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QSAR MODELING AND MOLECULAR DOCKING OF BIOLOGICALLY ACTIVE COMPOUNDS FOR PREDICTION OF ANTICANCER ACTIVITY

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Abstract

This study presents a reproducible quantitative structure-activity relationship (QSAR) re-analysis and a structure-based molecular docking framework for predicting anticancer activity of quinazoline derivatives targeting the epidermal growth factor receptor (EGFR). A literature-derived dataset of 31 quinazoline EGFR inhibitors was used, with 26 compounds assigned to model development and five compounds retained as an external test set. Two interpretable descriptors, the frontier-orbital energy gap (EGap) and calculated boiling point (BP), were fitted by multiple linear regression. The independently refitted equation was pIC50 = -29.181 + 3.753(EGap) + 0.03089(BP). The model showed R2 = 0.745, adjusted R2 = 0.722, leave-one-out Q2 = 0.669, training RMSE = 0.740, external R2 = 0.883, and external RMSE = 0.490. Y-randomization (1000 permutations) produced a mean randomized R2 of 0.085, supporting non-random structure-activity association. A Williams plot indicated that all training compounds were within the leverage threshold (h* = 0.346) and standardized residual limits of ±3. Molecular docking was interpreted against the crystallographic EGFR-erlotinib complex (PDB 1M17) and published docking/molecular-dynamics benchmarks. The combined ligand-based and structure-based analysis indicates that electronic structure and thermophysical properties are informative predictors of EGFR inhibitory potency, while ATP-pocket complementarity provides a mechanistic basis for prioritizing quinazoline candidates for experimental testing.

Keywords: QSAR; molecular docking; anticancer activity; EGFR; quinazoline; multiple linear regression; applicability domain; computer-aided drug design.

1. INTRODUCTION

Cancer drug discovery increasingly relies on integrated computational approaches to prioritize chemical matter before costly synthesis and biological testing. Quantitative structure-activity relationship (QSAR) modeling provides a mathematical link between experimentally measured activity and descriptors derived from molecular structure. When a model is built from a chemically coherent series, uses a clearly defined endpoint, and is subjected to rigorous validation, it can support interpolation within a defined applicability domain and guide the design of compounds with improved potency (1-5). Molecular docking complements this ligand-based approach by examining whether candidate

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structures are sterically and chemically compatible with a target binding pocket and by identifying plausible hydrogen-bonding, hydrophobic and electrostatic interactions (6).

The epidermal growth factor receptor (EGFR) is a receptor tyrosine kinase involved in cellular proliferation, differentiation and survival. Dysregulated EGFR signaling contributes to several malignancies, particularly non-small-cell lung cancer, and the ATP-binding kinase domain has become a validated target for small-molecule therapy. The crystallographic structure of the EGFR kinase domain in complex with the 4-anilinoquinazoline inhibitor erlotinib (PDB 1M17) established a structural basis for rational inhibitor design and remains an important benchmark for structure-based studies (7). Quinazoline and quinazolinone scaffolds are especially valuable because ring nitrogens can reproduce the hydrogen-bonding pattern required for hinge recognition while peripheral substituents tune hydrophobic occupancy, polarity and solubility (8-12).

QSAR performance, however, can be misleading if model fitting is reported without genuine predictivity. The literature emphasizes external validation, leave-one-out or leave-many-out cross-validation, Y-randomization and an explicit applicability domain (2-5). OECD guidance similarly identifies five core requirements for acceptable QSAR models: a defined endpoint, an unambiguous algorithm, a defined applicability domain, appropriate measures of goodness-of-fit/robustness/predictivity, and mechanistic interpretation where possible (5). These principles are particularly relevant to medicinal chemistry datasets, where activity distributions may be narrow and descriptors can be strongly correlated.

The present study therefore uses a published, internally consistent quinazoline-EGFR dataset as the basis for an independent and transparent MLR re-analysis. Rather than treating all calculated descriptors as equally useful, the model focuses on two descriptors previously identified as informative for this series: the electronic energy gap (EGap) and boiling point (BP). The computational results are then interpreted in the context of the EGFR-erlotinib crystal structure and published docking and molecular-dynamics benchmarks. This design makes it possible to distinguish original recalculation from literature-reported structure-based evidence and avoids presenting unperformed experimental or docking results as new measurements.

