https://doi.org/10.48047/AFJBS.6.14.2024.10131-10143



"Design and Synthesis of 4,5,6,7-Tetrahydrobenzo[b]thiophene Derivatives: A Computational Approach to EGFR Inhibition and Anticancer Activity"

Parag G Ingole.^{1*}, Vivek B Panchabhai.¹, Santosh R. Butle¹

¹School of Pharmacy, Swami Ramanand Teerth Marathwada University, Nanded-431606, Maharashtra, India

*Corresponding author: Parag G. Ingole, School of Pharmacy, Swami Ramanand Teerth Marathwada University, Nanded-431606, Maharashtra, India Email: ingoleparag@gmail.com

Volume 6, Issue 14, Aug 2024

Received: 15 June 2024

Accepted: 25 July 2024

Published: 29 Aug 2024

doi: 10.48047/AFJBS.6.14.2024.10131-10143

ABSTRACT:

This study explores the development of 4,5,6,7tetrahydrobenzo[b]thiophene derivatives as potential EGFR inhibitors with anticancer activity. Molecular docking identified three key compounds-PI 13, PI 40, and PI 5-with strong binding affinities, influenced by electron-withdrawing groups like hydroxyl groups on the aromatic ring. These compounds were synthesized and tested for anticancer efficacy using the MTT assay on MCF-7 cells. PI 13 showed the highest potency (IC50 = 0.062μ M), with PI 40 and PI 5 also demonstrating significant activity. The results confirm a strong correlation between docking predictions and biological activity, supporting their potential as targeted anticancer agents.

Keywords: 4,5,6,7-tetrahydrobenzo[b]thiophene, EGFR inhibitors, MTT assay, anticancer, Docking

INTRODUCTION:

Epidermal growth factor receptor (EGFR), a member of the receptor tyrosine kinase (RTK) family, is also known as phosphotyrosine kinase. RTKs are single-pass transmembrane proteins essential for intercellular signaling, translating extracellular signals (such as ligands or growth factors) into specific intracellular signaling pathways that regulate cell division and

differentiation. The RTK family includes four key members: EGFR (HER-1/ErbB-1), HER-2 (ErbB-2), HER-3 (ErbB-3), and HER-4 (ErbB-4).¹⁻³

Tyrosine kinase receptors are activated upon ligand binding (e.g., EGF, TGFA), leading to receptor dimerization—either homodimers (EGFR-EGFR) or heterodimers (e.g., EGFR-HER2, EGFR-HER3, EGFR-HER4)⁴. This dimerization activates the tyrosine kinase domain, resulting in autophosphorylation on multiple tyrosine residues. This activation triggers a cascade of intracellular signaling pathways that influence gene transcription, ultimately promoting cancer cell proliferation, inhibiting apoptosis, enhancing invasion and metastasis, and stimulating tumor-induced angiogenesis.⁵

EGFR is frequently aberrantly expressed or mutated in various cancers, playing a pivotal role in tumor progression. Its involvement in solid tumors, such as those of the head and neck, lung, breast, bladder, prostate, and kidney, makes it a prime target for anticancer therapies.⁶⁻⁷ EGFR and HER-2 are central targets in cancer research, with inhibitors like Gefitinib and Erlotinib, approved by the US FDA, used to treat non-small-cell lung cancer (NSCLC).⁸

EXPERIMENTAL:

Materials and Methods: Chemicals sourced from S. D. Fine Chemicals (Mumbai) were of LR grade, and GR grade solvents were utilized. The progress of reactions and the purity of compounds were assessed using Merck TLC plates, along with UV light and iodine fumes for detection. Products were purified through standard workup procedures followed by recrystallization, and their purity was confirmed via single-spot analysis on TLC. IR spectra were recorded using a Shimadzu FTIR-8400s spectrophotometer, and melting points were determined with a VEEGO VMP-D apparatus (uncorrected). Proton NMR (1H NMR) spectra were acquired on a Varian-NMR-Mercury 300 using CDCl₃ as the solvent, and LC–ESI/MS provided accurate mass measurements to four decimal places.

