

Normal
chromosomal 9



Normal
chromosomal 22



ABL

BCR



break



translocation

Transformed
chromosomal 9



Transformed
chromosomal 22



BCR-ABL
Fusion gene

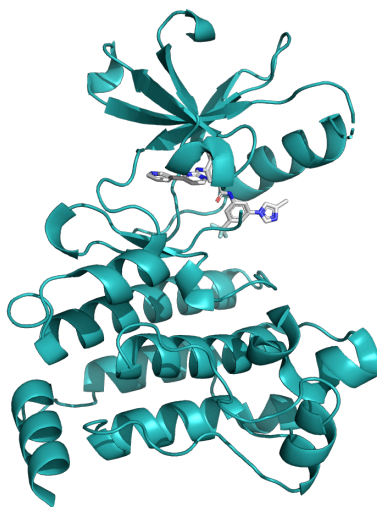
JCI 2007, 117, 2036.

Nat. Rev. Cancer 2007, 7, 345.

Transformed
chromosomal 22

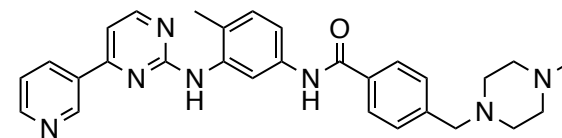


BCR-ABL
Fusion gene

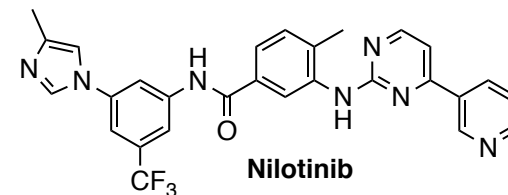


Constitutively-active
ABL tyrosine kinase

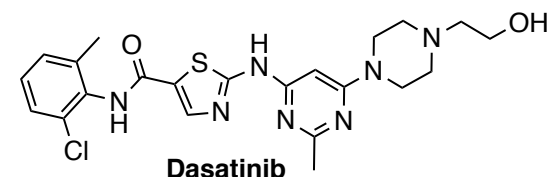
ABL Tyrosine Inhibitors



Imatinib



Nilotinib



Dasatinib

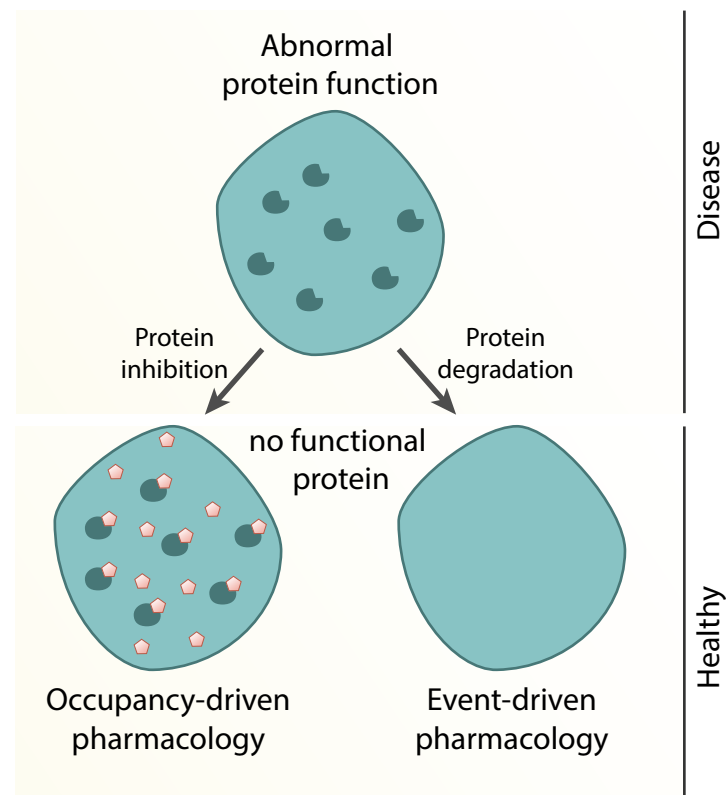
Pharmacology Models: Inhibition vs Degradation

- Occupancy-driven pharmacology

 - Stoichiometric activity
 - Mostly target active-site binding
 - Site occupancy to block function
 - Specificity defined by binding

