Supporting information

Design, synthesis, and biological evaluation of potent FAKdegrading PROTACs

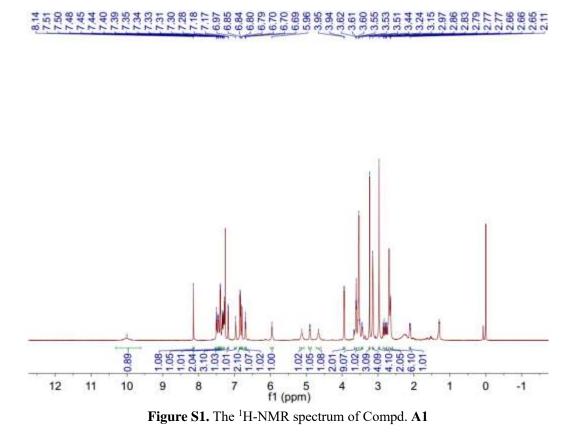
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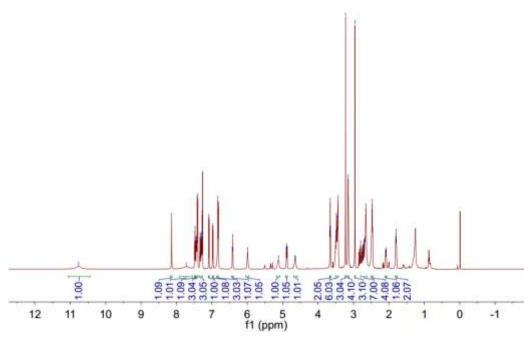
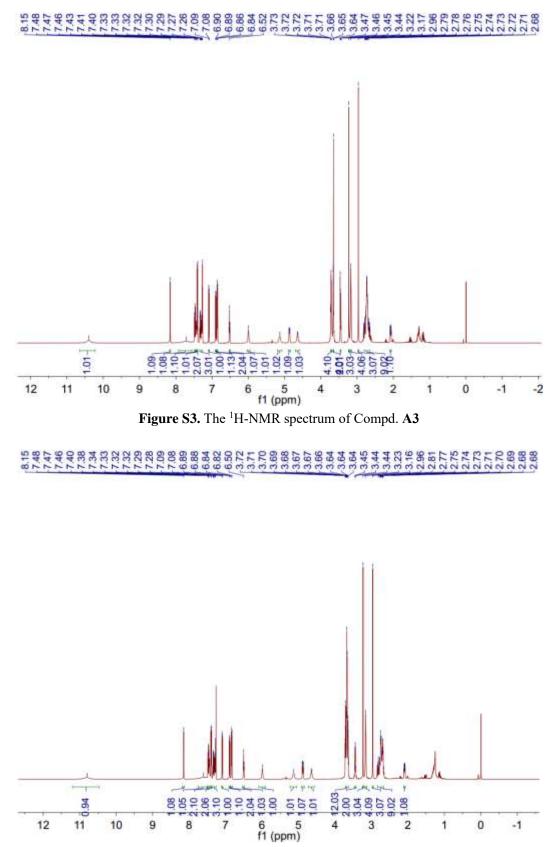
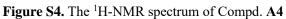