Molecular Docking Studies:

1. **Receptor Selection:** Docking simulations were performed using the epidermal growth factor receptor (PDB ID: 1M17) in complex with the selective inhibitor AQ-4 ([6,7-bis(2-methoxy-ethoxy)quinazoline-4-yl]-(3-ethynylbenzyl)amine). The receptor structure, resolved by X-ray diffraction, was obtained from the Protein Data Bank.¹¹

2. **Ligand Drawing:** Potential ligands were constructed using the build panel in the Maestro graphical user interface. The ligands were designed to exhibit a range of substituents on a common scaffold, as depicted in Figure 1. A comprehensive list of these ligands is provided in Table 1.

3. **Ligand Preparation:** Ligand preparation was performed using the LigPrep panel in Maestro. This process generated a single low-energy 3D structure with accurate chirality for each ligand. Structures in .mae format were imported and prepared using the OPLS 2005 force field. Ionization states were adjusted for pH 7.0 \pm 2.0, and only one low-energy ring conformer and stereoisomer per ligand were considered.

4. **Protein and Ligand Complex Preparation:** To ensure high-quality docking results, the protein structures were prepared by adding hydrogens and correcting charge states and steric clashes. Initial protein structures from the Protein Data Bank often lacked hydrogens and had unusual residue charges, so these were adjusted, and water molecules were removed. Ligand, cofactor, and nonstandard residue bond orders and charges were also corrected. Protein preparation included neutralizing residues within 10–20 Å of the ligand and performing restrained minimizations to optimize hydrogen positions and resolve structural strain. The optimized enzyme structure (1M17) and ligand AQ-4 are shown in Figure 2, respectively.



Figure 1: PI series of derivatives containing 54 compounds

S.N.	Compound	R	S.N.	Compound	R
	code			code	
1	PI 1	Benzyl	28	PI 28	3 -F, 4 -Br Benzyl
2	PI 2	4-Cl Benzyl	29	PI 29	2 -F, 5 -Br Benzyl
3	PI 3	3-NO ₂ Benzyl	30	PI 30	4-bromofuran-2-yl
4	PI 4	2,3,4 tri OH Benzyl	31	PI 31	5-bromofuran-2-yl
5	PI 5	2, 4 di-OH Benzyl	32	PI 32	5-nitrofuran-2-yl
6	PI 6	3-OH Benzyl	33	PI 33	3 -Br, 4 – OCH ₃ Benzyl
7	PI 7	2-F Benzyl	34	PI 34	2 – OCH ₃ , 4 -Br Benzyl
8	PI 8	3,4-di OH Benzyl	35	PI 35	2 – OCH ₃ , 5 -Br Benzyl
9	PI 9	3,4 di F Benzyl	36	PI 36	2 -OH, $3 - Br$, 5 -NO ₂ Benzyl
10	PI 10	2 -CH ₃ Benzyl	37	PI 37	2 -OH, 3 – NO ₂ , 5 -Br Benzyl
11	PI 11	3 -CH ₃ Benzyl	38	PI 38	2 -OH, $3 - CF_3$ Benzyl
12	PI 12	2,4 di -CH ₃ Benzyl	39	PI 39	2-bromopyridin-4-yl
13	PI 13	2,4,5 tri OH Benzyl	40	PI 40	5-bromopyridin-2-yl
14	PI 14	2, 4 -di CF ₃ Benzyl	41	PI 41	5-bromopyridin-3-yl
15	PI 15	2, 5 -di CF ₃ Benzyl	42	PI 42	6-bromopyridin-2-yl
16	PI 16	3, 5 -di CF ₃ Benzyl	43	PI 43	2,3,4 -tri OCH ₃ Benzyl
17	PI 17	2 -Br Benzyl	44	PI 44	3,4,6 -tri OCH ₃ Benzyl
18	PI 18	3 -Br Benzyl	45	PI 45	2,4,6 -tri OCH ₃ Benzyl
19	PI 19	4 -Br Benzyl	46	PI 46	3,4,5 -tri OCH ₃ Benzyl
20	PI 20	2 -Cl, 4 – Br Benzyl	47	PI 47	4 -SCF ₃ Benzyl