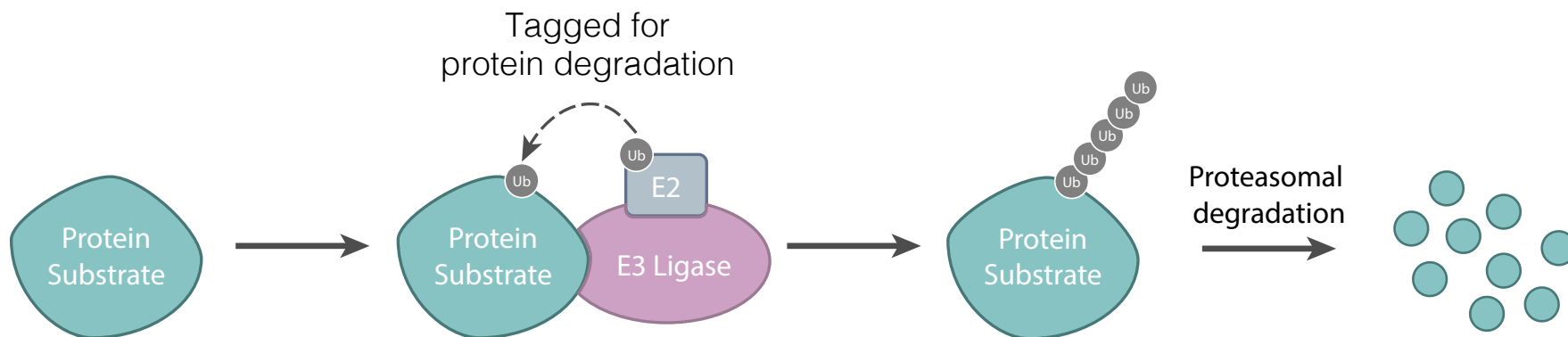
- Event-driven pharmacology

 - Sub-stoichiometric activity
 - Target active and allosteric sites
 - Additional layer of specificity
 - Restoration of function requires re-synthesis



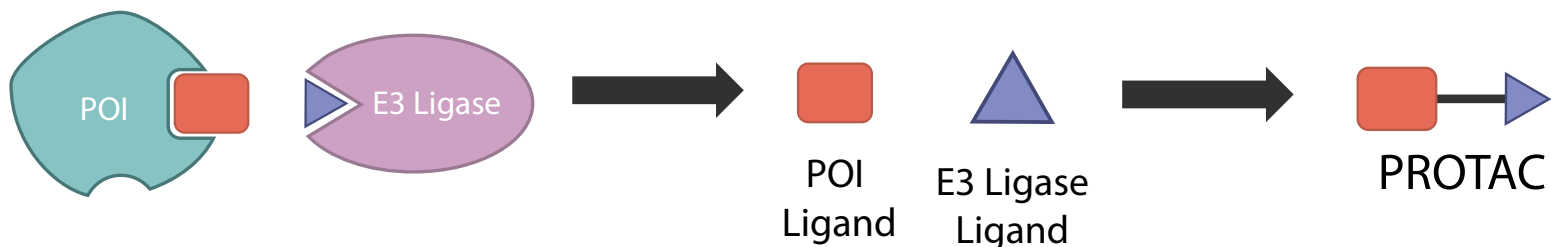
Nat. Drug. Disc. **2017**, 16, 101.
Cell Chemical Biology **2017**, 24, 1181.

Protein Degradation - Ubiquitin-Proteasome System (UPS)

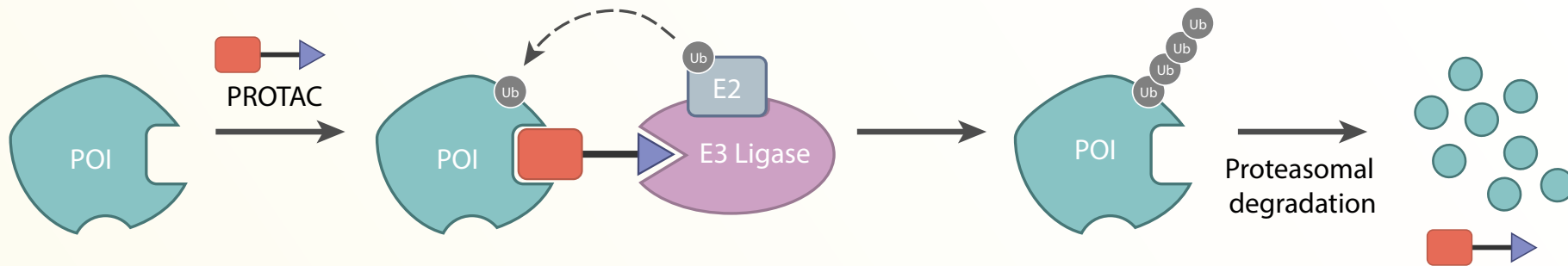


Nat. Rev. Mol. Cell Biol. **2008**, 9, 679.

Proteolysis Targeting Chimeras - PROTACs



Small-molecule-mediated Protein degradation:



Natl. Acad. Sci. USA 2001, 98, 8554.

