European Journal of Medicinal Chemistry 95 (2015) 424-434

Contents lists available at ScienceDirect

European Journal of Medicinal Chemistry

journal homepage: http://www.elsevier.com/locate/ejmech

Original article

Discovery of *N*-benzoxazol-5-yl-pyrazole-4-carboxamides as nanomolar SQR inhibitors



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ARTICLE INFO

Article history: Received 16 February 2015 Received in revised form 19 March 2015 Accepted 26 March 2015 Available online 28 March 2015

Keywords: Succinate—ubiquinone oxidoreductase Molecular design Computational simulations MM/PBSA Pyrazole-carboxamides

ABSTRACT

Succinate—ubiquinone oxidoreductase (SQR, EC 1.3.5.1, complex II), an essential component of cellular respiratory chain and tricarboxylic acid (or Krebs) cycle, has been identified as one of the most significant targets for pharmaceutical and agrochemical. Herein, with the aim of discovery of new antibacterial lead structure, a series of *N*-benzoxazol-5-yl-pyrazole-4-carboxamides were designed, synthesized, and evaluated for their SQR inhibitory effects. Very promisingly, one candidate ($K_i = 11$ nM, porcine SQR) was successfully identified as the most potent synthetic SQR inhibitor so far. The further inhibitory kinetics studies revealed that the candidate is non-competitive with respect to the substrate cytochrome *c* and DCIP. Computational simulations revealed that the titled compounds have formed hydrogen bond with D_Y91 and B_W173 and the pyrazole ring formed cation– π interaction with C_R46. In addition, in R¹ position, –CHF₂ group has increased the binding affinity and decreased the entropy contribution, while –CF₃ group displayed completely opposite effect when bound with SQR. The results of the present work showed that *N*-benzoxazol-5-yl-pyrazole-4-carboxamide is a new scaffold for discovery of SQR inhibitors and worth further study.

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1. Introduction

Succinate—ubiquinone oxidoreductase (SQR, EC 1.3.5.1, complex II) is an essential component of cellular respiratory chain and tricarboxylic acid (or Krebs) cycle. The function of SQR is to catalyse the oxidation of succinate into fumarate, and coupled to the reduction of ubiquinone into ubiquinol [1–5]. Due to its critical role in the life cycle, SQR has been identified as one of the most significant targets for the development of pharmaceuticals and agrochemicals. For example, several recent studies have shown that mutant forms of SQR are responsible for causing diverse physiological disorders [6,7], leading to the hypothesis that chain B, C, and D (the crystal structure of SQR contains A, B, C, and D chains) are tumour suppressors, and that SQR is a critical component of the

oxygen-sensing system [8]. A recent study reported that the 8aminoquinoline analogue sitamaquine (SQ), an oral antileishmanial drug currently undergoing phase II clinical trials for the treatment of visceral leishmaniasis, caused a dose-dependent inhibition of succinate dehydrogenase of the respiratory chain in digitonin-permeabilized promastigotes, together with a drop in intracellular ATP levels and a decrease of the mitochondrial electrochemical potential [9]. In addition, in the agricultural field, over 18 SQR inhibitors have been successfully developed as agricultural fungicides, including pyrazole-4-carboxamides, oxathiincarboxamides, phenyl-benzamides, pyridine-carboxamides, thiazole-carboxamides, phenyl-oxo-ethyl thiophene amide, pyridinylethyl benzamides and furan-carboxamides [10-12]. Apart from the synthetic SQR inhibitors, Satoshi et al. reported that the natural product Atpenin A5 is a very potent SQR inhibitor, with the IC₅₀ 3.6 nM against bovine heart SQR and 3.7 nM against rat liver SOR [13].

Very recently, by integrating the molecular docking, molecular dynamics simulation and molecular mechanics/Poisson-Boltzmann surface area (MM/PBSA) calculations methods, we have



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successfully established the binding mode of ten commercial carboxamide fungicides for the first time [11]. The acid moiety of carboxamide fungicides inserts into the Q-site of SQR, forming vander-Waals (VDW) interactions with C_R46, C_S42, B_1218, and B_P169, while the amine moiety extending toward the mouth of the Q-site, forming VDW interactions with C_W35, C_143, and C_130. The carbonyl oxygen atom of the carboxamide forms hydrogen bond with B_W173 and D_Y91. The uncovered interaction mechanism at atomic level suggested that, optimizing the important hydrogen bond interaction and improving the VDW interactions between side-chain of inhibitors and key residues in the Q-site should be an effective way to design and discover new SQR inhibitors with higher potency.

Many researches had proved that benzoxazol was an important fragment in both medicinal and agricultural chemistry. For example, fenoxaprop-P-ethyl and metamifop have been used as commercial herbicides for many years [14]. Furthermore, the benzoxazol derivatives are known to exhibit a wide range of biological activities, such as melatonin receptor agonists [15], antimicrobial [16] and anti-measles virus activities [17]. Meanwhile, pyrazole-4-carboxamides have gained a considerable attention in the field of pesticide chemistry in recent years. For example, André S et al. had reported that this type of inhibitor showed some insect activity [18]. So far, eight pyrazole-4carboxamide derivatives have been introduced into the market as agricultural fungicides [10,19] (Fig. 1). Based on the above consideration, we proposed that pyrazole-carboxamidebenzoxazol hybrid (7a.b-17a.b) (Fig. 2) would be an new scaffold of SOR inhibitor. According the above-mentioned interaction mechanism, the benzoxadzole ring was further prolonged with substituted benzylthio group in order to increase the VDW interaction between ligand and the corresponding residues in the binding pocket. As we expected, the newly designed N-(2-(benzylthio)benzoxazol-5-yl)-pyrazole-4-carboxamides indeed showed excellent inhibitory activity against porcine SCR with the IC_{50} values ranging from 0.56 to 0.038 μ M, significantly higher than penthiopyrad, a commercial fungicide selected as a positive control. Among these inhibitors, compound 13b was identified as the most promising candidate with a K_i value of 11 nM against porcine SQR. The further inhibitory kinetics studies against porcine SCR (succinate-cytochrome c reductase) and SQR revealed that compound 13b and penthiopyrad are both noncompetitive inhibitors with respect to the substrate cytochrome c and dichlorophenolindophenol (DCIP). The binding mode of the titled compounds was further studied by molecular docking, molecular dynamics simulations and MM/PBSA calculations. The present work showed that N-benzoxazol-5-yl-pyrazole-4carboxamide is a new scaffold for discovery of SQR inhibitors and worth further study.

2. Results and discussion

2.1. Chemistry

Title compounds **7a,b**–**17a,b** were prepared by the route shown in Scheme 1. 2-Amino-4-nitrophenol (1) was treated with potassium ethyl xanthate, (2), in ethanol to afford 5-nitrobenzo[*d*]xazol-2-thiol (3), which was reacted with commercially available benzyl chlorides or bromides *via* an S_N2 reaction to obtain the key intermediates **4a**–**k** in good yields. The nitrobenzoxazols **4a**–**k** were refluxed in ethanol/H₂O with powered iron in the presence of NH₄Cl to provide amines **5a**–**k**, which were used without purification. Finally, compounds **5a**–**k** were then subjected to an amide formation reaction with pyrazole carboxylic acids **6** by using EDCl as the coupling reagent to furnish the final products **7**–**17a/b** in 45–80% yield. Structures of all the target compounds were characterized by ¹H NMR, ¹³C NMR and HRMS spectral data.

2.2. Enzyme inhibition

Succinate—cytochrome *c* reductase (SCR) is the mixture of respiratory complex II and complex III, which was also deemed to form complex II—complex III super complexes. Complex II (SQR) firstly passes electrons from succinate to ubiquinone, and then complex III passes electrons from reduced ubiquinone to cytochrome *c*. The activity of SQR in SCR was selectively determined by using succinate and dichlorophenolindophenol (DCIP) as substrates, and the activity of only complex III in SCR was determined by using decylubiquinol (DBH₂) and cytochrome *c* as substrates, whereas the overall activity of SCR (both complex II and complex III) was determined using succinate and cytochrome *c* as substrates [11].

The enzymatic inhibition of all newly synthesized compounds 7–17 against porcine SCR was assayed and the determined IC_{50} values against porcine SCR were listed in Table 1. For comparison, the inhibitory activity of the corresponding pyrazole-4carboxamide commercial fungicide penthiopyrad was also presented. The results indicated that all of the compounds exhibited no effect on the activity of complex III (data not show), but markedly inhibited the activity of SCR. As shown in Table 1, 22 new synthesized compounds showed a significant improvement of SCR inhibitory activity than penthiopyrad, which indicated that the introduction of benzoxazol with substituted benzylthio group was reasonable. Remarkably, the analogues 7a-17a bearing the R^1 group of -CF₃ always displayed lower activity than **7b**-**17b** with -CHF₂. For instance, the IC₅₀ value against SCR of **13b** ($R^1 = -CHF_2$) was 0.038 μ M, while that of **13a** (R¹ = -CF₃) was 0.088 μ M. In addition, other compounds had also displayed the same phenomenon, suggesting that the -CHF₂ group is critical to maintain high potency and its molecular mechanism would be discussed in the



Fig. 1. Structures of pyrazole-4-carboxamides SQR inhibitors.



