Supporting Information

Discovery of Potent and Selective Inhibitors of Cdc2-like Kinase 1 (CLK1) as a New Class of Autophagy Inducers

Qi-Zheng Sun,^{†,⊥} Gui-Feng Lin,^{†,⊥} Lin-Li Li,^{‡,⊥} Xi-Ting Jin,[‡] Lu-Yi Huang,^{†,§} Guo Zhang,[‡] Wei Yang,[‡] Kai Chen,[†] Rong Xiang,[∥] Chong Chen,[†] Yu-Quan Wei,[†] Guang-Wen Lu,^{*,†} and Sheng-Yong Yang^{*,†,§}

[†]State Key Laboratory of Biotherapy and Cancer Center, West China Hospital, Sichuan University, and Collaborative Innovation Center for Biotherapy, Chengdu, 610041, PR China.

[‡]Key Laboratory of Drug Targeting and Drug Delivery System of Ministry of Education, West China School of Pharmacy, Sichuan University, Sichuan 610041, China.

[§]School of Chemical Engineering, Sichuan University, and Collaborative Innovation Center for Biotherapy, Chengdu, 610041, PR China.

^{II}Department of Clinical Medicine, School of Medicine, Nankai University, Tianjin 300071, China.

Table of Contents:

Table S1. Kinase inhibition profile of compound 25	3
Table S2. Crystallographic data collection and refinement statistics	8
Figure S1. Virtual screening led to the discovery of hit compoundS	9
Figure S2. Dendrogram representation of the kinase selectivity profile of 25	0
Figure S3. Overview of X-ray co-crystal structure of CLK1 complexed with 25 and	a
2D ligand-interaction diagram for 25	.1
Figure S4. Effects of 25 (20 nM and 100 nM) on the location and redistribution of S	R
proteins	2
Figure S5. Detection of autophagy and autophagic flux induced by 25 (20 nM and 10)0
nM)S1	3
Figure S6. In vitro effects of 18 on LC3	4

Figure S7. Pharmacokinetic characteristics of compound 25	S15
Figure S8. IC ₅₀ curves of compounds 1, 9e, 25, and 25R on CLK1 and 1	DYRK1A.S16
Figure S9. IC ₅₀ curves of compound 25	S17
Synthesis and Structure Confirmation of Compound 25R (the E	nantiomer of
Compound 25)	S24
Pharmacokinetic Assessments of Compound 25	S25
Copies of ¹ H- and ¹³ C-NMR Spectra	S26
Copies of MS Spectra	S55
HPLC Purity Analysis for Compound 25	S56
Confirmation of Enantiomeric Purity of Compound 25	S57

Kinase	IC ₅₀ (nM)	Kinase	IC ₅₀ (nM)
Abl(h)	>10000 ^b	MARK4(h)	>10000 ^b
Abl (H396P) (h)	>10000 ^b	MEKK2(h)	>10000 ^b
Abl (M351T)(h)	>10000 ^b	MELK(h)	>10000 ^b
Abl (Q252H) (h)	>10000 ^b	Mer(h)	2972
Abl(T315I)(h)	>10000 ^b	Met(h)	>10000 ^b
Abl(Y253F)(h)	>10000 ^b	Met(D1246H)(h)	>10000 ^b
ACK1(h)	>10000 ^b	Met(D1246N)(h)	>10000 ^b
ALK(h)	>10000 ^b	Met(M1268T)(h)	>10000 ^b
ALK1(h)	$>10000^{b}$	Met(Y1248C)(h)	>10000 ^b
ALK2(h)	$>10000^{b}$	Met(Y1248D)(h)	>10000 ^b
ALK4(h)	$>10000^{b}$	Met(Y1248H)(h)	>10000 ^b
ALK6(h)	>10000 ^b	MINK(h)	3623
Arg(h)	$>10000^{b}$	MKK6(h)	>10000 ^b
AMPKa1(h)	$>10000^{b}$	MKK7 β (h)	>10000 ^b
AMPKa2(h)	>10000 ^b	MLCK(h)	>10000 ^b
A-Raf(h)	>10000 ^b	MLK1(h)	7196
ARK5(h)	>10000 ^b	MLK2(h)	1260
ASK1(h)	>10000 ^b	Mnk2(h)	>10000 ^b
Aurora-A(h)	>10000 ^b	MOK(h)	>10000 ^b
Aurora-B(h)	>10000 ^b	MRCKa(h)	>10000 ^b
Aurora-C(h)	>10000 ^b	MRCKβ(h)	>10000 ^b
Axl(h)	>10000 ^b	MSK1(h)	1430
Blk(h)	9621	MSK2(h)	266
Bmx(h)	>10000 ^b	MSSK1(h)	>10000 ^b
BRK(h)	>10000 ^b	MST1(h)	>10000 ^b
BrSK1(h)	>10000 ^b	MST2(h)	1265
BrSK2(h)	>10000 ^b	MST3(h)	>10000 ^b
BTK(h)	>10000 ^b	MST4(h)	$>10000^{b}$
BTK(R28H)(h)	>10000 ^b	mTOR(h)	>10000 ^b
B-Raf(h)	>10000 ^b	mTOR/FKBP12(h)	>10000 ^b
B-Raf(V599E)(h)	>10000 ^b	MuSK(h)	>10000 ^b
CaMKI(h)	>10000 ^b	MYLK2(h)	>10000 ^b
CaMKIB(h)	>10000 ^b	MYO3B(h)	>10000 ^b
CaMKIy(h)	>10000 ^b	NEK1(h)	449
CaMKIIα(h)	>10000 ^b	NEK2(h)	>10000 ^b
CaMKIIβ(h)	>10000 ^b	NEK3(h)	>10000 ^b
CaMKII _γ (h)	>10000 ^b	NEK6(h)	>10000 ^b
CaMKI _δ (h)	>10000 ^b	NEK7(h)	>10000 ^b
CaMKII _(h)	>10000 ^b	NEK9(h)	>10000 ^b
CaMKIV(h)	>10000 ^b	NIM1(h)	>10000 ^b
CaMKK1(h)	>10000 ^b	NEK11(h)	2357
CaMKK2(h)	>10000 ^b	NLK(h)	3273

 Table S1. Kinase inhibition profile of compound 25^a

CDK1/cyclinB(h)	>10000 ^b	NUAK2(h)	>10000 ^b
CDK2/cyclinA(h)	>10000 ^b	p70S6K(h)	546
CDK2/cyclinE(h)	>10000 ^b	PAK1(h)	>10000 ^b
CDK3/cyclinE(h)	>10000 ^b	PAK2(h)	>10000 ^b
CDK4/cyclinD3(h)	$>10000^{b}$	PAK4(h)	$>10000^{b}$
CDK5/p25(h)	$>10000^{b}$	PAK3(h)	$>10000^{b}$
CDK5/p35(h)	$>10000^{b}$	PAK5(h)	>10000 ^b
CDK6/cyclinD3(h)	>10000 ^b	PAK6(h)	$>10000^{b}$
CDK7/cyclinH/MAT1(h)	>10000 ^b	PAR-1B $\alpha(h)$	>10000 ^b
CDK9/cyclin T1(h)	1428	PASK(h)	154
ChaK1(h)	>10000 ^b	PEK(h)	>10000 ^b
CHK1(h)	>10000 ^b	PDGFRa(h)	>10000 ^b
CHK2(h)	>10000 ^b	PDGFRa(D842V)(h)	5342
CHK2(I157T)(h)	>10000 ^b	PDGFRa(V561D)(h)	>10000 ^b
CHK2(R145W)(h)	>10000 ^b	PDGFRβ(h)	>10000 ^b
CK1y1(h)	>10000 ^b	PDHK4(h)	>10000 ^b
$CK1\gamma 2(h)$	>10000 ^b	PDK1(h)	>10000 ^b
CK1γ3(h)	>10000 ^b	PhKy2(h)	>10000 ^b
CK1\delta(h)	>10000 ^b	Pim-1(h)	3505
CK2(h)	>10000 ^b	Pim-2(h)	>10000 ^b
CK2α1(h)	>10000 ^b	Pim-3(h)	>10000 ^b
$CK2\alpha 2(h)$	>10000 ^b	PKA(h)	549
CLIK1(h)	1164	PKAcβ(h)	1153
CLK1(h)	2	PKBα(h)	4132
CLK2(h)	31	PKBβ(h)	>10000 ^b
CLK3(h)	5590	PKBγ(h)	1908
CLK4(h)	8	PKCα(h)	6565
cKit(h)	>10000 ^b	PKCβI(h)	1343
cKit(D816V)(h)	>10000 ^b	PKCβII(h)	>10000 ^b
cKit(D816H)(h)	>10000 ^b	PKCγ(h)	>10000 ^b
cKit(V560G)(h)	>10000 ^b	PKCδ(h)	>10000 ^b
cKit(V654A)(h)	>10000 ^b	PKCɛ(h)	>10000 ^b
CSK(h)	>10000 ^b	PKCη(h)	>10000 ^b
c-RAF(h)	>10000 ^b	PKCı(h)	>10000 ^b
cSRC(h)	>10000 ^b	PKCµ(h)	>10000 ^b
DAPK1(h)	>10000 ^b	PKCθ(h)	2629
DAPK2(h)	>10000 ^b	PKCζ(h)	>10000 ^b
DCAMKL2(h)	>10000 ^b	PKD2(h)	>10000 ^b
DCAMKL3(h)	$>10000^{b}$	PKD3(h)	>10000 ^b
DDR1(h)	>10000 ^b	PKG1a(h)	807
DDR2(h)	>10000 ^b	PKG1β(h)	248
DMPK(h)	$>10000^{b}$	PKR(h)	>10000 ^b
DRAK1(h)	>10000 ^b	Plk1(h)	>10000 ^b
DYRK1A(h)	138	Plk3(h)	>10000 ^b

DYRK1B(h)	690	PRAK(h)	>10000 ^b
DYRK2(h)	>10000 ^b	PRKG2(h)	344
DYRK3(h)	4976	PRK2(h)	229
eEF-2K(h)	>10000 ^b	PrKX(h)	>10000 ^b
EGFR(h)	>10000 ^b	PTK5(h)	>10000 ^b
EGFR(L858R)(h)	>10000 ^b	Pyk2(h)	>10000 ^b
EGFR(L861Q)(h)	>10000 ^b	Ret(h)	>10000 ^b
EGFR(T790M)(h)	>10000 ^b	Ret (V804L)(h)	>10000 ^b
EGFR(T790M,L858R)(h)	4818	Ret(V804M)(h)	>10000 ^b
EphA1(h)	>10000 ^b	RIPK2(h)	3571
EphA2(h)	>10000 ^b	ROCK-I(h)	>10000 ^b
EphA3(h)	>10000 ^b	ROCK-II(h)	>10000 ^b
EphA4(h)	>10000 ^b	Ron(h)	>10000 ^b
EphA5(h)	>10000 ^b	Ros(h)	1071
EphA7(h)	>10000 ^b	Rse(h)	>10000 ^b
EphA8(h)	>10000 ^b	Rsk1(h)	>10000 ^b
EphB2(h)	>10000 ^b	Rsk2(h)	>10000 ^b
EphB1(h)	>10000 ^b	Rsk3(h)	>10000 ^b
EphB3(h)	>10000 ^b	Rsk4(h)	>10000 ^b
EphB4(h)	>10000 ^b	SAPK2a(h)	>10000 ^b
ErbB2(h)	>10000 ^b	SAPK2a(T106M)(h)	>10000 ^b
ErbB4(h)	>10000 ^b	SAPK2b(h)	>10000 ^b
FAK(h)	>10000 ^b	SAPK3(h)	$>10000^{b}$
Fer(h)	>10000 ^b	SAPK4(h)	>10000 ^b
Fes(h)	>10000 ^b	SGK(h)	>10000 ^b
FGFR1(h)	$>10000^{b}$	SGK2(h)	>10000 ^b
FGFR1(V561M)(h)	>10000 ^b	SGK3(h)	>10000 ^b
FGFR2(h)	>10000 ^b	SIK(h)	>10000 ^b
FGFR2(N549H)(h)	>10000 ^b	SIK2(h)	>10000 ^b
FGFR3(h)	>10000 ^b	SIK3(h)	>10000 ^b
FGFR4(h)	>10000 ^b	SLK(h)	>10000 ^b
Fgr(h)	>10000 ^b	Snk(h)	>10000 ^b
Flt1(h)	>10000 ^b	SNRK(h)	>10000 ^b
Flt3(D835Y)(h)	>10000 ^b	Src(1-530)(h)	>10000 ^b
Flt3(h)	5283	Src(T341M)(h)	>10000 ^b
Flt4(h)	>10000 ^b	SRPK1(h)	>10000 ^b
Fms(h)	>10000 ^b	SRPK2(h)	>10000 ^b
Fms(Y969C)(h)	>10000 ^b	STK25(h)	>10000 ^b
Fyn(h)	>10000 ^b	STK33(h)	>10000 ^b
GCK(h)	>10000 ^b	Syk(h)	>10000 ^b
GCN2(h)	>10000 ^b	TAK1(h)	>10000 ^b
GRK1(h)	>10000 ^b	TAO1(h)	1154
GRK2(h)	>10000 ^b	TAO2(h)	1689
GRK3(h)	>10000 ^b	TAO3(h)	1205

