

Supporting Information

Targeting a Targeted Drug: An Approach Toward Hypoxia-Activatable Tyrosine Kinase Inhibitor Prodrugs

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Figure S1. ¹H NMR spectrum of compound **1a**.



Figure S2. ¹³C NMR spectrum (broadband proton decoupled, j-modulated) of compound 1a.



Figure S3. ¹H NMR spectrum of compound **1b**.



Figure S4. ¹³C NMR spectrum (broadband proton decoupled, j-modulated) of compound 1b.



Figure S5. ¹H NMR spectrum of compound **2a**.



Figure S6. ¹³C NMR spectrum (broadband proton decoupled, j-modulated) of compound 2a.



Figure S 7. ¹H NMR spectrum of compound 2b.



Figure S8. ¹³C NMR spectrum (broadband proton decoupled, j-modulated) of compound 2b.



Figure S9. ¹H NMR spectrum of compound **2c**.



Figure S10. ¹³C NMR spectrum (broadband proton decoupled, j-modulated) of compound 2c.



Figure S11. Time curve of compound **1a** in 10 mM phosphate buffer, 1% DMSO, pH 7.4, at 37°. Reactions were followed by HPLC.



Figure S12. Time curve of compound 1b in 10 mm phosphate buffer, 1% DMSO, pH 7.4, at 37°. Reactions were followed by HPLC.



Figure S13. Time curve of compound 2a in 10 mM phosphate buffer, 1% DMSO, pH 7.4, at 37°. Reactions were followed by HPLC.



Figure S14. Time curve of compound 2b in 10 mm phosphate buffer, 1% DMSO, pH 7.4, at 37°. Reactions were followed by HPLC.



Figure S15. Time curve of compound 2c in 10 mM phosphate buffer, 1% DMSO, pH 7.4, at 37°. Reactions were followed by HPLC.



Figure S16. Release of sunitinib from prodrug **1b** (2.5 μ M) upon incubation with NADH (50 μ M) and NTR (1.33 μ g/mL) at 37°C. Reactions were followed by HPLC.



Figure S17. Release of erlotinib from prodrug **2a** (2.5 μ M) upon incubation with NADH (50 μ M) and NTR (1.33 μ g/mL) at 37°C. Reactions were followed by HPLC.



Figure S18. Release of erlotinib from prodrug **2b** (2.5 μ M) upon incubation with NADH (50 μ M) and NTR (1.33 μ g/mL) at 37°C. Reactions were followed by HPLC.



Figure S19. Release of **2b** from prodrug **2c** (2.5μ M) upon incubation with NADH (50μ M) and NTR (1.33μ g/mL) at 37° C. Reactions were followed by HPLC.



Figure S20. Grid sizes for (A) sunitinib in complex with VEGFR-2 (PDB ID: 4AGD), and (B) erlotinib in complex with EGFR (PDB ID: 1M17). Proteins are depicted in ribbon representation while compounds are shown in capped stick representation. Pictures were generated using Pymol.

VGFR2 (4AGD)	Score (kcal/mol)	EGFR (1M17)	Score (kcal/mol)
Sunitinib docked	- 9.1	Erlotinib docked	- 10.6
1a	- 7.3	2a	- 8.3
1b	- 7.7	2c	- 8.4
		2b	- 7.8

Lys920 Han a Phe1047 mit HOH2037 Phe918 u840 Cys919 Val916 JULI 'IT Ala866 Leu1035 Glu917 Val899

Table S1. Docking scores of docked erlotinib, sunitinib, 1a, 1b, and 2a – c.

towards the ligand atoms they contact. The contacted atoms are shown with spokes radiating back.



Figure S22. Schematic 2D diagram of protein-ligand interactions for VEGFR-2 in complex with (A) **1a**, and (B) **1b**. VEGFR-2 structure was obtained from PDB ID: 4AGD. Hydrogen bonds are indicated by dashed lines, while hydrophobic contacts are represented by an arc with spokes radiating towards the ligand atoms they contact. The contacted atoms are shown with spokes radiating back.