Figure S2. The ¹H-NMR spectrum of Compd. A2





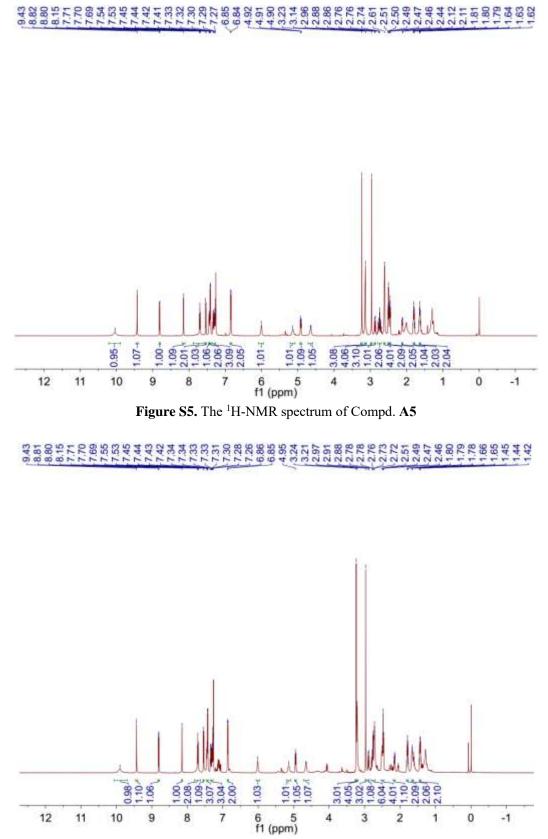
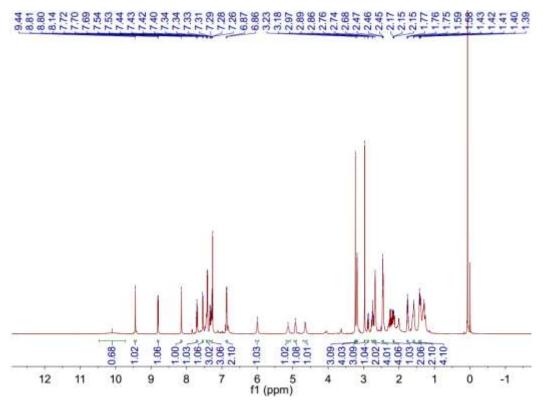


