Data Collection and Structure Determination:

X-ray diffraction data for the GID4 and UBF9092 complex was collected at 100K at beamline NSLS-II Beamline 17-ID-2 of Brookhaven National Laboratory. The data were processed using HKL3000 suite (Otwinowski Z, Minor W. Meth Enzymol 1997;276:307–326) and the structure was solved by REFMAC using the PDB entry 6WZZ as a model (Murshudov GN, Vagin AA, Dodson EJ. Acta Crystallogr D Biol Crystallogr 1997;53:240–255). REFMAC was also used for structure refinement. Geometry restraints for the compound refinement were prepared by using ACEDRG (Fei Long, Robert A Nicholls, Paul Emsley, Saulius GraZulis, Andrius Merkys, Antanas Vaitkus and Garib N Murshudov. Acta Cryst. (2017), D73, 112-122.). Graphics program COOT (Emsley P, Cowtan K. Acta Crystallogr D Biol Crystallogr 2004;60:2126–2132) was used for model building and visualization. Molprobity (Williams et al. (2018) MolProbity: More and better reference data for improved all-atom structure validation. Protein Science 27: 293-315.) was used for structure validation.

Supplementary Table 1. Crystallographic data and refinement statistics

	GID1 + UBF9092a
PDB Code	8V1P
Data collection	
Space group	$P4_12_12$
Cell dimensions	
a, *b*, *c* (Å)	40.1, 40.1, 201.0
α, β, γ (°)	90, 90, 90
Resolution (Å) (highest resolution shell)	50.0-2.21 (2.25-2.21)
Unique reflections	8994
R_{merge}	0.053(0.688)
$I/\sigma I$	42.6(2.0)
Completeness(%)	99.5(99.5)
Redundancy	9.8(5.9)
CC(1/2)	0.998(0.757)
Refinement	
Resolution (Å)	39.36-2.21
No. reflections (test set)	8016(895)
R_{work}/ R_{free} (%)	21.6/27.8
No. atoms	
Protein	1298
Compound	23
B-factors (Å^2)	
Protein	66.3
Compound	59.4
RMSD	
Bond lengths (Å)	0.010
Bond angles (°)	1.45
Ramachandran plot % residues	
Favored	94.5
Additional allowed	5.5
Generously allowed	0
Disallowed	0