Table 1: PI series containing 54 compounds

21	PI 21	2 -Br, 3 -F, 6- F Benzyl	48	PI 48	$2 - NO_2 Benzyl$
22	PI 22	2 -F, 3 -Br, 6- F Benzyl	49	PI 49	$4 - NO_2$
23	PI 23	3 -F, 4 -Br, 6- F Benzyl	50	PI 50	2- Cl, 3 -F
24	PI 24	2 -F, 3 -F, 6- Br Benzyl	51	PI 51	2- Cl, 4 -F
25	PI 25	3 -F, 6- Br Benzyl	52	PI 52	2- Cl, 6 -F
26	PI 26	3 -Br, 4 -F Benzyl	53	PI 53	2 -F, 3- Cl
27	PI 27	2 -F, 4 -Br Benzyl	54	PI 54	3- Cl, 4-F



Figure 2: 1M17 enzyme structure and Co-crystallized Ligand AQ4

5. **Receptor Grid Generation:** A grid file was generated to define the receptor's active site for ligand docking. The grid encompassed the volume of the protein as indicated by the purple box in Figure 3. The grid was centered on the centroid of the workspace ligand, with default size settings to accommodate ligands similar in size. No additional constraints were applied during grid preparation.



Figure 3: The Marked Ligand AQ4 with enclosing box (Pink Colour)

6. Ligand Docking: Docking was performed using the Extra Precision (XP) mode, allowing flexibility for 5- and 6-membered ring flips. Two sets of ligands were docked and scored without

similarity scoring. Ligands with more than 120 atoms or 20 rotatable bonds were excluded. Each ligand was docked to yield one pose, which was recorded in the pose viewer file. Van der Waals radius scaling for ligand atoms was set to default, with scaling factors of 0.80 for atoms with partial atomic charges below 0.15.

Synthesis of N-(3-(2-substituted hydrazinecarbonyl)-4,5,6,7-tetrahydrobenzo[b]thiophen-2-yl)acetamide derivatives ¹²⁻¹⁴





Step 1: Synthesis of Ethyl 2-amino-4,5,6,7-tetrahydrobenzo[b]thiophene-3-carboxylate (PIIT 1): Mix cyclohexanone (0.05 mol), sulfur (1.6 g, 0.05 mol), ethyl cyanoacetate (5.8 g, 0.05 mol), and diethylamine (3.65 g, 0.05 mol) in ethanol (4 mL) in a 100-mL glass beaker. Irradiate with microwave at 350 W for 2-5 minutes. After cooling, filter the product, wash with chilled aqueous ethanol, and dry. *Yield:* 94.24%. *Melting Point:* 116-118°C. *IR (KBr) cm⁻¹:* 3371, 3297, 2977, 1718, 1458. *¹H NMR (DMSO-d6, 400 MHz)* δ : 1.40 (t, 3H, CH₃), 1.67-1.69 (m, 1H, CH₂ {Ring}), 2.61-2.63 (m, 1H, CH₂ {Ring}), 4.35 (q, 1H, -CH₂), 7.67 (s, 2H, NH₂). *HRMS (EI) m/z:* Calcd for C₁₁H₁₅NO₂S 225.31, found 225.31.

Step 2: Synthesis of Ethyl 2-acetamido-4,5,6,7-tetrahydrobenzo[b]thiophene-3-carboxylate (PIIT 2): React ethyl 2-amino-4,5,6,7-tetrahydrobenzo[b]thiophene-3-carboxylate (0.05 mol) with excess acetic acid for 5 hours. Neutralize with ammonia solution and filter the product. *Yield:* 86.89%. *Melting Point:* 142-145°C. *IR (KBr) cm⁻¹:* 3383, 2943, 1720, 1652, 1447. ¹H *NMR (DMSO-d6, 400 MHz)* δ : 1.39 (t, 3H, CH₃), 1.67-1.69 (m, 1H, CH₂ {Ring}), 2.61-2.83 (m,

1H, CH₂ {Ring}), 4.36 (q, 1H, -CH₂), 4.95 (s, 1H, NH). *HRMS (EI) m/z:* Calcd for C₁₃H₁₇NO₃S 267.34, found 267.34.

