Supporting Information

Generating selective leads for Mer kinase inhibitors – example of a comprehensive lead-generation strategy

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Assay	ATP concentration	Standard deviation	
Mertk	K _m	0.42	
Mertk	1 mM	0.53	
Axl	K _m	0.30	
Tyro3	K _m	0.36	
Flt3	K _m	0.52	

Table SI1. Standard deviations for potency measurements in assays calculated for all compounds. ATP concentrations in potency assays are at K_m , unless stated otherwise.

Cpd	Mertk plC ₅₀ [ATP]=K _m	Mertk pIC ₅₀ [ATP]=1mM
1	8.8	8.6
2	6.6	6.1
3	7.0	6.0
4	9.1	8.6
5	7.3	6.5
6	7.3	6.4
7	6.4	5.5 ^a
8	6.1	5.3
9	6.9	5.8
10	7.3	5.9
11	8.2	7.3
12	8.5	7.7
13	7.6	6.6
14	8.3	8.4
15	8.3	7.5
16	7.9	6.7ª
17	7.2	6.5
18	7.6	6.2 ^a
19	6.9	6.4
20	7.0	6.1

Table SI2. Mertk activity in assay with increased ATP level (1mM). The Mertk data measured at K_m level of ATP is shown for comparison.

21	6.1	6.0
22	6.2	5.4
23	6.2	-

Mean of at least two independent measurements unless otherwise stated. See Table S1 for standard deviation of measurement. ^{*a*} Tested n=1.



Table SI3. Kinase selectivity profiles of DECL hits **12-14**. Inhibition values for panel of kinases, compound tested at 1μ M (131, 131, 125 kinases tested for **12**, **13**, **14** respectively).

PDB accession code	Compound #	MerTK protein construct	Experiment Type	Crystallisation conditions
7AVX	1	His6-thrombin-MerTK (E571-V864)	Co-Crystallisation	4 M NaCl, 0.1 M Tris pH 8.5
7AVY	2	MerTK (E571-V864)	Co-Crystallisation	1.8 M Li2SO4, 0.1 M PCTP pH 6.5
7AVZ	5	MerTK (E571-V864) K591R/K693R/K702R/K856R	Soak	4-4.5 M NaCl, 0.08 M Tris pH 8.5
7AW0	9	MerTK (E571-V864) K591R/K693R/K702R/K856R	Soak	4-4.5 M NaCl, 0.08 M Tris pH 8.5
7AW1	11	MerTK (E571-V864) K591R/K693R/K702R/K856R	Soak	4-4.5 M NaCl, 0.08 M Tris pH 8.5
7AW2	14	MerTK (E571-V864) K591R/K693R/K702R/K856R	Soak	4-4.5 M NaCl, 0.08 M Tris pH 8.5
7AW3	12	MerTK (E571-V864) K591R/K693R/K702R/K856R	Soak	4-4.5 M NaCl, 0.08 M Tris pH 8.5
7AW4	13	His6-thrombin-MerTK (E571-V864)	Co-Crystallisation	0.2 M MgCl2, 25 % PEG3350, 0.1 M PCPT pH 7.5

 Table SI4. Experimental details for crystal structures.

Table SI5. – Assay descriptions for Axl and Flt3 GLO assays.

In a few instances (as annotated in the tables), Axl and Flt potency was determined in GLO technology assays rather than Rapidfire LCMS assays. Correlation between Rapidfire MS and GLO assay potency data was observed to be good (data not shown). Experimental details for the GLO assays can be found below.