Figure S6. The ¹H-NMR spectrum of Compd. A6





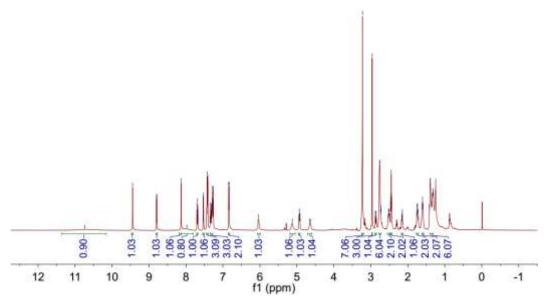


Figure S8. The ¹H-NMR spectrum of Compd. A8

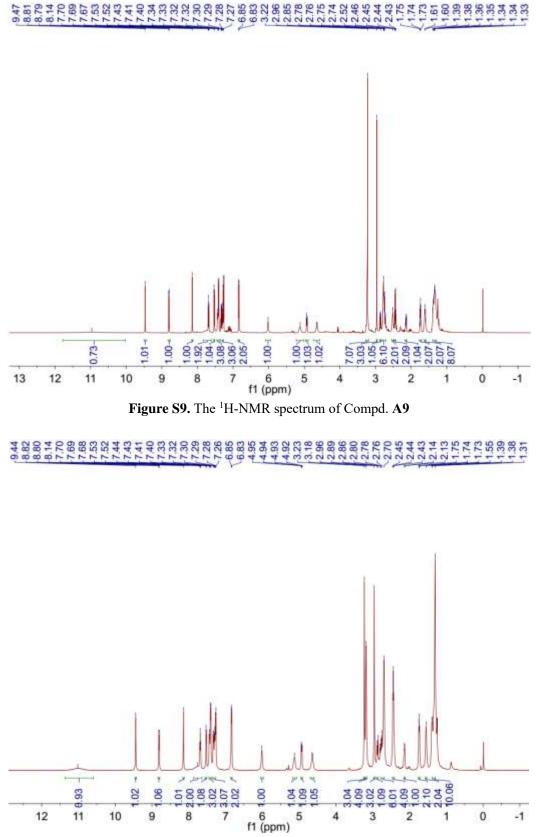
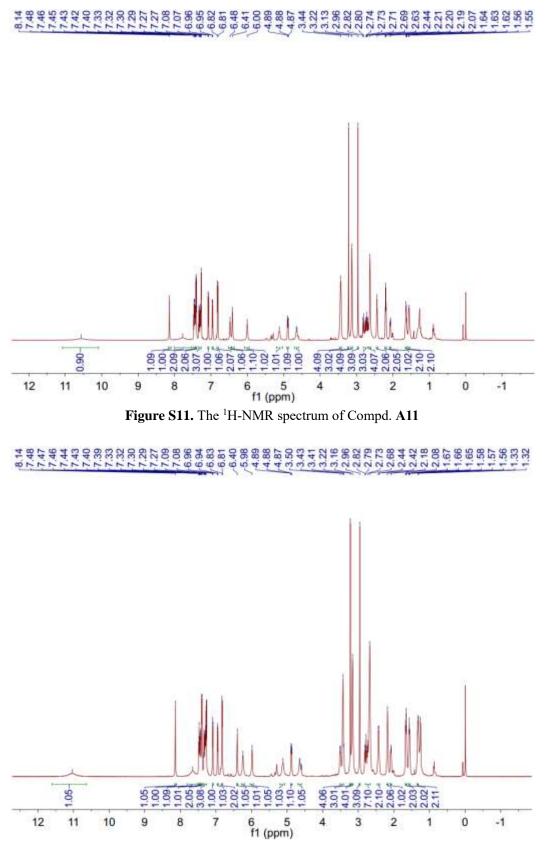
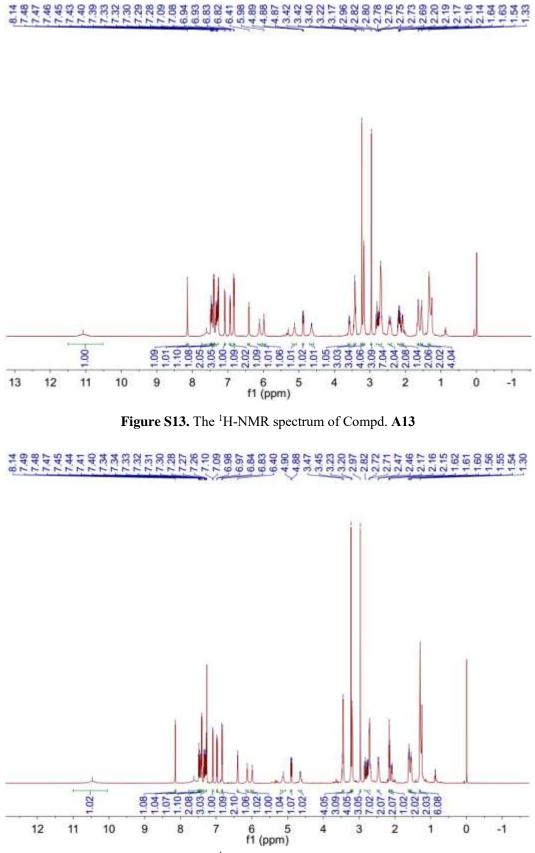


