

3D-QSAR, Molecular Docking and Molecular Dynamics Simulations of 3-Phenylsulfonylaminopyridine Derivatives as Novel PI3K α Inhibitors

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ABSTRACT The p110 α , catalytic subunit of PI3K α , was the primary phosphoinositide 3-kinases (PI3Ks) isoform involved in oncogenic RTK signaling and tumorigenesis. In this study, the three-dimensional quantitative structure-activity relationship (3D-QSAR), molecular docking and molecular dynamics simulation were employed to study the binding mode between 3-phenylsulfonylaminopyridine derivatives and PI3K α . The stable and reliable 3D-QSAR models were constructed based on the application of the comparative molecular field analysis (CoMFA) model ($q^2 = 0.704$, $r^2 = 0.994$) and comparative molecular similarity index analysis (CoMSIA) model ($q^2 = 0.804$, $r^2 = 0.996$). The contour maps illustrated relationship between structure and biological activity. The conformation obtained after MD simulation was more stable than the docked conformation. MD simulation was performed in a more realistic environment, and was much closer to physiological conditions. As a result, five novel PI3K α inhibitors were designed with better biological activity than the template compound **8**.

Keywords: PI3K inhibitor, 3D-QSAR, molecular docking, molecular dynamics simulation;

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1 INTRODUCTION

Phosphoinositide 3-kinases (PI3Ks), discovered in early 1980s^[1], phosphorylated the 3-hydroxyl group of the inositol ring presented in membrane-bound phosphatidylinositol (PtdIns) lipids^[2]. PI3Ks signaling pathways were involved in cell proliferation, growth, motility, metabolism and survival^[3, 4].

PI3Ks were divided into 3 classes (classes I, II, and III) based on their structure and substrate specificity^[2, 5, 6]. The class I PI3Ks, including PI3K α , PI3K β , PI3K δ and PI3K γ , were composed of one regulatory subunit and one of the four catalytic (p110) subunits such as p110 α , p110 β , p110 δ and p110 γ isoforms^[7-9]. In vivo, class I PI3Ks primarily generated phosphatidylinositol-3,4,5-trisphosphate (PIP₃), a critical second messenger that recruits AKT for activation of growth, proliferation and survival signaling, from phosphatidylinositol-4,5-bisphosphate (PIP₂) as a high-affinity substrate of p110 α ^[3, 4, 10]. It was worth mentioning that p110 α had a high correlation with the survival and resistance treatment of human cancer^[11]. Class II PI3Ks consisted of three mono-

mers of PI3K-C2 α , PI3K-C2 β , and PI3K-C2 γ , with high molecular weight due to the extension at both N-terminal and C-terminal^[12]. Class III PI3Ks also had a heterodimeric structure, composed of a regulatory subunit, Vps15 or p150, and a catalytic subunit Vps34^[13].

Many potent PI3K inhibitors, including several p110 α -specific inhibitors, had been disclosed since the discovery of the first generation inhibitors, Wortmannin and LY294002^[14]. Four of them had been approved by the FDA, and the corresponding structures are depicted in Fig. 1. Idelalisib (Gilead science)^[15] approved in 2014 indicated for the treatment of patients with Chronic Lymphocytic Leukemia (CLL), Small Lymphocytic Lymphoma (SLL) or Follicular Lymphoma (FL). Three years later, Copanlisib (Bayer Healthcare Pharmaceuticals)^[16] was approved for the treatment of patients with Non-Hodgkin Lymphoma (NHL). In the next year, Duvelisib (Verastem)^[17] received FDA approval for previously treated Chronic Lymphocytic Leukemia (CLL), Small Lymphocytic Lymphoma (SLL) or

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Follicular Lymphoma (FL). After a year, Alpelisib (Novartis)^[18] was initially approved to treat HR⁺/HER²- advanced breast cancer patients. Additionally, there were

many other PI3Ks inhibitors being currently in clinical trials^[17].

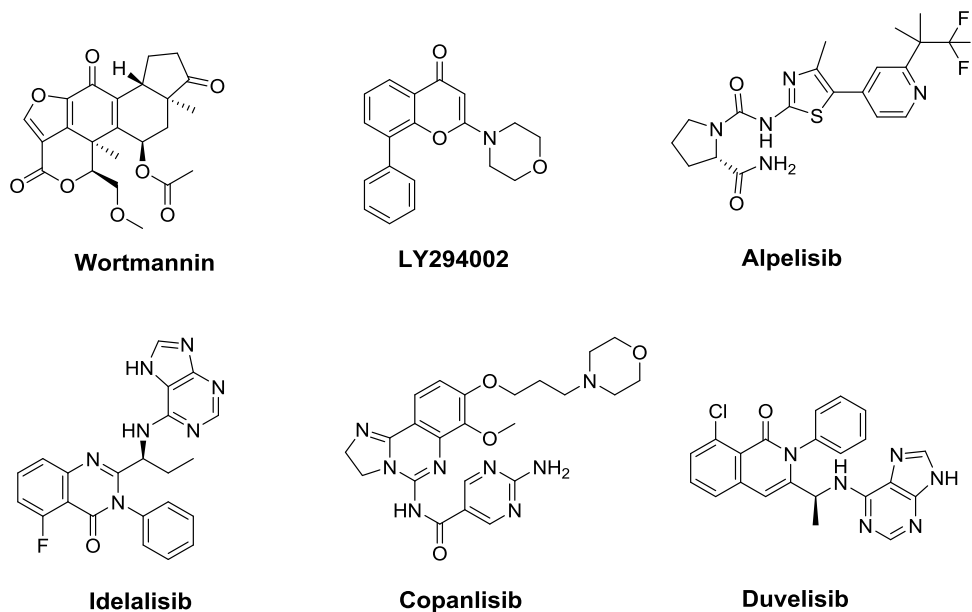


Fig. 1. Chemical structures of representative PI3Ks inhibitors

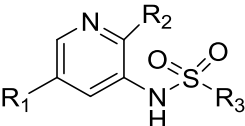
In this study, we developed 3D-QSAR models using CoMFA^[19] and CoMSIA^[20] technology on 65 3-phenylsulfonylaminopyridine derivatives^[21-25]. The structural and pharmacodynamic information obtained from 3D-QSAR model and its influence on the biological activity would be helpful for further drug design^[26-31]. Molecular docking and molecular dynamics simulation were carried out to analyze the binding mode between PI3K α and molecules. Molecular dynamics simulation studies on compounds with different selectivity would provide detailed information to explain and elucidate the mechanisms for improving selectivity^[32-35]. Finally, five new PI3K α inhibitors were designed, and this research aimed to provide a theoretical basis for the discovery of novel PI3K α inhibitors.