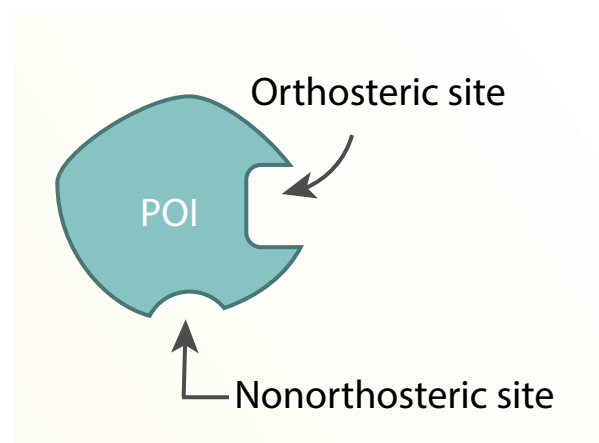
Targeting Protein of Interest

- Orthosteric/Active Site Modulators

- Structurally similar to endogenous ligand
 - Employ rational drug design
 - Varying degrees of specificity
 - Highly susceptible to drug resistance

- Nonorthosteric/Allosteric Modulators

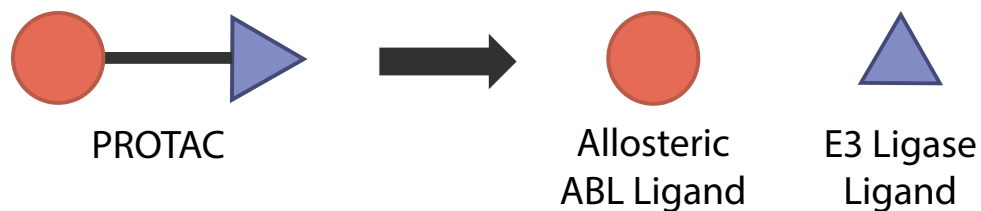
- Lack an endogenous ligand
 - Unique chemical structures
 - Elevated target selectivity
 - Reduced off-targets
 - Spatio-temporal specificity
 - Reduced susceptibility to drug resistance



ACS Cent. Sci. **2017**, 3, 925.
Med. Princ. Pract. **2013**, 22, 418.
Rev. Pharmacol. Toxicol. **2014**, 54, 165.

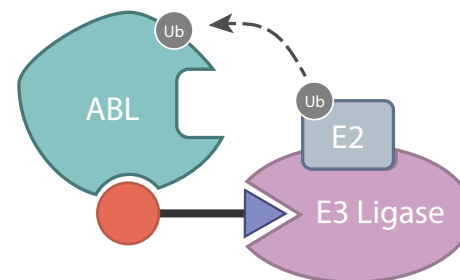
Hypothesis – Application of an allosteric BCR-ABL PROTAC induces BCR-ABL protein degradation