Fig. 2. Design strategy of the title compounds.

following section. Obviously, the inhibitory activities were varied with regard to the different groups at the 3-position and/or 4position of phenyl. It seemed that introducing electronwithdrawing group at phenyl 4-position produced a higher SCR inhibition effect than 3-position. Taking the chlorine substituent as an example, compounds **9a** (4-Cl, $IC_{50} = 0.111 \ \mu M$) and **9b** (4-Cl, $IC_{50} = 0.057 \,\mu\text{M}$) showed higher activity than compounds 15a (3-Cl, $IC_{50}=$ 0.149 $\mu M)$ and 15b (3-Cl, $IC_{50}=$ 0.082 $\mu M).$ Compounds 8a(4-F, $IC_{50}=$ 0.210 $\mu M)$ and $\boldsymbol{8b}$ (4-F, $IC_{50}=$ 0.101 $\mu M)$ also showed higher activity than 11a (3-F, IC_{50} = 0.418 $\mu M)$ and 11b (3-F, $IC_{50} = 0.244 \ \mu$ M). In addition, the electron-withdrawing R² groups had a favourable effect on the inhibitory activity than electrondonating group, except -CN. For example, compound **7** (4-CF₃) and 8 (4-F) showed higher activity than 14 (4-OMe) and 16 (4-Me), respectively. Compared with the single fluorine substituted derivatives (e.g. compounds 8 and 11), compounds 17 with 3,4-di-F at R² position displayed increased inhibitory activity upon porcine SCR, indicating that the disubstituted group at the phenyl might be more favourable for the activity than mono substituted group. One possibility for this phenomenon is that R¹ and R² would affect the bioactive conformation of inhibitors.

Kinetic properties are of great importance for understanding the molecular mechanism of SQR function. We therefore selected **13b** as an example to study the mechanism of SCR and SQR inhibition. As shown in Fig. 3A, double-reciprocal plots showed non-competitive inhibition of **13b** with respect to cytochrome *c*. Furthermore, we examined the effect of **13b** on the reactions of the SCR pathway catalysed by SQR. We determined the kinetics of SQR activity with respect to the substrate DCIP in the absence and presence of **13b**. As shown in Fig. 3B, **13b** was a non-competitive

inhibitor against SQR with respect to the substrate DCIP. These results indicate that **13b** would bind to the Q-site of SQR, consistent with our previous study [11] that the carboxamide inhibitors bind to the Q-site of SQR. A similar result was obtained for commercial fungicide penthiopyrad. As shown in Fig. 3C and D, penthiopyrad is a non-competitive inhibitor with respect to cytochrome c ($K_i = 1.393 \mu$ M) and DCIP ($K_i = 0.327 \mu$ M).

Next, we compared the inhibitory activities of both of compound against porcine SCR and SQR (Table 2 and Fig. 3). Compound 13b and penthiopyrad exhibited about 4-fold greater inhibition against the porcine SQR than SCR, as indicated by the K_i values. We also found that compound **13b** and penthiopyrad nearly did not show inhibitory effects against complex III at 10 µM concentrations (the inhibition rate was about 13% for 13b and lower than 10% for penthiopyrad). Furthermore, we also measured the IC₅₀ values of 13b and penthiopyrad against porcine SQR (Supporting information Fig. 1S). The difference in IC_{50} values was still very small. All these results indicated that the portion of complex III in SCR system did not display effect upon the SQR assay. In addition, 13b should have the same mechanism of biological action with commercial fungicide. As shown in Table 2, the K_i value of **13b** was 0.043 µM against porcine SCR and 0.011 µM against porcine SQR, which was about 30-fold higher activity than penthiopyrad. Therefore, to our knowledge, compound 13b is so far the most potent synthetic inhibitor of SQR.

2.3. The binding free energy calculation

To understand the structure—activity relationship at the atomic level, we performed the molecular docking and binding free energy



Scheme 1. Synthesis of compounds 7–17a/b. Reagents and conditions: (*a*) EtOH, reflux; (*b*) substituted benzyl chloride/bromide, K₂CO₃, acetone, reflux; (*c*) EtOH/H₂O, NH₄Cl, reflux, addition of Fe; (*d*) carboxylic acid **6**, EDCl, DMAP, CH₂Cl₂, r. t.

Table 1

Inhibitory activities and the binding free energy of compounds 7–17 against porcine SCR.



No.	\mathbb{R}^1	R ²	$\Delta E_{\rm ele}$	ΔE_{vdw}	$\Delta G_{\rm np}$	$\triangle G_{\text{pol}}$	ΔH	$-T\Delta S$	ΔG_{cal}	ΔG_{\exp}^{a}	IC ₅₀ (μM)
7a	CF ₃	4-CF ₃	-19.32	-45.72	-5.37	43.96	-26.44	10.61	-15.83	-9.62	0.083 ± 0.001
7b	CHF ₂	4-CF3	-24.21	-44.94	-5.31	46.54	-27.91	11.47	-16.44	-10.07	0.039 ± 0.001
8a	CF ₃	4-F	-19.98	-44.19	-5.22	44.53	-24.86	10.20	-14.66	-9.07	0.210 ± 0.019
8b	CHF ₂	4-F	-23.36	-43.23	-5.15	45.41	-26.33	10.94	-15.39	-9.51	0.101 ± 0.012
9a	CF ₃	4-Cl	-18.59	-44.53	-5.24	42.92	-25.44	10.43	-15.01	-9.45	0.111 ± 0.001
9b	CHF ₂	4-Cl	-22.67	-44.19	-5.20	44.83	-27.23	11.10	-16.13	-9.84	0.057 ± 0.001
10a	CF ₃	4-CN	-22.99	-44.64	-5.40	48.90	-24.13	11.23	-12.90	-8.49	0.562 ± 0.011
10b	CHF ₂	4-CN	-21.97	-43.56	-5.04	44.56	-26.01	12.39	-13.62	-8.70	0.397 ± 0.012
11a	CF ₃	3-F	-18.20	-43.83	-5.21	42.45	-24.80	10.82	-13.98	-8.67	0.418 ± 0.011
11b	CHF ₂	3-F	-21.93	-43.48	-5.14	44.51	-26.03	11.79	-14.24	-8.99	0.244 ± 0.012
12a	CF ₃	3-Br	-22.49	-43.97	-5.19	45.53	-26.12	10.54	-15.58	-9.41	0.119 ± 0.001
12b	CHF ₂	3-Br	-24.07	-45.98	-5.24	48.13	-27.17	11.14	-16.03	-9.79	0.062 ± 0.001
13a	CF ₃	$4-OCF_3$	-17.84	-47.78	-5.44	45.76	-25.29	9.70	-15.59	-9.59	0.088 ± 0.010
13b	CHF ₂	$4-OCF_3$	-26.86	-43.74	-5.34	47.52	-28.41	11.46	-16.95	-10.08	0.038 ± 0.001
14a	CF ₃	4-OMe	-20.67	-45.38	-5.40	45.73	-25.73	11.50	-14.23	-8.90	0.284 ± 0.012
14b	CHF ₂	4-OMe	-23.03	-45.88	-5.35	46.31	-27.95	13.82	-14.13	-9.08	0.208 ± 0.013
15a	CF ₃	3-Cl	-15.11	-43.49	-5.19	42.37	-21.41	7.00	-14.41	-9.28	0.149 ± 0.015
15b	CHF ₂	3-Cl	-23.16	-45.78	-5.20	47.73	-26.41	10.70	-15.71	-9.63	0.082 ± 0.001
16a	CF ₃	4-Me	-23.31	-43.28	-5.22	47.93	-23.88	10.04	-13.84	-8.93	0.269 ± 0.012
16b	CHF ₂	4-Me	-25.68	-44.44	-5.21	48.49	-26.85	12.26	-14.59	-9.05	0.216 ± 0.010
17a	CF ₃	3,4-di-F	-14.77	-45.63	-5.25	42.01	-23.65	8.50	-15.15	-9.36	0.130 ± 0.012
17b	CHF ₂	3,4-di-F	-22.21	-41.35	-4.86	42.92	-25.49	10.17	-15.32	-9.51	0.100 ± 0.001
Penthiopyrad			-13.84	-41.91	-5.10	34.28	-26.57	13.54	-13.03	-7.99	1.321 ± 0.11

^a $\Delta G_{exp} = -RTLnIC_{50}$.