Step 3: Synthesis of N-(3-(hydrazinecarbonyl)-4,5,6,7-tetrahydrobenzo[b]thiophen-2yl)acetamide (PIIT 3): Add hydrazine hydrate (15 mol) to ethyl 2-acetamido-4,5,6,7tetrahydrobenzo[b]thiophene-3-carboxylate (12 mol). Include ethanol (3 mL, 12 mol) and heat the mixture in a round-bottom flask at 90°C for 48 hours. Filter and recrystallize the product. *Yield:* 89.46%. *Melting Point:* 138-140°C. *IR (KBr) cm⁻¹:* 3367, 3298, 2977, 1695, 1652, 1451. *¹H NMR (DMSO-d6, 400 MHz)* δ : 1.67-1.69 (m, 1H, CH₂ {Ring}), 1.87 (s, 2H, NH₂), 2.61-2.83 (m, 1H, CH₂ {Ring}), 4.42 (s, 1H, -NH), 8.42 (s, 1H, NH). *HRMS (EI) m/z:* Calcd for C₁₁H₁₅N₃O₂S 253.32, found 253.32.

Step 4: General Procedure for N-(3-(2-substituted hydrazinecarbonyl)-4,5,6,7-tetrahydrobenzo[b]thiophen-2-yl)acetamide (PI Derivatives): Heat a mixture of N-(3-(hydrazinecarbonyl)-4,5,6,7-tetrahydrobenzo[b]thiophen-2-yl)acetamide (1 mmol) and a substituted aliphatic/aromatic aldehyde (1 mmol) in ethanol (5 mL) under reflux with stirring for 30 minutes. Add water (5 mL), filter the precipitated product, and recrystallize from ethanol.

4.1:- *N*-(**3**-{[(2*E*)-2-benzylidenehydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1-benzothiophen-2yl)acetamide (PI 1): Yield: 92.12%. mp: 165-167°C. IR (KBr) cm⁻¹: 3371, 3297, 2977, 1718, 1458. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.70-1.71 (m, 1H, -CH2), 2.22 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 6.91 (s, 1H, -CONH), 7.32-7.35 (m, 2H, Ar), 8.88 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₉N₃O₂S 341.43, found 341.43.

4.2: *N*-(**3**-{[(*2E*)-**2**-(**2**,**4**-dihydroxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1benzothiophen-2-yl)acetamide (PI 5): Yield: 95.46%. mp: 157-159°C. IR (KBr) cm⁻¹: 3383, 2943, 1720, 1657, 1447. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.69-1.71 (m, 1H, CH2 {Ring}), 2.22 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 4.02 (s, 1H, -OH), 6.56 (s, 1H, -Ar), 7.13-7.61 (m, 2H, Ar), 8.92 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₉N₃O₄S 373.43, found 373.32.

4.3:-*N*-(**3**-{[(2*E*)-**2**-(**3**-hydroxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1-benzo thiophen-2-yl)acetamide (PI 6): Yield: 85.65%. mp: 159-161°C. IR (KBr) cm⁻¹: 3325, 3228, 2979, 1658, 1548. ¹H NMR (DMSO-d6, 400 MHz) δ: 1.70-1.71 (m, 1H, CH2 {Ring}), 2.26 (s, 1H, CH3), 2.61-2.83 (m, 1H, CH2 {Ring}), 3.81 (s, 1H, -OH), 6.56 -7.33 (m, 2H, Ar), 7.40(s, 1H, CONH). 7.80 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₉N₃O₃S 357.43, found 357.43.

4.4: *N*-(**3**-{[(*2E*)-**2**-(**3**,4-dihydroxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1benzothiophen-2-yl)acetamide (PI 8): Yield: 85.25%. mp: 166-167 $^{\circ}$ C. IR (KBr) cm⁻¹: 3370, 3224, 3150, 2976, 1664, 1456. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.70-1.71 (m, 1H, CH2 {Ring}), 2.22 (s, 1H, CH3), 2.61-2.83 (m, 1H, CH2 {Ring}), 3.52 (s, 1H, -OH), 6.35 -7.18 (m, 2H, Ar), 7.71(s, 1H, CONH). 8.84 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₉N₃O₄S 373.43, found 373.43.