Phase I

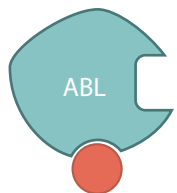


Development of an allosteric BCR-ABL PROTAC

Phase II

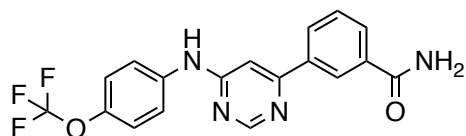


BCR-ABL protein degradation

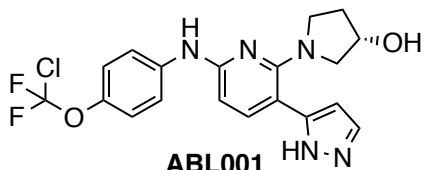


ABL Allosteric-site Inhibitors

Target Myristate-binding site

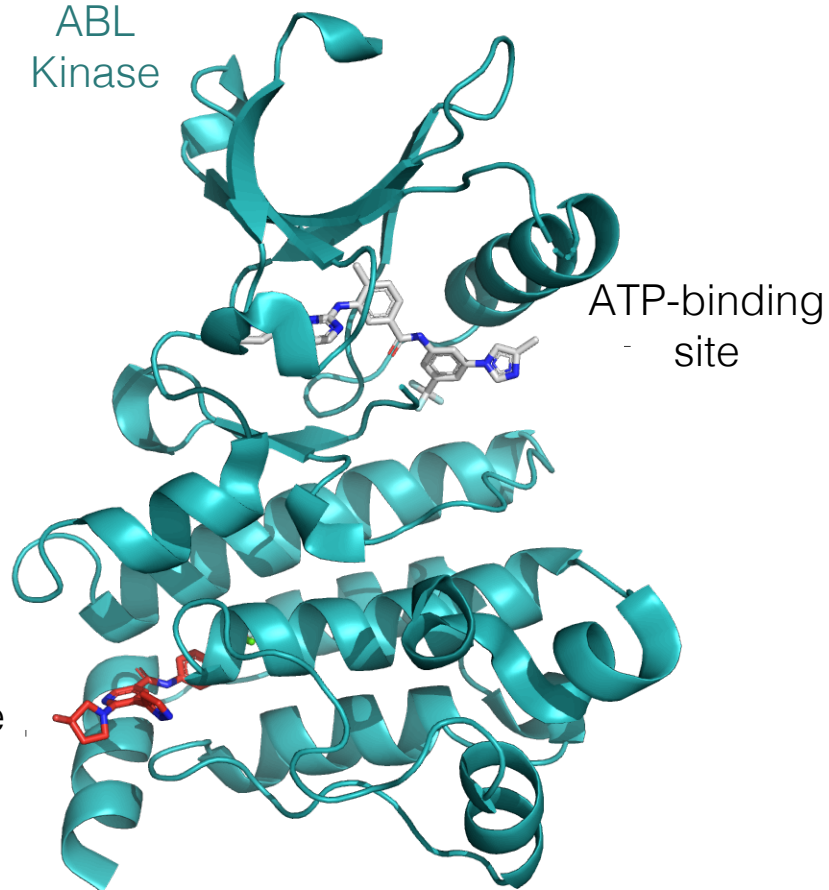


GNF-2



ABL001

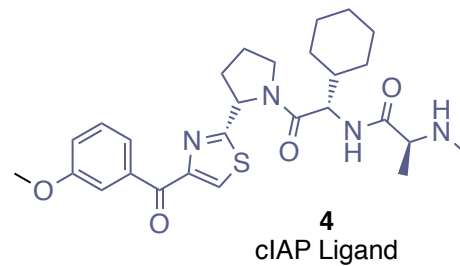
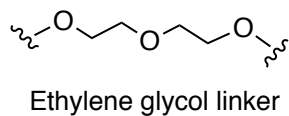
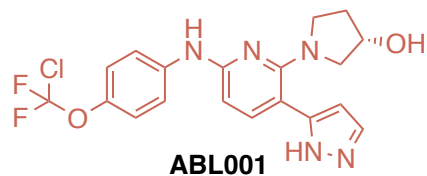
ABL
Kinase

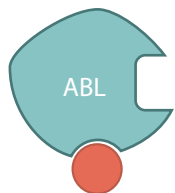


PDB: 5MO4

Nature **2010**, 463, 28.
Nature **2017**, 543, 733.