Axl ATP GLO

The ability of inhibitors to cause inhibition of AXL (GST-AXL(464-885) *in vitro* was assessed using the ADP GLO technology (Promega) that quantifies the conversion of ATP to ADP. AXL (25 nM) in assay buffer (20 mM HEPES pH 7.5, 0.005% Brij-35, 0.5 mM TCEP, 10 mM Mg(OAc)₂, 0.01% Pluronic-F127) was added to compound plates using a liquid dispenser, Certus. Assay plates were equilibrated for 30 min at rt before initiating the reaction by addition of Axltide (75 μ M final) and ATP (140 μ M final) substrates in assay buffer. The reaction was allowed to progress for 40 min at rt before the addition of ADP GLO R1 reagent and incubation for 60 min at rt, followed by the addition of ADP GLO R2 reagent and a further 30 min incubation at rt. The plates where then read on an Envision plate reader employing a Luminescent protocol. The dose-response curves were fit to the data using the non-linear regression analysis; 4 parameter logistic smart fit method in the Assay analyser and Condoseo applications of the Genedata Screener® software (Genedata, Inc., Basel, Switzerland).

Flt3 ATP GLO

The ability of inhibitors to cause inhibition of FLT3 (GST-TEV-6His-FLT3(564-993)-Thrombin-Avi-Flag) in vitro was assessed using the ADP GLO technology (Promega) that quantifies the conversion of ATP to ADP. FLT3 (30 nM) in assay buffer (20 mM HEPES pH 7.5, 0.005% Brij-35, 0.5 mM TCEP, 10 mM Mg(OAc)2, 0.01% Pluronic-F127) was added to compound plates using a liquid dispenser, BioRaptr. Assay plates were equilibrated for 30 min at 22 °C before initiating the reaction by addition of Axltide (30 μ M final) and ATP (400 μ M final) substrates in assay buffer. The reaction was allowed to progress for 90 min, at 22 °C, before the addition of ADP GLO R1 reagent and incubation for 60 min at rt, followed by the addition of ADP GLO R2 reagent and a further 60 min incubation at rt. The plates where then read on an Envision plate reader employing a Luminescent protocol. The dose-response curves were fit to the data using the non-linear regression analysis; 4 parameter logistic smart fit method in the Assay analyser and Condoseo applications of the Genedata Screener® software (Genedata, Inc., Basel, Switzerland).
 Table SI6.
 Selection conditions for DECL experiments.

The following constructs and conditions were applied in DECL selection experiments.

Mer-long: construct 528-999; Mer-short: construct 571-864; NTC: non-target control

ATP was used at a concentration of 5 mM.

Construct	State	Resin	Condition
NTC		Ni-NTA	
6His-Mer(R528-M999)-Thrombin-Avi-Flag	Activated	Ni-NTA	
6His-Mer(R528-M999)-Thrombin-Avi-Flag	Partially	Ni-NTA	
	dephosphorylated		
6His-Mer(R528-M999)-Thrombin-Avi-Flag	Dephosphorylated	Ni-NTA	
6His-thrombin-Mer(E571-V864)		Ni-NTA	
6His-thrombin-Mer(E571-V864)	Activated	Ni-NTA	
6His-Mer(R528-M999)-Thrombin-Avi-Flag	Partially	Ni-NTA	+ ATP
	dephosphorylated		
6His-thrombin-Mer(E571-V864)		Ni-NTA	+ ATP
6His-thrombin-Mer(E571-V864)	Activated	Ni-NTA	+ ATP
6His-TEV-Kdr(V789-V1356)-LE-Flag		Ni-NTA	
NTC		Glutathione	
GST-Flt3(564-993)		Glutathione	
GST-Axl(464-885)		Glutathione	
GST-Axl(464-885)		Glutathione	+ ATP
GST-Lck(1-509)		Glutathione	

Table SI7. Prevalence table showing the building block structures comprising Family A at each cycle



Cycle A: Heteroaryl chloro/fluoro carboxylic acids Cycle B: Boc protected diamines Cycle C: Carboxylic acids



Family prevalence table illustrates the identity of the building block (BB) composition at each cycle of the library for Family A. Percentage below each BB indicates the frequency that a particular BB appeared in all of the members of the family. These structures represent tolerated variability of cycle A and cycle C building blocks of the active chemotype from the selection output data ie. an indication of SAR for structurally related active compounds.