Fig. 3. Kinetic analysis of inhibition by **13b** (A for SCR and B for SQR) and penthiopyrad (C for SCR and D for SQR) against porcine SCR and SQR. The inhibition of porcine SCR by (A) **13b** (1, 0 nM; 2, 10 nM; 3, 20 nM; 4, 30 nM and 5, 50 nM), (C) penthiopyrad (1, 0 nM; 2, 300 nM; 3, 500 nM; 4, 1000 nM and 5, 2000 nM). Each reaction mixture contains 100 mM PBS (pH 7.4), 0.3 mM EDTA, 20 mM succinate, 0.1 nM enzyme, 0.29–10.36 μ M cytochrome *c* and the indicated penthiopyrad or **13b**. *K*₁ was estimated to be 0.043 \pm 0.002 μ M for **13b** and 1.393 \pm 0.087 μ M for penthiopyrad by assuming non-competitive inhibition. The inhibition of porcine SQR by (B)**13b** (1, 0 nM; 2, 3 nM; 3, 5 nM; 4, 10 nM and 5, 20 nM), (D) penthiopyrad (1, 0 nM; 2, 100 nM; 3, 200 nM; 4, 300 nM and 5, 500 nM). Each reaction mixture contains 100 mM PBS (pH 7.4), 0.3 mM EDTA, 20 mM succinate, 2 nM SCR, 1.18–4.122 μ M DCIP and the indicated amount of penthiopyrad or **13b**. *K*₁ was estimated to be 0.011 \pm 0.003 μ M for **13b** and 0.327 \pm 0.0092 μ M for penthiopyrad by assuming non-competitive inhibition.

Table 2

The inhibitory effect of some inhibitors against porcine SCR and SQR.

Inhibitor	SCR (succinate-cy	yt. c system 23 °C)		SQR (DCIP-system 23 °C)			
	IC ₅₀ (μM)	Inhibition type (with cyt. <i>c</i>)	<i>K</i> _i (μM)	IC ₅₀ (μM)	Inhibition type (with DCIP)	$K_{\rm i}$ (μ M)	
13b Penthiopyrad	$\begin{array}{c} 0.038 \pm 0.001 \\ 1.321 \pm 0.110 \end{array}$	Non-competitive Non-competitive	$\begin{array}{c} 0.043 \pm 0.002 \\ 1.3931 \pm 0.087 \end{array}$	$\begin{array}{c} 0.011 \pm 0.0011 \\ 0.527 \pm 0.111 \end{array}$	Non-competitive Non-competitive	$\begin{array}{c} 0.011 \pm 0.0003 \\ 0.327 \pm 0.0092 \end{array}$	

calculations for all newly synthesized compounds. As summarized in Table 1, the calculated binding free energies (ΔG_{cal}) range from -12.90 kcal/mol to -16.95 kcal/mol, whereas the experimental binding free energies (ΔG_{exp}) range from -8.49 kcal/mol to -10.08 kcal/mol. Obviously, the MM/PBSA calculations systematically overestimated the absolute binding affinities of the ligand toward SOR. However, the relative order of the calculated binding affinities of the compounds is qualitatively consistent with the order of potency. A good linear correlation between ΔG_{cal} and ΔG_{exp} was obtained with a correlation coefficient of $R^2 = 0.93$ (Fig. 4), confirming the reliability of the computational models constructed in this study. At the same time, the correlation coefficients between ΔG_{exp} and individual energy terms are 0.16 for sum of the electrostatic energies (ΔE_{ele}), 0.12 for sum of the VDW energies (ΔE_{vdw}), 0.03 for nonpolar solvation energies (ΔG_{np}), 0.18 for polar solvation energies (ΔG_{pol}), 0.13 for enthalpy contribution (ΔH), and 0.10 for entropy compensation $(-T\Delta S)$. The results of the individual energy terms suggest that, although the enthalpy contribution (ΔH) is important for binding, the binding free energy arises from a more complex interplay among these components. Indeed, the ELE (ranging from -14.77 to -26.86 kcal/mol) and VDW (ranging from -41.35 to -47.78 kcal/mol) energies are the larger favourable components of the binding free energy for each complex. This result indicates that the affinities of these inhibitors for SQR are dominated by electronic interaction and shape complementarily.

As shown in Table 1, compound **13b** was the most potent inhibitor with the K_i value of 0.011 μ M against porcine SQR. The simulated binding mode **13b** (Fig. 5A) showed that the carbonyl oxygen atom formed hydrogen bond with the residue of D_Y91 and B_W173 and pyrazole ring formed cation- π interaction with the residue of C_R46, which were nearly the same as the commercial carboxamide fungicides obtained in our previous work [11]. In addition, the hydrogen atom in –CHF₂ group also formed hydrogen bond with the residue of D_D90 and the phenyl ring formed hydrophobic interaction with D_Y91. Other compounds also displayed the similar binding mode. As shown in Table 1, the compounds **7b**–**17b** always showed higher activities against SCR than **7a–17a**.



Fig. 4. Correlation between the calculated and experimental binding free energy.

In order to illustrate the phenomena, the binding modes of **7b–17b** were superimposed and we found that there were about two space conformations for the hydrogen atom in -CHF₂ group in R¹ position. One was the same as **13b**, in which the hydrogen atom in -CHF₂ group formed hydrogen bond with D_D90. The other was that the hydrogen atom in $-CHF_2$ group pointed to carbonyl oxygen atom and then formed intramolecular hydrogen bond with it (Fig. 5B). One possible reason for this phenomenon might be due to the group effect in \mathbb{R}^2 position. The $-CHF_2$ in **7b**, **8b**, **10b**, **12b**, **13b**, 15b, 16b and 17b (Fig. 5B) displayed the same conformation with 13b, and others (including 9b, 11b, and 14b, Fig. 5C) took on another conformation. Therefore, when replacing the $-CHF_2$ group at R^1 position with -CF₃, 7a-17a compounds would lose hydrogen bond with D_D90 or intramolecular hydrogen bond with carbonyl oxygen atom, which contributed greatly to the potency of SQR inhibitors (Fig. 5D).

Based on above analysis, it seemed that $-CF_3$ group in R¹ position would lead to unfavourable interaction when bound with SQR. From the energy component analysis (Table 1), we concluded that the compounds **7b**–**17b** always showed more favourable electronic energy (ΔE_{ele}) and binding affinity (ΔH) bound with SQR than **7a**–**17a**. On the contrary, the entropy compensation ($-T\Delta S$) in **7b**–**17b** was less favourable than **7a**–**17a**. All these results indicated that, in R¹ position, $-CHF_2$ group would increase the binding affinity and decrease the entropy contribution when bound with SQR, while $-CF_3$ group displayed completely opposite effect.

At the same time, we also found that the substituted phenyl ring showed different conformations when bound with SQR. This might be due to rotatable single bonds between benzoxazol and phenyl ring. For example (Fig. 5C), 4-Cl substituted phenyl in **9b** would form edge-to-edge π - π interaction with C_W35, and 3-F substituted phenyl in **11b** would point to another direction forming hydrophobic interaction with C_I30 and C_T31 (data not show).

When the R² group changed from 4-OCF₃ to 4-CN, 4-OMe, 4-Me or 3-F, compounds would show less activity, such as 10a and 10b, 14a and 14b, 16a and 16b. In order to understand the molecular basis of this phenomenon, the interaction energy between inhibitor and key residues was calculated via Anal module. For instance, the interaction energy, including electronic and VDW energy, between ligands with B_W173 and D_Y91 respective are -9.83 and -8.98 kcal/mol for **10a** ($R^2 = 4$ -CN), -10.50 and -9.30 kcal/mol for **10b** ($R^2 = 4$ -CN), -11.99 and -9.60 kcal/mol for **14a** ($R^2 = 4$ -OMe), -8.38 and -5.79 kcal/mol for **14b** ($R^2 = 4$ -OMe), -12.30and -10.95 kcal/mol for **16a** ($R^2 = 4$ -Me), -15.09 and -12.08 kcal/ mol for **16b** ($R^2 = 4$ -Me), -14.71 and -12.03 kcal/mol for **13b** $(R^2 = 4$ -OCF₃), respectively. Hence, excepting **16b**, the replacement of 4-OCF₃ with 4-CN, 4-OMe, 4-Me or 3-F may result in the lower interaction energy with key residues and then less binding free energy with SQR. As for 16b, less favourable entropy contribution $(-T\Delta S)$ might be used to explain its lower activity.