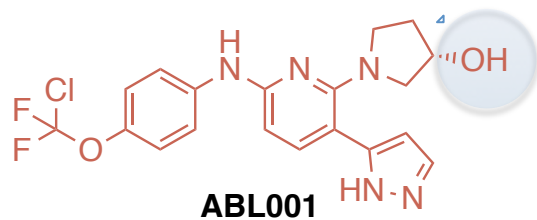
Design of PROTAC



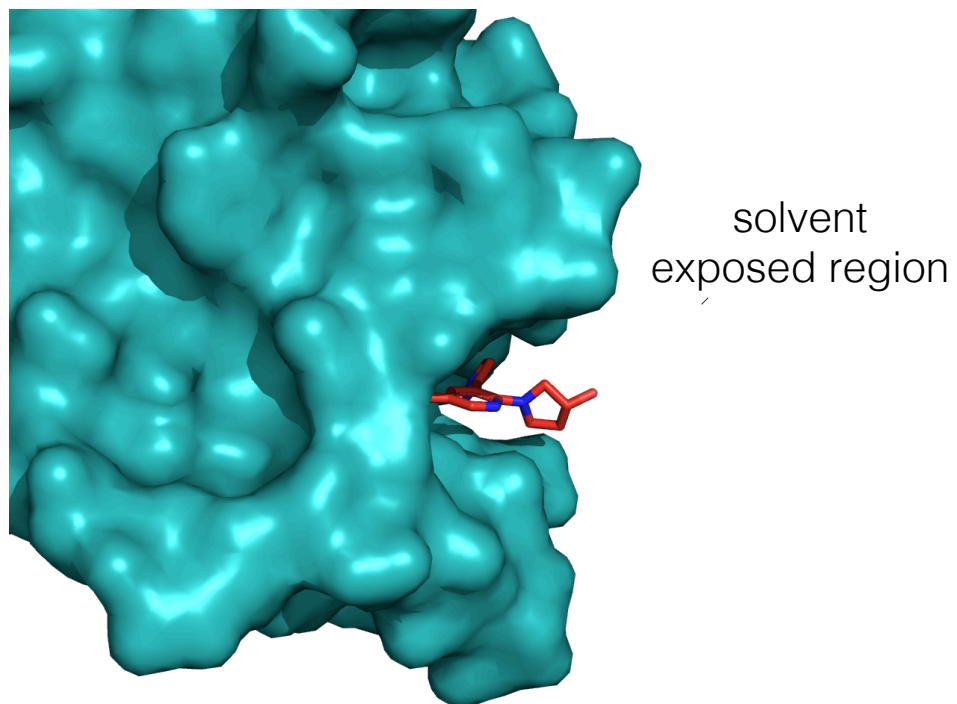


Structural Analysis of ABL001 bound ABL Kinase

Positioning of the linker

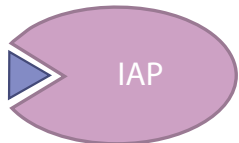


Surface view of ABL Kinase



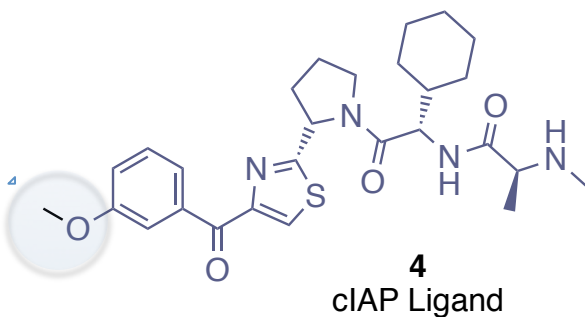
PDB: 5MO4

Nature 2017, 543, 733.