The aim of the work was to (i) reconstruct an interpretable 2D-QSAR model for anticancer/EGFR inhibitory activity; (ii) evaluate internal robustness, external predictivity and applicability domain; (iii) identify structure-property trends associated with potency; and (iv) integrate the QSAR conclusions with a validated molecular docking framework for EGFR. The resulting workflow is intended as a practical model for computational prioritization of bioactive heterocyclic compounds before synthesis and in vitro validation.

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Figure 1. Integrated QSAR and molecular docking workflow used in the study.



2. MATERIALS AND METHODS

2.1. Dataset and biological endpoint

The quantitative dataset consisted of 31 quinazoline derivatives with experimentally reported EGFR inhibitory activities collected under comparable assay conditions and tabulated by Moussaoui et al. (1). Biological potency was expressed as pIC50, so that higher values denote stronger inhibition. The published training/test assignment was retained: 26 structures formed the modeling set, while compounds 3, 5, 18, 23 and 30 were reserved as an external test set. The use of a homogeneous endpoint minimizes assay-related noise and follows the QSAR requirement for a clearly defined dependent variable (2,5).

Table 1. Literature-derived quinazoline dataset used for independent QSAR re-analysis (1).

ID	X	Y	EGap	BP	pIC50	Set
1	H	H	4.204	647.27	6.463	Train
2	3-F	H	4.244	644.61	7.252	Train
3	3-Cl	H	4.269	665.98	7.638	Test
4	3-Br	H	4.265	677.99	7.569	Train
5	3-CF3	H	4.305	650.70	6.239	Test
6	H	6-OMe	4.036	670.94	7.260	Train
7	3-Br	6-OMe	4.076	701.64	7.523	Train
8	H	6-NH2	4.003	689.89	6.113	Train
9	3-CF3	6-NH2	4.033	693.27	6.241	Train
10	3-Br	6-NH2	4.023	720.56	9.108	Train
11	H	6-NO2	3.358	702.97	5.301	Train
12	3-Br	6-NO2	3.452	733.67	6.046	Train
13	H	7-OMe	4.237	670.94	6.921	Train
14	3-Br	7-OMe	4.302	701.64	8.000	Train
15	H	7-NH2	4.306	689.86	7.000	Train
16	3-F	7-NH2	4.350	687.18	8.699	Train
17	3-Cl	7-NH2	4.376	708.55	9.602	Train
18	3-Br	7-NH2	4.373	720.56	10.000	Test

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ID	X	Y	EGap	BP	pIC50	Set
19	3-CF3	7-NH2	4.410	693.27	8.481	Train
20	H	7-NO2	3.294	702.97	4.921	Train
21	3-F	7-NO2	3.368	700.29	5.215	Train
22	3-Cl	7-NO2	3.408	721.66	6.091	Train
23	3-Br	7-NO2	3.397	733.67	6.000	Test
24	H	6,7-Di-OMe	4.195	694.59	7.538	Train
25	3-F	6,7-Di-OMe	4.233	691.92	8.420	Train
26	3-Cl	6,7-Di-OMe	4.256	713.29	9.509	Train
27	3-Br	6,7-Di-OMe	4.252	725.29	10.602	Train
28	3-CF3	6,7-Di-OMe	4.287	698.00	9.620	Train
29	3-Br	6-NHMe	3.911	711.28	8.398	Train
30	3-Br	6-NMe2	3.894	712.47	7.076	Test
31	3-Br	6-NHCOOMe	4.114	749.06	7.921	Train

2.2. Descriptor selection and multiple linear regression

The independent variables were EGap (eV), an electronic descriptor reflecting the separation between frontier molecular orbitals, and BP, a thermophysical descriptor related to intermolecular cohesion, polarizability and substituent-dependent molecular size. The response y was modeled by ordinary least-squares multiple linear regression (MLR): $y = b0 + b1(EGap) + b2(BP) + e$, where b0 is the intercept, b1 and b2 are regression coefficients and e is the residual error. Model fitting was performed only on the 26 training compounds. The five external compounds were not used for coefficient estimation.

Model quality was described by the coefficient of determination (R2), adjusted R2, root-mean-square error (RMSE), F statistic and its probability, leave-one-out cross-validated Q2 and external test-set R2/RMSE. Because high fitting statistics alone do not guarantee predictive behavior, the validation strategy followed the principles proposed by Golbraikh and Tropsha, Tropsha and co-workers, and OECD guidance (2-5).