GRK5(h)	>10000 ^b	TBK1(h)	>10000 ^b
GRK6(h)	>10000 ^b	Tec(h) activated	>10000 ^b
GRK7(h)	>10000 ^b	TGFBR1(h)	>10000 ^b
$GSK3\alpha(h)$	418	Tie2 (h)	>10000 ^b
$GSK3\beta(h)$	1594	Tie2(R849W)(h)	>10000 ^b
Hck(h)	>10000 ^b	Tie2(Y897S)(h)	>10000 ^b
Hck(h) activated	>10000 ^b	TLK1(h)	>10000 ^b
HIPK1(h)	>10000 ^b	TLK2(h)	>10000 ^b
HIPK2(h)	>10000 ^b	TNIK(h)	1969
HIPK3(h)	>10000 ^b	TrkA(h)	179
HIPK4(h)	748	TrkB(h)	457
HPK1(h)	>10000 ^b	TrkC(h)	526
ICK(h)	>10000 ^b	TSSK1(h)	>10000 ^b
IGF-1R(h)	>10000 ^b	TSSK2(h)	>10000 ^b
IGF-1R(h), activated	>10000 ^b	TSSK3(h)	>10000 ^b
IKKα(h)	>10000 ^b	TSSK4(h)	>10000 ^b
IKKβ(h)	>10000 ^b	TTBK1(h)	>10000 ^b
IKKe(h)	>10000 ^b	TTBK2(h)	>10000 ^b
IR(h)	>10000 ^b	TTK(h)	>10000 ^b
IR(h), activated	>10000 ^b	Txk(h)	8500
IRE1(h)	>10000 ^b	TYK2(h)	3700
IRR(h)	220	ULK1(h)	>10000 ^b
IRAK1(h)	4450	ULK2(h)	>10000 ^b
IRAK4(h)	1516	ULK3(h)	>10000 ^b
Itk(h)	4582	Wee1(h)	>10000 ^b
JAK1(h)	>10000 ^b	WNK2(h)	>10000 ^b
JAK2(h)	>10000 ^b	WNK3(h)	>10000 ^b
JAK3(h)	>10000 ^b	VRK2(h)	>10000 ^b
JNK1a1(h)	>10000 ^b	Yes(h)	>10000 ^b
JNK2a2(h)	>10000 ^b	ZAK(h)	>10000 ^b
JNK3(h)	$>10000^{b}$	ZAP-70(h)	>10000 ^b
KDR(h)	>10000 ^b	ZIPK(h)	>10000 ^b
Lck(h)	>10000 ^b	ATM(h)	279
Lck(h) activated	>10000 ^b	ATR/ATRIP(h)	$>10000^{b}$
LIMK1(h)	>10000 ^b	DNA-PK(h)	412
LKB1(h)	>10000 ^b	PI3 Kinase (p110β/p85α)(h)	1606
LOK(h)	>10000 ^b	PI3 Kinase (p120γ)(h)	1745
Lyn(h)	>10000 ^b	PI3 Kinase (p110δ/p85α)(h)	1212
LRRK2(h)	>10000 ^b	PI3 Kinase (p110α/p85α)(h)	2023
LTK(h)	>10000 ^b	PI3 Kinase (p110α(E542K)/p85α)(h)	6569
MAPK1(h)	>10000 ^b	PI3 Kinase (p110α(H1047R)/p85α)(h)	1026
MAPK2(h)	>10000 ^b	PI3 Kinase (p110α(E545K)/p85α)(h)	2793
MAP4K4(h)	>10000 ^b	PI3 Kinase (p110 α /p65 α)(h)	2541
MAP4K5(h)	>10000 ^b	PI3KC2a(h)	$>10000^{b}$

MAPKAP-K2(h)	>10000 ^b	PI3KC2γ(h)	362
MAPKAP-K3(h)	>10000 ^b	PIP4K2 α (h)	>10000 ^b
MEK1(h)	$>10000^{b}$	PIP5K1a(h)	$>10000^{b}$
MEK2(h)	$>10000^{b}$	$PIP5K1\gamma(h)$	$>10000^{b}$
MARK1(h)	$>10000^{b}$		

^{*a*}IC₅₀ values were determined using the KinaseProfiler of Eurofins. In case of CLKs and DYRKs, the data represent the mean values of two independent experiments. In other cases, the data represent the results of a single experiment. [ATP] = 10 μ M. ^{*b*}Inhibition% @ 10 μ M was lower than 50%. [ATP] = 10 μ M. For detailed protocols, see http://www.eurofins.com/pharmadiscovery.

CLK1 + compound 25		
PDB ID	5X8I	
Data collection		
Space group	P65	
Cell dimension		
$a, b, c(\text{\AA})$	68.33, 68.33, 285.72	
<i>α, β, γ</i> (°)	90, 90, 120	
Resolution (Å) ^a	50.00 -1.90 (1.97-1.90)	
Rmerge	0.086 (0.431)	
I / δ^{Ia}	30.72 (8.07)	
Completeness (%) ^a	99.7 (100.0)	
Redundancy ^a	15.9 (15.9)	
Refinement		
Resolution (Å)	33.60-1.90	
No. reflections	58718	
Rwork/ Rfree	0.166/0.206	
No. atoms		
Protein	5386	
Ligand/ion	62	
Water	630	
B-factors		
Protein	23.96	
Ligand/ion	18.37	
Water	35.03	
R.m.s. deviations		
Bond lengths (Å)	0.007	
Bond angles (°)	1.129	
Ramachandran analysis		
Favored (%)	97.4	
Allowed (%)	2.6	
Outliers(%)	0.0	

Table S2. Crystallographic data collection and refinement statistics^a

^{*a*} Values for the outmost resolution shell are given in parentheses.

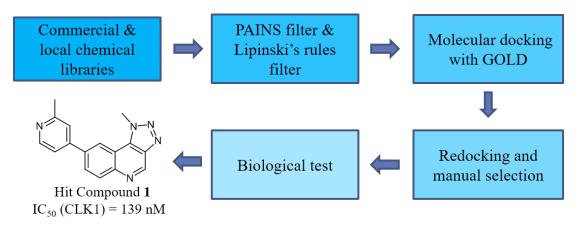


Figure S1. Virtual screening led to the discovery of hit compound^a

^aTo identify new CLK1 inhibitors as autophagy inducers, we first of all performed a virtual screening against various commercial chemical libraries including Chemdiv, Specs, Enamine, Pharmakon, Selleck, and MCE, as well as our in-house chemical library. Before the virtual screening, all the compound databases were filtered by Lipinski's rules of five, and the "pan-assay interference compounds" (PAINS) were also removed. The receptor structure was taken from the crystal structure of CLK1 (PDB ID 1Z57). The preparation and pre-process of receptor and ligand were made on the platform of Discovery Studio 3.1 (Accelrys Inc., San Diego, CA, USA). The CHARMm force field was used. The binding pocket was defined as a sphere with a radius of 9 Å, an area large enough to cover the ATP-binding region at the catalytic site. The GOLD version 5.1 program (CCDC, Cambridge, UK) was adopted for the molecular docking. GoldScore incorporated into the GOLD program package was employed to evaluate and rank the binding poses. After finishing the first round of docking, top 1% of the docking-ranked molecules were re-docked on a more flexible condition. Finally, highranking candidates were carefully selected for biological assays, which led to the discovery of the hit compound 1.

Figure S2. Dendrogram representation of the kinase selectivity profile of 25. The figurewasgeneratedusingKinomeRender1.4(http://bcb.med.usherbrooke.ca/kinomerenderLig.php).

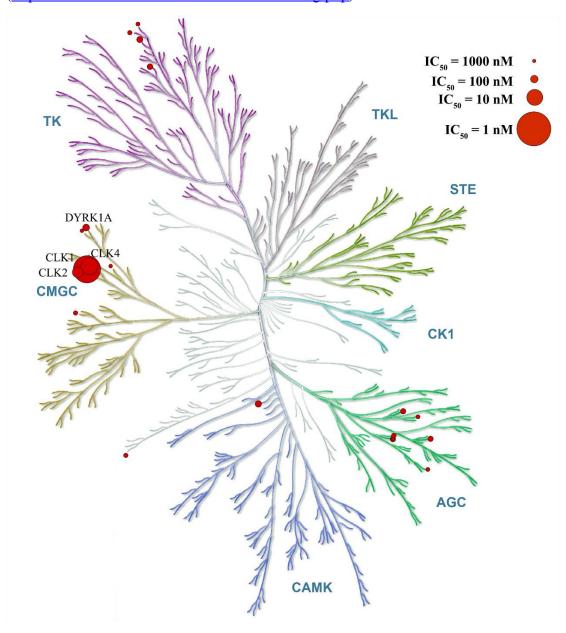


Figure S3. (A) Overview of X-ray co-crystal structure of CLK1 in complex with **25**. (B) A 2D ligand-interaction diagram for **25**. The ligand-interaction plot was generated using maestro 10.

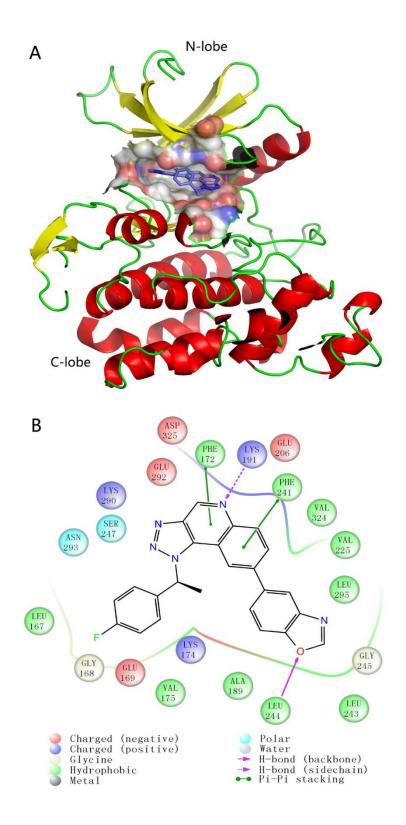
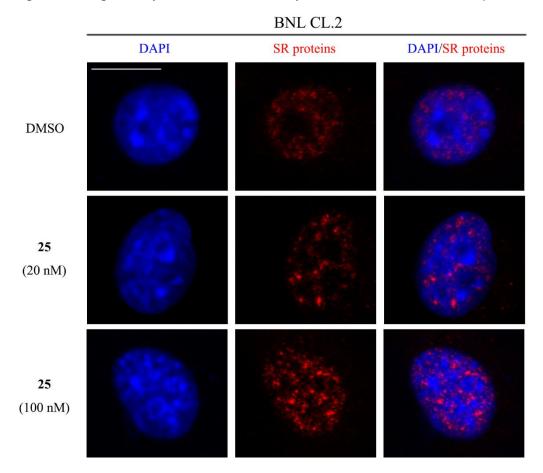
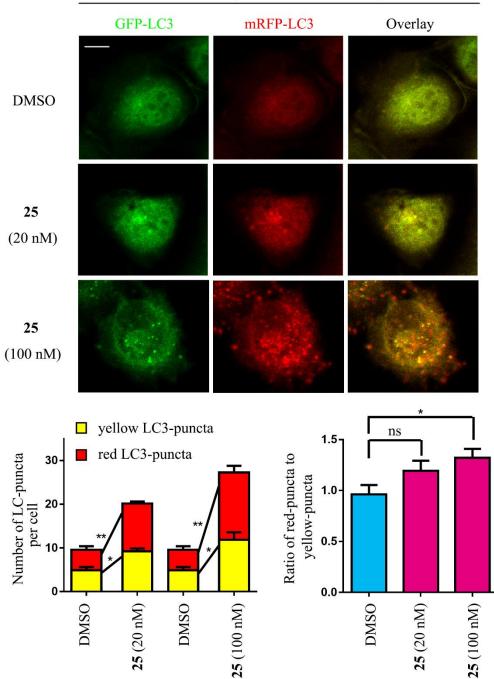


Figure S4. Effects of **25** (20 nM and 100 nM) on the location and redistribution of SR proteins. BNL CL.2 cells treated with DMSO (0.1%) or **25** (20 nM and 100 nM) for 24 h were fixed and probed with anti-SR proteins antibody (mAb1H4G7). Diffuse staining and typical speckles demonstrated by mAb1H4G7 represent active and stored forms of SR proteins respectively. DAPI was used to dye the nucleus. Scale bar: 10 µm.