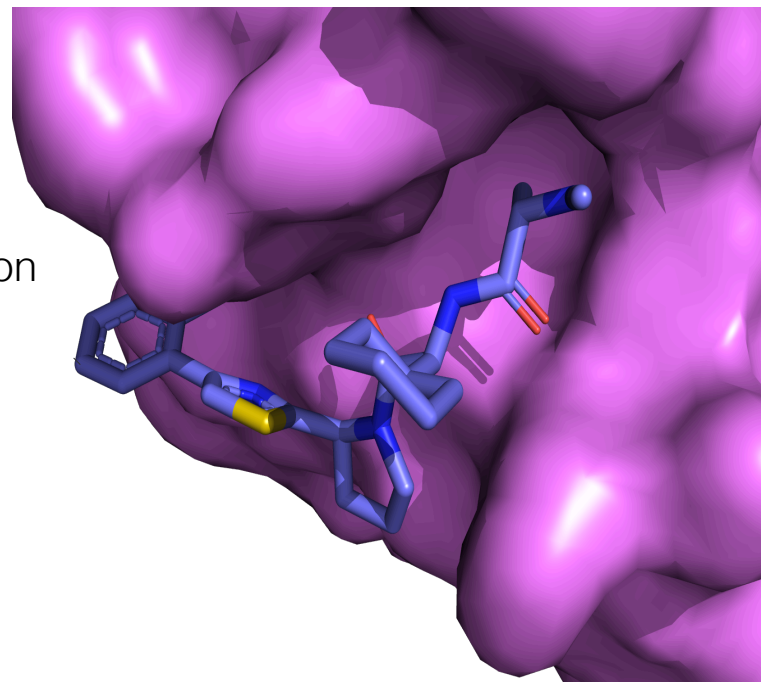
Structural Analysis of IAP Ligand

Positioning of the linker



Surface view of IAP

solvent
exposed region



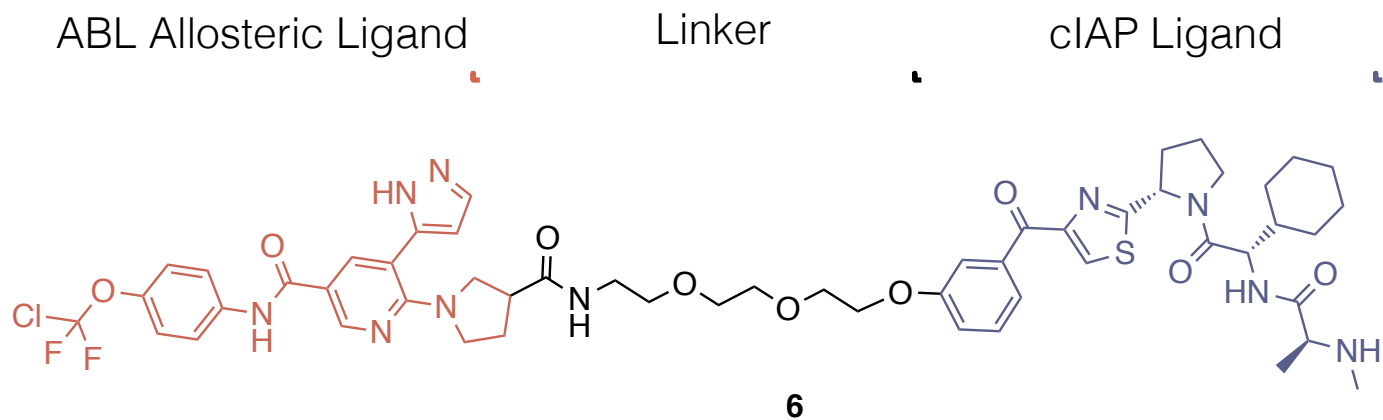
PDB: 3GT9

J. Biological Chemistry **2017**, 292, 4556.

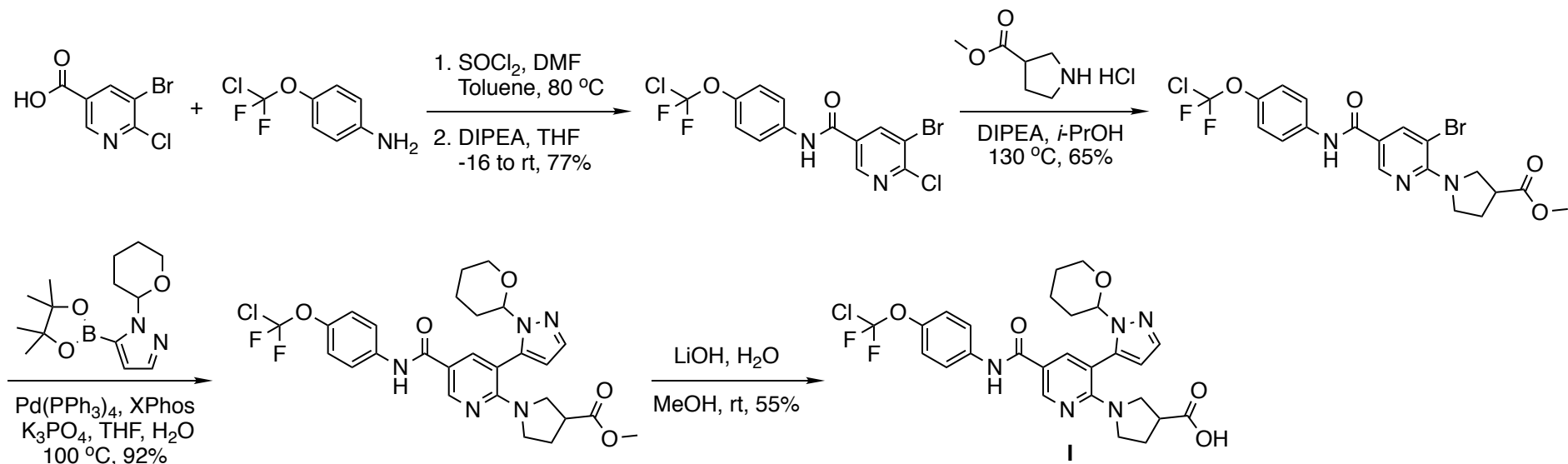
J. Med. Chem. Article ASAP

Bioorg. & Medi.Chem. Lett. **2010**, 20, 2229.