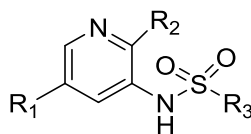
2 MATERIALS AND METHODS

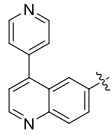

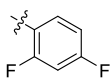
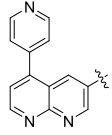

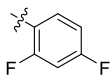
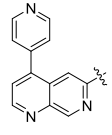

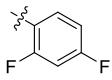
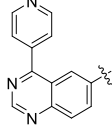

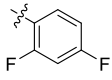
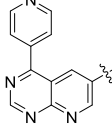

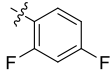
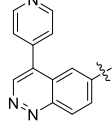

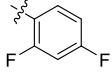
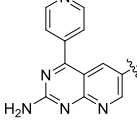

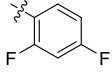
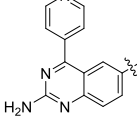

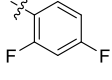
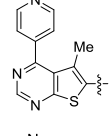

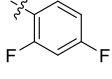
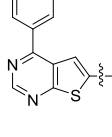

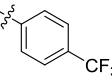
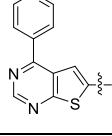

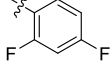
2.1 Datasets and biological activity

The 3D-QSAR research was based on a database of 65 3-phenylsulfonylaminopyridine derivatives as potent inhibitors against PI3K α , which were collected from literatures^[21-25]. Their molecular structures and corresponding biological activities in IC_{50} values are listed in Table 1. All molecules were divided into the training and test sets. 45 molecules were selected as the training set to generate the 3D-QSAR model. 20 molecules were selected as the test set to validate the quality of the models. Energies of all molecules were minimized by using Powell conjugate gradient methods at the Tripos force field^[36] under the conditions of a gradient convergence of 0.005 kcal/mol-Å in Gasteiger-Huckel charge^[37] and the maximum number of iterations was set to 10000.

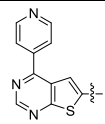

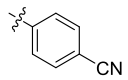
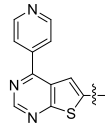

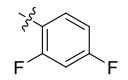
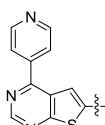

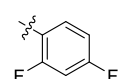
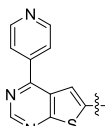

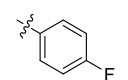
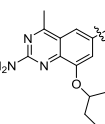

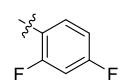
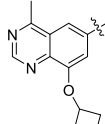

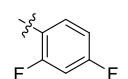
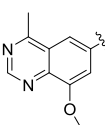

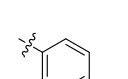
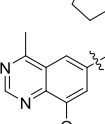

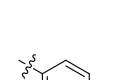
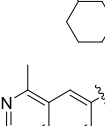


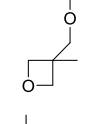

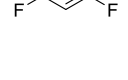
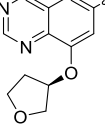

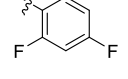
Table 1. Molecular Structures and Activity Values of Compounds

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Compd.	Substituent			IC_{50} (nM)
	R ₁	R ₂	R ₃	
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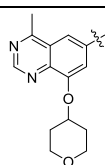

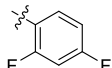
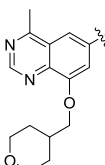

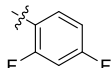
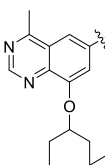

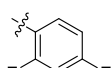
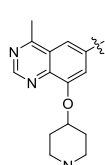

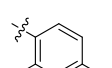
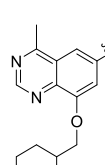

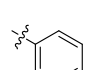
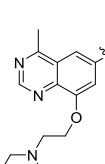

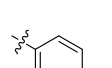
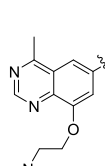

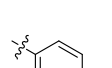
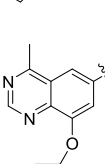

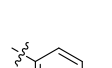
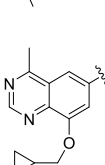

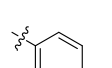


1				0.100
2				34.700
3 ^{TS}				1.020
4				0.095
5				51.700
6 ^{TS}				0.270
7				35.600
8				0.070
9				72.300
10				17.000
11				2.070

To be continued

12 ^{TS}				3.600
13 ^{TS}				1.700
14				0.230
15				0.300
16				0.800
17				1.000
18				1.000
19				1.500
20				0.870
21				0.880
22				0.950

To be continued

23				0.600
24				0.920
25				0.890
26				2.100
27				1.600
28 ^{TS}				2.300
29				6.800
30				5.300
31				1.500

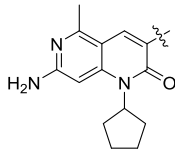

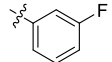
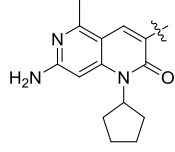


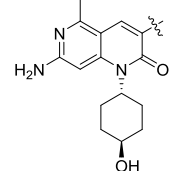

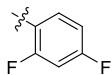
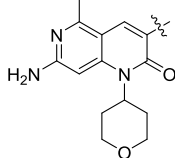

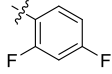
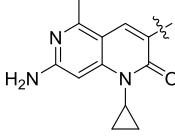