3. Conclusions

In summary, a series of novel *N*-(2-(benzylthio)benzoxazol-5yl)-pyrazole-4-carboxamide **7**–**17** were designed and synthesized as potent SQR inhibitors, among which 3-(difluoromethyl)-1-

Fig. 5. (A) The binding mode of **13b**. The blue dashed line represent the hydrogen bond between **13b** and key residues; (B) The binding mode overlay of **7b** (ice green), **8b** (dark blue), **10b** (grey), **12b** (yellow), **15b** (pink), **16b** (ice blue), and **17b** (dark red). For clarity, only hydrogen bond between **7b** and key residues was shown as blue dashed line; (C) The binding mode overlay of **9b** (brown), **11b** (grey), and **14b** (blue). For clarity, only hydrogen bond between **9b** and key residues was shown as blue dash line and the intramolecule hydrogen bond was coloured by yellow; (D) The binding mode of **13a**. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

methyl-N-(2-((4-(trifluoromethoxy)benzyl)thio)-benzoxazol-5vl)-1H-pyrazole-4-carboxamide **13b** was identified as the most potent candidate with K_i value of 11 nM against porcine SOR. The further inhibitory kinetics studies showed that 13b is a noncompetitive inhibitor with respect to substrate cytochrome *c* and DCIP. In addition, the results of computational simulations revealed that the title compound binds with the Q-site of SQR, forming hydrogen-bonds with D_Y91 and B_W173 and cation- π interaction between its pyrazole ring and C_R46. Meanwhile, the –CHF₂ group at R¹ position formed additional hydrogen bond with D_D90 and/or intramolecular hydrogen bond with carbonyl oxygen, contributing significantly to the potency of SQR inhibitors. According to the results of energy component analysis, we concluded that the -CHF₂ group at R¹ position would increase the binding affinity and decrease the entropy contribution, while -CF₃ group at this position took on opposite effect. Therefore, how to balance the binding affinity and entropy contribution would be the primary concern in our future work.

4. Materials and methods

4.1. Reagents and equipment

Unless otherwise noted, all chemical and biological reagents were commercially available and treated with standard methods before use. Solvents were dried in a routine way and redistilled before use. ¹H NMR and ¹³C NMR spectra were recorded on a VARIAN Mercury-Plus 600 or a 400 spectrometer in CDCl₃ or DMSO-*d*₆ with TMS as internal reference. Mass spectral data were obtained on a Thermo Fisher Mass platform DSQII by electrospray ionization (ESI-MS). High resolution mass spectra (HRMS) were acquired in positive mode on a WATERS MALDI SYNAPT G2 HDMS (MA, USA). Melting points were taken on a Büchi B-545 melting point apparatus and were uncorrected. All chemical yields were not optimized and generally represent the result of a single experiment.

4.2. Synthesis of the intermediate **3** [20]

A solution of 2-amino-4-nitrophenol (7.7 g, 50 mmol) in ethanol (100 mL) was heated to reflux, and potassium ethyl xanthate (8.4 g, 55 mmol) was added at reflux temperature. The resulting mixture was refluxed for 4 h and then it was allowed to cool to ambient temperature, then the solution was poured into water and aqueous hydrochloric acid was added. The resulting precipitate was collected by filtration, washed with water and dried to afford 16.5 g (84%) 5-nitrobenzoxazol-2-thiol.

4.3. General procedure for synthesis of the intermediate **4a**–**k** [21]

Potassium carbonate (6.0 mmol) and the corresponding halide derivative (5.5 mmol) were added to 5 mmol of stirred solution of intermediate **3** in acetone (50 mL). When the reaction was completed, as monitored by TLC detection, the reaction mixture was filtered and the solvent was removed under reduced pressure. The residue was purified by column chromatography on silica gel.

4.3.1. Data for 4a

Yellow solid; yield: 78%; mp 130–132 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (s, 1H), 8.24 (d, *J* = 9.0 Hz, 1H), 7.62–7.60 (m, 4H), 7.54 (d, *J* = 9.0 Hz, 1H), 4.61 (s, 2H); MS (EI) *m/z*: 354.12 (M)⁺.

4.3.2. Data for 4b

White solid; yield: 72%; mp 133–135 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, *J* = 2.4 Hz, 1H), 8.24 (dd, *J* = 9.0, 2.4 Hz, 1H), 7.54 (d, *J* = 9.0 Hz, 1H), 7.47 (dd, *J* = 8.4, 4.2 Hz, 2H), 7.06 (t, *J* = 9.0 Hz, 2H), 4.56 (s, 2H); MS (EI) *m/z*: 304.25 (M)⁺.

4.3.3. Data for 4c

White solid; yield: 73%; mp 132–133 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, *J* = 1.8 Hz, 1H), 8.24 (dd, *J* = 8.4, 1.8 Hz, 1H), 7.54 (d, *J* = 9.0 Hz, 1H), 7.43 (d, *J* = 9.6 Hz, 2H), 7.33 (s, 2H), 4.54 (s, 2H); MS (EI) *m*/*z*: 320.15 (M)⁺.

4.3.4. Data for 4d

White solid; yield: 75%; mp 160–162 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, *J* = 1.8 Hz, 1H), 8.25 (dd, *J* = 9.0, 2.4 Hz, 1H), 7.66 (d, *J* = 7.8 Hz, 2H), 7.63 (d, *J* = 8.4 Hz, 2H), 7.54 (d, *J* = 9.0 Hz, 1H), 4.59 (s, 2H); MS (EI) *m/z*: 311.16 (M)⁺.

4.3.5. Data for 4e

White solid; yield: 79%; mp 101–103 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, J = 1.8 Hz, 1H), 8.24 (dd, J = 9.0, 2.4 Hz, 1H), 7.54 (d, J = 9.0 Hz, 1H), 7.33 (d, J = 5.4 Hz, 1H), 7.25 (s, 1H), 7.21 (d, J = 9.6 Hz, 1H), 7.02(t, J = 8.4 Hz, 1H), 4.56 (s, 2H); MS (EI) m/z: 304.17 (M)⁺.

4.3.6. Data for **4f**

White solid; yield: 85%; mp 104–105 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, J = 1.8 Hz, 1H), 8.25(dd, J = 9.0, 2.4 Hz, 1H), 7.65 (s, 1H), 7.45 (dd, J = 8.4, 2.4 Hz, 2H), 7.26 (s, 1H), 7.24 (d, J = 7.8 Hz, 1H), 4.53 (s, 2H); MS (EI) m/z: 364.15 (M)⁺.

4.3.7. Data for 4g

White solid; yield: 68%; mp 126–128 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.52 (d, *J* = 2.4 Hz, 1H), 8.24 (dd, *J* = 9.0, 2.4 Hz, 1H), 7.44 (d, *J* = 9.0 Hz, 1H), 6.98 (d, *J* = 8.4 Hz, 2H), 6.88 (d, *J* = 9.0 Hz, 2H), 4.56 (s, 2H); MS (EI) *m/z*: 370.22 (M)⁺.

4.3.8. Data for 4h

White solid; yield: 76%; mp 135–137 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.49 (s, 1H), 8.23 (d, J = 8.4 Hz, 1H), 7.53(dd, J = 8.4, 2.4 Hz, 1H), 7.40 (d, J = 7.8 Hz, 2H), 6.89 (d, J = 7.8 Hz, 2H), 4.55 (s, 2H), 3.80 (s, 3H); MS(EI) m/z: 316.18 (M)+.

4.3.9. Data for 4i

White solid; yield: 82%; mp 100–102 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.49 (d, *J* = 1.8 Hz, 1H), 8.23 (dd, *J* = 8.4, 1.8 Hz, 1H), 7.53 (d, *J* = 9.0 Hz, 1H), 7.37 (d, *J* = 7.8 Hz, 2H), 7.17 (d, *J* = 7.2 Hz, 2H), 4.53 (s, 2H); MS (EI) *m/z*: 320.16 (M)⁺.

4.3.10. Data for 4j

White solid; yield: 84%; mp112-114 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (d, *J* = 1.8 Hz, 1H), 8.24 (dd, *J* = 8.4, 1.8 Hz, 1H), 7.53 (d,

J = 8.4 Hz, 1H), 7.37 (d, J = 7.8 Hz, 2H), 7.17 (d, J = 7.2 Hz, 2H), 4.56 (s, 2H), 2.35 (s, 3H); MS (EI) m/z: 300.33 (M)⁺.

4.3.11. Data for 4k

White solid; yield: 70%; mp 101–102 °C; ¹H NMR (600 MHz, CDCl₃) δ 8.50 (s, 1H), 8.25 (dd, *J* = 7.2, 1.8 Hz, 1H), 7.54 (d, *J* = 9.0 Hz, 1H), 7.35–7.33 (m, 1H), 7.23 (dd, *J* = 6.6, 1.8 Hz, 1H), 7.16 (dd, *J* = 18.0, 8.4 Hz, 1H), 4.52 (s, 2H); MS(EI) *m/z*: 322.16 (M)⁺.