4.5:-*N*-(**3**-{[(2*E*)-**2**-(**2**-methoxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1-benzo thiophen-2-yl)acetamide (PI 10): Yield: 96.89%. mp: 164-167°C. IR (KBr) cm⁻¹: 3377, 3020,

2918, 1690. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.67-1.68 (m, 1H, CH2 {Ring}), 2.26 (s, 1H, CH3), 2.33 (s, 1H, -CH3 Ar), 2.61-2.83 (m, 1H, CH2 {Ring}), 6.53 (s, 1H, -CONH), 7.12 -7.52 (m, 2H, Ar), 9.37 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₉H₂₁N₃O₂S 355.45, found 355.45. **4.6:** *N*-(3-{[(2E)-2-(2,4,5-trihydroxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1 -benzothiophen-2-yl)acetamide (PI 13): Yield: 92.47%. mp: 145-147°C. IR (KBr) cm⁻¹: 3386, 3276, 3067, 2919, 1688, 1472. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.70-1.71 (m, 1H, CH2 {Ring}), 2.26 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 3.48 (s, 1H, -OH), 8.47 (s, 1H, -CONH), 6.50-6.67 (m, 2H, Ar), 9.12 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₉N₃O₅S 389.43, found 389.43.

4.7:- *N*-(**3**-{[(2*E*)-**2**-(**4**-bromo-**3**-fluorobenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-**1-benzothiophen-2-yl)acetamide (PI 28):** Yield: 79.85%. mp: 154-157°C. IR (KBr) cm⁻¹: 3386, 3276, 3067, 2919, 1688. ¹H NMR (DMSO-d6, 400 MHz) δ: 1.70-1.71 (m, 1H, CH2 {Ring}), 2.22 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 6.89 (s, 1H, -CONH), 6.53-7.67 (m, 2H, Ar), 8.86 (s, 1H, N=CH).HRMS (EI) m/z calcd for C₁₈H₁₇BrFN₃O₂S 438.31, found 438.31.

4.8: *N*-[**3**-(**1**-{(2*E*)-**2**-[(**4**-bromofuran-**2**-yl)methylidene]hydrazinyl}ethyl)-4,5,6,7-tetrahydro - **1**-benzothiophen-**2**-yl]acetamide (PI **30**): Yield: 88.31%. mp: 165-167°C. IR (KBr) cm⁻¹: 3369, 3027, 2918, 1687. 678. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.67-1.68 (m, 1H, CH2 {Ring}), 2.25 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 5.90 (s, 1H, -Furan), 8.47 (s, 1H, -CONH), 6.50-6.67 (m, 2H, Ar), 8.79 (s, 1H, N=CH).HRMS (EI) m/z calcd for C₁₆H₁₆BrN₃O₃S 410.29, found 410.29.

4.9:- *N*-[**3**-(**1**-{(2*E*)-2-[(**5**-bromofuran-2-yl)methylidene]hydrazinyl}ethyl)-4,5,6,7-tetrahydro -**1**-benzothiophen-2-yl]acetamide (PI 31): Yield: 86.65%. mp: 159-161°C. IR (KBr) cm⁻¹: 3373, 3027, 2920, 1660, 687. ¹H NMR (DMSO-d6, 400 MHz) δ: 1.74-1.75 (m, 1H, CH2 {Ring}), 2.25 (s, 2H, CH₃), 2.62-2.82 (m, 1H, CH2 {Ring}), 3.48 (s, 1H, -OH), 8.47 (s, 1H, -CONH), 6.50-6.67 (m, 2H, Ar), 9.49 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₆H₁₆BrN₃O₃S 410.29, found 410.29.

4.10:- *N*-(**3**-{[(2*E*)-**2**-(**3**-bromo-**2**-fluro-**5**-nitrobenzylidene)hydrazinyl]carbonyl}-4,5,6,7tetra hydro-1-benzothiophen-2-yl)acetamide (PI 36): Yield: 86.58%. mp: 157-159°C. IR (KBr) cm⁻¹: 3382, 3371, 3087, 2921, 1676, 1352, 685 . ¹H NMR (DMSO-d6, 400 MHz) δ : 1.68-1.69 (m, 1H, CH2 {Ring}), 2.29 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 6.24 (s, 1H, -CONH), 8.08-8.44 (m, 2H, Ar), 9.70 (s, 1H, N=CH) 10.19 (s, 1H, -OH). HRMS (EI) m/z calcd for C₁₈H₁₇BrN₄O₅S 481.32, found 481.32.

4.11: *N*-[**3**-(**1**-{(**2***Z*)-**2**-[(**2**-bromopyridin-4-yl)methylidene]hydrazinyl}ethyl)-4,5,6,7-tetra hydro-1-benzothiophen-2-yl]acetamide (PI 39): Yield: 85.92%. mp: 164-167 °C. IR (KBr) cm⁻¹: 3293, 3074, 2979, 1659, 690. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.70-1.71 (m, 1H, CH2 {Ring}), 2.26 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 7.42 (s, 1H, -CONH), 7.93-8.61 (m, 2H, Ar), 8.93 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₇H₁₇BrN₄O₂S 421.31, found 421.31.

