

Discovery of Boron-conjugated 4-Anilinoquinazoline as a Prolonged Inhibitor of EGFR Tyrosine Kinase

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1. Molecular Docking and Quantum Mechanical Simulations

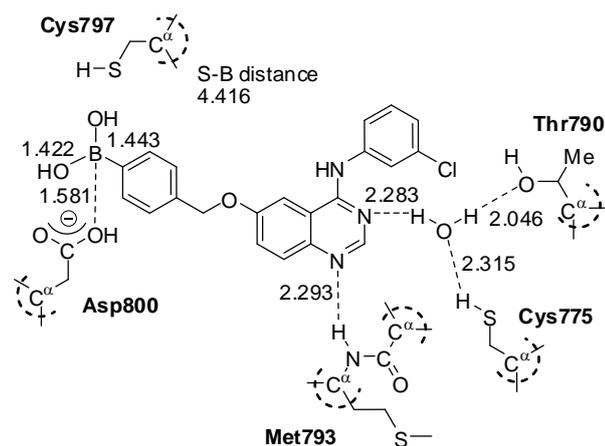


Fig. S1 QM/MM optimized geometries for an EGFR-compound **7d** docking mode (model 1).

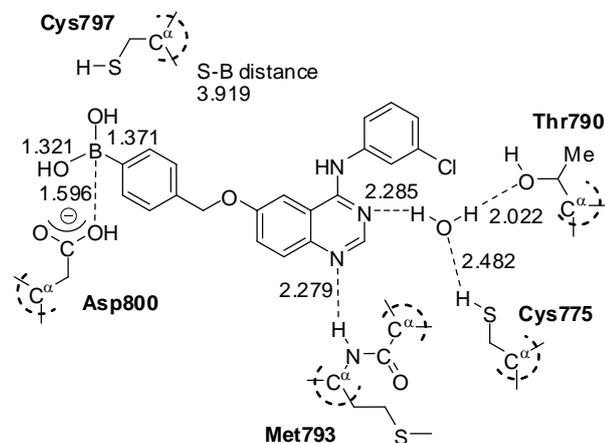


Fig. S2 QM/MM optimized geometries for an EGFR-compound **7d** docking mode (model 2).

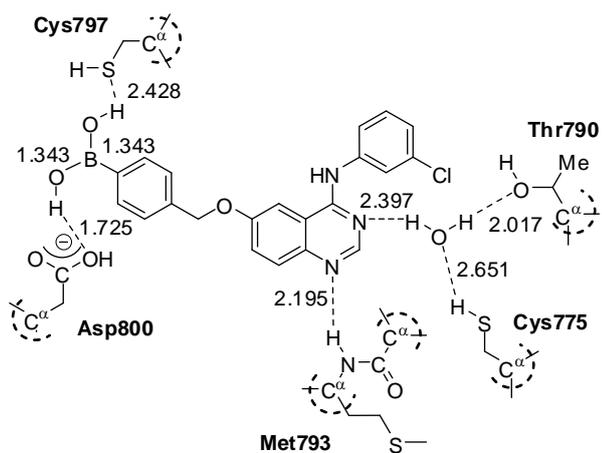
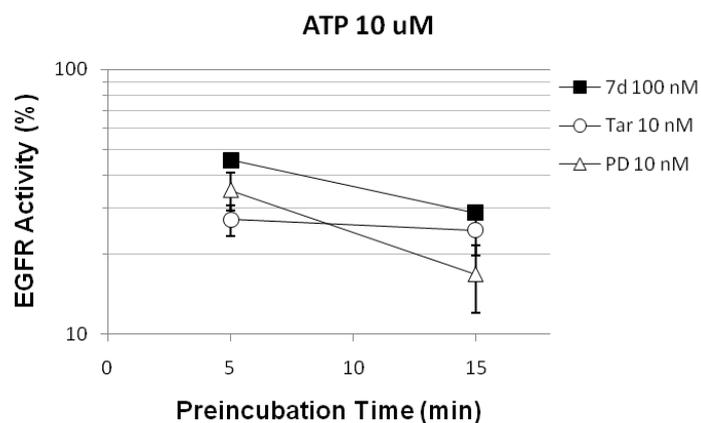


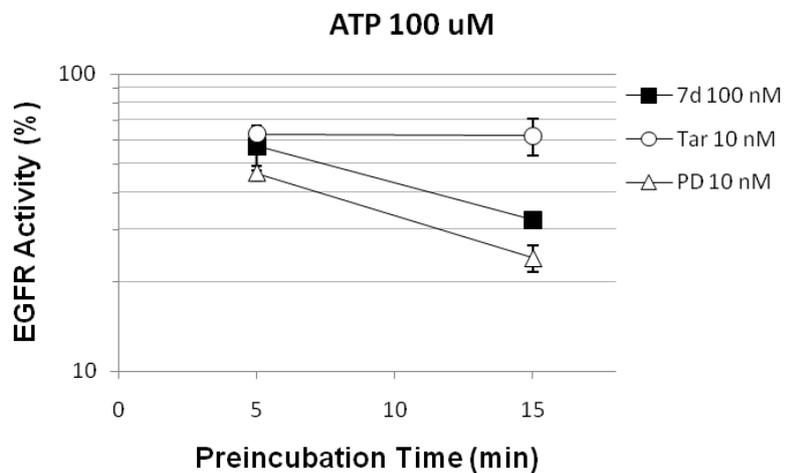
Fig. S3. QM/MM optimized geometries for an EGFR-compound **7d** docking mode (model 3).