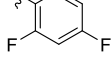
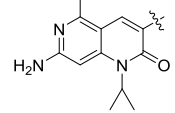

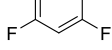
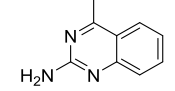

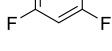
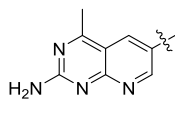


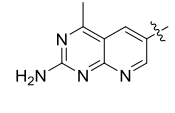

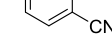
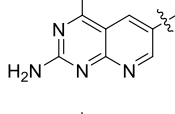

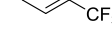
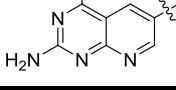


To be continued

32 ^{TS}				2.000
33				1.700
34				1.200
35				2.000
36				6.100
37 ^{TS}				2.400
38 ^{TS}				1.300
39				1.300
40 ^{TS}				2.200
41				2.200
42				9.300
43				3.000

To be continued

44 ^{TS}				1.100
45 ^{TS}				2.200
46 ^{TS}				1.600
47 ^{TS}				2.300
48				1.600
49				12.030
50 ^{TS}				2.420
51				174.280
52				14.270
53				174.880
54				72.590

To be continued

55 ^{TS}				60.510
56				37.330
57				9.900
58				8.600
59 ^{TS}				39.650
60 ^{TS}				42.840
61 ^{TS}				3.430
62				63.100
63				2.820
64 ^{TS}				8.410
65 ^{TS}				67.000

^{TS} = test set.

2.2 Molecular modeling and alignment

The prediction accuracy and statistical quality of the 3D-QSAR model depended heavily on alignment. Molecules of the training sets were aligned onto the template molecule

(compound **8**) which had the highest activity against PI3K α . The alignments were used for further 3D-QSAR study. The results are shown in Fig. 2.

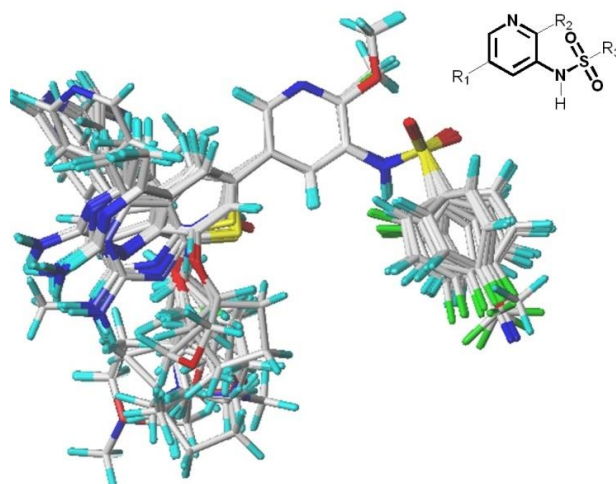


Fig. 2. Molecular alignments of all compounds in the data set. Compound 8 was employed as the template for alignment, and the common substructure was shown in bold

2.3 3D-QSAR models studies

The reliability and predictive ability of the 3D-QSAR models were evaluated through internal and external validation. In the Partial least squares (PLS) analysis, the Leave-one-out (LOO) method was used to determine the optimum number of components (*NOC*). In the 3D-QSAR

models validation, non-cross-validated correlation coefficient (r^2_{ncv}), standard error estimate (*SEE*) and F-statistic values (*F*) were obtained. Each molecule's predicted value and their actual value are in linear relationship and respectively shown in Fig. 3. The predicted pIC_{50} values via CoMFA and CoMSIA models are listed in Table 2.

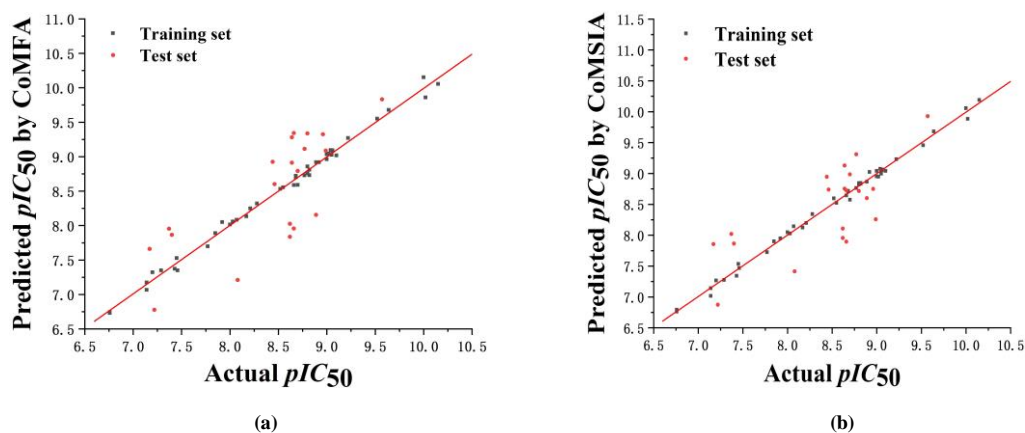


Fig. 3. Correlation plots of the predicted pIC_{50} values versus the actual pIC_{50} values using the training and test sets based on the CoMFA (a) and CoMSIA (b) models, respectively

Table 2. Actual and Predicted pIC_{50} Values of All Compounds

Compd.	Actual	CoMFA		CoMSIA	
		Predicted	Residues	Predicted	Residues
1	10.000	10.152	0.152	10.057	0.057
2	7.460	7.349	0.111	7.467	0.007
3	8.990	9.087	0.097	8.256	0.734
4	10.020	9.858	0.162	9.883	0.137
5	7.290	7.348	0.058	7.274	0.016
6	9.570	9.831	0.261	9.927	0.357
7	7.450	7.527	0.077	7.535	0.085
8	10.150	10.054	0.096	10.190	0.040