PROTAC Development

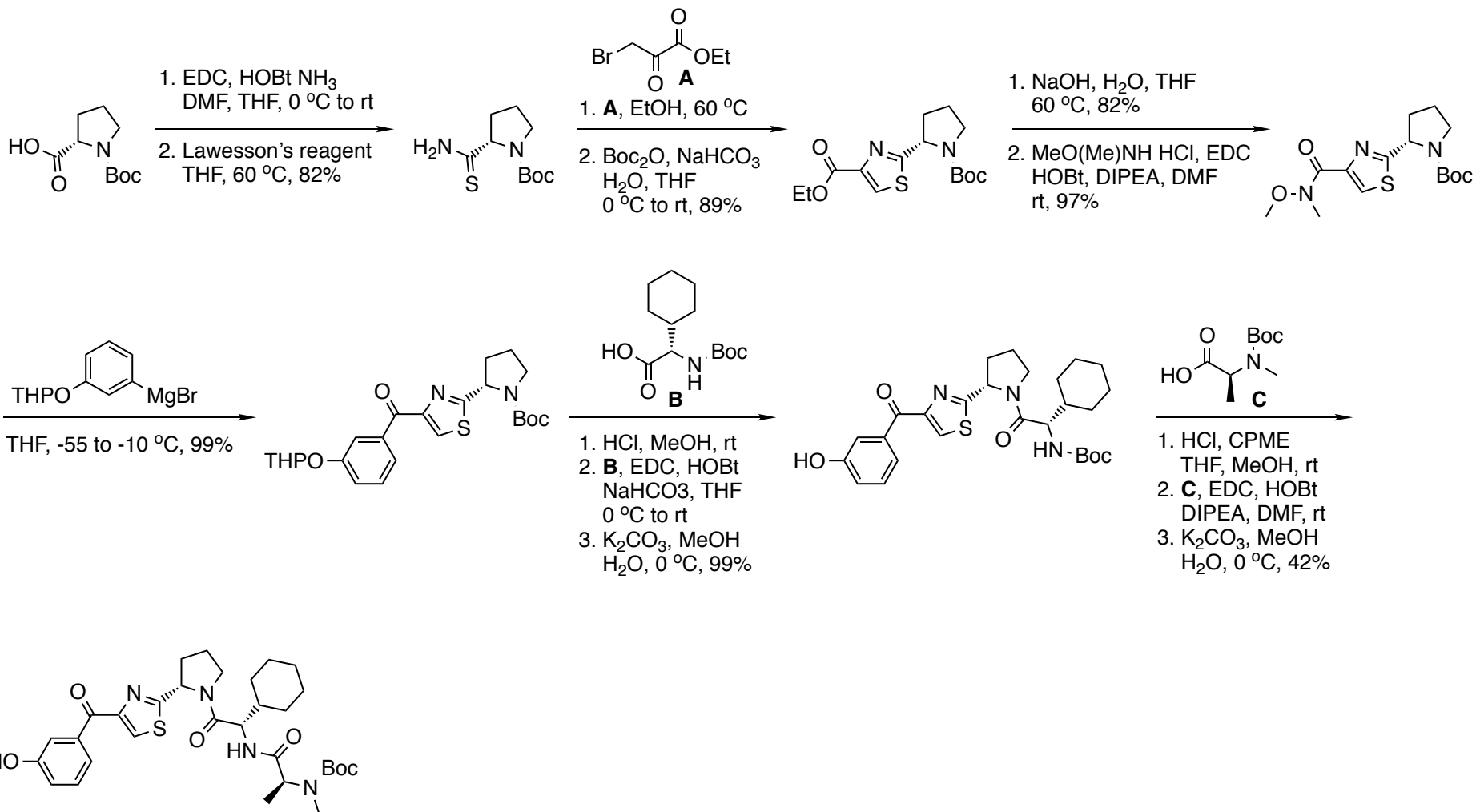


Synthesis of the ABL Allosteric Ligand



Nature **2010**, 463, 28.
Nature **2017**, 543, 733.