Figure S10. The ¹H-NMR spectrum of Compd. A10









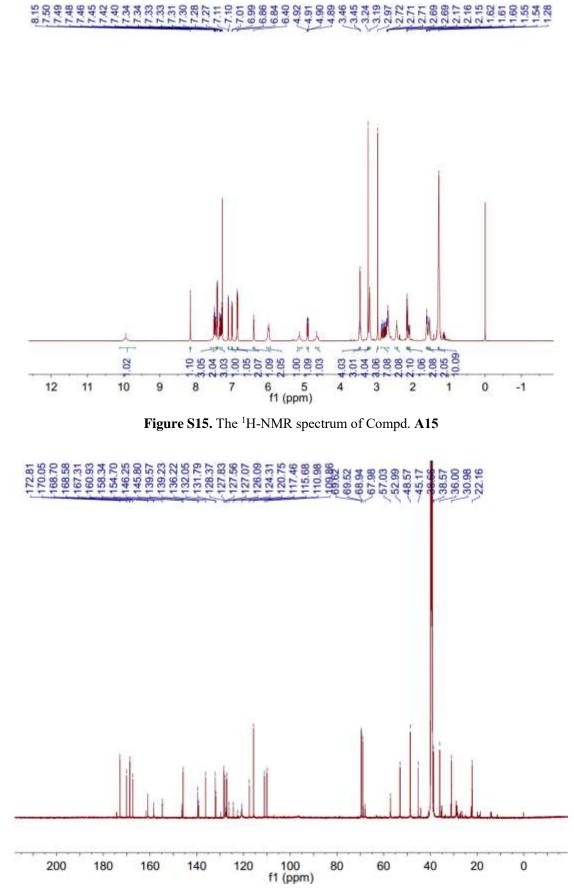


Figure S16. The ¹³C-NMR spectrum of Compd. A1

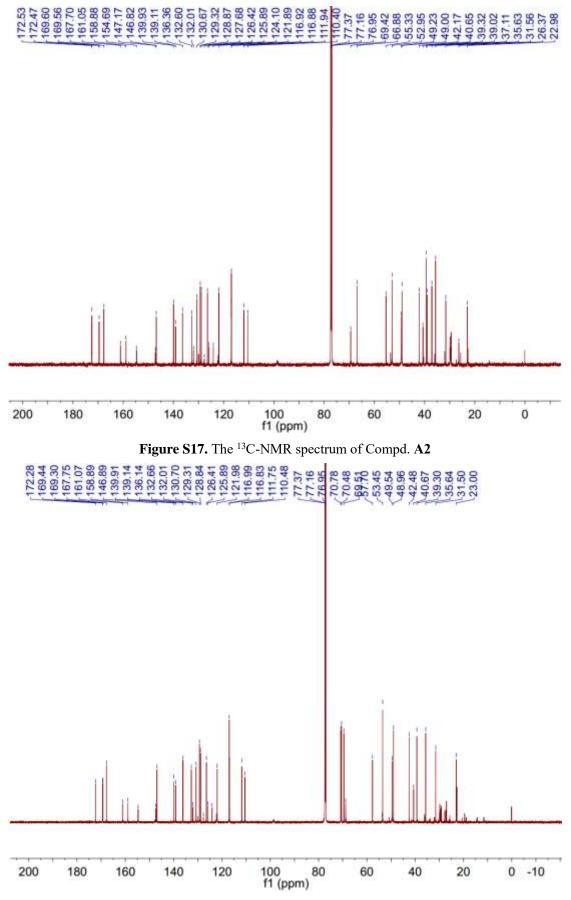
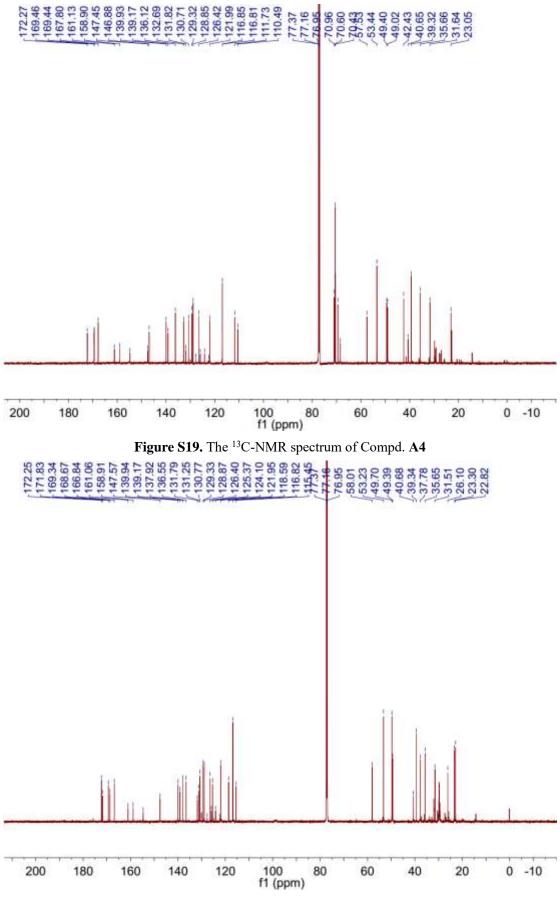


