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SUPPLEMENTARY INFORMATION

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Crystal structure of the SALL4–pomalidomide–cereblon–DDB1 complex

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Supplementary Table 1. Data collection and refinement statistics

	SALL4-pomalidomide-cereblon-DDB1 (6UML)
Data collection	
Space group	P 1 21 1
Cell dimensions	
a, *b*, *c* (Å)	77.4 127.7 110.2
α, β, γ (°)	90 109.7 90
Resolution (Å)	37.04 - 3.577(3.705 - 3.577)[a]
R_{merge}	0.1637 (0.5699)
R_{meas}	0.1948 (0.6734)
R_{pim}	0.1042 (0.3551)
$I/\sigma(I)$	5.04 (2.21)
$CC_{1/2}$	0.964 (0.734)
Completeness (%)	98.42 (98.11)
Redundancy	3.4 (3.5)
Refinement	
Resolution (Å)	37.04 - 3.577
No. reflections	23629 (2331)
R_{work} / R_{free}	0.2038 / 0.2671
No. atoms	
Protein	11082
Ligand/ion	20/2
Water	0
B factors	
Protein	85.17
Ligand/ion	80.729 / 77.34
Water	N/A
R.m.s. deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.68
Methods	
Ramachandran (%)	
Favored	92.98
Outliers	0.35
Clash score	9.49
MolProbity score	1.95

Data was collected from a single crystal. [a]Values in parentheses are for highest-resolution shell.