To be continued

9	7.140	7.172	0.032	7.140	0.000
10	7.770	7.699	0.071	7.723	0.047
11	8.680	8.723	0.043	8.705	0.025
12	8.440	8.924	0.484	8.944	0.504
13	8.770	9.112	0.342	9.311	0.541
14	9.640	9.677	0.037	9.679	0.039
15	9.520	9.550	0.030	9.455	0.065
16	9.100	9.018	0.082	9.040	0.060
17	9.000	8.961	0.039	8.953	0.047
18	9.000	9.035	0.035	9.039	0.039
19	8.820	8.730	0.090	8.829	0.009
20	9.060	9.080	0.020	9.061	0.001
21	9.060	9.092	0.032	9.051	0.009
22	9.020	9.044	0.024	8.946	0.074
23	9.220	9.270	0.050	9.228	0.008
24	9.040	9.093	0.053	9.074	0.034
25	9.050	9.024	0.026	8.994	0.056
26	8.680	8.698	0.018	8.716	0.036
27	8.800	8.856	0.056	8.842	0.042
28	8.640	8.911	0.271	9.129	0.489
29	8.170	8.133	0.037	8.122	0.048
30	8.280	8.319	0.039	8.340	0.060
31	8.820	8.809	0.011	8.844	0.024
32	8.700	8.791	0.091	8.984	0.284
33	8.770	8.727	0.043	8.761	0.009
34	8.920	8.919	0.001	9.022	0.102
35	8.700	8.589	0.111	8.574	0.126
36	8.210	8.248	0.038	8.195	0.015
37	8.620	7.837	0.783	8.108	0.512
38	8.890	8.156	0.734	8.600	0.290
39	8.890	8.919	0.029	8.864	0.026
40	8.660	7.957	0.703	7.896	0.764
41	8.660	8.586	0.074	8.644	0.016
42	8.030	8.058	0.028	8.026	0.004
43	8.520	8.530	0.010	8.594	0.074
44	8.960	9.325	0.365	8.750	0.210
45	8.660	9.342	0.682	8.723	0.063
46	8.800	9.338	0.538	8.715	0.085
47	8.640	9.280	0.640	8.751	0.111
48	8.800	8.755	0.045	8.822	0.022
49	7.920	8.050	0.130	7.946	0.026
50	8.620	8.024	0.596	7.954	0.666
51	6.760	6.743	0.017	6.792	0.032
52	7.850	7.889	0.039	7.900	0.050
53	6.760	6.731	0.029	6.762	0.002
54	7.140	7.066	0.074	7.017	0.123
55	7.220	6.776	0.444	6.872	0.348
56	7.430	7.371	0.059	7.340	0.090
57	8.000	8.015	0.015	8.045	0.045
58	8.070	8.083	0.013	8.142	0.072
59	7.400	7.864	0.464	7.864	0.464
60	7.370	7.953	0.583	8.018	0.648
61	8.460	8.601	0.141	8.738	0.278
62	7.200	7.320	0.120	7.265	0.065

To be continued

63	8.550	8.553	0.003	8.522	0.028
64	8.080	7.211	0.869	7.414	0.666
65	7.170	7.661	0.491	7.854	0.684

2.4 Molecular docking

Molecular docking studies were carried out using the Surflex-Dock module in Sybyl-x 2.0, which aimed to analyze the detailed binding mode of small molecules and PI3K α , and to validate the 3D-QSAR models. The 3D structures of

PI3K α (PDB code: 4ykn) were downloaded from RCSB protein database. The protein ligands and water were removed and the pocket which was used to combine with molecules was exposed before docking (Fig. 4).

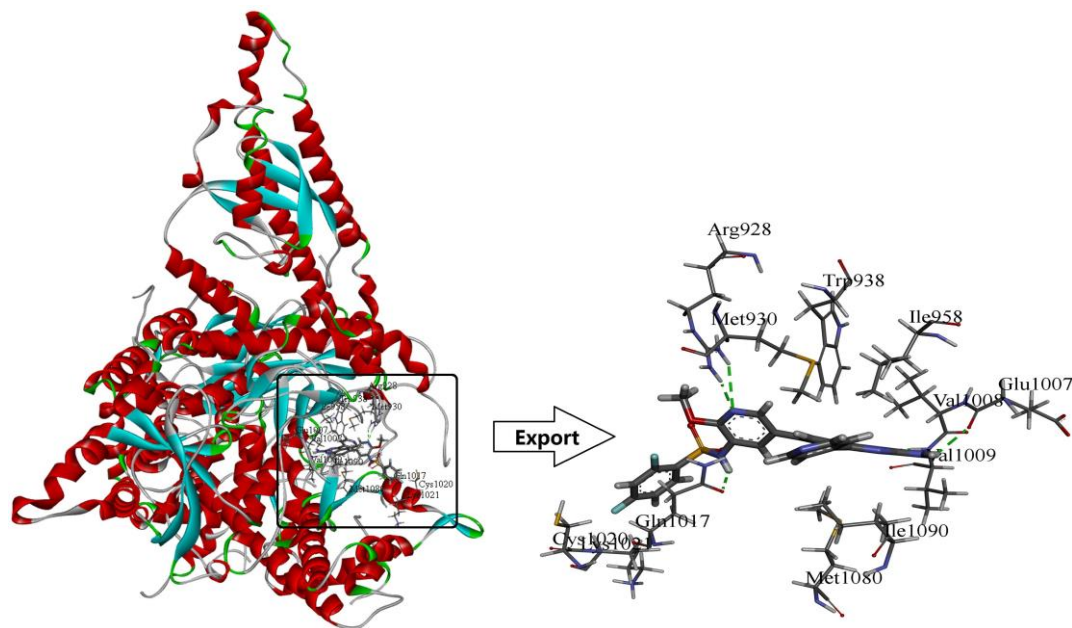


Fig. 4. Docking of the representative ligand compound 8 into the binding site of PI3K α . Ligands and the important residues for binding interaction were depicted by stick and line models

2.5 Molecular dynamics simulation

Molecular dynamics simulation was carried out with 8-4ykn complex as the initial structure by using amber 12.0 software^[38]. The general AMBER force field (GAFF) was employed on the ligands and the Amber ff99SB was used for the proteins^[39]. Na⁺ was added to achieve the system charge balance within a cubic water box. The entire simulation followed the procedures for minimization, heating, density balance, and production. The initial configurations of the receptor and ligand were obtained from docking studies. The energy of the whole system was minimized by the steepest descent and conjugate gradient method. Then, the minimized system was heated from 0 to 300 K over 10000 ps under the NVT ensemble, followed by density equilibration in the NPT ensemble at 300 K over 10000 ps. All hydrogen atoms were constrained by SHAKE method^[40]. After MD simulation, the root-mean-square deviation (RMSD) was calculated to evaluate the stability of the complex system. The image display softwares of VMD^[41] were used to extract and

analyze the trajectories.