S12

Figure S5. Detection of autophagy and autophagic flux induced by **25** (20 nM and 100 nM) in SKOV-3 cells^{*a*}



SKOV-3 (Ad-mRFP-GFP-LC3)

^{*a*}Ad-mRFP-GFP-LC3-infected SKOV-3 cells were treated with DMSO or **25** (20 nM and 100 nM) for 24 h and fixed before examination by confocal microscopy. Representative photographs are presented. Scale bar: 10 μ m. Alignment of green and red signals appears yellow. The number of LC3-puncta (mean ± SEM) in overlays was quantified and is shown below. More than 90 cells were counted in each individual experiment (n = 3). * *P* < 0.05, ** *P* < 0.01; ns, no statistical significance.

Figure S6. In vitro effects of 18 on LC3. SKOV-3 cells were treated with DMSO, 25 (the positive control, 10 μ M) or 18 (10 μ M) for 24 h. Then whole cell lysates were subjected to immunoblot assay to detect LC3.

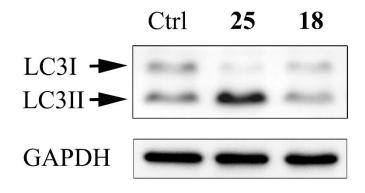


Figure S7. Pharmacokinetic characteristics of compound **25**. (A) Plasma concentration—time curve of **25** in SD rats after a single intravenous dose of 10 mg/kg. Blood was collected at indicated time points (0.03, 0.08, 0.25, 0.5, 1, 2, 3, 4, 6, 8, 12 h), and the plasma concentrations were determined by LC-MS. Points, mean; bars, SEM; n = 6. Pharmacokinetic parameters of **25** (iv) is shown in the right panel. (B) Plasma concentration—time curve of **25** in SD rats after a single intraperitoneal dose of 10 mg/kg. Blood was collected at indicated time points (0.16, 0.25, 0.5, 1, 2, 3, 4, 6, 8, 12 h), and the plasma concentrations were determined by LC-MS. Points, mean; bars, SEM; n = 6. Pharmacokinetic parameters of **25** in SD rats after a single intraperitoneal dose of 10 mg/kg. Blood was collected at indicated time points (0.16, 0.25, 0.5, 1, 2, 3, 4, 6, 8, 12 h), and the plasma concentrations were determined by LC-MS. Points, mean; bars, SEM; n = 6. Pharmacokinetic parameters of **25** (ip) is shown in the right panel.

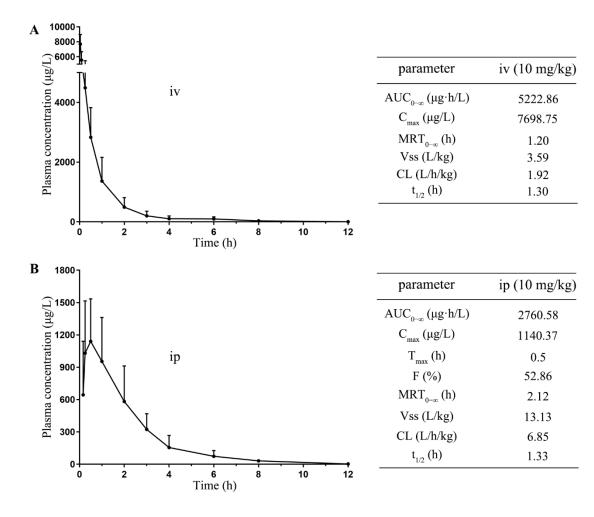
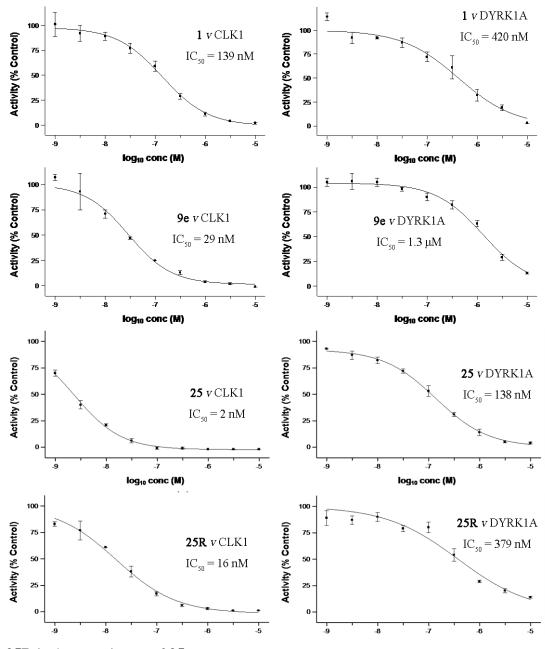
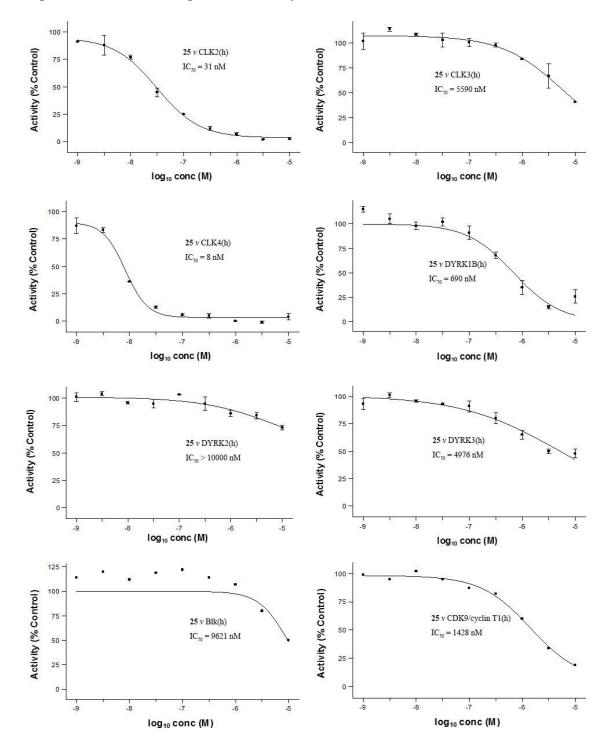


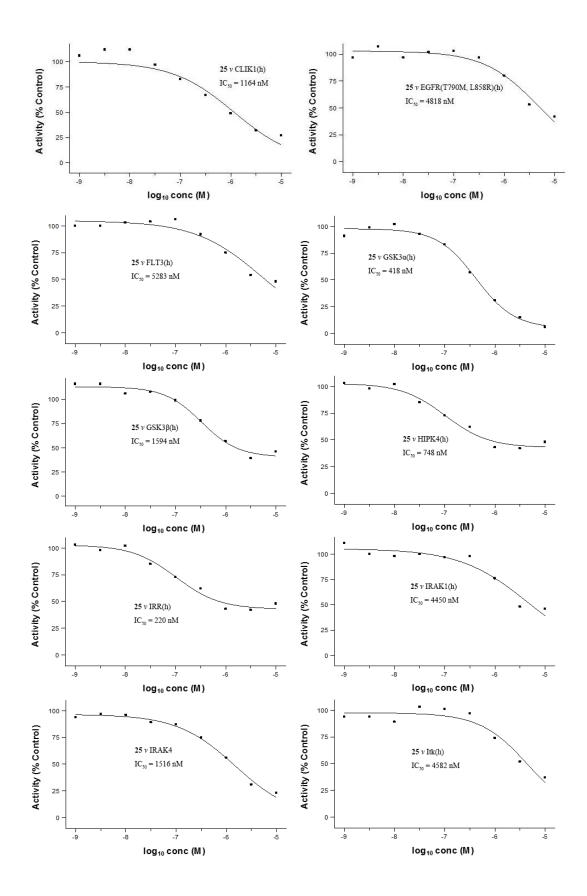
Figure S8. IC₅₀ curves of compounds **1**, **9e**, **25**, and **25** \mathbb{R}^{a} on CLK1 and DYRK1A. The values were determined using the KinaseProfiler of Eurofins, in duplicates at 10 different concentrations with an ATP concentration of 10 μ M. For detailed protocols, see http://www.eurofins.com/pharmadiscovery.

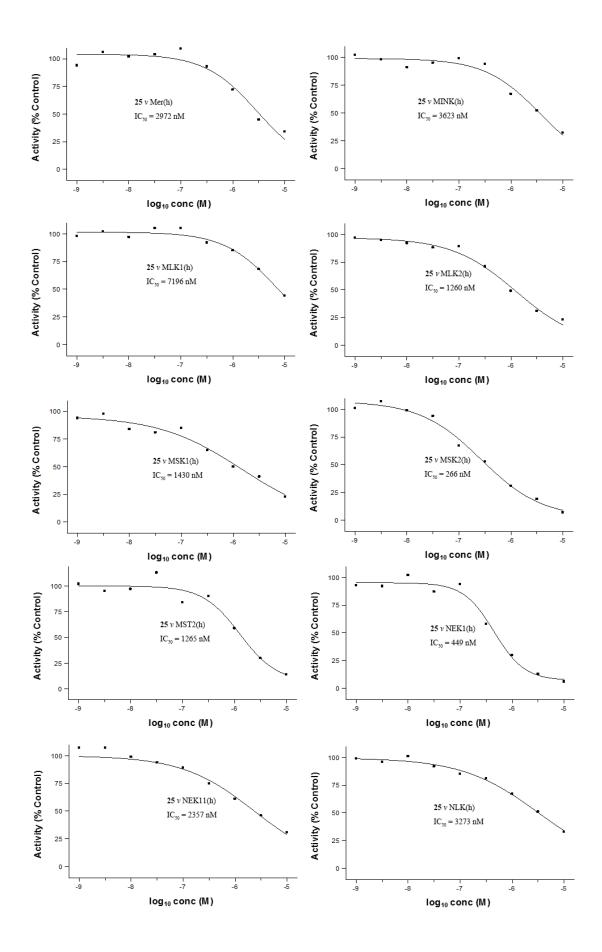


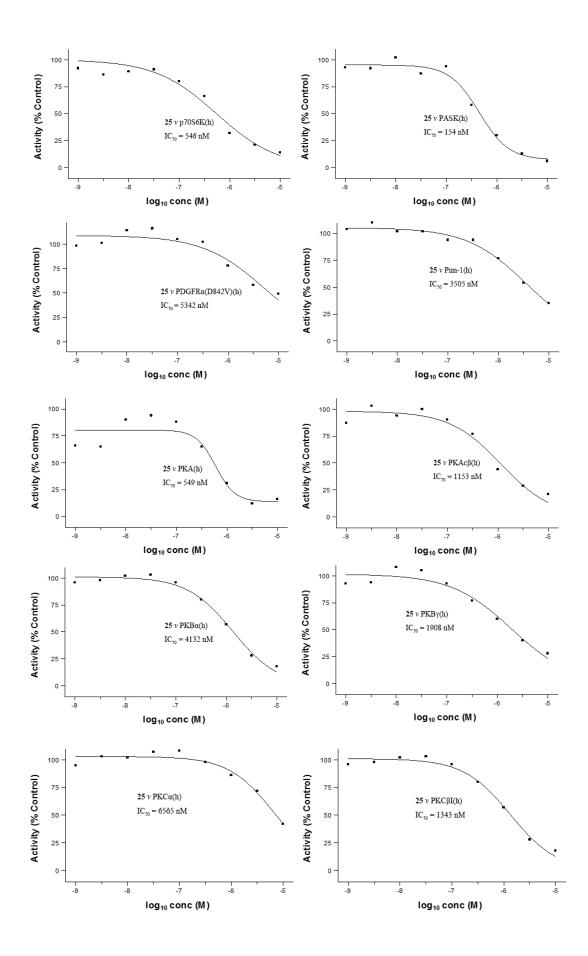
^{*a*}**25R** is the enantiomer of **25**.