Figure S18. The ¹³C-NMR spectrum of Compd. A3





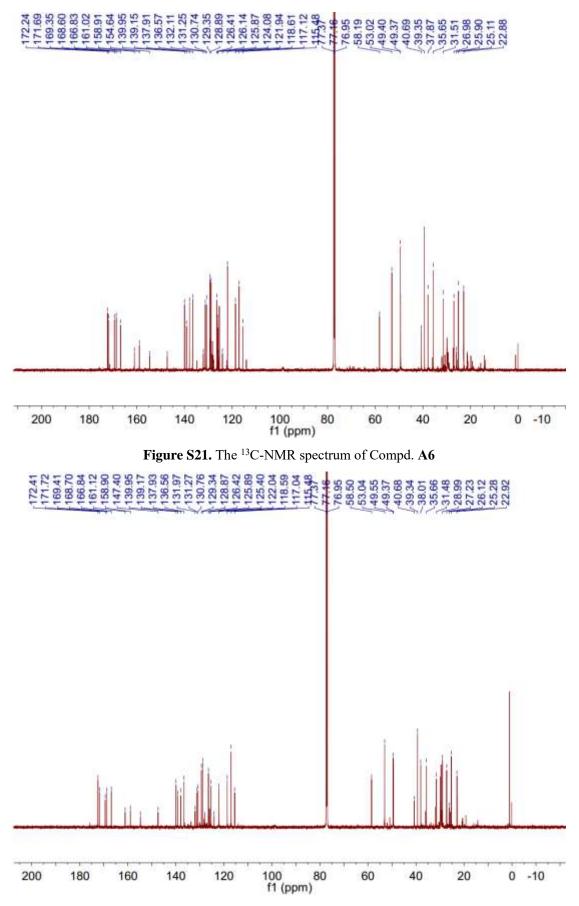


Figure S22. The ¹³C-NMR spectrum of Compd. A7

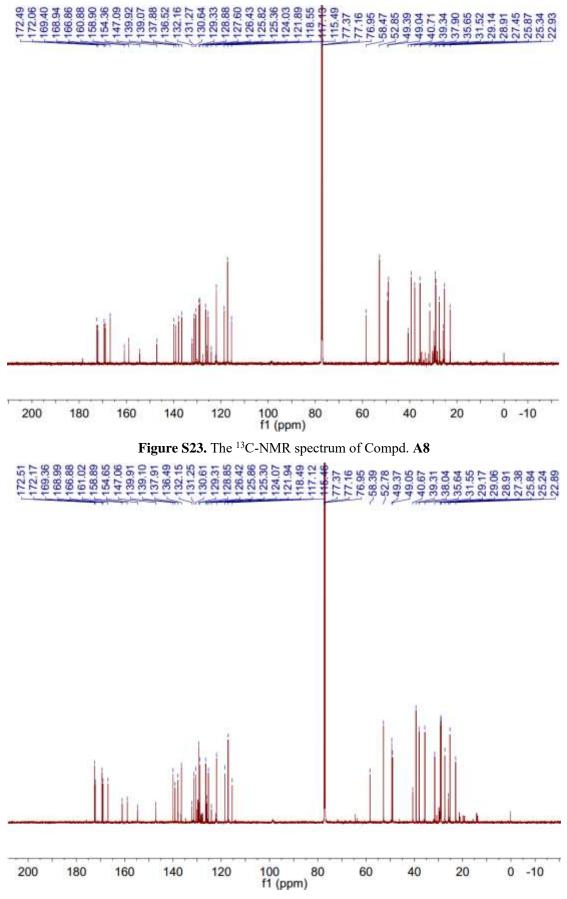


Figure S24. The ¹³C-NMR spectrum of Compd. A9

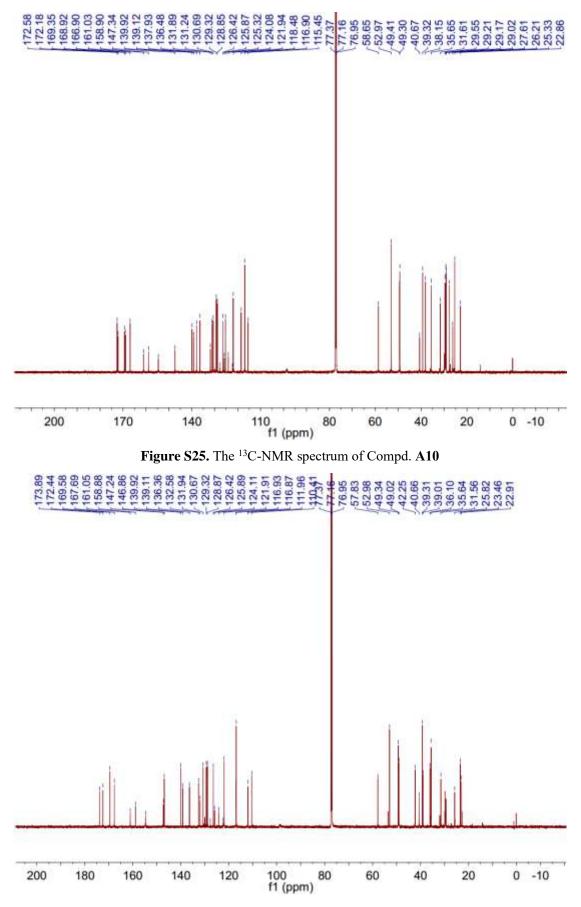


Figure S26. The ¹³C-NMR spectrum of Compd. A11