3 RESULTS AND DISCUSSION

3.1 CoMFA and CoMSIA statistical results

Table 3 shows the statistics obtained by the CoMFA and CoMSIA models. In the CoMFA model study, the cross-validation correlation coefficient (q^2) and non-cross-validation correlation coefficient (r^2_{ncv}) are 0.704 and 0.994, respectively. The *ONC* is 10 in the training set. The *SEE* is 0.075 and the *F* value is 564.104. The Steric field contribution is 47.4%. Meanwhile, the electrostatic field contribution is 52.6%. Analogously, in the CoMSIA model study, q^2 , r^2_{ncv} , *ONC*, *SEE* and *F*-value are 0.804, 0.996, 10, 0.064 and 768.981, respectively. The Steric field contribution, electrostatic field contribution, donor field contribution, acceptor field contribution and hydrophobic field contribution are 9.4%, 30.7%, 31.0%, 19.5% and 9.4%, respectively.

Table 3. Best Results of the CoMFA and CoMSIA PLS Statistical Results

Statistical parameters	CoMFA	CoMSIA
q^2	0.704	0.804
r^2_{ncv}	0.994	0.996
ONC	10	10
SEE	0.075	0.064
F	564.106	768.981
Field contribution (%)		
Steric (S)	47.4	9.4
Electrostatic (E)	52.6	30.7
Hydrophobic (H)		31.0
Acceptor (A)		19.5
Donor (D)		9.4

3.2 3D-QSAR contour maps results and analysis

The contour maps of CoMFA and CoMSIA models provided information that explained the relationship between structural features and biological activity. Figs. 5 and 6 showed the contour maps around compound **8** with the

highest biological activity.

3.2.1 CoMFA contour maps

The steric and electrostatic fields from the best CoMFA model are shown in Fig. 5.

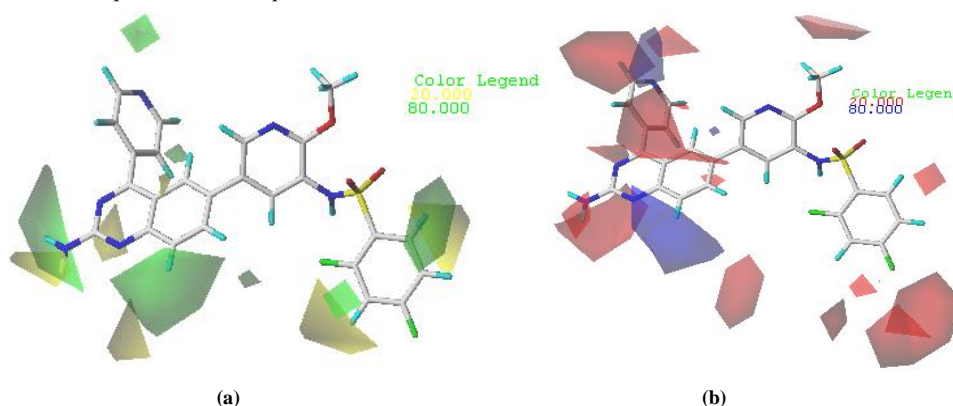


Fig. 5. Contour maps of compound 8. (a) Steric contour maps of CoMFA: favored (green) and disfavored (yellow); (b) Electrostatic contour maps of CoMFA: electrostatic (blue) and electronegative (red)

Areas where steric bulk substituents increased the potency were represented by green polyhedrons, while those in which steric bulk substituents decreased the potency were represented by yellow polyhedra (Fig. 5a). As shown in the steric map (Fig. 5a), a small yellow contour occurring around the 2'-site of quinazoline ring at R₁ of compound **8** indicated that compounds with small substituents at this site would have better biological activity. This could explain why the biological activity of compound **39** (pIC_{50} = 8.89) with -NH₂ group was slightly better than that of compound **48** (pIC_{50} = 8.80) with -NCH₃ group. A large green contour around the 8'-site of quinazoline ring at R₁ of compound **8** indicated that bulk substituents were beneficial to the biological activity. The biological activity of compound **37** (pIC_{50} = 8.62) with -NCH₃ group was higher than that of compound **36** (pIC_{50} = 8.21) with -NH group.

As shown in the electrostatic map (Fig. 5b), the blue area

indicated that the electropositive group was beneficial to the biological activity, and the red area indicated that the electronegative group was beneficial to the biological activity. The blue contours were distributed around the 8'-site of quinazoline ring at R₁ of compound **8**, indicating that the biological activity of compounds **1** (pIC_{50} = 10.00) and **8** (pIC_{50} = 10.15) with the carbon atom at the 8'-site of quinazoline ring was better than that of compound **2** (pIC_{50} = 7.46) with nitrogen atom. A medium red contour map was located near R₂, suggesting that the electronegative groups at this position would be favorable to increase the biological activity. The biological activity of compound **14** (pIC_{50} = 9.64) with chlorine atom at R₂ was better than that of compound **12** (pIC_{50} = 8.44) with a methyl group and compound **13** (pIC_{50} = 8.77) with a methoxy group.