2. Additional *in vitro* irreversible inhibition study of EGFR tyrosine kinase activity

(A)



(B)



(C)

	ATP (μM)	EGFR Activity (%)	
		5 min	15 min
7d (100 nM)	10	45.6 ± 0.8	28.7 ± 1.2
	100	57.1 ± 9.8	32.3 ± 1.6
Tar (10 nM)	10	27.0 ± 3.6	24.7 ± 4.9
	100	62.8 ± 1.6	61.9 ± 8.6
PD (10 nM)	10	34.9 ± 5.7	16.8 ± 4.9
	100	46.4 ± 2.6	24.0 ± 2.4

Fig. S4. Effects of ATP concentration on *in vitro* preincubation-time-dependent EGFR inhibition by compound **7d**. EGFR was incubated in kinase assay buffer with 100 nM compound **7d**, 10 nM Tarceva (Tar), or 10 nM PD168393 (PD). After incubation for 5 and 15 min, kinase assay was initiated by adding 10 μM ATP (A) or 100 μM ATP (B), and phosphorylation of the poly(Glu:Tyr) substrate was detected. (C) Percent of EGFR activity represent mean \pm s.d.

3. ^1H NMR spectra for compounds 2-4

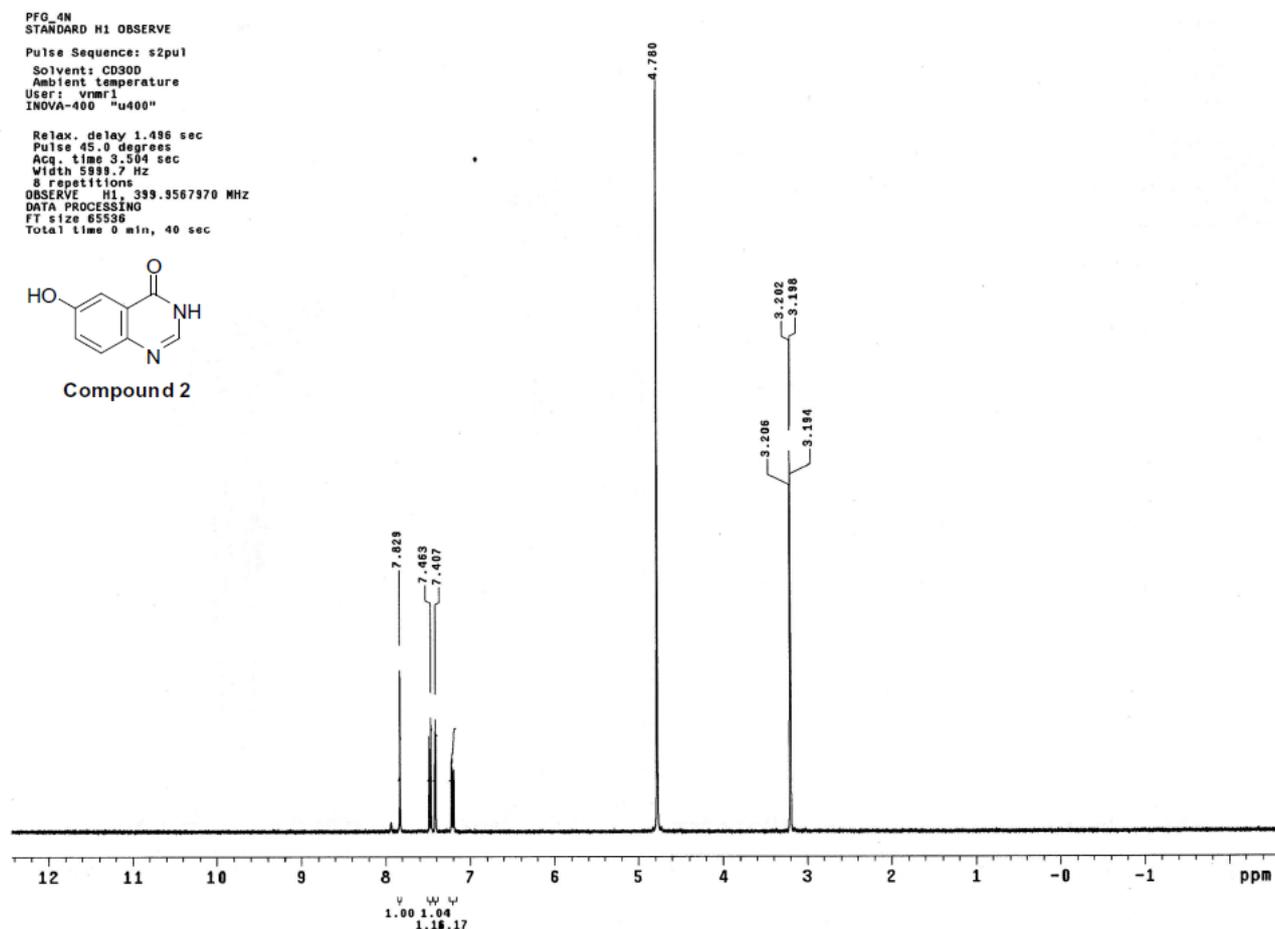


Fig. S5. ^1H NMR (400 MHz, CDCl_3) of compound **2**.

