

Proteome-wide identification of the druggable CRBN interactome

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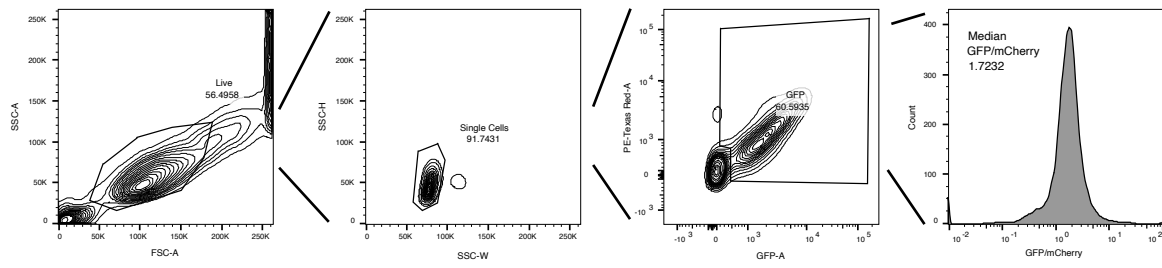
Supplementary Figure 1

Supplementary Table 1

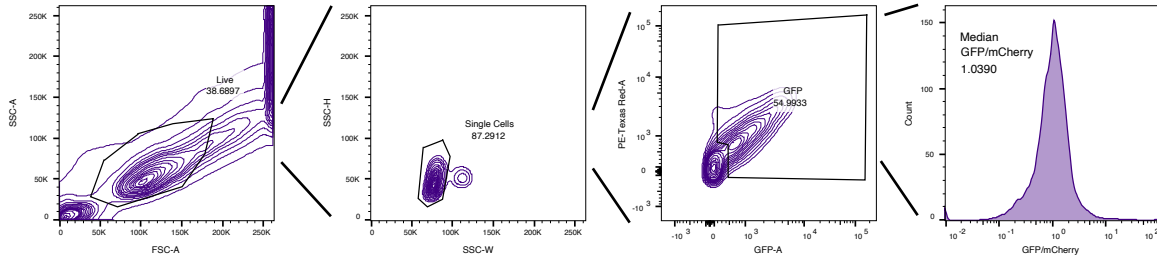
Supplementary Table 2 (provided as a separate Excel file)

Supplementary Table 3

IKZF2-ZF2 DMSO



IKZF2-ZF2 500 μ M pomalidomide



Supplementary Figure 1: Gating strategy.

Figure which shows the gating strategy used in the degradation experiments in Fig. 1 d, f, g, and h.

Supplementary Table 1: Cryo-EM data collection, refinement, and validation statistics

1) Sharpening was done with DeepEMhancer

	SALL4 ^{ZF12Helix}	Ikaros ^{ZF23}	Helios ^{ZF123}
Data collection and processing			
EMDB ID	EMD-55106	EMD-55107	EMD-55108
PDB ID	9SQ4	9SQ5	9SQ6
Detector	Falcon 4	Falcon 4i	Falcon 4i
Magnification	120,000	75,000	75,000
Voltage (kV)	200	300	300
Electron exposure (e-/Å)	50	50	50
Defocus range (μm)	-2.0 to -0.8	-2.0 to -0.8	-2.0 to -0.8
Pixel size (Å)	0.84	0.845	0.845
Symmetry imposed	C1	C1	C1
Initial particle images (no.)	3,278,449	437,387	1,150,503
Final particle images (no.)	280,439	102,811	87,668
Map resolution (Å)	3.49	3.68	3.64
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	3-9	3-15	3-12
Refinement			
Initial models used (PDB codes)	N.A.	4CI3	9E2U
Model resolution (Å)	3.49	3.68	3.64
FSC threshold	0.143	0.143	0.143
Map sharpening B factor (Å)	N.A. ¹	N.A. ¹	N.A. ¹
Model composition			
Non-hydrogen atoms	9992	10037	9907
Protein residues	1256	1263	1241
Ligands	LIG: 1 ZN: 2	LIG: 1 ZN: 3	LIG: 1 ZN: 4
B factors (Å)			
Protein	121.27	202.71	81.55
Ligands	138.58	294.41	122.43
R.m.s deviations			
Bond lengths (Å)	0.004	0.003	0.004
Bond angles (°)	0.662	0.567	0.695
Validation			
MolProbity score	0.93	1.37	1.22
Clashscore	0.68	2.64	1.8
Poor rotamers (%)	0.19	0.48	0.39
Ramachandran plot			
Favored (%)	96.67	95.33	95.95
Allowed (%)	3.25	4.5	3.88
Disallowed (%)	0.08	0.17	0.17
Model-to-data fit			
CCmask	0.75	0.79	0.68
CCbox	0.76	0.89	0.67
CCpeaks	0.72	0.71	0.65
CCvolume	0.75	0.79	0.69

Supplementary Table 3: Table of primers used in this study and their sequence

All primers were synthesized by microsynth.

Name	Seq
pPG1	CTGCAGGTCGACGATCCTTTTGTTGTTTCCGGGTG
pPG2	TTGGAGTTGATTGTATGCTTGGTATAG
pPG3	AAGCATACAATCAACTCCAAGCTGGCCGCGGTACCATGTCGTACAACACTACGTGGTAAC
pPG4	GTCCAAAGCTACTAGTTCTAGACTAATGGATCCGAGTTAGCTCCTC
pPG5	ATCGGGAGAGACATCTAAGC
pPG6	AGTCCTTATTGAGCTCACGC
OGD241	GCCTACATACCTCGCTCTGC
OGD242	CAACCCGGTAAGACACGACT
ODL832	CCCTACACGACGCTCTTCCGATCTTTCAGGAGCATCTGCTAGC
ODL833	TTCAGACGTGTGCTCTTCCGATCTAGCGTGACATAACTAATAAGC