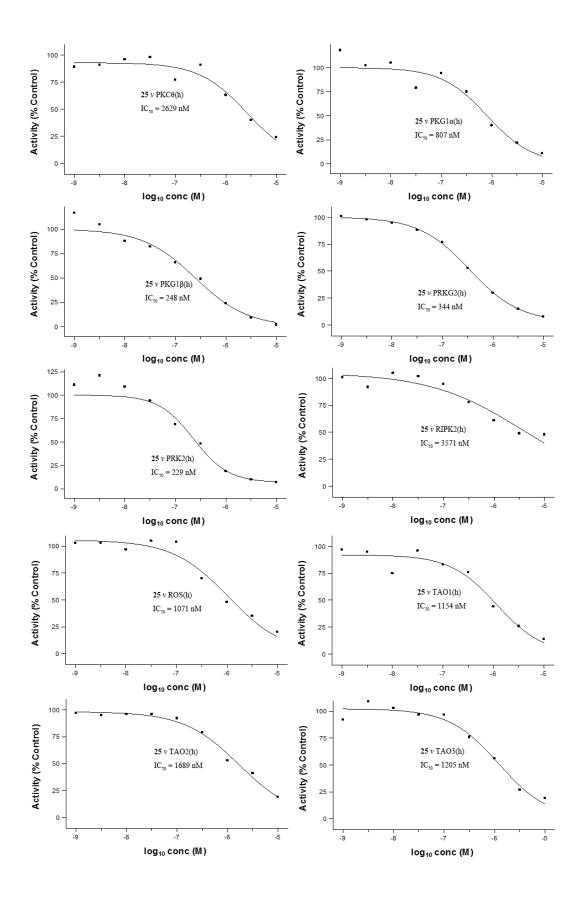
Figure S9. IC₅₀ curves of compound **25** on remaining kinases whose activity% @ 10 μ M is lower than 50%. In cases of CLKs and DYRKs, IC₅₀ values were determined in duplicates at 10 different concentrations. In other cases, IC₅₀ values were determined in singlicate at 10 different concentrations. [ATP] = 10 μ M. For detailed protocols, see http://www.eurofins.com/pharmadiscovery.

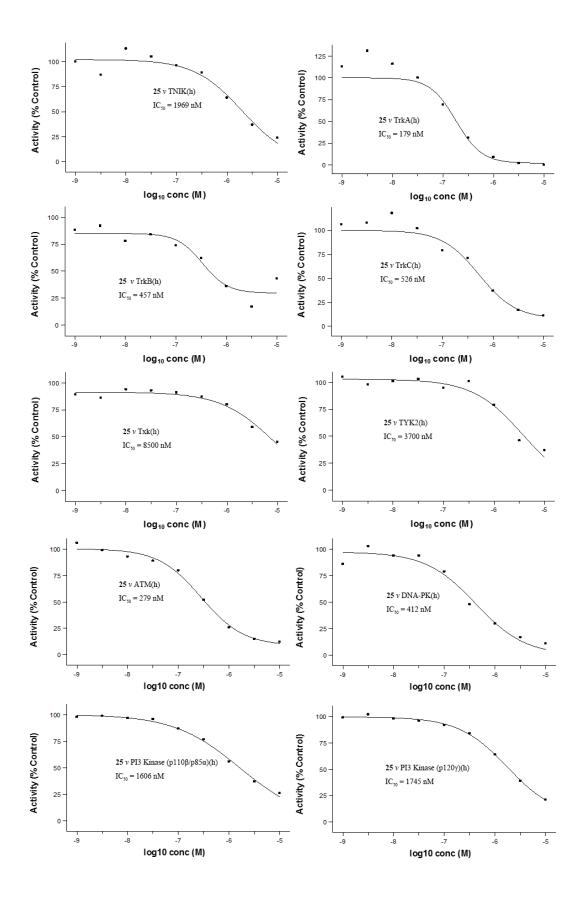


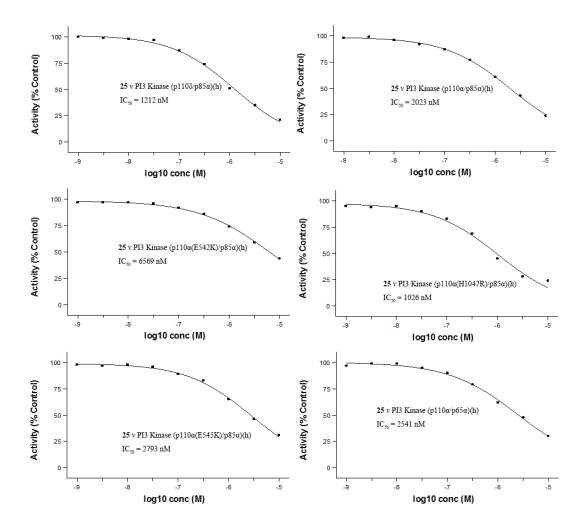




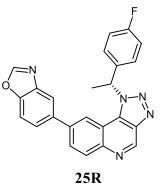








Synthesis and Structure Confirmation of Compound 25R (the Enantiomer of Compound 25)



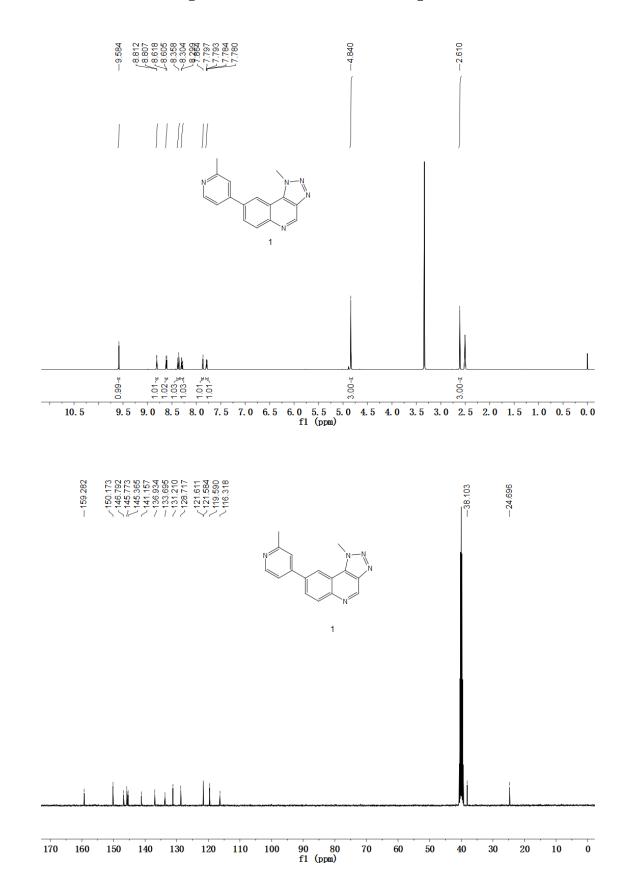
(*R*)-(+)-5-(1-(1-(4-Fluorophenyl)ethyl)-1*H*-[1,2,3]triazolo[4,5-*c*]quinolin-8yl)benzo[d]oxazole (25R). The title compound was prepared from 8f (50 mg, 135 μmol) and self-prepared 28 (33 mg, 135 μmol) using the procedure described for compound 1 in 84.3% yield as a white powder. [α] $_{D}^{25}$ = +238.74 (c = 0.191, CH₃Cl, ee 100%). ¹H NMR (400 MHz, DMSO) δ 9.63 (s, 1H), 8.87 (s, 1H), 8.52 (d, *J* = 1.6 Hz, 1H), 8.32 (d, *J* = 8.7 Hz, 1H), 8.24 (dd, *J* = 8.7, 1.9 Hz, 1H), 8.18 (d, *J* = 1.2 Hz, 1H), 8.00 (d, *J* = 8.3 Hz, 1H), 7.77 (dd, *J* = 8.3, 1.6 Hz, 1H), 7.32 (dd, *J* = 8.7, 5.4 Hz, 2H), 7.19 (t, *J* = 8.8 Hz, 2H), 7.06 (q, *J* = 6.7 Hz, 1H), 2.22 (d, *J* = 6.7 Hz, 3H). ¹³C NMR (101 MHz, DMSO) δ 163.26, 160.83, 155.64, 150.71, 145.43, 144.87, 141.37, 140.21, 139.22, 138.00, 137.97, 137.35, 133.14, 131.26, 129.35, 128.48, 128.39, 124.82, 121.53, 120.99, 116.59, 116.38, 115.70, 110.48, 60.08, 23.55. ESI-MS m/z 410.1 [M + H]⁺. HRMS m/z (ESI) calcd for C_{24H17}FN₅O [M + H]⁺ 410.1412; found, 410.1406. Chiral HPLC analysis (mobile phase: 2-propanol/n-hexane = 30/70, flow rate = 1.0 mL/min, λ = 255.9 nm, t_R = 45.89 min).

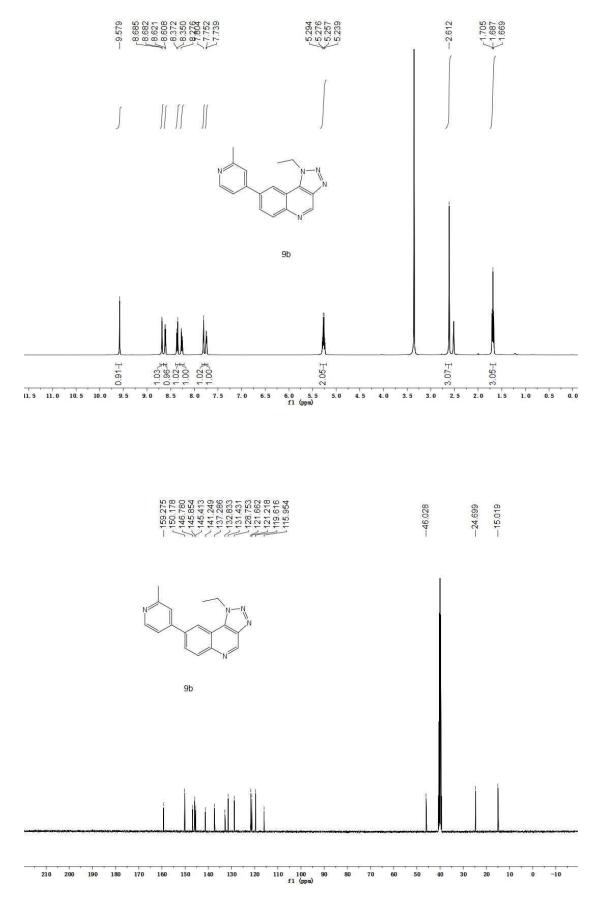
S24

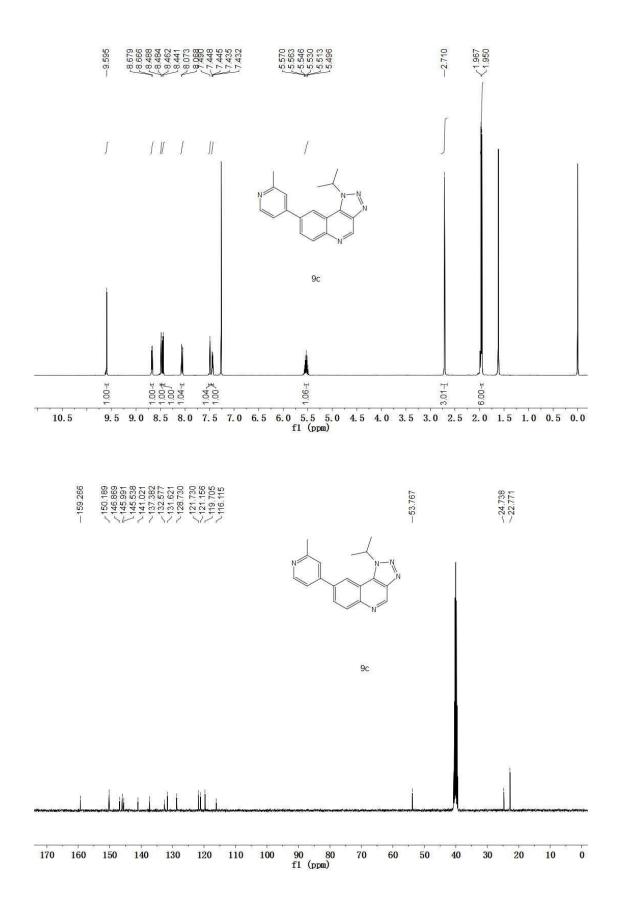
Pharmacokinetic Assessments of Compound 25.