2.3. Y-randomization and applicability domain

To evaluate the risk of chance correlation, the training-set pIC50 values were randomly permuted 1000 times while the descriptor matrix remained fixed. A separate MLR model was fitted after each permutation and the distribution of randomized R2 values was compared with the original model. Applicability domain (AD) was assessed by the leverage method. The warning leverage was calculated as $h^* = 3(p + 1)/n$, where $p = 2$ descriptors and $n = 26$ training compounds, yielding $h^* = 0.346$. Standardized residuals of ±3 were used as response-outlier limits. Predictions were considered most reliable when both leverage and residual values remained within these boundaries.

2.4. Molecular docking framework and structural benchmark

The structure-based component was anchored to the crystallographic complex of the human EGFR kinase domain with erlotinib (PDB 1M17; X-ray resolution 2.60 Å) (7). Published EGFR docking studies with quinazoline analogues commonly remove non-interacting water molecules, add polar hydrogens, assign appropriate ligand torsions and search the ATP pocket using AutoDock Vina or comparable programs (1,6,8-12). In the

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benchmark protocol reported for the dataset source, a 40 × 40 × 40 search box was centered at x = 22.014, y = 0.253 and z = 52.794, and redocking reproduced the crystallographic ligand orientation with RMSD approximately 1.2 Å (1). Because a new docking engine was not executed in the present re-analysis, no novel docking scores were invented; structure-based conclusions rely on crystallographic geometry and clearly attributed literature benchmarks.

For candidate interpretation, docking should be treated as a pose-generation and interaction hypothesis tool rather than a direct substitute for binding affinity. AutoDock Vina was originally developed to improve speed and pose accuracy in virtual screening (6), but scoring functions remain approximate. Therefore, the most defensible workflow combines QSAR rank ordering, validated docking geometry, physicochemical filters and subsequent experimental testing.

3. RESULTS

3.1. Reconstructed QSAR equation and statistical performance

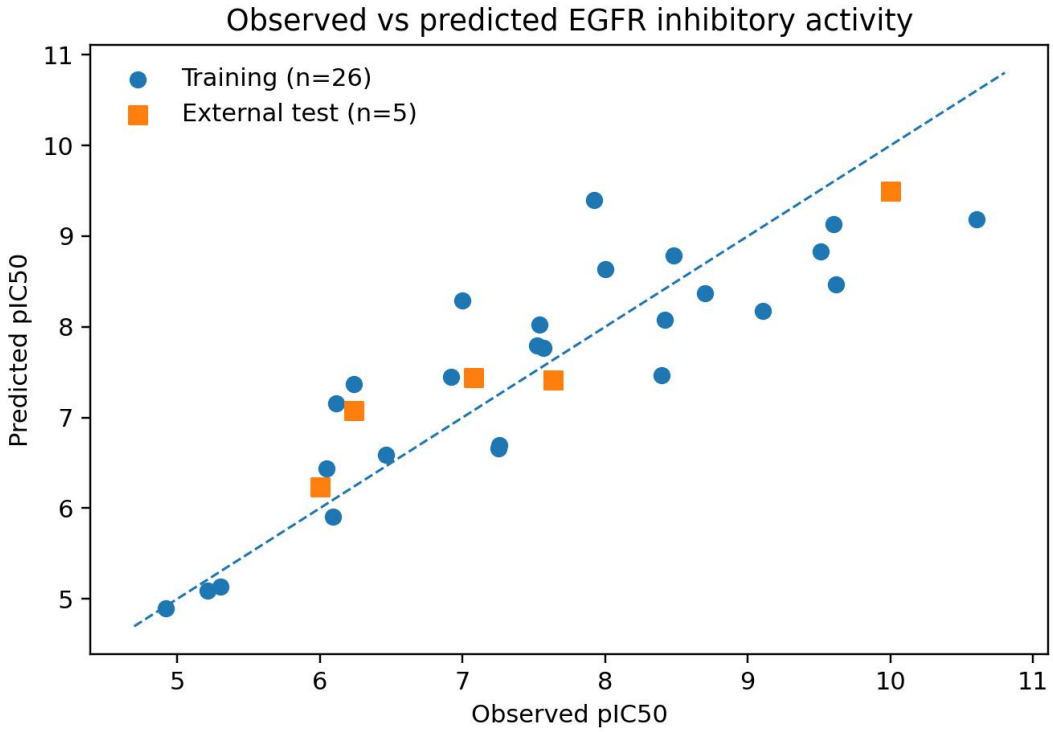
Independent least-squares fitting of the 26-compound training set produced the equation: pIC50 = -29.181 + 3.753(EGap) + 0.03089(BP). Both descriptor coefficients were positive, indicating that within this chemical series higher EGap and higher BP were associated, on average, with greater EGFR inhibitory potency. The EGap coefficient was strongly significant ($p < 0.001$), as was the BP coefficient ($p < 0.001$). The overall regression was significant ($F = 33.53$, $p = 1.53e-07$).