PFG_4H
STANDARD H1 OBSERVE
Pulse Sequence: s2pu1
Solvent: CDCl3
Ambient temperature
User: vnmr1
INOVA-400 "u400"

Relax. delay 1.496 sec
Pulse 45.0 degrees
Acq. time 3.504 sec
Width 5999.7 Hz
8 repetitions
OBSERVE H1, 399.9551780 MHz
DATA PROCESSING
FT size 65536
Total time 0 min, 40 sec

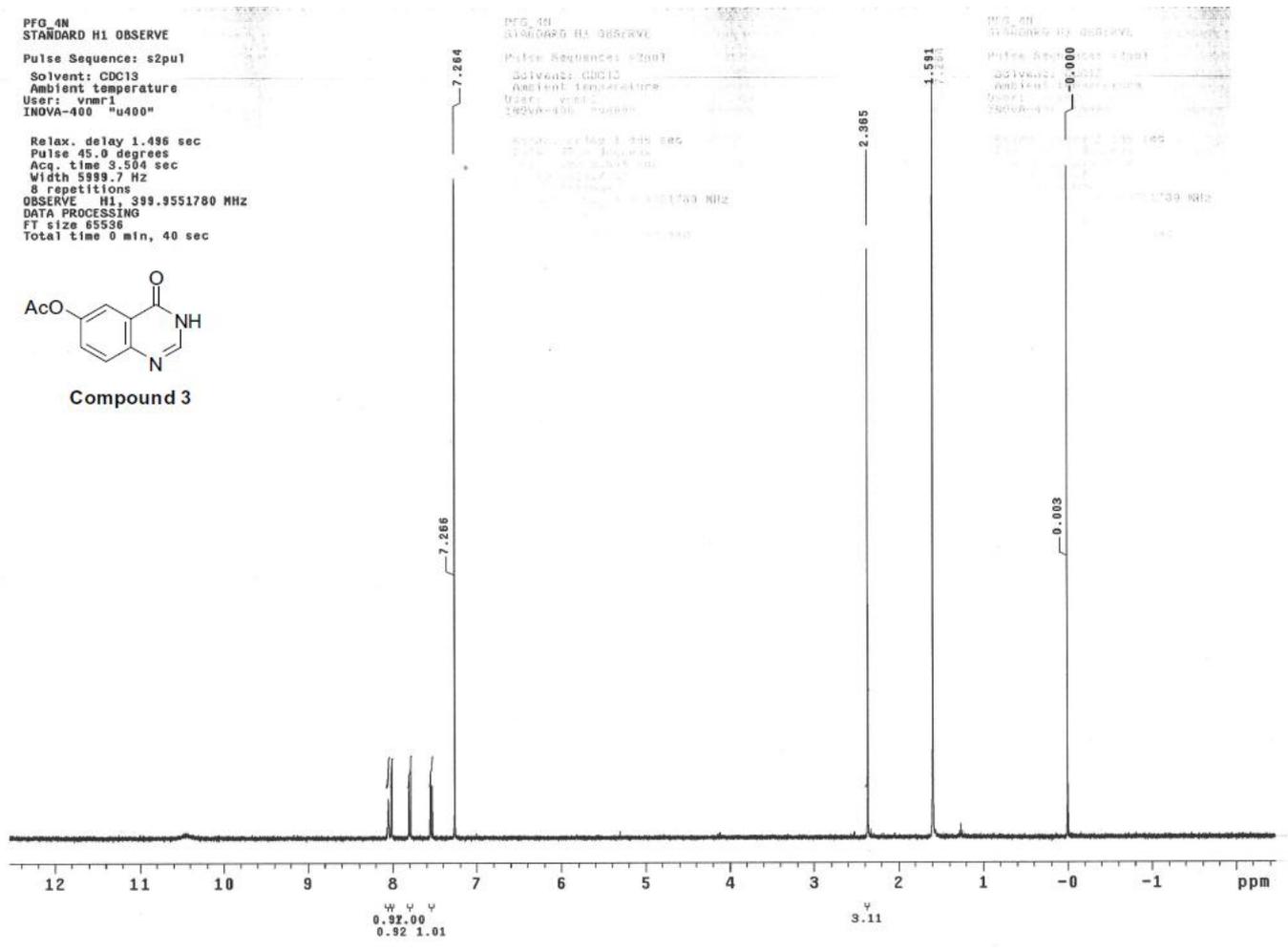


Fig. S6. ¹H NMR (400 MHz, CDCl₃) of compound 3.