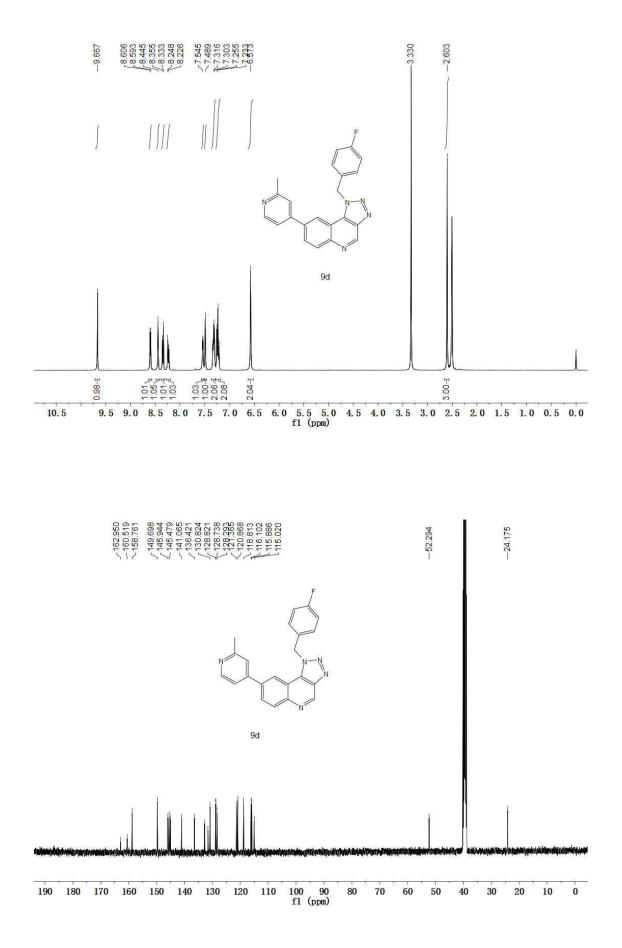
Catheters were surgically placed into the jugular veins of male Sprague–Dawley rats (Chinese Academy of Medical Science, Beijing, China) to collect serial blood samples. The animals were fasted overnight prior to dosing, and food was withheld until 4 h after dosing. Compound **25** was dissolved in 2.5% ethanol, 2.5% castor oil, and 95% saline for a concentration of 1 mg/mL. The rats $(200 \pm 10 \text{ g})$ were administered with a single dose of compound **25** (10 mg/kg) by intraperitoneal injection (n = 6) or intravenous injection (n = 6). Blood was collected in heparin-containing tubes at indicated time points and centrifuged at 4 °C immediately to obtain plasma. The plasma concentration of **25** were measured by high performance liquid chromatography (HPLC) with tandem mass spectrometric detection (3200 QTRAP system, Applied Biosystems). Non-compartmental pharmacokinetic parameters were obtained from the plasma concentration–time profiles using DAS software (Enterprise, version 2.0, Mathematical Pharmacology Professional Committee of China). At last, all surviving animals were transferred to the repository or euthanized after completing the test.