4.4. Synthesis of the intermediate **5a**–**k** [22]

The intermediate **4** (3.2 mmol) and ammonium chloride (0.171 g, 3.2 mmol) were dissolved in a mixture of ethanol (50 mL) and water (6 mL). The reaction mixture was heated to reflux and powered iron (0.536 g, 9.6 mmol) was added at reflux temperature. After completing the reaction, the resulting mixture was filtered through diatomaceous earth and the filtrate was concentrated under reduced pressure. The residue was extracted with ethyl acetate, and the combined extracts were washed with saturated brine. Finally, the residue was purified by column chromatography on silica gel.

4.4.1. Data for **5a**

White solid; yield: 81%; mp 99–101 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.58–7.56 (m, 4H), 7.21 (d, *J* = 8.4 Hz, 1H), 6.90 (s, 1H), 6.60 (d, *J* = 7.8 Hz, 1H), 4.54 (s, 2H); MS (EI) *m/z*: 324.15 (M)⁺.

4.4.2. Data for 5b

White solid; yield: 83%; mp 94–96 °C; ¹H NMR (600 MHz, DMSO-*d*₆) δ 7.55 (dd, *J* = 8.4, 5.4 Hz, 2H), 7.28 (d, *J* = 8.4 Hz, 1H), 7.18–7.15 (m, 2H), 6.76–6.75 (m, 1H), 6.56–6.54 (m, 1H), 5.09 (s, 2H), 4.56 (s, 2H); MS (EI) *m/z*: 274.17 (M)⁺.

4.4.3. Data for 5c

White solid; yield: 69%; mp 105–106 °C; ¹H NMR (600 MHz, DMSO-*d*₆) δ 7.52 (d, *J* = 8.4 Hz, 1H), 7.40 (d, *J* = 8.4 Hz, 2H), 7.27 (d, *J* = 8.4 Hz, 2H), 6.76 (d, *J* = 1.8 Hz, 1H), 6.54 (d, *J* = 2.4 Hz, 1H), 5.10 (s, 2H), 4.55 (s, 2H); MS (EI) *m/z*: 290.15 (M)⁺.

4.4.4. Data for **5d**

White solid; yield: 65%; mp 118–121 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 7.87 (d, J = 8.4 Hz, 2H), 7.70 (d, J = 8.4 Hz, 2H), 7.27 (d, J = 3.6 Hz, 1H), 6.74 (d, J = 7.2 Hz, 1H), 6.55 (d, J = 7.2 Hz, 1H), 5.09 (s, 2H), 4.64 (s, 2H); MS (EI) m/z: 281.19 (M)⁺.

4.4.5. Data for 5e

White solid; yield: 84%; mp 83–84 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.28 (s, 1H), 7.26 (s, 1H), 7.22 (d, *J* = 9.6 Hz, 1H), 7.19 (d, *J* = 8.4 Hz, 1H), 6.97–6.96 (m, 1H), 6.60 (d, *J* = 8.4 Hz, 1H), 4.52 (s, 2H), 3.68 (s, 2H); MS (EI) *m*/*z*: 274.24 (M)⁺.

4.4.6. Data for **5**f

White solid; yield: 78%; mp 79–81 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.61 (d, J = 8.4 Hz, 1H), 7.41 (d, J = 4.8 Hz, 1H), 7.39 (d, J = 5.4 Hz, 1H), 7.26 (s, 1H), 7.21 (d, J = 3.6 Hz, 2H), 6.60 (d, J = 7.2 Hz, 1H), 4.47 (s, 2H), 3.71 (s, 2H); MS (EI) m/z: 334.18 (M)⁺.

4.4.7. Data for **5g**

White solid; yield: 76%; mp 100–102 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 7.63 (d, J = 8.4 Hz, 2H), 7.35 (d, J = 8.4 Hz, 2H), 7.28 (d, J = 9.0 Hz, 1H), 6.75 (s, 1H), 6.55 (d, J = 8.4 Hz, 1H), 5.09 (s, 2H), 4.60 (s, 2H); MS (EI) m/z: 340.21 (M)⁺.

4.4.8. Data for **5h**

White solid; yield: 71%; mp 139–141 °C; ¹H NMR (600 MHz,

CDCl₃) δ 8.49 (s, 1H), 8.23 (d, J = 9.0 Hz, 1H), 7.53 (d, J = 8.4 Hz, 1H), 7.41 (d, J = 8.4 Hz, 2H), 6.89 (d, J = 9.0 Hz, 2H), 4.55 (s, 2H), 3.80 (s, 2H); MS (EI) m/z: 286.34 (M)⁺.

4.4.9. Data for 5i

White solid; yield: 84%; mp 83–84 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.45 (s, 1H), 7.33 (s, 1H), 7.26 (s, 1H), 7.20 (d, *J* = 7.8 Hz, 1H), 6.91 (s, 1H), 6.60 (d, *J* = 9.0 Hz, 1H), 4.48 (s, 2H), 3.69 (s, 2H); MS (EI) *m*/*z*: 290.21 (M)⁺.

4.4.10. Data for 5j

White solid; yield: 88%; mp 94–95 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.33 (d, J = 7.8 Hz, 2H), 7.20 (d, J = 8.4 Hz, 1H), 7.14 (d, J = 7.8 Hz, 2H), 6.91 (s, 1H), 6.59 (d, J = 6.6 Hz, 1H), 4.50 (s, 2H), 3.68 (s, 2H), 2.33 (s, 3H); MS (EI) m/z: 270.20 (M)⁺.

4.4.11. Data for **5k**

White solid; yield: 75%; mp 72–74 °C; ¹H NMR (600 MHz, CDCl₃) δ 7.37 (s, 1H), 7.35–7.4 (m, 2H), 7.31–7.29 (m, 1H), 7.19 (d, *J* = 9.0 Hz, 1H), 7.13 (dd, *J* = 9.0, 2.4 Hz, 1H), 7.00 (d, *J* = 8.4 Hz, 1H), 4.48 (s, 2H), 3.69 (s, 2H); MS (EI) *m/z*: 292.17 (M)⁺.

4.5. General procedure for synthesis of the title compounds (**7–17**) [23]

Intermediate **5** (1.0 mmol) and 4-dimethylaminopyridine (0.1 mmol) were added to a mixture of the corresponding carboxylic acid 6 (1.3 mmol) and (EDCI, 2 mmol) in CH₂Cl₂ (20 mL). The reaction system was stirred at room temperature overnight and then diluted with CH₂Cl₂ (50 mL). The resulting mixture was consecutively washed with 10% citric acid solution and brine. Then the organic phase was dried with sodium sulphate and filtered, and concentrated under reduced pressure. The residue was purified on a silica gel column to afford the title compounds **7–17**.

4.5.1. Data for 7a

White solid; yield: 56%; mp 174–175 °C; ¹H NMR (600 MHz. DMSO- d_6) δ 10.29 (s, 1H), 8.55 (s, 1H), 8.08 (s, 1H), 7.77 (d, J = 8.4 Hz, 2H), 7.73 (d, J = 7.8 Hz, 2H), 7.63 (d, J = 8.4 Hz, 1H), 7.52 (d, J = 8.4 Hz, 1H), 4.70 (s, 2H), 4.00 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 164.99, 158.78, 149.00, 141.99, 140.16, 138.61, 135.27, 134.08, 130.12, 129.90, 129.40, 125.63, 120.04, 117.29, 110.98, 109.85, 39.86 (s), 35.74 (s); HRMS (MALDI): Calcd for C₂₁H₁₄F₆N₄O₂S [M+H]⁺ 501.0820. Found: 501.0823.

4.5.2. Data for 7b

White solid; yield: 61%; mp 142–143 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.17 (s, 1H), 8.50 (s, 1H), 8.09 (s, 1H), 7.77 (d, J = 7.8 Hz, 2H), 7.73 (d, J = 7.8 Hz, 2H), 7.63 (d, J = 9.0 Hz, 1H), 7.53 (d, J = 9.0 Hz, 1H), 7.36 (t, J = 54.0 Hz, 1H), 4.70 (s, 2H), 3.99 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 164.83, 159.49, 148.84, 143.06, 141.97, 140.18, 135.26, 134.44, 130.19, 129.87, 129.52, 125.61, 124.80, 122.99, 117.18, 116.75, 113.21, 111.67, 110.78, 110.12, 109.80, 39.60, 35.72; HRMS (MALDI): Calcd for C₂₁H₁₅F₅N₄O₂S [M+H]⁺ 483.0914.

