR DOCKING April-June 2010, 2(1):219-231*
9. *(9)A textbook of computer aided drug design of pv publication by Dr. Sahil k. Mehta and dr.*
10. *Rajesh k. Singh.*