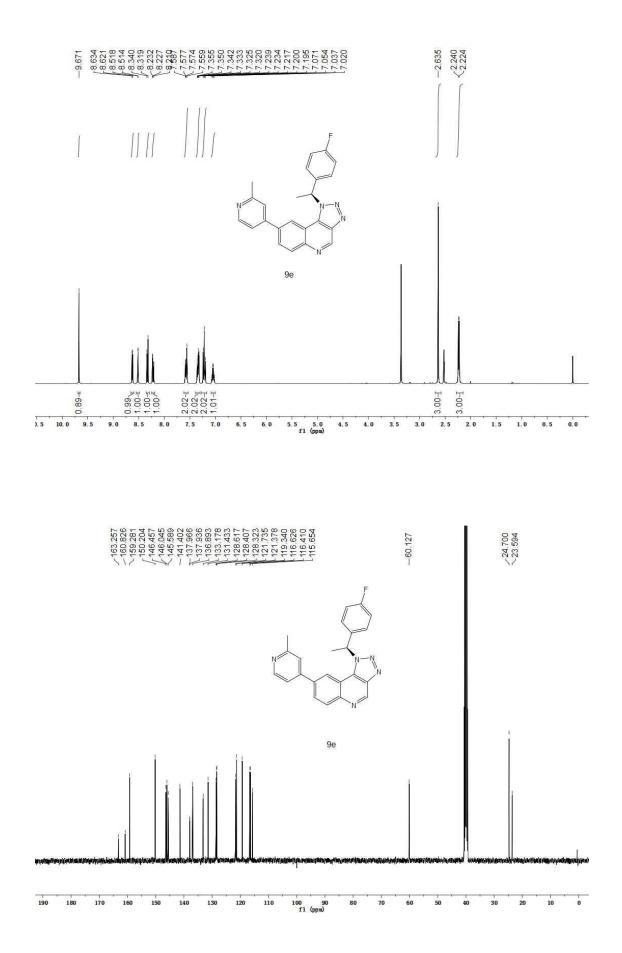
Copies of ¹H- and ¹³C-NMR Spectra

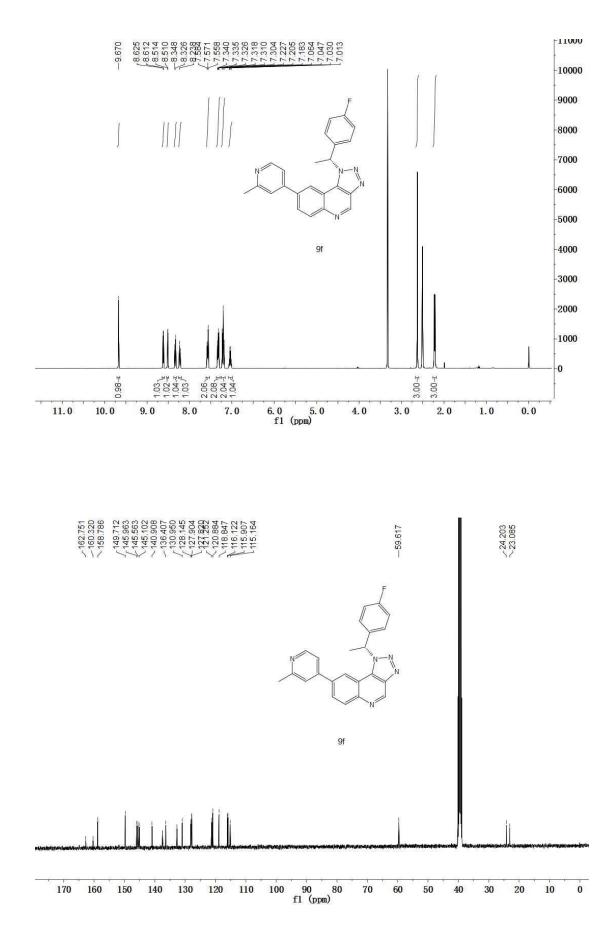




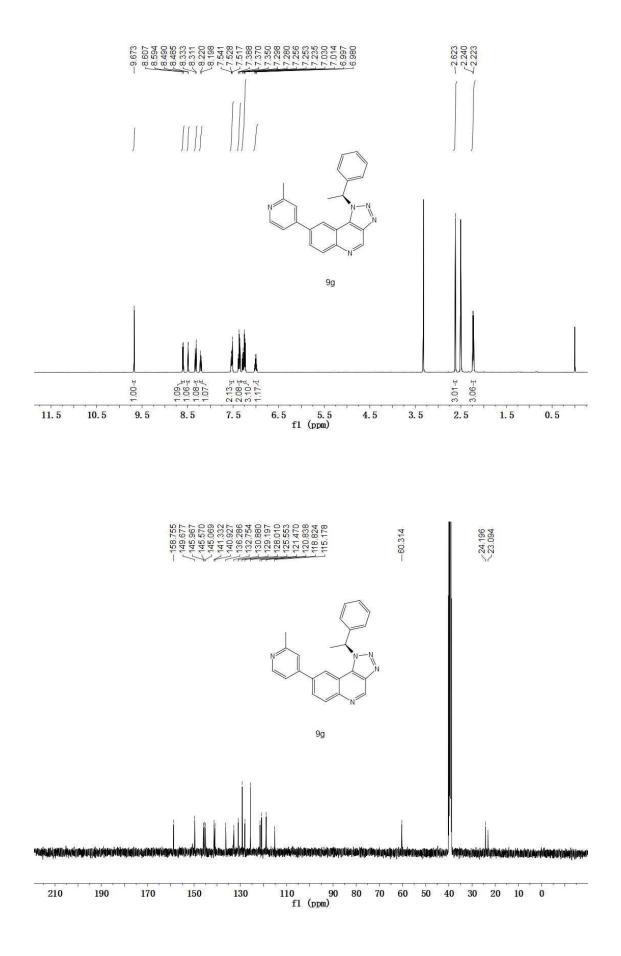


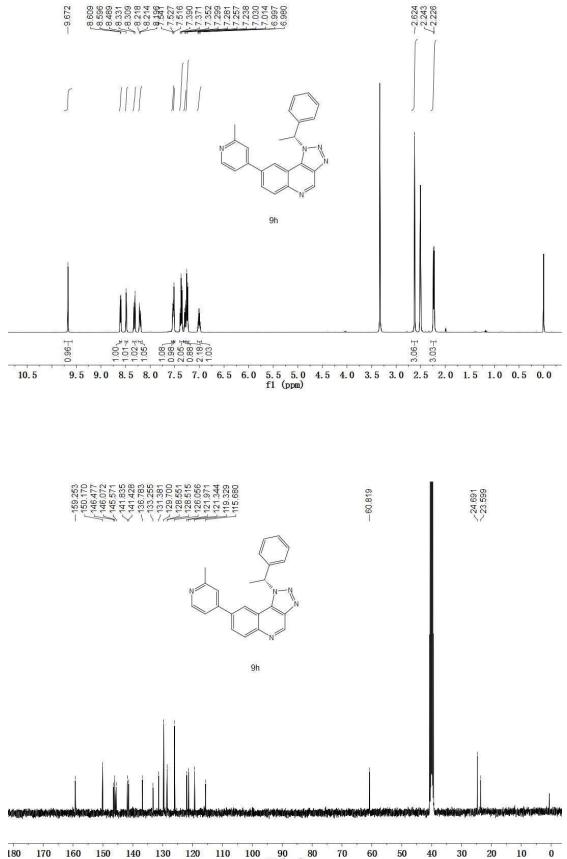


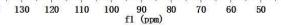


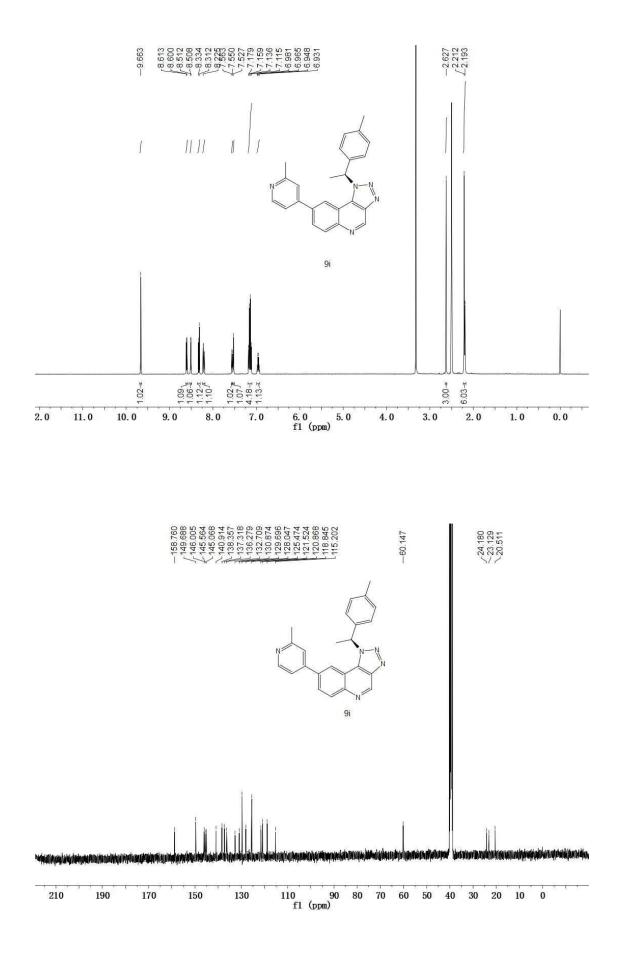


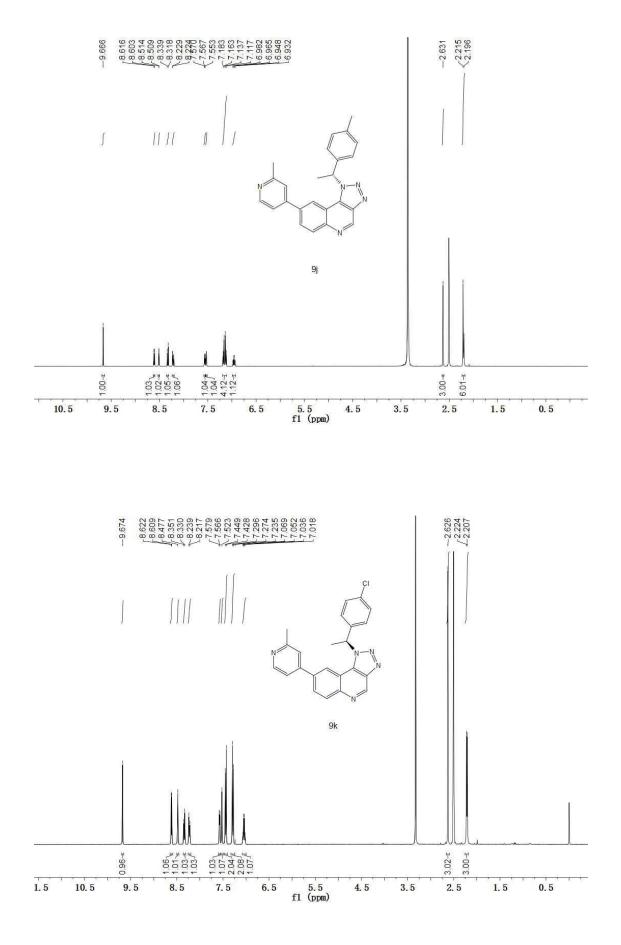


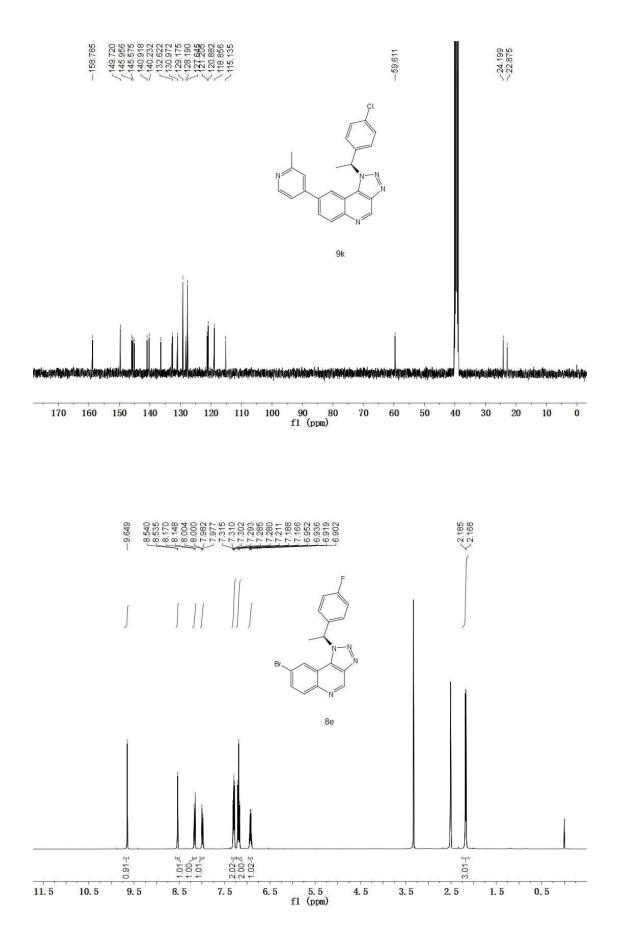


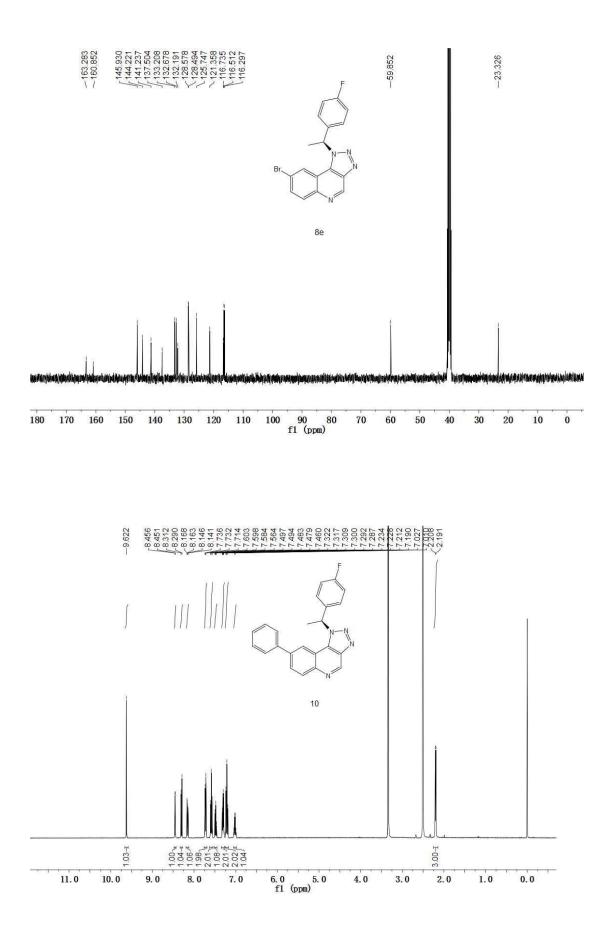


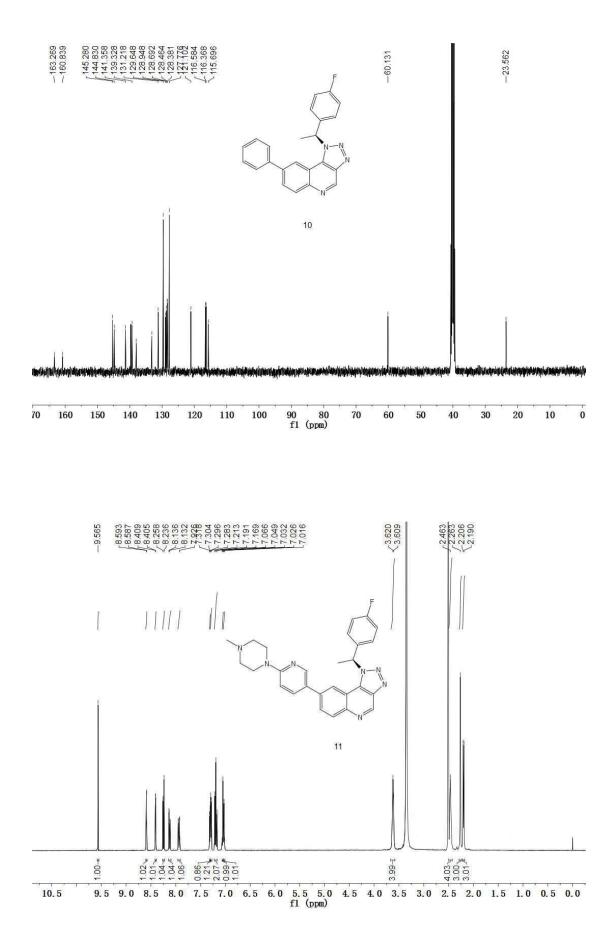


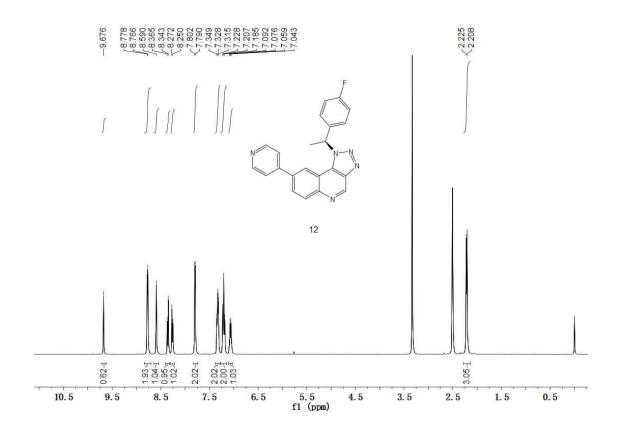


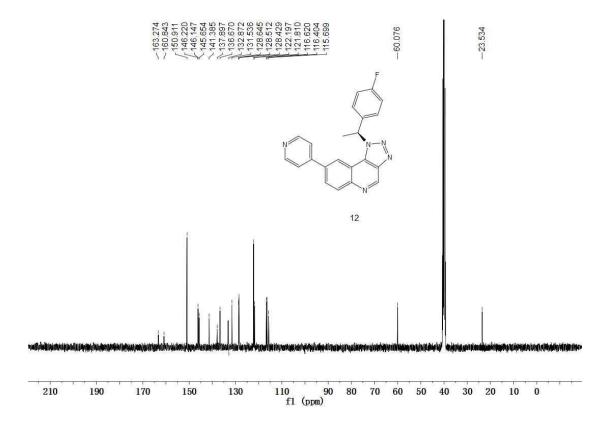