4.5.3. Data for **8a**

White solid; yield: 47%; mp 109–111 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.29 (s, 1H), 8.54 (s, 1H), 8.07 (s, 1H), 7.63 (d, J = 8.4 Hz, 1H), 7.59 (d, J = 8.4 Hz, 2H), 7.57 (d, J = 8.4 Hz, 1H), 7.18 (t, J = 9.0 Hz, 2H), 4.62 (s, 2H), 4.00 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.34, 163.10, 161.46, 148.88, 142.21, 133.97, 131.65, 130.74, 117.13, 115.88, 115.60, 110.96, 109.75, 39.81, 35.69; HRMS (MALDI): Calcd for C₂₀H₁₄F₄N₄O₂S [M+H]⁺ 451.0852. Found: 451.0850.

4.5.4. Data for 8b

White solid; yield: 52%; mp 154–156 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.18 (s, 1H), 8.50 (s, 1H), 8.08 (d, J = 2.4 Hz, 2H), 7.63 (d, J = 8.4 Hz, 1H), 7.59 (dd, J = 8.4, 5.4 Hz, 2H), 7.53 (dd, J = 8.4, 1.8 Hz, 1H), 7.37 (d, J = 7.8 Hz, 2H), 7.36 (t, J = 54.6 Hz, 1H), 7.19 (t, J = 9.0 Hz, 1H), 4.64 (s, 2H), 3.98 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.23, 163.09, 148.77, 142.09, 134.37, 131.66, 130.75, 116.99, 115.60, 109.73, 39.51, 35.69; HRMS (MALDI): Calcd for C₂₀H₁₅F₃N₄O₂S [M+H]⁺ 433.0946. Found: 433.0949.

4.5.5. Data for **9a**

White solid; yield: 70%; mp 143–144 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.28 (s, 1H), 8.54 (s, 1H), 8.07 (d, J = 1.6 Hz, 1H), 7.62 (d, J = 8.8 Hz, 1H), 7.57 (s, 1H), 7.55 (s, 1H), 7.53 (dd, J = 8.8, 2.0 Hz, 1H), 7.42 (s, 1H), 7.41 (d, J = 1.6 Hz, 1H), 4.61 (s, 2H), 4.01 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.20, 158.93, 148.84, 141.91, 139.06, 138.93, 134.86 (s), 134.35, 133.99, 133.72, 130.37, 128.81, 121.74, 119.96, 118.17, 117.33, 116.95, 110.94, 109.71, 39.74, 35.65; HRMS (MALDI): Calcd for C₂₀H₁₄ClF₃N₄O₂S [M+H]⁺ 467.0556. Found: 467.0558.

4.5.6. Data for **9b**

White solid; yield: 72%; mp 169–171 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.16 (s, 1H), 8.50 (s, 1H), 8.08 (d, J = 1.6 Hz, 1H), 7.62 (d, J = 8.8 Hz, 1H), 7.57 (s, 1H), 7.54 (dd, J = 8.8, 2.0 Hz, 1H), 7.49 (s, 1H), 7.43 (d, J = 2.0 Hz, 1H), 7.41 (d, J = 2.0 Hz, 1H), 7.36 (t, J = 54.0 Hz, 1H), 4.61 (s, 2H), 3.99 (s, 3H); ¹³C NMR (150 MHz, DMSO- d_6) δ 164.70, 160.33, 148.06, 145.60, 141.79, 136.20, 133.23, 132.79, 131.26, 128.88, 117.31, 116.59, 110.23, 35.13; HRMS (MALDI): Calcd for C₂₀H₁₅ClF₂N₄O₂S [M+H]⁺ 449.0651. Found: 449.0648.

4.5.7. Data for 10a

White solid; yield: 79%; mp 166–168 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.29 (s, 1H), 8.55 (s, 1H), 8.08 (s, 1H), 7.84 (d, J = 7.8 Hz, 2H), 7.75 (d, J = 8.4 Hz, 2H), 7.63 (d, J = 8.4 Hz, 1H), 7.52 (d, J = 8.4 Hz, 1H), 4.69 (s, 2H), 4.01 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 164.60, 158.84, 149.05, 142.00, 135.03, 134.14, 132.44, 129.83, 121.83, 120.04, 118.60, 117.33, 117.15, 111.55, 111.10, 109.99, 109.84, 39.85, 35.76; HRMS (MALDI): Calcd for C₂₁H₁₄F₃N₅O₂S [M+H]⁺ 458.0899. Found: 458.0903.

4.5.8. Data for 10b

White solid; yield: 80%; mp 223–225 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.17 (s, 1H), 8.49 (s, 1H), 8.07 (s, 1H), 7.83 (d, J = 7.8 Hz, 2H), 7.74 (d, J = 7.8 Hz, 2H), 7.63 (d, J = 9.0 Hz, 1H), 7.51 (d, J = 8.4 Hz, 1H), 7.35 (t, J = 53.4 Hz, 1H), 4.64 (s, 2H), 3.98 (s, 3H); ¹³C NMR (150 Hz, DMSO- d_6) δ 164.50, 160.33, 148.08, 141.70, 136.22, 133.27, 132.83, 130.43, 117.38, 116.54, 111.00, 110.21, 110.21, 35.32; HRMS MALDI: Calcd for C₂₁H₁₅F₂N₅O₂S [M+H]⁺ 440.0993. Found: 440.0999.

4.5.9. Data for **11a**

White solid; yield: 51%; mp 108–110 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.28 (s, 1H), 8.54 (s, 1H), 8.06 (d, J = 2.0 Hz, 1H), 7.63 (d, J = 8.8 Hz, 1H), 7.53 (dd, J = 8.8, 2.0 Hz, 1H), 7.41 (s, 1H), 7.39 (d, J = 1.6 Hz, 1H), 7.37 (s, 1H), 7.15–7.11 (m, 1H), 4.64 (s, 2H), 4.01 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.26, 163.54, 161.90, 158.73, 149.03, 142.17, 138.35, 135.48, 134.05, 130.24, 124.73, 121.87, 117.23, 116.10, 115.95, 115.00, 114.86, 110.96, 109.86, 39.86, 35.88; HRMS (MALDI): Calcd for C₂₀H₁₄F₄N₄O₂S [M+H]⁺ 451.0852. Found: 451.0856.

4.5.10. Data for 11b

White solid; yield: 67%; mp 128–130 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.16 (s, 1H), 8.50 (s, 1H), 8.07 (s, 1H), 7.63 (d, *J* = 8.4 Hz, 1H), 7.54 (d, *J* = 9.0 Hz, 1H), 7.39–7.37 (m, 3H), 7.36 (t, *J* = 54.0 Hz,

1H), 7.13–7.11 (m, 1H), 4.63 (s, 2H), 3.99 (s, 3H); 13 C NMR (150 MHz,CDCl₃) δ 164.86, 159.55, 150.77, 149.07, 148.90, 142.12, 135.18, 134.43, 133.19, 125.47, 118.08, 117.50, 117.28, 116.79, 113.23, 111.69, 110.86, 110.14, 109.99, 109.81, 39.55, 35.37; HRMS (MALDI): Calcd for $C_{20}H_{15}F_{3}N_{4}O_{2}S$ [M+H]⁺ 433.0946. Found: 433.0939.

4.5.11. Data for 12a

White solid; yield: 74%; mp 108–110 °C; ¹H NMR (400 MHz, DMSO-*d*₆) δ 10.27 (s, 1H), 8.53 (s, 1H), 8.05 (s, 1H), 7.75 (s, 1H), 7.61 (d, *J* = 8.8 Hz, 1H), 7.53 (d, *J* = 7.6 Hz, 2H), 7.48 (d, *J* = 7.6 Hz, 1H), 7.31 (t, *J* = 7.6 Hz, 1H), 4.61 (s, 2H), 4.00 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.08, 158.81, 148.96, 142.08, 138.82, 138.57, 138.19, 135.06, 133.98, 131.95, 130.98, 130.22, 127.68, 122.52, 121.78, 119.99, 117.19, 116.94, 110.99, 109.76, 39.78, 35.67; HRMS (MALDI): Calcd for C₂₀H₁₄BrF₃N₄O₂S [M+Na]⁺ 551.0051. Found: 551.0058.

4.5.12. Data for 12b

White solid; yield: 67%; mp 145–146 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.15 (s, 1H), 8.49 (s, 1H), 8.05 (s, 1H), 7.75 (s, 1H), 7.63 (d, J = 8.4 Hz, 1H), 7.54 (d, J = 6.4 Hz, 2H), 7.35 (m, 2H), 7.33 (t, J = 53.6 Hz, 1H), 4.61 (s, 2H), 3.98 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 164.93, 159.50, 148.81, 143.07, 142.88, 142.08, 138.21, 135.00, 134.32, 131.94, 130.95, 130.20, 127.67, 122.50, 116.92, 116.63, 113.10, 111.55, 110.80, 110.00, 109.82, 39.50, 35.67; HRMS (MALDI): Calcd for C₂₀H₁₅BrF₂N₄O₂S [M+H]⁺ 493.0145. Found: 493.0152.

