Supplementary Table 6. Data collection and refinement statistics for structural model of co-crystalized MLL1-SET and Borealin K143 peptide

	MLL1-SET$_{3785-3969}$ + Borealin peptide$_{137-145}$
Data collection	
Wavelength (Å)	1.12705
Space group	P31 2 1
Cell dimensions	
a , *b* , *c* (Å)	54.48, 54.48, 105.63
α, β, γ (°)	90, 90, 120
Resolution (Å)	47.18 - 2.59 (2.63 - 2.59)
R_{sym} or R_{merge} (%)	4.6 (78.9)
I / σI	11.2 (0.8)
Completeness (%)	97.96 (79.46)
Redundancy	5.7
Refinement	
Resolution (Å)	43.08 - 2.59 (2.68 – 2.59)
No. reflections	5878
R_{work} / R_{free}	24.77 / 30.36
No. atoms	
Protein	1000
Ligand/ion	1 (Zn2+), 26 (AdoHcy),
B-factors	
Protein	61.12
Ligand/ion	142.86 (Zn2+), 61.92 (AdoHcy)
R.m.s. deviations	
Bond lengths (Å)	0.01
Bond angles (°)	1.16
Ramachandran plot (%)	
Favored	93
Outliers	0
Protein Data Bank code	7U5V