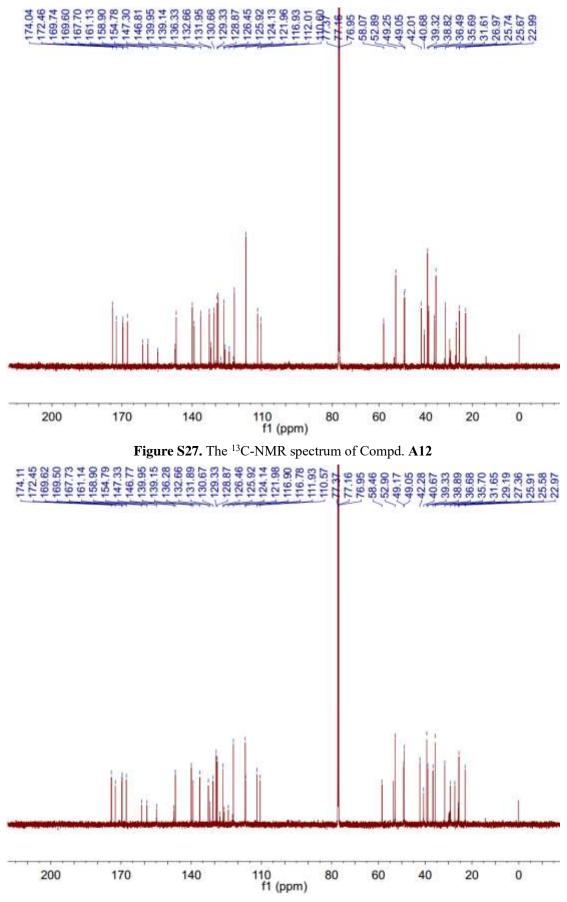


Figure S28. The ¹³C-NMR spectrum of Compd. A13

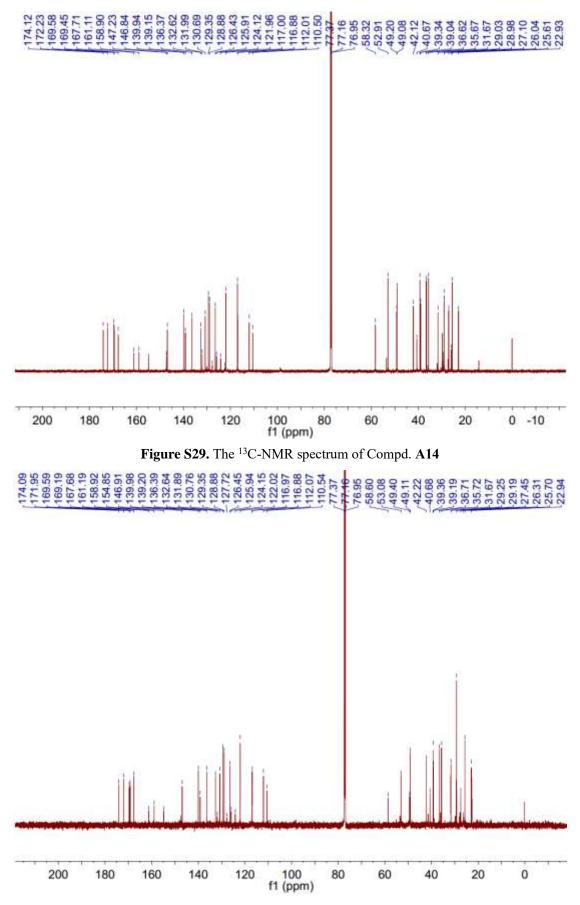
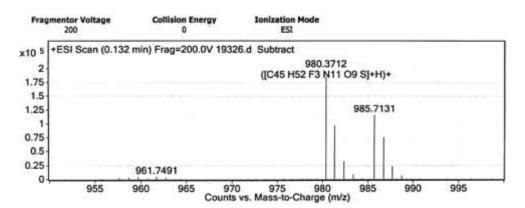
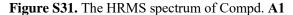
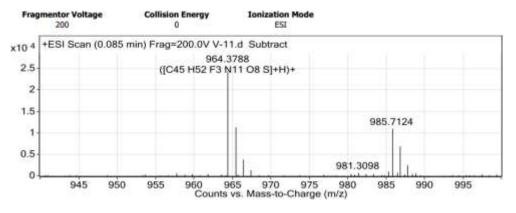
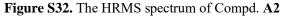