4.5.13. Data for 13a

White solid; yield: 65%; mp 163–165 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.29 (s, 1H), 8.55 (s, 1H), 8.08 (s, 1H), 7.68 (d, J = 8.4 Hz, 2H), 7.63 (d, J = 9.0 Hz, 1H), 7.53 (dd, J = 8.4, 1.8 Hz, 1H), 7.36 (d, J = 7.8 Hz, 2H), 4.65 (s, 2H), 4.01 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.17, 158.77, 148.84, 148.67, 142.10, 138.73, 138.49, 135.18, 134.74, 134.03, 130.51, 121.81, 121.13, 120.95, 120.03, 119.47, 117.20, 110.97, 109.96, 109.79, 39.78, 35.53; HRMS (MALDI): Calcd for C₂₁H₁₄F₆N₄O₂S [M+H]⁺ 517.0769. Found: 517.0774.

4.5.14. Data for **13b**

White solid; yield: 45%; mp 111–113 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.18 (s, 1H), 8.51 (s, 1H), 8.09 (s, 1H), 7.68 (d, J = 8.4 Hz, 2H), 7.64 (d, J = 9.0 Hz, 1H), 7.54 (d, J = 9.0 Hz, 1H), 7.37 (d, J = 7.8 Hz, 2H), 7.36 (t, J = 54.0 Hz, 1H), 4.64 (s, 2H), 3.98 (s, 3H); ¹³C NMR (150 MHz, DMSO- d_6) δ 165.07, 159.51, 148.75, 143.03, 141.99, 135.15, 134.72, 134.41, 130.51, 121.12, 119.46, 117.14, 116.74, 113.17, 111.62, 110.74, 110.08, 109.76, 39.56, 35.52; HRMS (MALDI): Calcd for C₂₁H₁₅F₅N₄O₂S [M+H]⁺ 499.0863. Found: 499.0857.

4.5.15. Data for 14a

White solid; yield: 62%; mp 166–168 °C; ¹H NMR (400 MHz, DMSO-*d*₆) δ 10.27 (s, 1H), 8.54 (s, 1H), 8.05 (d, *J* = 1.6 Hz, 1H), 7.62 (d, *J* = 8.8 Hz, 1H), 7.53 (d, *J* = 1.6 Hz, 1H), 7.44 (d, *J* = 8.4 Hz, 2H), 6.91 (d, *J* = 8.4 Hz, 2H), 4.57 (s, 2H), 4.00 (s, 3H), 3.73 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.71, 159.20, 158.87, 148.84, 142.17, 138.73, 134.82, 133.90, 130.26, 127.48, 121.77, 119.98, 117.12, 114.05, 110.94, 109.65, 55.20, 39.70, 36.08; HRMS (MALDI): Calcd for C₂₁H₁₇F₃N₄O₃S [M+Na]⁺ 485.0871. Found: 485.0868.

4.5.16. Data for 14b

White solid; yield: 64%; mp 163–165 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.16 (s, 1H), 8.50 (s, 1H), 8.07 (s, 1H), 7.62 (d, J = 8.8 Hz, 1H), 7.52 (d, J = 8.8 Hz, 1H), 7.45 (d, J = 8.4 Hz, 2H), 7.35 (t, J = 56.0 Hz, 1H), 6.90 (d, J = 8.4 Hz, 2H), 4.57 (s, 2H), 3.98 (s, 3H), 3.73 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.68, 159.57, 159.25, 148.80, 142.30, 134.99, 134.33, 130.33, 127.63, 117.06, 114.12, 111.60, 110.81, 109.73, 55.27, 39.55, 36.16; HRMS (MALDI): Calcd for C₂₁H₁₈F₂N₄O₃S [M+H]⁺ 445.1146. Found: 445.1145.

4.5.17. Data for 15a

White solid; yield: 62%; mp 95–97 °C; ¹H NMR (600 MHz, CDCl₃) δ 10.27 (s, 1H), 8.54 (s, 1H), 8.06 (s, 1H), 7.94 (s, 1H), 7.91 (s 1H), 7.53 (s, 1H), 7.47 (s, 1H), 7.38 (s, 1H), 7.36 (d, *J* = 4.2 Hz, 1H), 4.51 (s, 2H), 3.99 (s, 3H); ¹³C NMR (151 MHz, CD₃OD-*d*₆) δ 167.07, 161.80, 150.39, 143.46, 142.39, 140.71, 137.04, 135.81, 135.31, 131.66, 130.57, 129.41, 128.99, 119.15, 118.33, 112.19, 111.26, 40.41 (s), 36.79 (s); HRMS (MALDI): Calcd for C₂₀H₁₄ClF₃N₄O₂S [M+H]⁺ 467.0556. Found: 467.0562.

4.5.18. Data for 15b

White solid; yield: 66%; mp 151–152 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.25 (s, 1H), 8.25 (s, 1H), 8.06 (s, 1H), 7.97 (s, 1H), 7.47 (s, 1H), 7.43 (d, J = 8.4 Hz, 1H), 7.39–7.35 (m, 2H), 7.27 (s, 1H), 6.92 (t, J = 54.6 Hz, 1H), 4.52 (s, 2H), 3.96 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.00, 159.37, 148.82, 142.84, 142.04, 137.94, 135.35, 134.42, 129.94, 129.09, 128.07, 127.22, 117.10, 116.84, 113.29, 111.71, 110.73, 109.97, 39.61, 35.78; HRMS (MALDI): Calcd for C₂₀H₁₅ClF₂N₄O₂S [M+H]⁺ 449.0651. Found: 449.0648.

4.5.19. Data for 16a

White solid; yield: 76%; mp 139–140 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.29 (s, 1H), 8.55 (s, 1H), 8.06 (s, 1H), 7.63 (d, J = 9.0 Hz, 1H), 7.54 (d, J = 9.0 Hz, 1H), 7.40 (d, J = 7.8 Hz, 2H), 7.16 (d, J = 7.8 Hz, 2H), 4.58 (s, 2H), 4.01 (s, 3H), 2.27 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 165.64, 159.10, 148.69, 141.82, 139.75, 139.32, 137.71, 134.39, 133.92, 132.32, 129.35, 128.86, 121.69, 119.91, 117.41, 116.77, 110.94, 109.54, 39.59 36.21, 21.03; HRMS (MALDI): Calcd for C₂₁H₁₇F₃N₄O₂S [M+H]⁺ 447.1103. Found: 447.1095.

4.5.20. Data for **16b**

White solid; yield: 54%; mp 117–119 °C; ¹H NMR (600 MHz, DMSO- d_6) δ 10.17 (s, 1H), 8.50 (s, 1H), 8.06 (s, 1H), 7.63 (s, 1H), 7.62 (d, J = 8.4 Hz, 1H), 7.53 (d, J = 8.4 Hz, 1H), 7.40 (d, J = 7.8 Hz, 2H), 7.36 (t, J = 54.6 Hz, 1H), 4.58 (s, 2H), 3.98 (s, 3H), 2.27 (s, 3H); ¹³C NMR (100 MHz, DMSO- d_6) δ 164.47, 159.89, 147.58, 141.44, 136.96, 133.34, 132.85, 129.08, 129.00, 116.87, 116.14, 109.79, 35.40, 20.63; HRMS (MALDI): Calcd for C₂₁H₁₈F₂N₄O₂S [M+H]⁺ 429.1197. Found: 429.1204.

4.5.21. Data for 17a

White solid; yield: 59%; mp 121–123 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.28 (s, 1H), 8.55 (s, 1H), 8.07 (s, 1H), 7.64 (s, 1H), 7.61 (d, J = 5.2 Hz, 1H), 7.53 (d, J = 8.8 Hz, 1H), 7.42 (t, J = 6.8 Hz, 2H), 4.61 (s, 2H), 4.01 (s, 3H). ¹³C NMR (150 MHz, CDCl₃) δ 164.99, 158.69, 150.80, 149.02, 142.08, 135.45, 134.06, 133.12, 125.21, 121.84, 120.05, 118.07, 117.49, 117.31, 110.97, 109.86, 39.86, 35.37; HRMS (MALDI): Calcd for C₂₀H₁₃F₅N₄O₂S [M+H]⁺ 469.0758. Found: 469.0760.

4.5.22. Data for 17b

White solid; yield: 49%; mp 142–144 °C; ¹H NMR (400 MHz, DMSO- d_6) δ 10.17 (s, 1H), 8.51 (s, 1H), 8.09 (d, J = 1.6 Hz, 1H), 7.65 (d, J = 5.6 Hz, 1H), 7.62–7.60 (m, 1H), 7.55 (dd, J = 8.8, 2.0 Hz, 1H), 7.43–7.40 (m, 2H), 7.37 (t, J = 54 Hz, 1H), 4.62 (s, 2H), 3.99 (s, 3H); ¹³C NMR (150 MHz, CDCl₃) δ 164.80, 159.49, 150.71, 149.02, 148.85, 142.07, 135.13, 134.37, 133.14, 125.41, 118.03, 117.45, 117.23, 116.74 (s), 113.18, 111.63, 110.81, 110.09, 109.93, 109.75, 39.50, 35.32; HRMS (MALDI): Calcd for C₂₀H₁₄F₄N₄O₂S [M+H]⁺ 451.0852. Found: 451.0850.

