

SUPPLEMENTAL MATERIAL

Nathanson et al., <http://www.jem.org/cgi/content/full/jem.20131738/DC1>

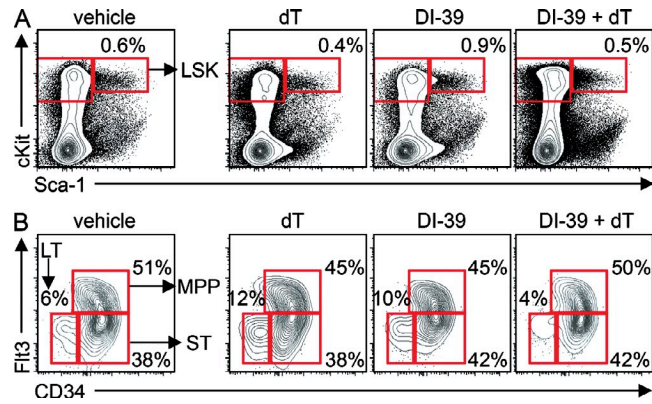


Figure S1. FACS gating strategy to identify hematopoietic progenitor populations quantified in Fig. 8 (E and F).

Table S1. Data collection and refinement statistics for the DI-39-dCK crystal structure

Parameters	Values
Complex	DI-39 + UDP
PDB code	4KCG
Data collection statistics	
x-ray source and detector	LS-CAT ID-G MARCCD 300
Wavelength (Å)	0.97856
Temperature (K)	100
Resolution ^a (Å)	2.09 (2.09 – 2.22)
Number of Reflections	
Observed	187,731
Unique	32,222
Completeness (%)	97.7 (94.4)
R _{sym} (%)	4.5 (68.9)
Average I/σ(I)	18.73 (2.24)
Space group	P 4 ₁
Unit cell (Å)	
a = b	68.73
c	120.59
Refinement statistics	
Refinement program	REFMAC5
Twinning fraction	0.5
R _{cryst} (%)	17.6
R _{free} (%)	24.8
Resolution range (Å)	30–2.09
Protein molecules per a.u.	2
Number of atoms	
Protein (ProtA, ProtB)	1,910, 1,905
Inhibitor	34 × 2
UDP	25 × 2
Water	96
R.m.s. deviation from ideal	
Bond length (Å)	0.012
Bond angles (°)	1.724
Average B-factors (Å ²) /chain	
Protein (ProtA, ProtB)	54.1, 54.0
Inhibitor (ProtA, ProtB)	54.9, 56.1
UDP (ProtA, ProtB)	54.5, 60.1
Waters	50.1
Ramachandran plot (%)	
Most favored regions	87.9
Additionally allowed regions	10.7
Generously allowed regions	1.2
Disallowed regions	0.2

^aLast shell in parenthesis.