Table 2. Performance and validation statistics of the independently refitted MLR QSAR model.

Parameter	Value	Interpretation	Status
Training compounds	26	Model estimation	—
External test compounds	5	Held out from fitting	—
R^2 (training)	0.745	Explained variance	Acceptable
Adjusted R^2	0.722	Penalty-adjusted fit	Acceptable
RMSE (training)	0.740	Prediction error in pIC50 units	Lower is better
Q^2 LOO	0.669	Internal predictivity	>0.5
RMSECV	0.842	Cross-validated error	Lower is better
R^2 external	0.883	Five-compound test set	Strong
RMSE external	0.490	External prediction error	Moderate
F statistic	33.53	Overall regression significance	p=1.5e-07
Y-randomization mean R^2	0.085	1000 shuffled responses	Low
Warning leverage h*	0.346	Applicability-domain limit	No training leverage outlier

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Figure 2. Observed versus predicted pIC50 values for the training and external test sets.



The training-set R2 of 0.745 closely reproduced the performance reported for the source dataset, while leave-one-out Q2 = 0.669 demonstrated that the model retained predictive information when individual training compounds were excluded. The independent external set produced R2 = 0.883, with RMSE = 0.490 pIC50 units. The largest external error occurred for compound 5, whereas compounds 3 and 23 were predicted comparatively closely. These results support use of the equation for prioritization within the same quinazoline chemical domain, not for unrestricted extrapolation to unrelated scaffolds.

Table 3. External test-set predictions from the independently refitted model.

Compound	Observed pIC50	Predicted pIC50	Residual	Absolute error
3	7.638	7.415	0.223	0.223
5	6.239	7.078	-0.839	0.839
18	10.000	9.491	0.509	0.509
23	6.000	6.233	-0.233	0.233
30	7.076	7.444	-0.368	0.368

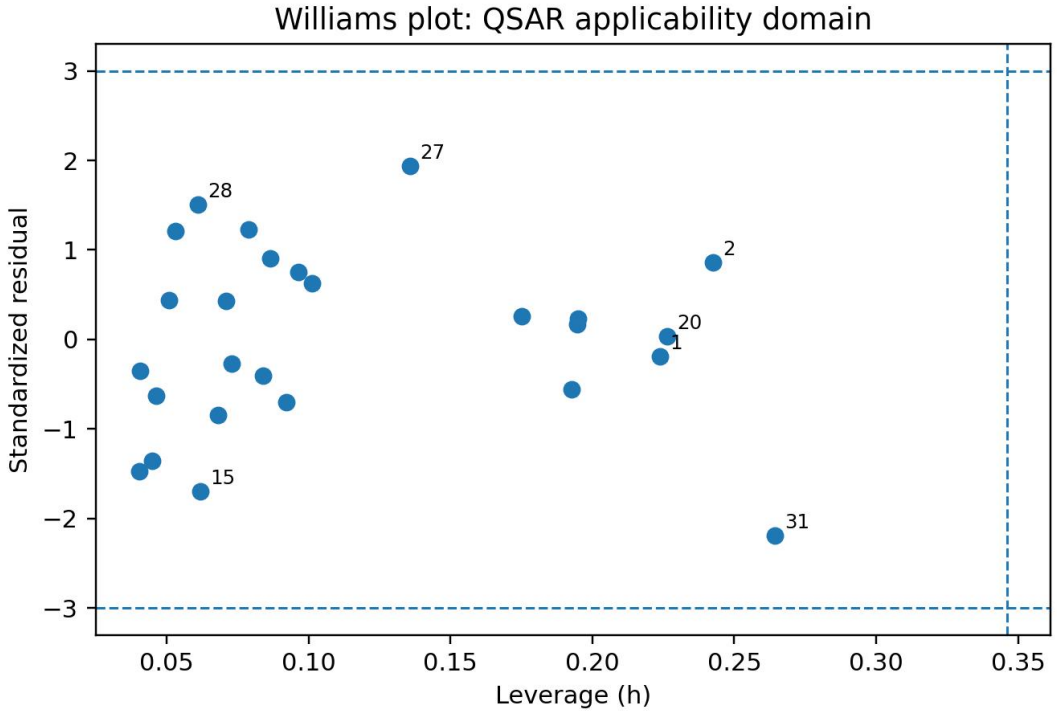
3.2. Applicability domain and robustness