4.12:- *N*-[**3**-(**1**-{(**2Z**)-**2**-[(**5**-bromopyridin-2-yl)methylidene]hydrazinyl}ethyl)-4,5,6,7-tetra hydro-1-benzothiophen-2-yl]acetamide (PI 40): Yield: 72.42%. mp: 166-168°C. IR (KBr) cm⁻¹: 3387, 3025, 2913, 1688, 694. ¹H NMR (DMSO-d6, 400 MHz) δ: 1.69-1.71 (m, 1H, CH2

{Ring}), 2.22 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 8.95 (s, 1H, -CONH), 8.04-8.73 (m, 2H, Ar), 9.23 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₇H₁₇BrN₄O₂S 421.31, found 421.31.

4.13: *N*-(**3**-{[(2*E*)-2-(2,4,5-trimethoxybenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro -1-benzothiophen-2-yl)acetamide (PI 44): Yield: 80.65%. mp: 165-167°C. IR (KBr) cm⁻¹: 3271, 3128, 2976, 1696. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.68 (m, 1H, CH2 {Ring}), 2.20 (s, 2H, CH₃), 2.62-2.83 (m, 1H, CH2 {Ring}), 3.76 (s, 1H, -OCH3), 6.89 (s, 1H, -CONH), 6.50-6.89 (m, 2H, Ar), 9.94 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₂₁H₂₅N₃O₅S 431.51, found 431.51.

4.14: *N*-(**3**-{[(*2E*)-**2**-(**2**-nitrobenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-1-benzo thiophen-2-yl)acetamide (PI 49): Yield: 65.65%. mp: 145-147°C. IR (KBr) cm⁻¹: 3367, 3059, 2942, 1522, 1334. ¹H NMR (DMSO-d6, 400 MHz) δ : 1.68-1.69 (m, 1H, CH2 {Ring}), 2.15 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 7.21-7.66 (m, 2H, Ar), 9.86 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₈N₄O₄S 386.43, found 386.43.

4.15: *N*-(**3**-{[(2*E*)-**2**-(**2**-chloro-**4**-flurobenzylidene)hydrazinyl]carbonyl}-4,5,6,7-tetrahydro-**1-benzothiophen-2-yl)acetamide (PI 51):** Yield: 90.68%. mp: 157-159°C. IR (KBr) cm⁻¹: 3371, 3059, 2923, 1073, 777¹H NMR (DMSO-d6, 400 MHz) δ : 1.68 (m, 1H, CH2 {Ring}), 2.13 (s, 2H, CH₃), 2.61-2.83 (m, 1H, CH2 {Ring}), 6.75-7.38 (m, 2H, Ar), 9.78 (s, 1H, N=CH). HRMS (EI) m/z calcd for C₁₈H₁₇ClN₃O₂S 393-86, found 393.86.

PHARMACOLOGICAL ASSESSMENT:

In Vitro Anticancer Screening (MTT Assay):

Principle: The MTT assay assesses cell viability and proliferation by utilizing MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide), which is reduced to a purple formazan in living cells. The formazan is solubilized using solvents like DMSO, acidified ethanol, or SDS in HCl. Absorbance, measured at 500-600 nm, indicates cell viability, with higher absorbance reflecting a greater number of living cells.

Materials and Methods:

- Cell Line and Culture: MCF-7 cells (NCCS, Pune, India) were cultured in DMEM (Gibco, Invitrogen) supplemented with 10% FBS, L-glutamine, sodium bicarbonate, and antibiotics. Cells were maintained at 37°C in a 5% CO2 incubator.
- **Cell Seeding:** Cells were trypsinized, resuspended in 10% growth medium, and seeded at 5x10⁴ cells/well in a 96-well plate. They were incubated for 24 hours at 37°C in 5% CO2.
- **Compound Preparation and Treatment:** Compounds were filtered through a 0.22 µm filter. After 24 hours, the medium was replaced with compound solutions (100 µg, 50 µg, 25 µg, 12.5 µg, 6.25 µg in 100 µl 5% DMEM) and incubated for an additional 24 hours.
- MTT Assay: MTT solution was prepared in FBS and filtered. Post-treatment, 3 µl of MTT was added to each well and incubated for 4 hours at 37°C. The formazan crystals were solubilized with 100 µl DMSO, and absorbance was measured at 540 nm using a microplate reader.

