

Supplemental materials

Distinct effects of two HIV-1 capsid assembly inhibitor families that bind the same site within the N-terminal domain of the viral CA protein

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Table S1

Amino acid substitutions selected by culture of virus in the presence of various inhibitors

Compound	EC₅₀ / CC₅₀ (μM)	Major substitutions*	Minor substitutions* *
BD 2	1.1 / >84	G61E	-
BD 1	0.07 / >28	V36T, G208R	V27A/I, A31D, T58I, L138P
BM 2	0.26 / >25	T58I	K30R, S33G, M144V, G208R, E213G
BM 3	0.11 / 14	T58I, G208R	V27A, K30R, A31T, M68I, M144I/V

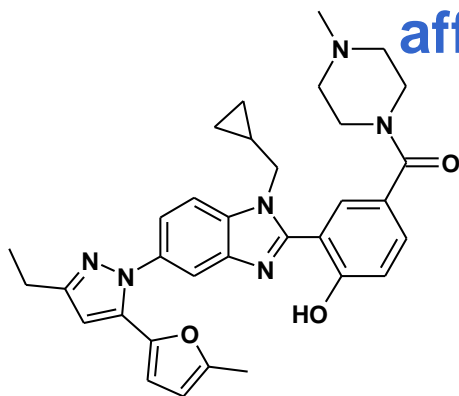
*Major substitutions are those observed in at least 40% of sequenced clones.

**Size and boldness of font indicates relative frequency of mutation found in clonal analysis (includes substitutions observed only once and in any passage).

Table S2 Reductions in affinities for additional BM compounds by resistance substitutions

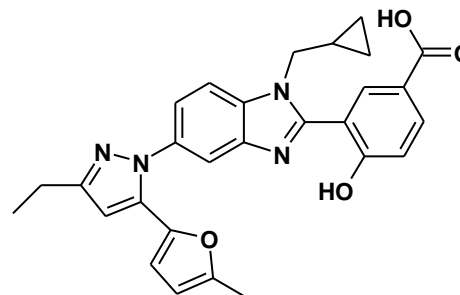
BM Cmps \ K_D (μ M)	BM ^r				BD ^r	
	WT	T58I	K30R	S33G	V27A	V36T
BM 2	0,21	0,19 (0.9x)	ND	2,7 (13x)	1,2 (6x)	3,3 (16x)
BM 6	0,057	0,078 (1.4x)	0,080 (1,4x)	0,98 (17x)	0,55 (10x)	1,2 (21x)
BM 7	0,18	0,24 (1.4x)	0,14 (0,8x)	2,9 (17x)	1,8 (10x)	2,7 (15x)
BM 5	0,17	0,18 (1.1x)	0,15 (0,9x)	2,2 (14x)	1,2 (10x)	3,0 (18x)

No effect on affinity



BM 6

Significant effect on affinity



BM 7

Table S3 Energetics of BM2 binding to wildtype and mutant CA_{NTD}

BM 2	K_D <i>(μM)</i>	ΔG <i>(kcal/mole)</i>	ΔH <i>(kcal/mole)</i>	-TΔS <i>(kcal/mole)</i>
WT	0.210	-9.12	-18.3	9.21
T58I	0.191	-9.17	-18.0	8.84
V27A	1.20	-8.08	-15.3	7.21
S33G	2.74	-7.59	-15.2	7.57
V36T	3.29	-7.48	-15.6	8.13