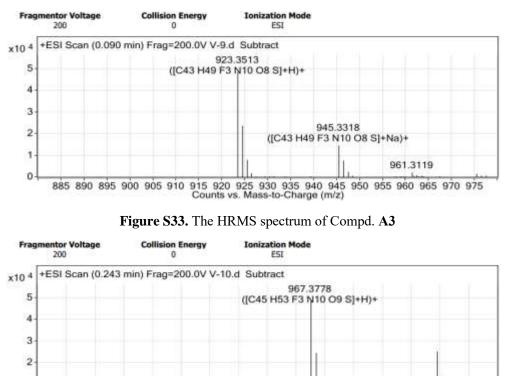
Figure S30. The ¹³C-NMR spectrum of Compd. A15



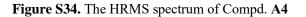


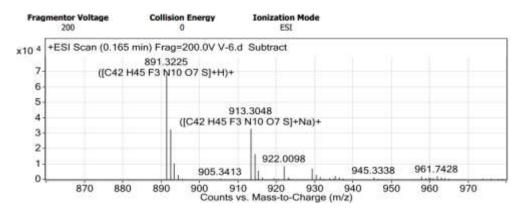




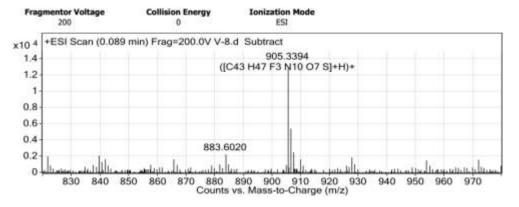


944.9872 961.7666 11, 11, 11, 11, 930 935 940 945 950 955 960 965 970 975 980 985 990 Counts vs. Mass-to-Charge (m/z)

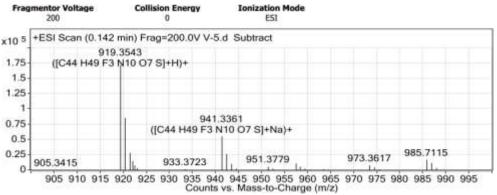


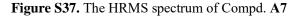












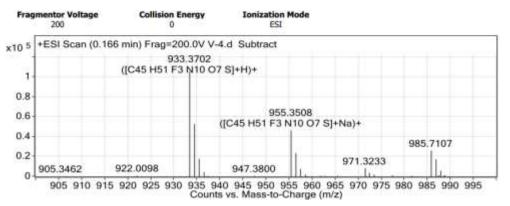
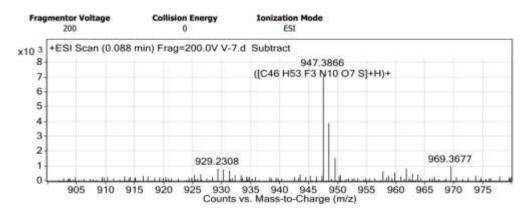
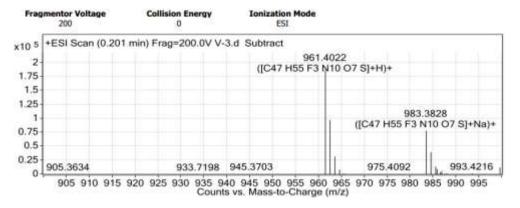