3.2.2 CoMSIA contour maps

Fig. 6a depicted the CoMSIA steric contour map of the

optimal model with compound **8** overlaid. A small area of green contour was located around the 8'-site of quinazoline ring at R_1 of compound **8**, indicating that the bulk substituents which were beneficial to the biological activity. It could be interpreted by the fact that compound **37** ($pIC_{50} = 8.62$) with $-NCH_3$ group had higher activity than compound **36** ($pIC_{50} = 8.21$) with $-NH$ group. A small yellow contour

covered behind quinazoline ring at R_1 of compound **8**, indicating the presence of a small substituent was good for the biological activity. Compound **18** ($pIC_{50} = 9.00$) with the cyclopentyloxy group was more active than compound **19** ($pIC_{50} = 8.82$) with a slightly smaller substituent, cyclohexyloxy group.

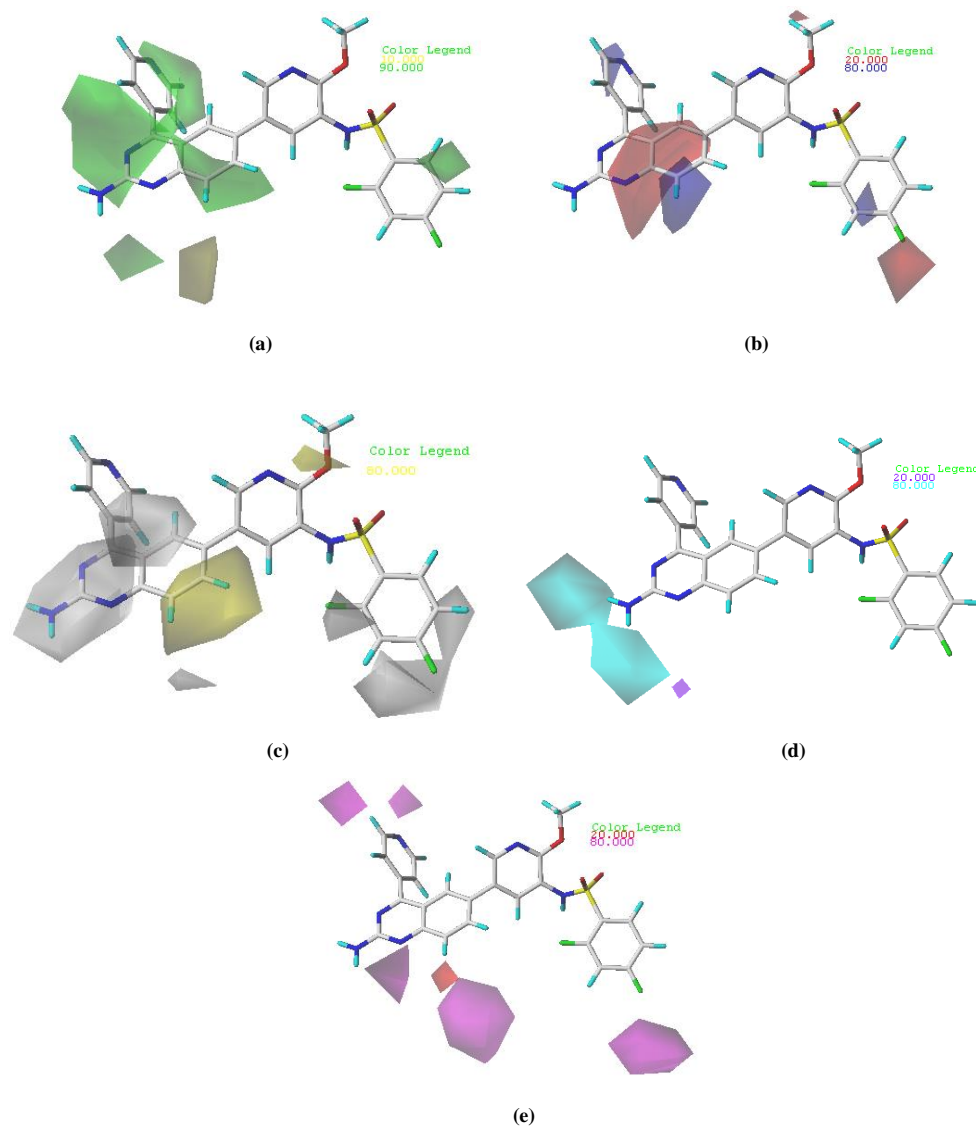


Fig. 6. (a) Steric contour maps of CoMSIA; (b) Electrostatic contour maps of CoMSIA; (c) Hydrophobic contour maps of CoMSIA: favored (yellow) and disfavored (grey); (d) Hydrogen bond donor contour maps of CoMSIA: favored (cyan) and disfavored (purple); (e) Hydrogen bond acceptor contour maps of CoMSIA: favored (magenta) and disfavored (red)

The electrostatic contour map of the CoMSIA model was displayed in Fig. 6b. A small area of red contour was located around the R_2 , indicating that the electronegative group was beneficial to the biological activity. It could be interpreted by the fact that compound **41** ($pIC_{50} = 8.66$) with chlorine atom had higher activity than compound **42** ($pIC_{50} = 8.03$) with the methyl group. A medium blue contour occurring around the

8'-site of quinazoline ring at R_1 of compound **8** indicated that compounds with electropositive groups at this site would have better biological activity. The biological activity of compound **4** ($pIC_{50} = 10.02$) with the quinazoline ring was higher than that of compound **5** ($pIC_{50} = 7.29$) with the pyrido[2,3-d]pyrimidine ring.

The CoMSIA contour map of hydrophobic contribution is

described in Fig. 6c. In this figure, the yellow (hydrophobic favorable) and white (hydrophobic unfavorable) contours represented 80% and 20% level contributions, respectively. A large white contour covered around the -NH₂ group at R₁ of compound **8**, indicating the presence of a hydrophilic group was good for the biological activity. Compound **7** (pIC_{50} = 7.45) with -NH₂ group was more active than compound **5** (pIC_{50} = 7.29) without such group.

In Fig. 6d, the cyan and purple contour maps indicated favorable and unfavorable H-bond donor groups, representing 80% and 20% level contributions, respectively. A medium cyan contour occurring near the -NH₂ group at R₁ of compound **8** indicated that compounds with H-bond donor substituent at this site preferred to produce higher PI3K α inhibitory activity. Compound **8** (pIC_{50} = 10.15) with -NH₂ group was more active than compound **4** (pIC_{50} = 10.02)

without this group.