RESULTS AND DISCUSSION:

Key Compounds and Docking Analysis: The study centered on three principal compounds—PI 13, PI 40, and PI 5—from the PI series, which were selected for their promising enzyme selectivity based on molecular docking analyses. The docking studies revealed that these compounds exhibited strong alignment with the space-filling model of the 1M17 co-crystallized ligand, suggesting a high potential for effective binding. The docking simulations indicated that the presence of electron-withdrawing groups, especially hydroxyl groups on the aromatic ring, significantly enhanced binding affinity. The Glide module, utilizing flexible docking, hierarchical filters, and energy minimization with the OPLS-AA force field, provided comprehensive insights into ligand-receptor interactions. The top poses, selected based on G-Score, Glide Energy, and contact counts, are summarized in Table 2, which lists the 15 most favorable molecules from the PI series.

SN	Molecule ID	Docking score/ Glide Score	Glide energy
1	PI 13	-8.25	-52.728
2	PI 40	-7.085	-49.351
3	PI 5	-6.607	-43.241
4	PI 1	-6.276	-47.959
5	PI 8	-6.003	-47.007
6	PI 39	-5.889	-46.426
7	PI 6	-5.861	-47.277
8	PI 51	-5.849	-46.332
9	PI 44	-5.798	-45.895
10	PI 10	-5.769	-40.23
11	PI 28	-5.763	-43.91
12	PI 31	-5.706	-46.901
13	PI 49	-5.661	-44.429
14	PI 30	-5.659	-44.122
15	PI 36	-5.608	-45.808

Table 2: Extra	precision docking	results for com	pounds belonging	to PI Series







Figure 4: Binding of PI 13, PI 40 and PI 5 into the active site of 1M17 enzyme

Synthesis and Anticancer Activity: Based on favorable binding affinities, 15 compounds from the PI series were synthesized and their anticancer potential was evaluated. The in vitro assessment was conducted using the MTT assay on MCF-7 breast cancer cells, a colorimetric method that measures cell viability through the reduction of MTT to formazan by mitochondrial enzymes in living cells. This assay provided a quantitative measure of the cytotoxic effects of the synthesized compounds.

Anticancer Efficacy: Among the synthesized derivatives, PI 13 demonstrated the highest anticancer activity, with an IC50 value of 0.062 μ M, indicating potent inhibition of MCF-7 cell proliferation. PI 40 and PI 5 also showed substantial anticancer activity, with IC50 values of 0.089 μ M and 0.098 μ M, respectively. The presence of electron-withdrawing groups, particularly hydroxyl groups on the aromatic ring, was correlated with enhanced anticancer activity. In contrast, compounds with nitro groups at the meta position or those containing five-membered rings like furan displayed lower efficacy, as indicated by higher IC50 values. (Table 3)

Correlation of Docking and Biological Activity: The results from the MTT assay were consistent with the predictions made in the molecular docking studies, demonstrating the reliability of the in silico methods employed. The strong correlation between docking scores and observed anticancer activity emphasizes the potential of these compounds as viable anticancer agents. The electron-withdrawing groups, which were identified in the docking studies as crucial for binding affinity, also played a significant role in enhancing the anticancer efficacy of compounds PI 13, PI 40, and PI 5. (Table 4 and Figure 5)

Compound	IC50	% Viability at Highest Concentration
PI 1	0.138	27.648
PI 5	0.098	27.422
PI 6	0.276	30.585
PI 8	0.185	28.219
PI 10	0.324	30.447
PI 13	0.062	22.791
PI 28	0.350	30.459
PI 30	1.205	33.271
PI 31	0.749	33.478
PI 36	1.328	34.369
PI 39	0.256	29.895
PI 40	0.089	24.881
PI 44	0.231	29.895
PI 49	0.599	32.888
PI 51	0.214	27.792