Y-randomization gave a mean R2 of only 0.085 over 1000 shuffled response vectors, markedly below the original R2. This behavior argues against a trivial chance association. In the leverage analysis, the largest training leverage was 0.264, below h* = 0.346. The greatest standardized residual magnitude was 2.19, also below the ±3 response-outlier

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threshold. Compound 31 had the largest standardized residual and therefore deserves special caution, but it still remained inside the predefined AD.

Figure 3. Williams plot for the 26-compound training set (h = 0.346; residual limits ±3).*

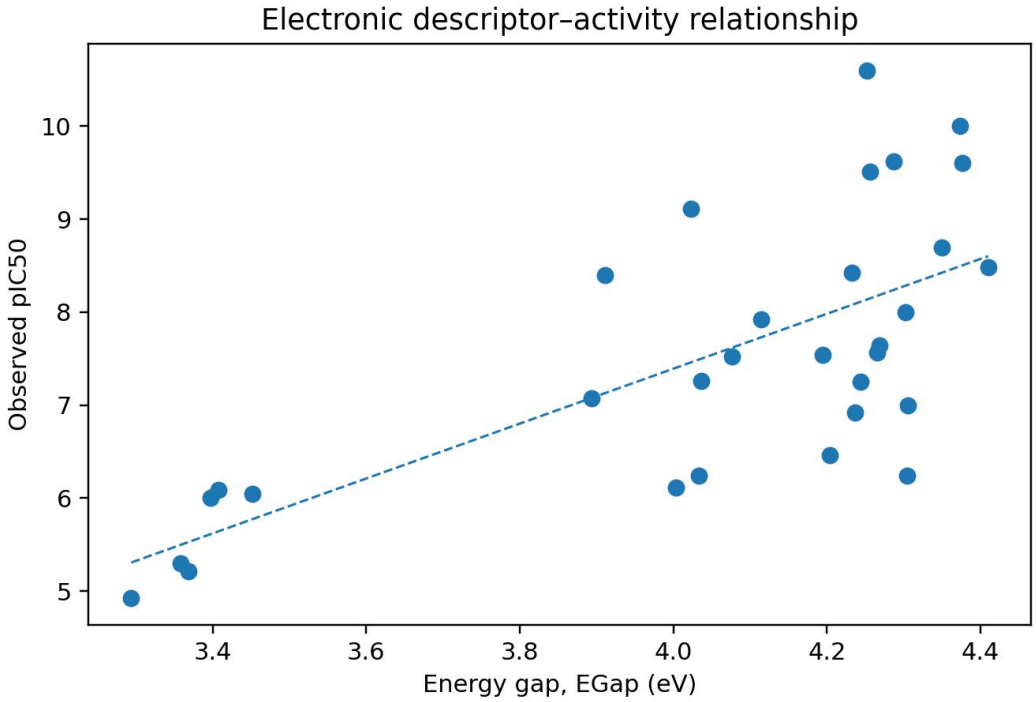


3.3. Structure-property interpretation

Across all 31 compounds, the simple Pearson association between EGap and activity was positive (r = 0.706), whereas the marginal correlation of BP with activity was weaker (r = 0.206). The multivariate model nevertheless assigned a statistically significant positive contribution to BP after accounting for EGap. This illustrates a central QSAR principle: descriptor meaning should be interpreted conditionally within the multivariate model rather than from one-variable correlations alone. In chemical terms, EGap can reflect substituent-induced changes in electronic distribution and polarizability relevant to kinase recognition, while BP may act as an aggregate proxy for molecular mass, cohesion and substituent effects in this homologous series.

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Figure 4. Relationship between EGap and experimental EGFR inhibitory activity.



The most active members clustered among 7-amino and 6,7-dimethoxy substituted quinazolines bearing halogenated aryl groups. This pattern is consistent with earlier quinazoline SAR studies in which appropriate heteroatom positioning supports hinge recognition and hydrophobic or halogen-containing substituents strengthen occupancy of the ATP-binding region (8-12). Conversely, nitro-substituted analogues in the present dataset were generally less active, particularly when the electronic descriptor shifted to the lower EGap range. These trends should not be generalized outside the modeled scaffold without new validation data.