As shown in Fig. 6e, the hydrogen bond acceptor field of the CoMSIA model was represented by magenta (hydrogen bond acceptor favorable) and red (hydrogen bond acceptor unfavorable), representing 80% and 20% level contributions, respectively. The small red contours near the 8'-site of quinazoline ring at R₁ of compound **8** suggested that the introduction of hydrogen bond acceptor substituents to these regions would decrease activity. Compound **1** (pIC_{50} = 10.00) with -C at the 8'-site of the quinoline ring was more active than compound **2** (pIC_{50} = 7.46) with -N at the same site of the same ring.

In conclusion, the above mentioned contour analysis of CoMFA and CoMSIA are summarized in Fig. 7, which provided effective help for the future design of new PI3K α inhibitors.

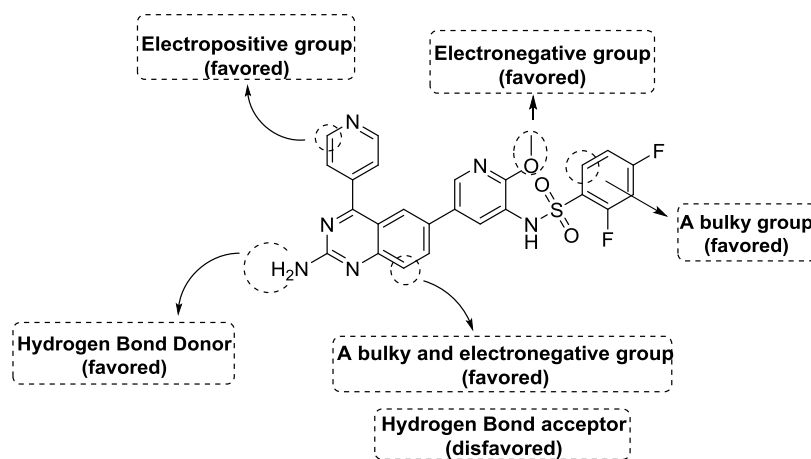


Fig. 7. Structural modification tips derived from 3D-QSAR studies

3.3 Molecular docking results and analysis

Docking studies revealed the interaction of selected ligands with target proteins, allowing us to understand the 3D-QSAR models. In this study, in order to explore the binding environment in which the ligand interacts within the 4ykn, docking studies were performed on compound **8** as the template.

As shown in Fig. 4, template compound **8** was docked in the binding cavity of the 4ykn with five H-bonds. The hydrogen bond distances observed are 2.27 Å (Glu1007 -C=O...H-HN-). The 1'-site nitrogen atom of quinazoline ring also acted as a hydrogen bond acceptor to form a hydrogen bond with the Val1009 (-N...H-, 2.24 Å). The nitrogen atom of the public skeleton's pyridine ring formed two hydrogen bonds with -NH₂ group of Arg928 (-N...H-, 2.12 Å, -N...H-, 2.97 Å). The hydrogen atom of the

sulfonylamino group interacted through H-bonding with -C=O group of Gln1017 (-C=O...H-, 2.24 Å). All the above results indicated that the binding pocket was appropriate for the study of PI3K α inhibitors.

3.4 Molecular dynamics simulation results and analysis

In this study, a 10 ns MD simulation was performed on a complex of compound **8** docked to the PI3K α protein. As shown in Fig. 8a, the root mean square deviation (RMSD) of the skeleton atom of protein PI3K α changed with time. The RMSD of PI3K α and compound **8** kept stable at about 3.6 and 4.0 Å. The superposition of the stable structure in all MD simulations (following 10 ns) and the initial docked structure is shown in Figs. 8b and 8c. After MD simulation, the interaction between compound **8** and the receptor was analyzed to explore the similarity and difference between molecular docking and MD simulation. From the most stable

structure extracted from the MD simulation, the model also revealed five hydrogen bonds formed between compound **8** and PI3K α (Fig. 9). An intramolecular H-bond ($\text{-F}\cdots\text{HN-}$, 2.24 Å) was built between the fluorine atom and -NH group. The sulfonyl group had formed two H-bonds with Arg928 ($\text{-S=O}\cdots\text{H-}$, 2.15 Å, $\text{-S=O}\cdots\text{H-}$, 2.85 Å). The 1'-site nitrogen atom of quinazoline ring interacted through H-bonding with -NH group of Val1009 ($\text{-N}\cdots\text{H-}$, 2.07 Å). The hydrogen atom

of amino group interacted through H-bonding with -C=O group of Glu1007 ($\text{-C=O}\cdots\text{H-}$, 1.80 Å). In general, the length of each hydrogen bond in this result was shorter than that in the docking model. Therefore, the conformation obtained after MD simulation was more stable than the docked conformation. MD simulation was performed in a more realistic environment, and much closer to physiological conditions.