4.6. Enzymatic kinetics [24–26]

The preparation of succinate-cytochrome c reductase (SCR, mixture of respiratory SQR and complex III) from porcine heart was essentially as reported. The activity of SCR was measured by

monitoring the increase of cytochrome c at 550 nm, by using the extinction coefficient of 18.5 mM⁻¹ cm⁻¹. The succinate--ubiquinone reductase (SQR) activity was measured by monitoring the decrease of 2,6-dichlorophenolindophenol (DCIP) at 600 nm, by using the extinction coefficient of 21 mM⁻¹ cm⁻¹. The reaction mixture may be scaled down to 1.8 mL with final concentrations of PBS (pH 7.4), 100 mM: EDTA, 0.3 mM: succinate, 20 mM: oxidized cvtochrome c. 60 uM (or DCIP, 53 uM); and appropriate amounts of enzyme to start the reaction. The ubiquinol-cytochrome *c* reductase (complex III) activity in catalysing the oxidation of DBH₂ by cytochrome c was assayed in 100 mM PBS (pH 7.4), 0.3 mM EDTA, 750 μ M lauryl maltoside (*n*-dodecyl- β -D-maltoside), 100 μ M DBH₂, 100 µM oxidized cytochrome *c*, and an appropriate amount of SCR. The preparation of DBH₂ from DB was carried out according to the procedure described in previous publications [11], and the concentration of DBH₂ was determined by measuring the absorbance difference between 288 and 320 nm using an extinction coefficient of 4.14 nM^{-1} cm⁻¹ for the calculation [27,28].

For the steady state studies, the reaction was carried out in the absence or presence of various concentrations of the inhibitor. To obtain the K_i and IC₅₀ values, all reactions were initiated by the addition of enzyme and monitored continuously by following the absorbance change at certain wavelengths on a Perkin–Elmer Lambda 45 spectrophotometer equipped with a magnetic stirrer at 23 °C.

4.7. Data analysis [29]

First, according to the measured substances extinction coefficient, the change of absorbance was converts to product variation, then making linear fitting of time, the slope is the enzymatic reaction velocity. Compared with the control sample, the inhibition rates of inhibitors were calculated. The concentrations at 50% inhibition (absolute IC_{50} values) for experiments with SCR were obtained from a nonlinear regression of the activity data according to a four parameter logistic model. The absolute IC_{50} was calculated according to Eq. (1)

$$y = \min + \frac{\max - \min}{1 + 10^{x - \log IC_{50}}}$$
(1)

Where y is the percentage of maximal rate, max and min are the y values at which the curve levels off, x is the logarithm of inhibitor concentration, and IC_{50} is the concentration of inhibitor that caused 50% of the total inhibition.

The inhibition type was determined by Lineweaver–Burk plots, and computer fitted to the appropriate equations like Eqs. (2) and (3). Sigma Plot software 9.0 was used to determine all kinetic constants.

$$\nu = \frac{V_{\max}[S]}{\left(1 + \frac{[I]}{K_i}\right)K_m + [S]}$$
(2)

$$v = \frac{V_{\max}[S]}{\left(1 + \frac{[I]}{K_i}\right)(K_m + [S])}$$
(3)

4.8. Molecular docking

The crystal structure of 1ZOY from porcine was selected as receptor. As we know, SQR consisted of four subunits (A, B, C, and D) and the binding site (Q-site) of ligand was formed by the subunits B, C, and D. So, chain A was deleted in the following molecular docking and binding free energy calculations.

The docking procedure was similar with our previous study [11]. The AutoDock 4.2 program [30] was applied to dock these inhibitors into the Q-site. Gasteiger charges were used for these inhibitors. In the docking process, a conformational search was performed for ligand, using the Solis and Wets local search method. The Lamarkian genetic algorithm (LGA) [31,32] was applied for the conformational search of the binding complex of ligand with porcine 1ZOY. Among a series of docking parameters, the grid size was set as $40 \times 32 \times 40$, and the grid space used was set to the default value of 0.375 Å. The interaction energy, which resulted from probing the porcine SQR with ligand, was assessed using the standard AutoDock scoring function. Among a set of 256 candidates of the docked complex structures, the best one was first selected based on the interaction energy and the binding mode of commercial carboxamide fungicides obtained from our previous study [11].

All the complex structures derived from molecular docking were used as starting structures for further energy minimizations, using the Sander module of the Amber8 [33] program before the final binding structures were achieved. Firstly, the ligand was minimized with the protein fixed. Secondly, the backbone atoms of the protein were fixed, and other atoms were relaxed. The final minimization was performed with both the ligand and the protein relaxed. In each step, the energy minimization was executed by using the steepest descent method for the first 1000 cycles, and the conjugated gradient method for the subsequent 2000 cycles with a convergence criterion of 0.1 kcal mol^{-1} Å⁻¹. Then, an additional 20 ps MD simulation was performed. For temperature regulation, the Langevin thermostat was used to maintain a temperature of 300 K. The atomic coordinates were saved per ps. Subsequently, the last snapshot of the MD simulation was minimized to a convergence criterion of 0.1 kcal mol⁻¹ Å⁻¹. Then, the Δ H calculation was performed on the minimized complex. The bcc charges were used as the atomic charges for these inhibitors. The energy minimization process was the same as previously described [11].

4.9. Binding energy calculation

On the basis of the modelled complex structure of porcine SQR bound with inhibitors, the binding free energy for each of the minimized complexes was estimated using the molecular mechanics-Possion-Boltzmann surface area (MM-PBSA) method [34]. In this method, the binding free energy of the protein-ligand complex (ΔG_{bind}) is obtained from the difference between the free energies of the protein-ligand complex (ΔG_{cpx}) and the unbound receptor (ΔG_{rec}) and the free ligand (ΔG_{lig}) as follows: [35].

$$\Delta G_{\rm bind} = \Delta G_{\rm cpx} - \Delta G_{\rm rec} - \Delta G_{\rm lig} \tag{4}$$

Binding free energy (ΔG_{bind}) can be evaluated as sum of the changes in molecular mechanical (MM) gas-phase binding energy (ΔE_{MM}), solvation free energy (ΔG_{sol}), and entropic contribution ($-T\Delta S$). The ΔE_{MM} was evaluated as a sum of electrostatic energy (ΔE_{ele}) and van der Waals interaction energy (ΔE_{vdw}).

$$\Delta G_{\rm bind} = \Delta E_{\rm MM} + \Delta G_{\rm sol} - T\Delta S \tag{5}$$

$$\Delta E_{\rm MM} = \Delta E_{\rm ele} + \Delta E_{\rm vdw} \tag{6}$$

The solvation free energy ΔG_{sol} was composed of two parts:

$$\Delta G_{\rm sol} = \Delta G_{\rm PB} + \Delta G_{\rm np} \tag{7}$$

$$\Delta G_{\rm nD} = \gamma {\rm SASA} + \beta \tag{8}$$

The electrostatic contribution to the solvation free energy (ΔG_{PB}) was evaluated using Poisson-Boltzmann (PB) methods [36,37]. The nonpolar solvation energy, ΔG_{np} , can be estimated by an empirical relation of $\Delta G_{np} = \gamma SASA + \beta$, where SASA is defined as the solvent-accessible surface area, and the solvation parameters γ and β were set to 0.00542 kcal mol⁻¹ Å⁻² and 0.92 kcal mol⁻¹ respectively. The dielectric constant for the molecule and surrounding solvent were set to 1 and 80, respectively, while the probe radius of the solvent was set to 1.4 Å.

The entropy contribution to the binding free energy can be divided into two parts: the solvation free entropy (ΔS_{solv}) and the conformational free entropy (ΔS_{conf}).

$$\Delta S_{\rm sol} = \Delta S_{\rm solv} + \Delta S_{\rm conf} \tag{9}$$

The solvation free entropy is gained by the tendency of water molecules to minimize their contacts with hydrophobic groups in protein. The conformational free entropy is related to the change of the number of rotatable bonds during the binding process. The detailed computational procedure used to evaluate the entropy contribution $(-T\Delta S)$ to the binding free energy was the same as previously described [38].

Acknowledgements

The research was supported in part by the National Key Technologies R&D Program (2011BAE06B05) and the National Natural Science Foundation of China (No. 21332004 and 21272092).

Appendix A. Supplementary data

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.ejmech.2015.03.060.

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