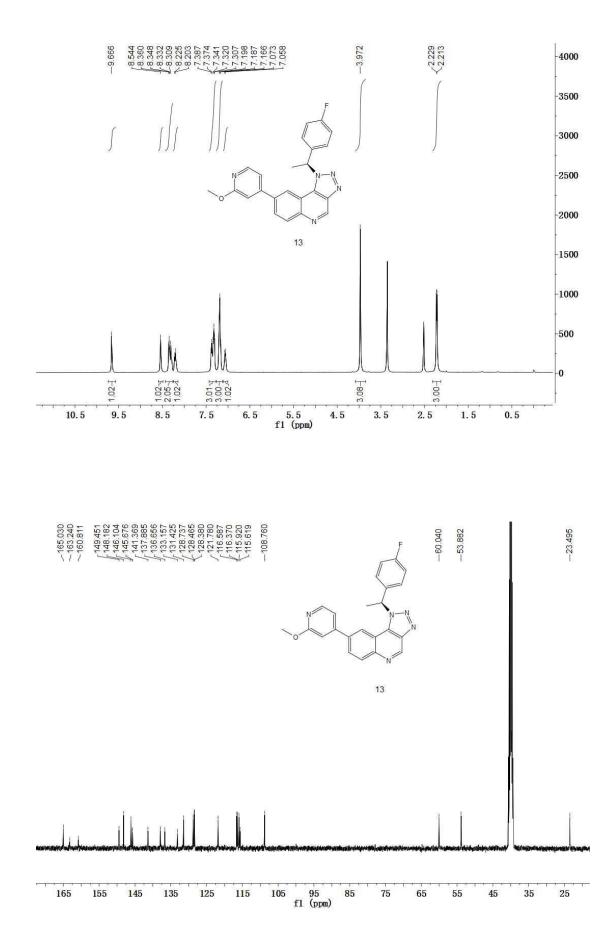


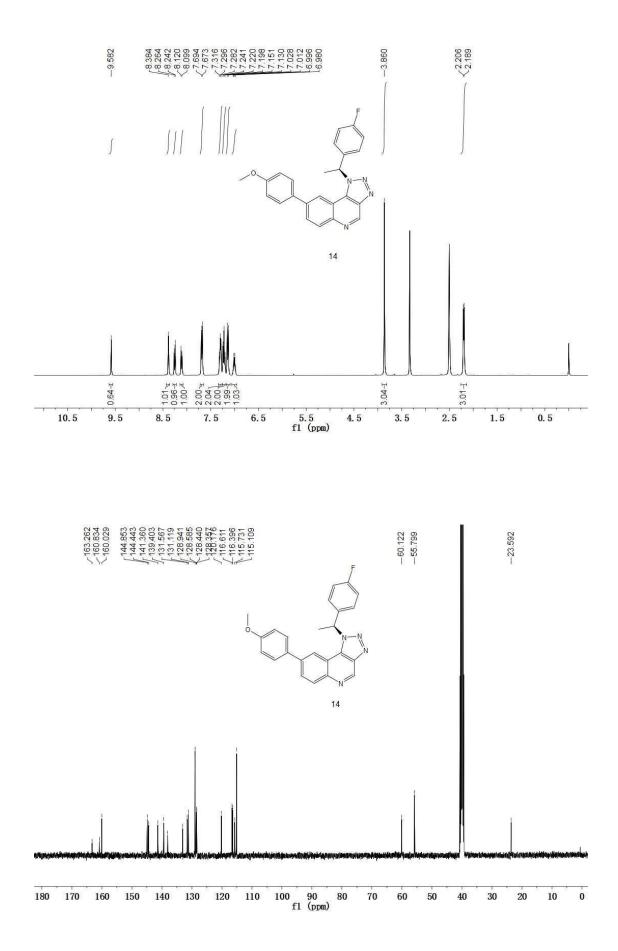




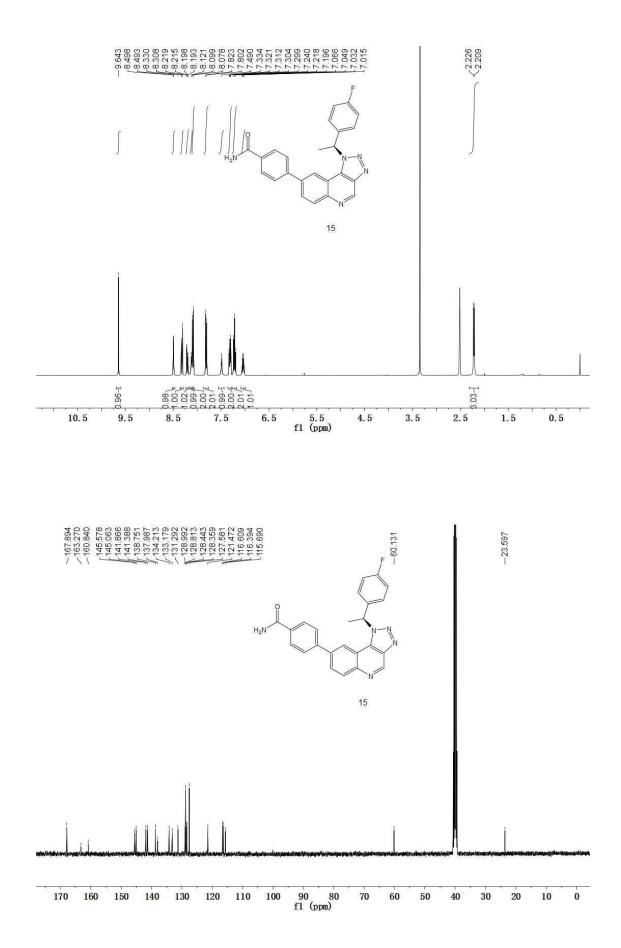




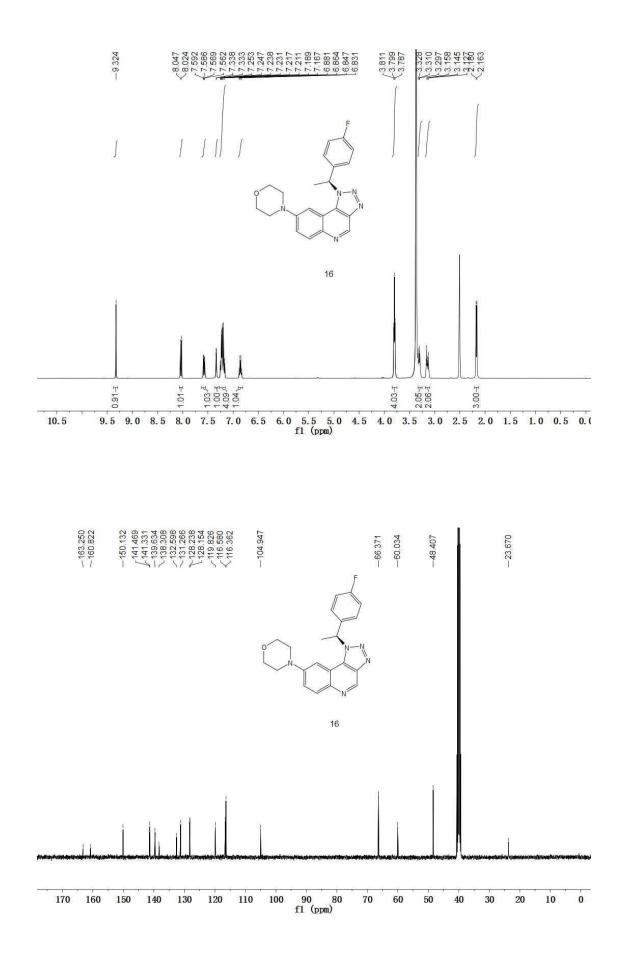


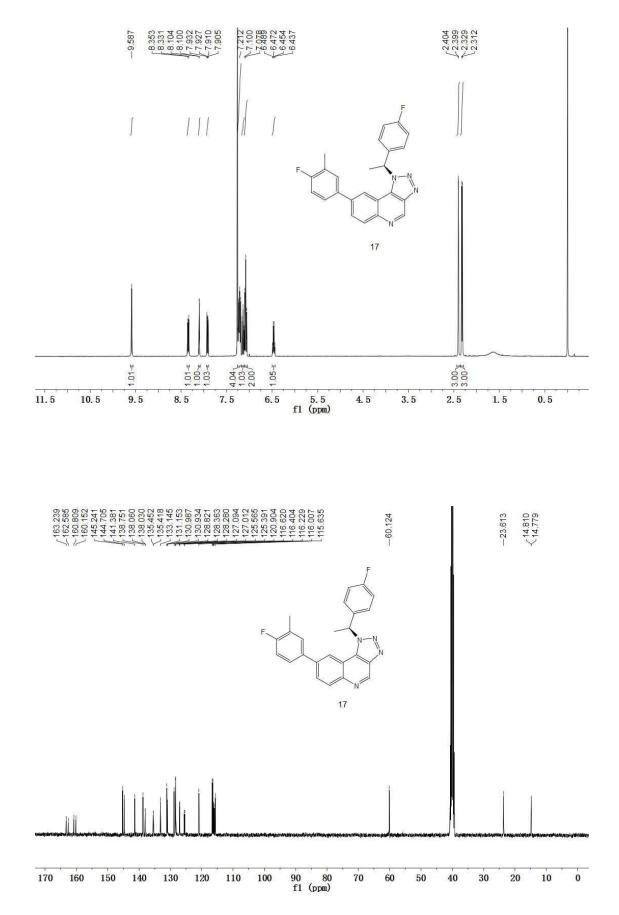


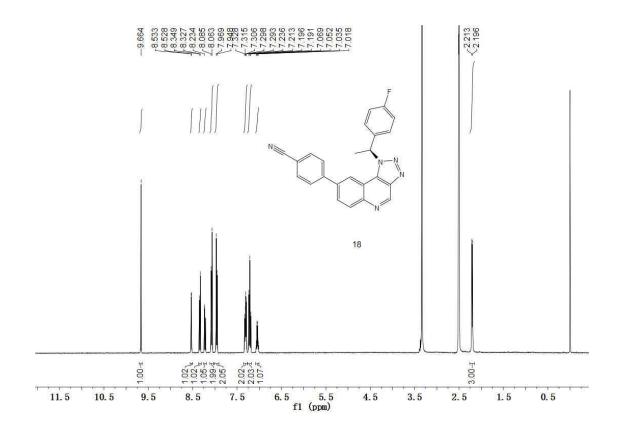
S41

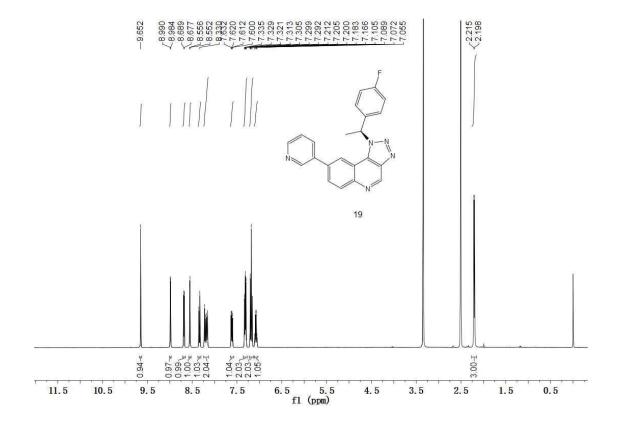


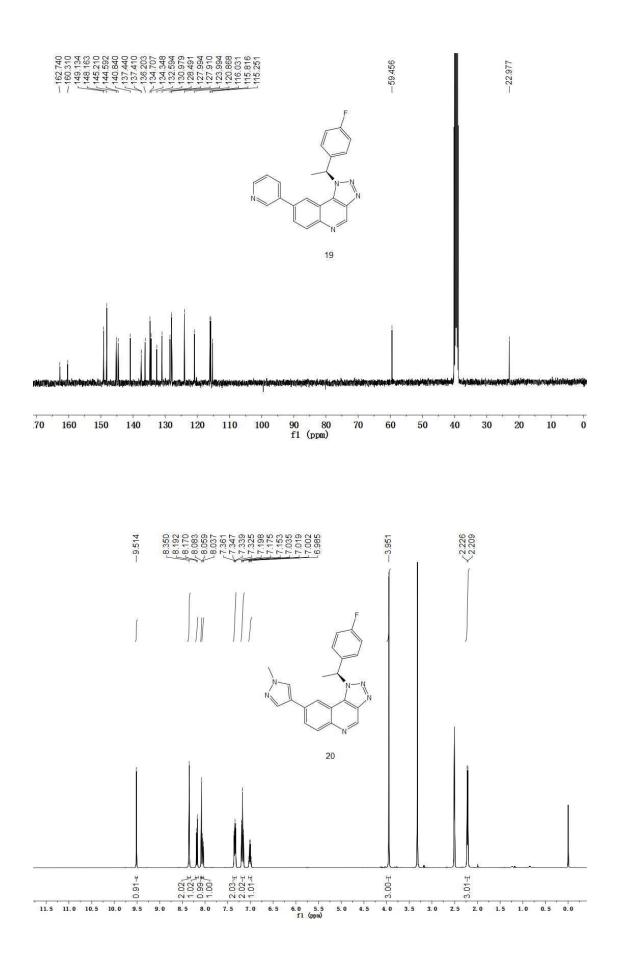
S42

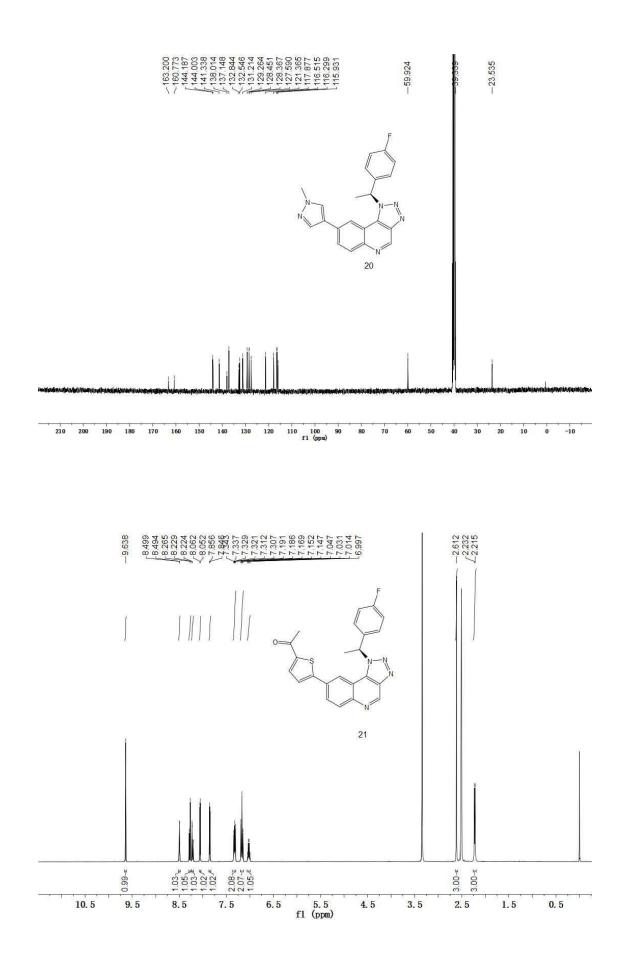


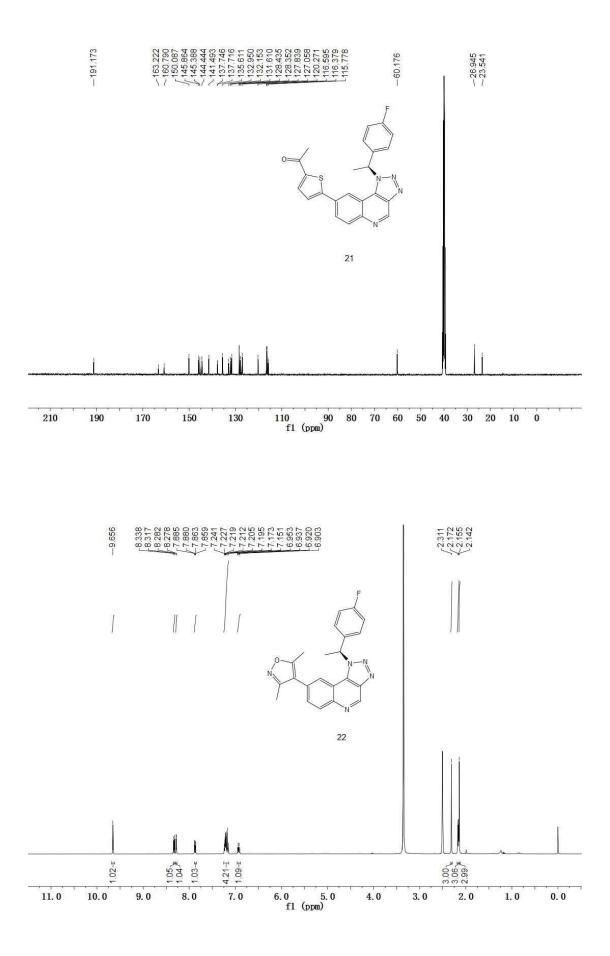




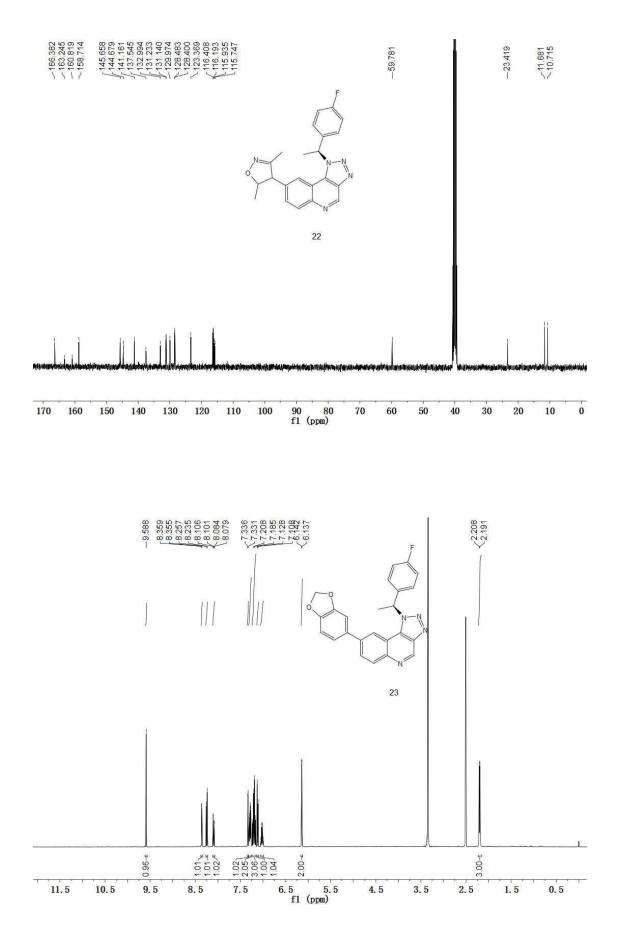


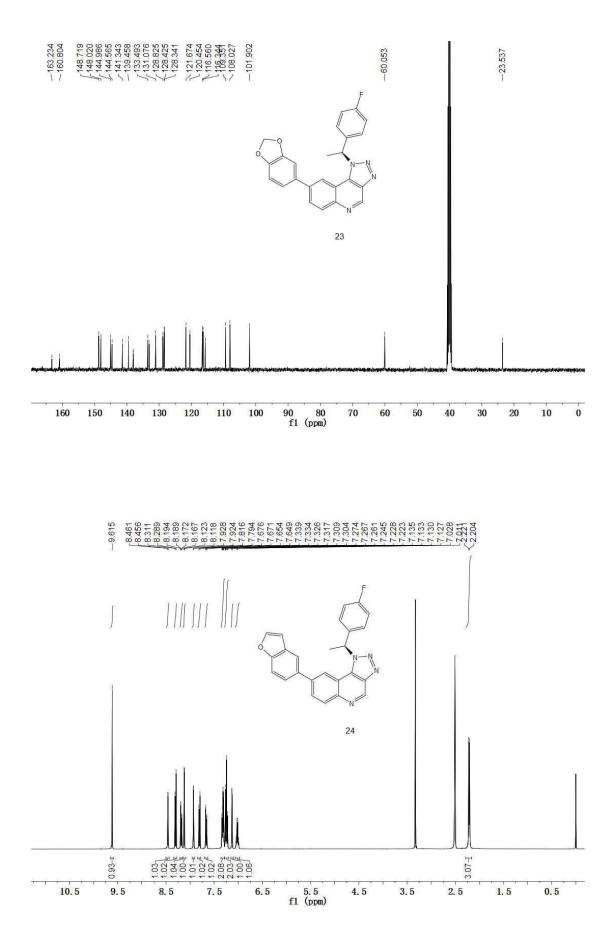