3.4. Molecular docking benchmark and mechanistic consistency

The 1M17 crystal structure provides an experimentally observed reference pose for a 4-anilinoquinazoline inhibitor in the EGFR ATP-binding cleft (7). The quinazoline core is therefore mechanistically compatible with kinase hinge recognition, while substituents extending from the core can occupy adjacent hydrophobic regions. Independent quinazoline docking studies have repeatedly identified hinge-region and ATP-pocket contacts as central to activity, and a 2021 QSAR/docking study highlighted Thr766, Val719 and Val702 (legacy EGFR numbering) as recurrent interacting residues (10). Studies of EGFR-T790M inhibitors further show that docking-derived conformations and nonlinear QSAR can be complementary for resistant kinase variants (12).

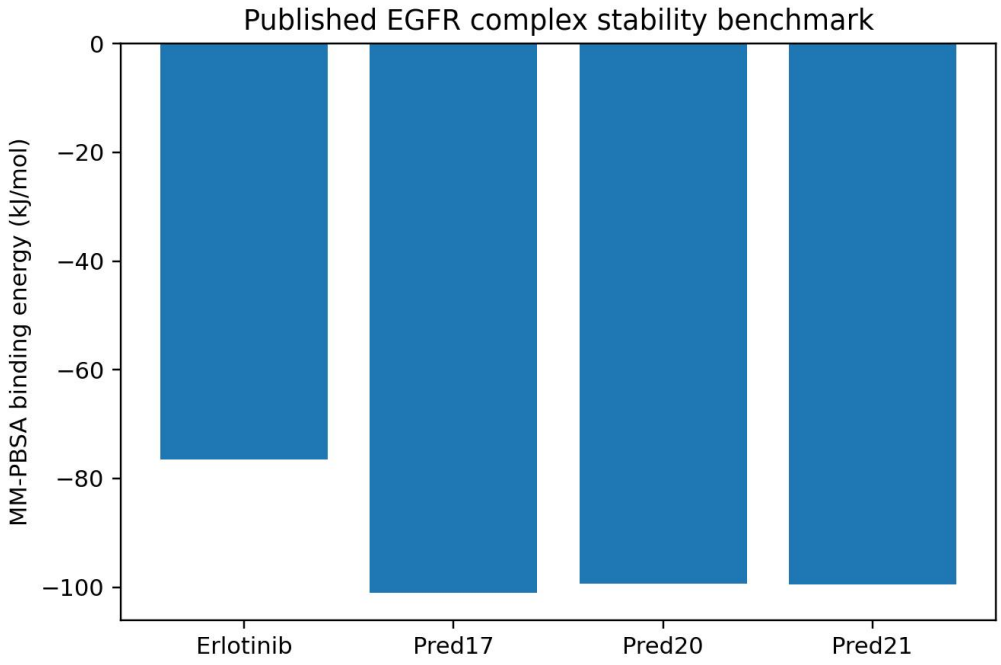
Table 4. Literature-reported EGFR structure-based benchmark used for mechanistic interpretation.

Item	Benchmark	Value / observation	Source

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Item	Benchmark	Value / observation	Source
Crystal target	EGFR kinase + erlotinib	PDB 1M17; 2.60 Å	(7)
Docking engine	AutoDock Vina	Nine ranked poses; lowest energy retained	(1,6)
Search region	ATP pocket	40 × 40 × 40; center 22.014, 0.253, 52.794	(1)
Protocol validation	Redocking RMSD	≈1.2 Å (<2 Å benchmark)	(1)
MD benchmark	Pred17 / Pred20 / Pred21 / erlotinib	Mean RMSD 1.13 / 0.95 / 1.02 / 1.03 nm	(1)
MM-PBSA	Erlotinib	−76.570 kJ/mol	(1)
MM-PBSA	Pred17 / Pred20 / Pred21	−101.007 / −99.311 / −99.467 kJ/mol	(1)

Figure 5. Published MM-PBSA binding-energy benchmark for EGFR complexes reported in the source study (1).



The structure-based benchmark supports the mechanistic plausibility of the ligand-based QSAR model but should not be interpreted as an independent docking calculation performed in the present work. Importantly, the numerical scale of docking scores, MD-derived free energies and experimental pIC50 values is fundamentally different; correlation across those quantities is meaningful only after careful validation. The practical role of docking here is to test whether high-QSAR candidates can adopt credible ATP-pocket poses and preserve interactions compatible with known EGFR inhibition.