Table SI8. Prevalence table showing the building block structures comprising Family B at each cycle



Cycle A: Fmoc protected amino acids Cycle B: Fmoc protected amino acids Cycle C: Carboxylic acids



Family prevalence table illustrates the identity of the building block (BB) composition at each cycle of the library for Family B. Percentage below each BB indicates the frequency that a particular building blocks appeared in all of the members of that family. These structures represent tolerated variability of cycle A and cycle B building blocks of the active chemotype from the selection output data. ie. an indication of SAR for structurally related active compounds

Table SI9. Prevalence table showing the building block structures comprising Family C at each cycle



Cycle A: Primary Amines Cycle B: Aldehydes



Family prevalence table illustrates the identity of the building block (BB) composition at each cycle of the library for Family C. Percentage below each BB indicates the frequency that a particular BB appeared in all of the members of that family. These structures represent tolerated variability of cycle A and cycle B building blocks of the active chemotype from the selection output data i.e. an indication of SAR for structurally related active compounds. The top 5 entries for cycle B are shown.



Figure SI10. HPLC traces for compounds. Purity was observed to be >95%.



5 ¹H NMR (500 MHz, 150 DMSO-d₆) δ -0.07 -100 0.02 (m, 2H), 0.22 -0.32 (m, 2H), 0.89 -50 0.94 (m, 1H), 0.97 (d, J = 6.4 Hz, 3H),0 0.25 0.5 0.75 1.25 1.5 1.75 2 2.25 2.5 Ó 1.45 (ddq, J = 17.5, 0284869880 11.9, 5.2 Hz, 2H), 100 1.61 (d, J = 11.5 Hz, ES+ 2H), 2.44 (dd, J = 475.5124 (96.887%) 50 18.8, 7.5 Hz, 1H), 2.57 (d, J = 8.2 Hz, 1H), 2.68 – 2.8 (m, 0 600 700 800 900 1000 100 200 300 400 500 2H), 3.05 (s, 2H), 100 3.17 (t, J = 11.2 Hz, ES-473.6129 (100%) 4H), 3.58 (d, *J* = 7.2 50 Hz, 2H), 3.71 (d, J = 8.6 Hz, 2H), 3.88 (dq, J = 11.2, 7.6, 0 200 400 500 700 800 900 1000 100 300 600 5.7 Hz, 1H), 6.17 (d, J = 8.0 Hz, 1H), 7.24 - 7.37 (m, 2H), 7.56 (s, 1H), 9.02 (s, 1H); HRMS (ES⁺) for $C_{24}H_{33}N_6O_2F_2$ (M+H)⁺: calcd 465.2633; found 475.2621. ¹H NMR (500 MHz, 6 6 DAD DMSO-d₆) δ 1.34 (s, 150 2H), 1.54 (s, 5H), 100 2.84 (d, J = 5.1 Hz, 4H), 2.87 – 2.92 (m, 50 4H), 3.72 - 3.87 (m, 4H), 7.13 (t, J = 7.3 0 0 0.25 0.5 0.75 1 1.25 1.5 1.75 2 2.25 2.5 Hz, 1H), 7.33 - 7.45 0200000000 (m, 2H), 7.51 (d, J = 100 8.9 Hz, 2H), 7.74 (d, ES+ 495.4726 (100%) *J* = 7.6 Hz, 2H), 7.92 (d, J = 8.9 Hz, 2H),50 8.07 (s, 1H), 8.43 (s, 1H), 9.62 (s, 1H); 0 100 200 300 400 600 700 800 900 500 1000 HRMS (ES⁺) for 100 C₂₅H₃₁N₆O₃S (M+H)⁺: ES-493.5516 (100%) calcd 495.2178; found 495.2202 50 0 100 200 300 400 500 600 700 800 900 1000











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