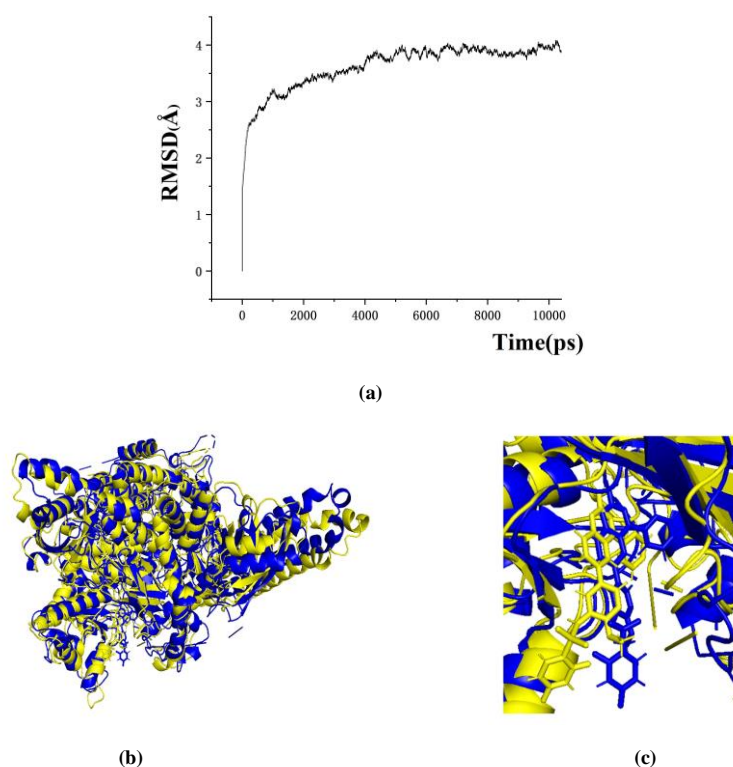


Fig. 8. MD simulation results. (a) Plot of the RMSD of docked complex versus MD simulation time in the MD-simulated structures; (b) and (c) View of superimposed backbone atoms of the lowest energy structure of the MD simulation (blue) and the initial structure (yellow) for compound **8**-PI3K α complex. Compound **8** was represented as carbon-chain in yellow for the initial complex and carbon-chain in blue for the lowest energy complex

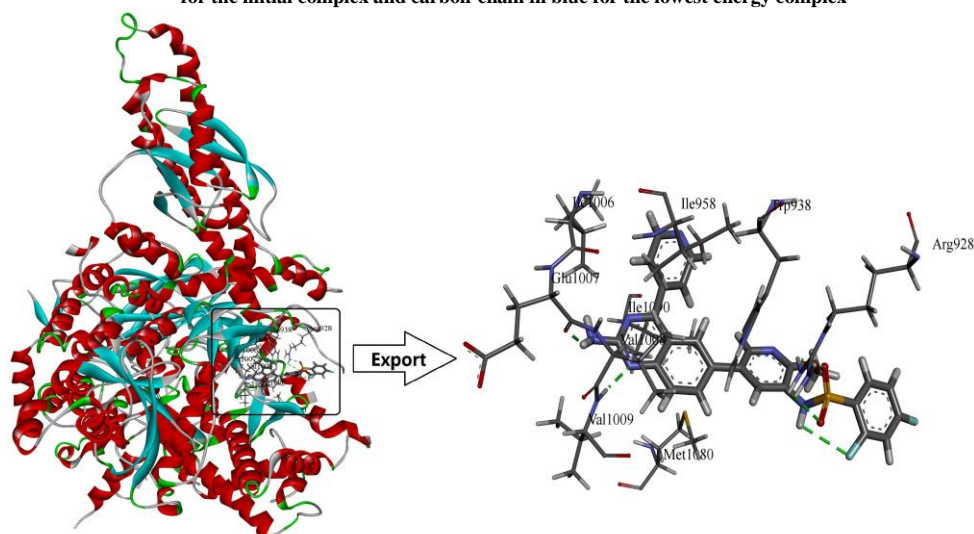


Fig. 9. Plot of the MD-simulated structure of the binding site with ligand. Compound **8** was in the active site of PI3K α . H-bonds were shown as dotted green lines; Active site amino acid residues were represented as sticks; The inhibitors were shown as stick and ball model

3.5 Design and prediction

On the basis of the above mentioned analysis, five novel structures (compounds **66** ~ **70**) with -CH₃/-CH₂CH₃/-CH₂CH₂CH₃ for R₄, -CH₃ for R₅, -OCH₃ for R₆, and -CH₃ for R₇/R₈ were designed based on the template compound **8** (Fig. 10). In addition to the 3D-QSAR of **66**~**70**, five

molecules **71**~**75** with potent PI3K α inhibitory activity, synthesized by Song and his colleagues^[42], were employed to validate the reliability of this 3D-QSAR model. The experimental activities and predicted values are shown in Table 4.

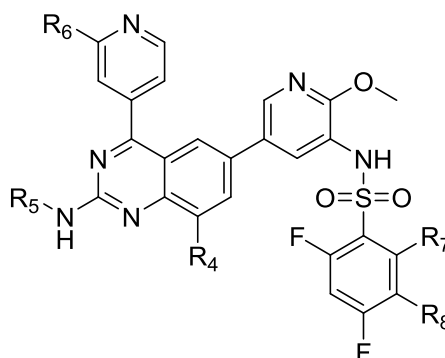


Fig. 10. Structure of the designed compounds based on the template compound 8

Table 4. Structures of the Compounds with Experimental and Predicted Activity

Compd.	Structure	Actual	CoMFA		CoMSIA	
			Pred.	Res.	Pred.	Res.
66		-	10.686	-	10.335	-
67		-	10.633	-	10.209	-
68		-	10.541	-	10.167	-
69		-	10.318	-	10.361	-
70		-	10.281	-	10.245	-
71		8.850	8.975	0.125	9.374	0.524

To be continued

72		8.800	9.237	0.437	9.701	0.901
73		9.040	9.303	0.263	9.413	0.373
74		9.200	9.980	0.780	9.474	0.274
75		8.890	8.885	0.005	9.697	0.807

The results of CoMFA and CoMSIA models showed that the pIC_{50} values of these compounds were close to the experimental activities, which further verify the superiority of the models. Compounds **66** ~ **70** had higher predicted activities than the template compound **8** in the 3D-QSAR models; it was indicated that these designed compounds might become potential candidates as PI3K α inhibitors.

4 CONCLUSION

In this work, the binding modes between 3-phenylsulfonylaminopyridine derivatives and PI3K α were studied by the

integration of 3D-QSAR, molecular docking, and molecular dynamics simulations. The contour maps explained the relationship between chemical structures and bioactivities. The molecular docking and molecular dynamics results implied that relevant hydrogen bonds were very important for ligand-receptor binding. The results from 3D-QSAR models, molecular docking, and MD simulation illustrated the chemical structure characteristics of 3-phenylsulfonylaminopyridine derivatives, which provided important guidance for further development of potent PI3K α inhibitors with improved biological activity.

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