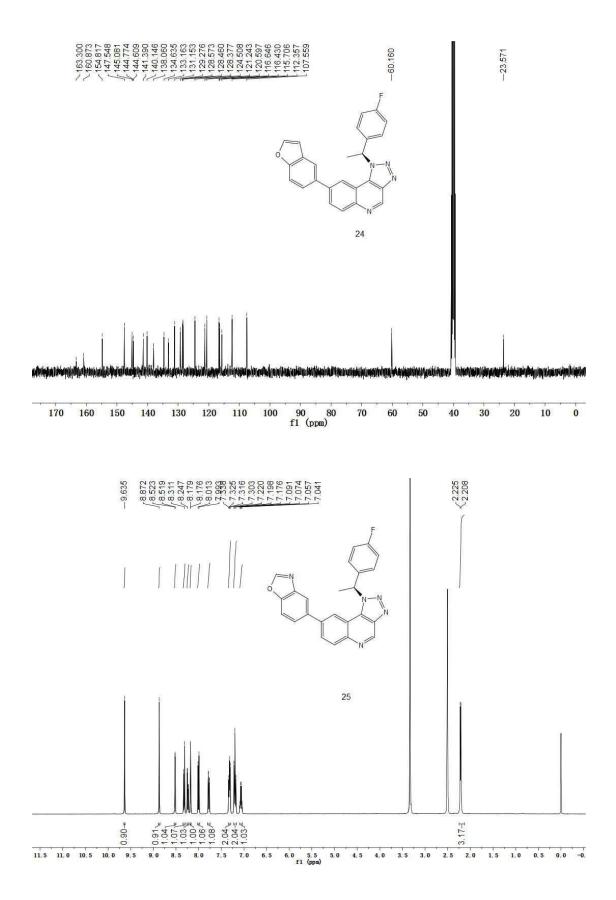


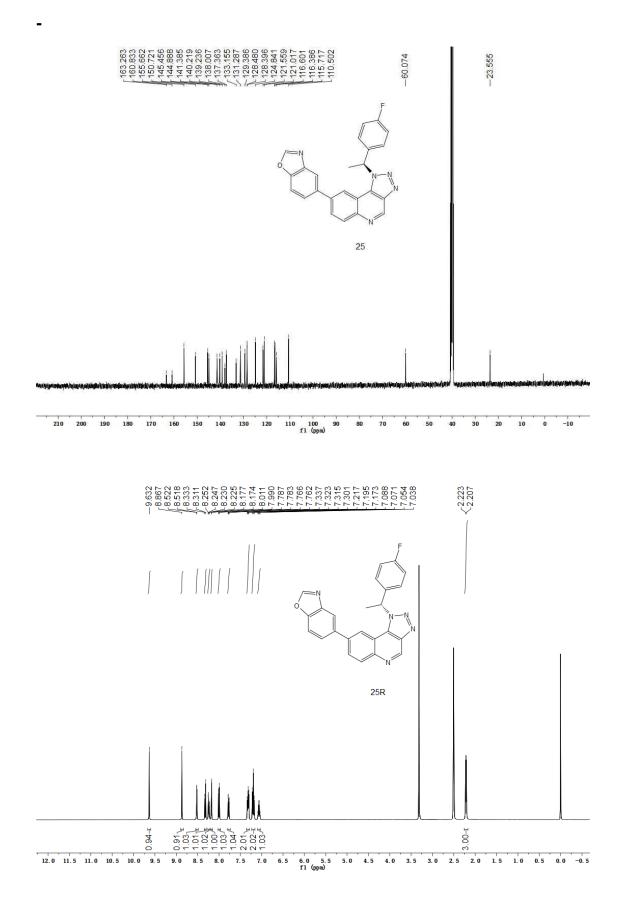


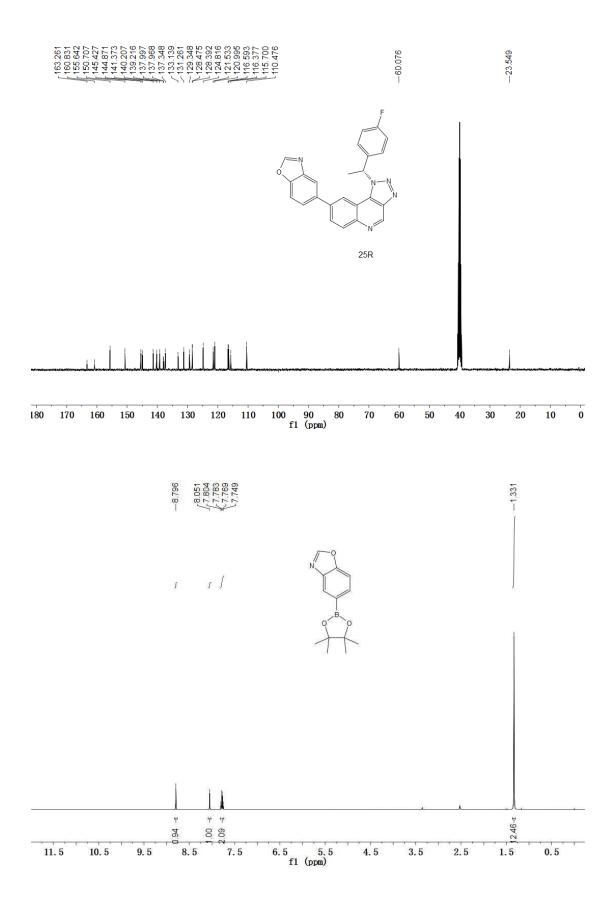
S48

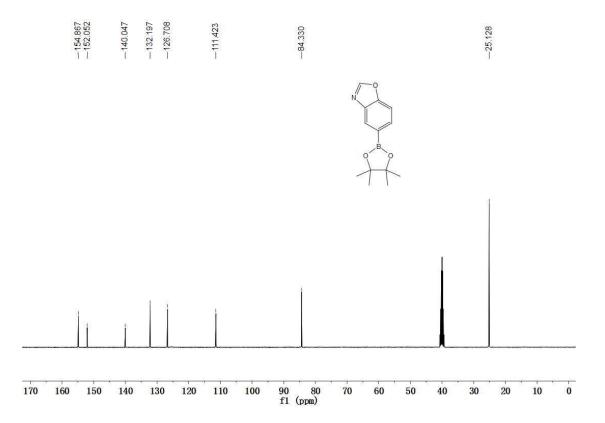


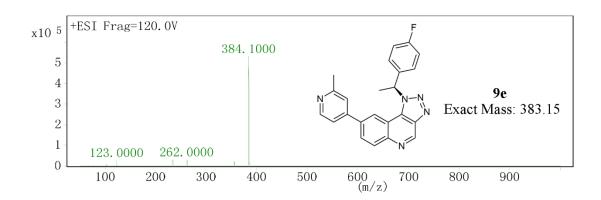




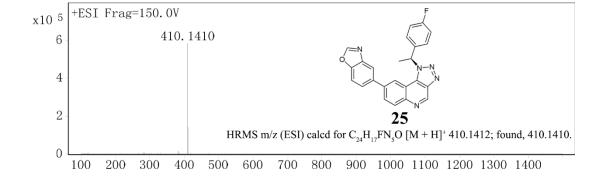


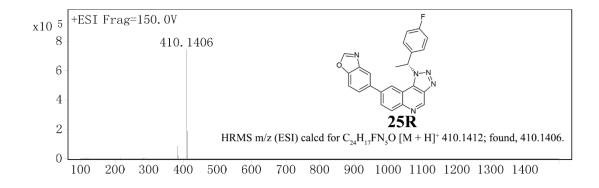


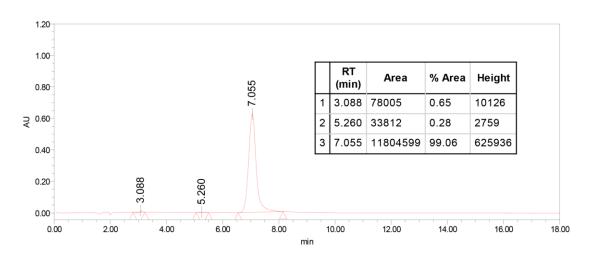




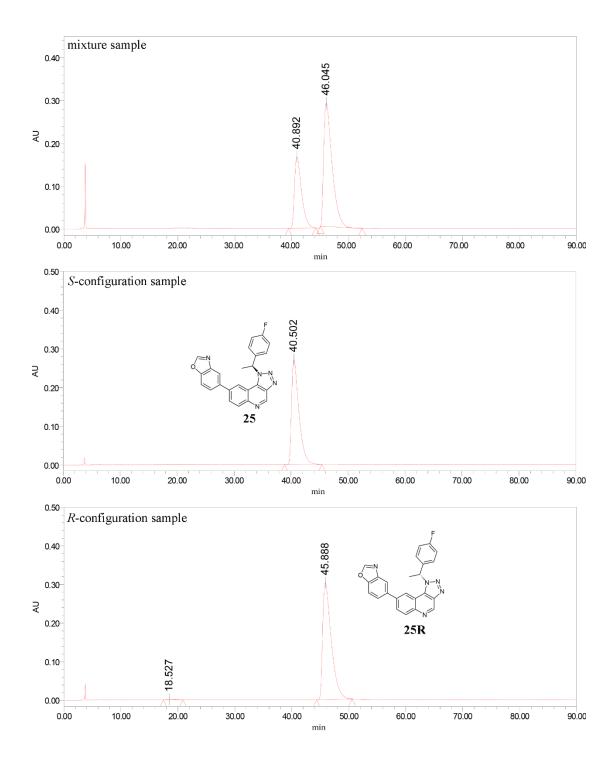
Copies of MS Spectra







HPLC Purity Analysis for Compound 25



Confirmation of Enantiomeric Purity of Compound 25