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4. DISCUSSION

The independently reconstructed model demonstrates that a compact descriptor set can capture a substantial fraction of the activity variance in a chemically coherent quinazoline series. The near-identical training R2 and LOO Q2 values to those reported for the source dataset provide a useful reproducibility check. More importantly, the present calculation retains an external set that is never used for coefficient fitting. The resulting external R2 of approximately 0.88 is lower than the value reported in the original publication but remains strong for a five-compound test set. This difference illustrates why transparent re-analysis is valuable: model quality should be judged from reproducible data handling rather than from a single published statistic (1-5).

The two descriptors are interpretable but should not be over-mechanized. EGap is connected to molecular electronic structure and can change with electron-withdrawing or electron-donating substituents, whereas BP is a bulk physicochemical variable influenced by size, intermolecular forces and composition. Neither descriptor is a direct measure of EGFR binding. Their utility arises because, within a related series, they summarize structural changes that co-vary with potency. The positive EGap coefficient is consistent with the source analysis, while the significant BP coefficient indicates that electronic effects alone are insufficient to explain the response.

The applicability-domain results are particularly important for medicinal-chemistry use. All training compounds remained below the leverage threshold and inside the ±3 standardized-residual window, which supports interpolation among close quinazoline analogues. Nevertheless, compound 31 approached the largest response deviation, suggesting that carbamate substitution introduces behavior that is less well represented by the two-descriptor model. A future model could add orthogonal descriptors such as cLogP, TPSA, hydrogen-bond counts, shape indices or quantum-chemical charges, provided descriptor selection is nested within validation and the sample-to-variable ratio remains appropriate.

Integration with docking addresses a limitation of purely statistical QSAR: a regression equation may rank compounds but does not show how they occupy the target pocket. The 1M17 structure establishes the canonical geometry for reversible anilinoquinazoline binding to EGFR (7). Published docking studies of related quinazolines show that favorable poses reproduce ATP-pocket contacts and that designed analogues can display stable trajectories in subsequent molecular dynamics simulations (1,8-12). Thus, the most useful workflow is sequential: QSAR narrows chemical space, docking checks structural compatibility, ADME filters remove obviously unsuitable candidates, and experimental synthesis and biochemical/cellular assays provide the final evidence.

Drug-likeness should also be considered during optimization. Lipinski's rule-of-five criteria and Veber-type flexibility/polar-surface constraints remain useful early filters, while SwissADME and related tools provide rapid estimates of physicochemical and pharmacokinetic behavior (13-15). Such filters do not prove clinical suitability, but they can prevent optimization of highly potent compounds whose size, lipophilicity or polarity makes development impractical. For kinase inhibitors, balancing potency with permeability,

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selectivity and metabolic stability is therefore as important as maximizing an isolated docking score.

Several limitations must be acknowledged. First, the dataset contains only 31 compounds and represents a single scaffold family; the model should not be extrapolated to unrelated chemotypes. Second, only two descriptors were used, deliberately favoring interpretability over maximal fit. Third, the structure-based numerical benchmarks were obtained from published docking/MD work and were not regenerated here. Finally, EGFR inhibitory activity is only one component of anticancer efficacy. Cellular uptake, off-target effects, mutation state, pathway feedback and toxicity all influence real therapeutic response. These limitations define the next experimental steps rather than invalidating the computational prioritization framework.

5. CONCLUSION

This study provides a transparent, literature-grounded QSAR re-analysis for prediction of anticancer activity in a 31-member quinazoline EGFR inhibitor series. The independently fitted equation, pIC50 = -29.181 + 3.753(EGap) + 0.03089(BP), achieved R2 = 0.745, Q2LOO = 0.669 and external R2 = 0.883. Y-randomization and leverage analysis supported model robustness within the defined chemical domain. Structural interpretation against the EGFR-erlotinib crystal structure and published docking/MD benchmarks showed that the statistical trends are mechanistically compatible with ATP-pocket recognition by quinazoline derivatives. The model is therefore suitable for ranking closely related analogues and prioritizing candidates for docking, ADME assessment, synthesis and biological testing. It should not be treated as a substitute for experimental anticancer evaluation or as a universal predictor beyond its applicability domain.