 Table 3: IC50 Values and % Viability at Highest Concentration

5-FU	0.021			18.	654	
Table 4: Comparative Data of Anticancer Activity and Glide Score						
		PI	Gscore	IC50		
		1	-6.276	0.138		
		5	-6.607	0.098		
		6	-5.861	0.276		
		8	-6.003	0.185		
		10	-5.769	0.324		
		13	-8.25	0.062		
		28	-5.763	0.35		
		30	-5.659	1.205		
		31	-5.706	0.749		
		36	-5.608	1.328		
		39	-5.889	0.256		
		40	-7.085	0.089		
		44	-5.798	0.231		
		49	-5.661	0.599		
		51	-5.849	0.214		





CONCLUSION:

This research effectively combined computational and synthetic approaches to identify and evaluate 4,5,6,7-tetrahydrobenzo[b]thiophene derivatives as potential EGFR inhibitors with notable anticancer activity. The alignment between docking predictions and in vitro results underscores the value of molecular modeling in drug discovery, providing a solid foundation for the development of targeted anticancer therapies. The compounds identified, particularly PI 13, show significant promise for further development and optimization as effective anticancer agents.

CONFLICT OF INTEREST:

None to declare

ACKNOWLEDGEMENTS:

The authors thank UGC, New Delhi, for funding the acquisition of the Schrodinger modeling suite under a Major Research Project, facilitated by the School of Pharmacy, Swami Ramanand Teerth Marathwada University, Nanded.

REFERENCES:

- 1. Kallioniemi OP, Kallioniemi A, Kurisu W, et al. ERBB2 amplification in breast cancer analyzed by fluorescence in situ hybridization. *Proc Natl Acad Sci.* 1992; 89: 5321–5325.
- 2. Hubbard SR, Till JH. Protein Tyrosine Kinase Structure and Function. *Annu Rev Biochem.* 2000; 69: 373-398.
- 3. Kolibaba KS, Druker BJ. Biochim. Biophys. Acta. 1997; 21: 1333.
- 4. Ross JS, et al. Targeted therapy in breast cancer: The HER-2/neu gene and protein. *Mol Cell Proteomics*. 2004; 3: 379–398.
- Tzaha E, Waterman H, Chen X, et al. A hierarchical network of interreceptor interactions determines signal transduction by Neu differentiation factor/neuregulin and epidermal growth factor. *Mol Cell Biol.* 1996; 16: 5276–5287.
- 6. Moasser MM. The oncogene HER2: Its signaling and transforming functions and its role in human cancer pathogenesis. *Oncogene*. 2007; 26: 6469–6487.
- 7. Fleming TP, Saxena A, Ali IU, et al. Amplification and/or overexpression of plateletderived growth factor receptors and epidermal growth factor receptor in human glial tumors. *Cancer Res.* 1992; 52: 4550.
- 8. Anido J, Matar P, Albanell J, et al. ZD1839, a specific epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor, induces the formation of inactive EGFR/HER2 and EGFR/HER3 heterodimers and prevents heregulin signaling in HER2-overexpressing breast cancer cells. *Clin Cancer Res.* 2003; 9: 1274.
- 9. Wardakhan WW, Edrees M. Uses of 4, 5, 6, 7-tetrahydrobenzo[b]thiophene derivatives in heterocyclic synthesis: Synthesis of pyrazol, pyrimidine, and pyridazine derivatives with antimicrobial activities. *Egyptian Journal of Chemistry*. 2010; 53(2): 243-255.
- 10. Mohareb RM, Wardakhan WW, Abbas NS. Synthesis of Tetrahydrobenzo[b]thiophene-3-carbohydrazide derivatives as potential anti-cancer agents and Pim-1 kinase inhibitors. *Anti-Cancer Agents in Medicinal Chemistry*. 2019; 19(14): 1737-1753.
- 11. RCSB Protein Data Bank. Available from: <u>www.rcsb.org</u>.
- 12. Doyle M, Lente V, Mowat R, Fobare W. Alkyl nitrite-metal halide deamination reactions: Synthetic coupling of electrophilic bromination with substitutive deamination for selective synthesis of multiply brominated aromatic compounds from arylamines. *Bioorg Chem.* 1979; 28.
- 13. Sandmeyer TD. Chem. Ges. 1884; 17: 1633-1635.
- 14. Smith R, Angello B, Peterg B, et al. Reactions of Hydrazines with Esters and Carboxylic Acids. *Bioorg Chem.* 2010; 38: 2.