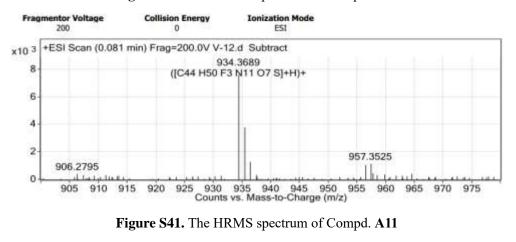
Figure S38. The HRMS spectrum of Compd. A8

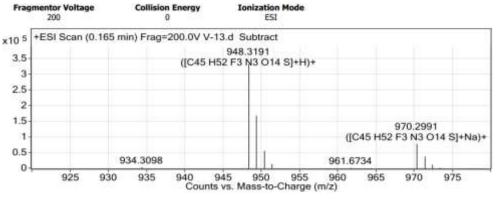


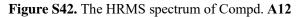


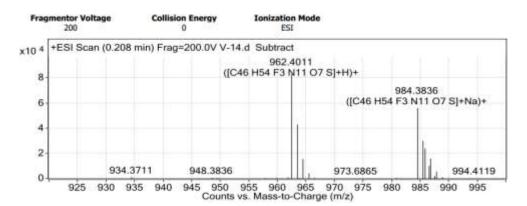


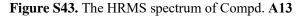


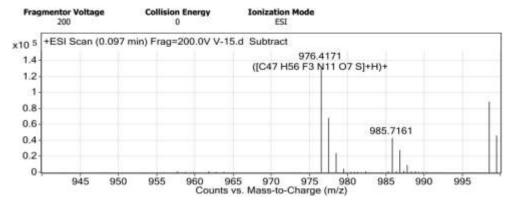


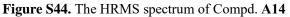












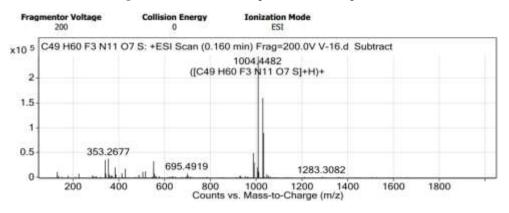


Figure S45. The HRMS spectrum of Compd. A15

We split compound **A13** into two parts for docking. Firstly, we docked the FAK ligandlinker moiety with the FAK protein. Molecular docking studies showed that the 2,4diaminopyrimidine core formed two donor-acceptor interactions with Cys502 in the hinge region, *N*-methyl sulfonamide fragment formed a hydrogen bond interaction with Asp564 in the DFG-motif, the trifluoromethyl group contained a hydrophobic interaction with the gatekeeper residue Met499, the linker extended from the solvent region to the outside of the protein pocket (Fig. S46). Secondly, we docked the Pomalidomide-linker moiety with the CRBN protein. Molecular docking studies showed that piperidine-2,6-dione formed three donor-acceptor interactions with His380 and Trp382, the linker also extended from the solvent region to the outside of the protein pocket (Fig. S47).

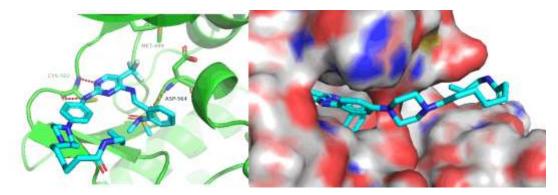


Fig. S46 Molecular docking model of FAK ligand-linker moiety of compound A13 with FAK protein (PDB ID:

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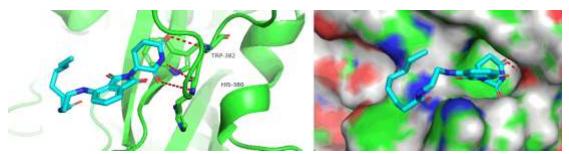


Fig. S47 Molecular docking model of pomalidomide-linker moiety of compound A13 with CRBN protein (PDB ID:

4CI3)