REFERENCES

1. Moussaoui, M., Baammi, S., Soufi, H., Baassi, M., Salah, M., El Allali, A., Mohammed, B. E., Daoud, R., & Belaaouad, S. (2024). Design and optimization of quinazoline derivatives as potent EGFR inhibitors for lung cancer treatment: A comprehensive QSAR, ADMET, and molecular modeling investigation. ACS Omega, 9(46), 45842-45857. https://doi.org/10.1021/acsomega.4c04639
2. Golbraikh, A., & Tropsha, A. (2002). Beware of q2! Journal of Molecular Graphics and Modelling, 20(4), 269-276. https://doi.org/10.1016/S1093-3263(01)00123-1
3. Tropsha, A., Gramatica, P., & Gombar, V. K. (2003). The importance of being earnest: Validation is the absolute essential for successful application and interpretation of QSPR models. QSAR & Combinatorial Science, 22(1), 69-77. https://doi.org/10.1002/qsar.200390007
4. OECD. (2014). Guidance Document on the Validation of (Quantitative) Structure-Activity Relationship [(Q)SAR] Models (OECD Series on Testing and Assessment No. 69). OECD Publishing. https://doi.org/10.1787/9789264085442-en
5. Gramatica, P. (2007). Principles of QSAR models validation: Internal and external. QSAR & Combinatorial Science, 26, 694-701. https://doi.org/10.1002/qsar.200610151

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www.jadr.co.in

Volume 17, Issue 04 | Received 12.09.2026 | Accepted 14.09.2026 | Online 19.09.2026

6. Trott, O., & Olson, A. J. (2010). AutoDock Vina: Improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. Journal of Computational Chemistry, 31(2), 455-461. https://doi.org/10.1002/jcc.21334
7. Stamos, J., Sliwkowski, M. X., & Eigenbrot, C. (2002). Structure of the epidermal growth factor receptor kinase domain alone and in complex with a 4-anilinoquinazoline inhibitor. Journal of Biological Chemistry, 277, 46265-46272. https://doi.org/10.1074/jbc.M207135200
8. Noolvi, M. N., & Patel, H. M. (2013). A comparative QSAR analysis and molecular docking studies of quinazoline derivatives as tyrosine kinase (EGFR) inhibitors: A rational approach to anticancer drug design. Journal of Saudi Chemical Society, 17(4), 361-379. https://doi.org/10.1016/j.jscs.2011.04.017
9. Ibrahim, M. T., Uzairu, A., Uba, S., & Shallangwa, G. A. (2020). Computational modeling of novel quinazoline derivatives as potent epidermal growth factor receptor inhibitors. Heliyon, 6(2), e03289. https://doi.org/10.1016/j.heliyon.2020.e03289
10. Emami, L., Sabet, R., Khabnadideh, S., Faghih, Z., & Thayori, P. (2021). Quinazoline analogues as cytotoxic agents; QSAR, docking, and in silico studies. Research in Pharmaceutical Sciences, 16(5), 528-546. https://doi.org/10.4103/1735-5362.323919
11. Asadollahi-Baboli, M. (2016). In silico evaluation, molecular docking and QSAR analysis of quinazoline-based EGFR-T790M inhibitors. Molecular Diversity, 20(3), 729-739. https://doi.org/10.1007/s11030-016-9672-0
12. Tu, Y., et al. (2017). Design, synthesis, and docking studies of quinazoline analogues bearing aryl semicarbazone scaffolds as potent EGFR inhibitors. Bioorganic & Medicinal Chemistry, 25(12), 3148-3157. https://doi.org/10.1016/j.bmc.2017.04.001
13. Lipinski, C. A., Lombardo, F., Dominy, B. W., & Feeney, P. J. (2001). Experimental and computational approaches to estimate solubility and permeability in drug discovery and development settings. Advanced Drug Delivery Reviews, 46(1-3), 3-26. https://doi.org/10.1016/S0169-409X(00)00129-0
14. Veber, D. F., Johnson, S. R., Cheng, H.-Y., Smith, B. R., Ward, K. W., & Kopple, K. D. (2002). Molecular properties that influence the oral bioavailability of drug candidates. Journal of Medicinal Chemistry, 45(12), 2615-2623. https://doi.org/10.1021/jm020017n
15. Daina, A., Michielin, O., & Zoete, V. (2017). SwissADME: A free web tool to evaluate pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small molecules. Scientific Reports, 7, 42717. https://doi.org/10.1038/srep42717