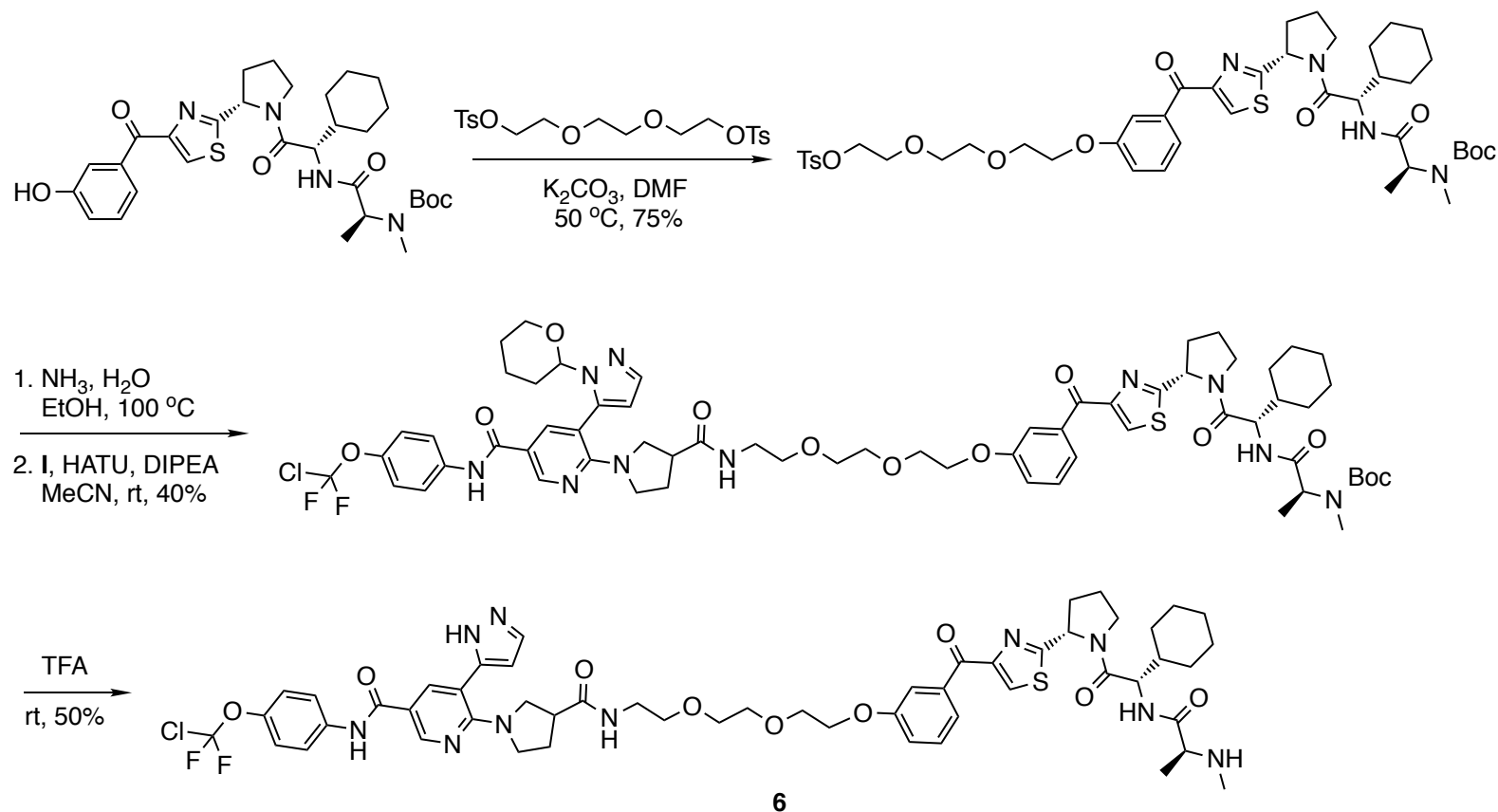
Synthesis of the cIAP Ligand



J. Biological Chemistry **2017**, 292, 4556.



Synthesis of PROTAC – Compound 6



ACS Med. Chem. Lett. 2017, 8, 1042.

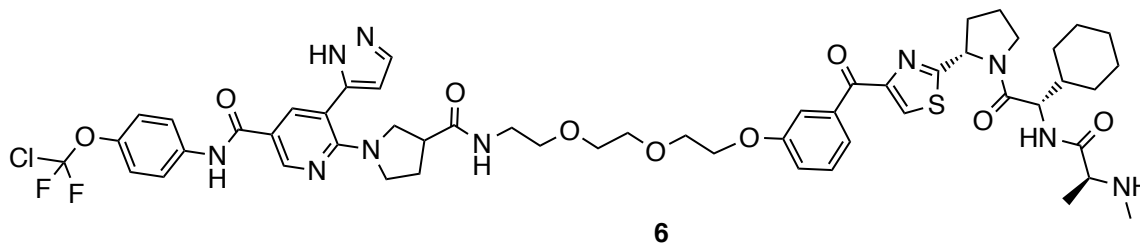
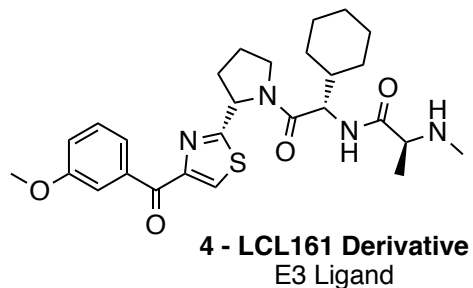
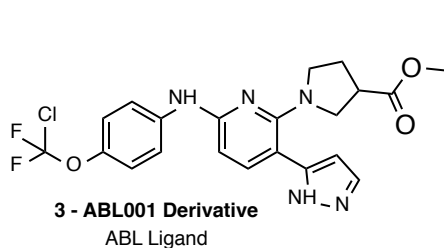
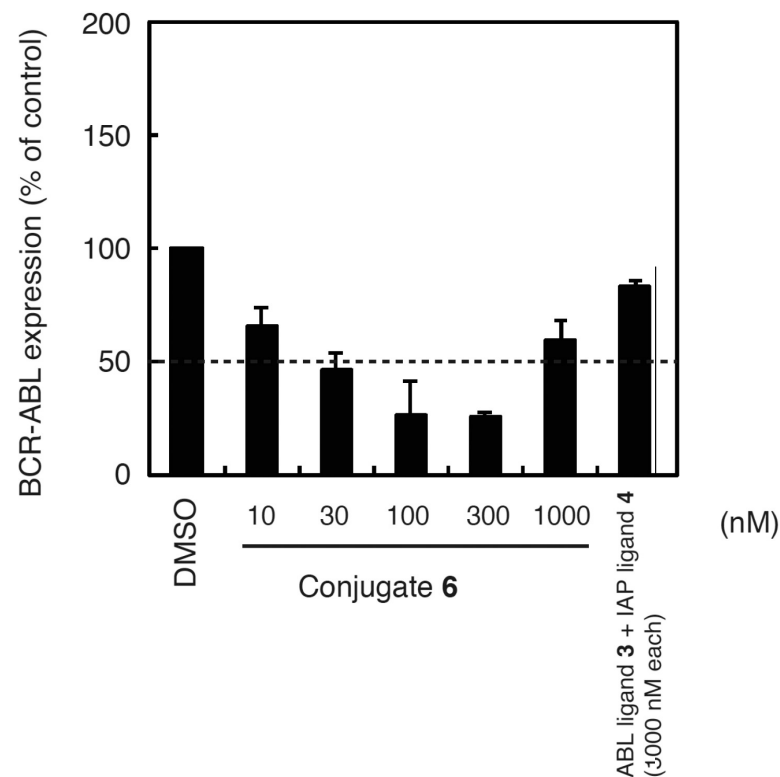
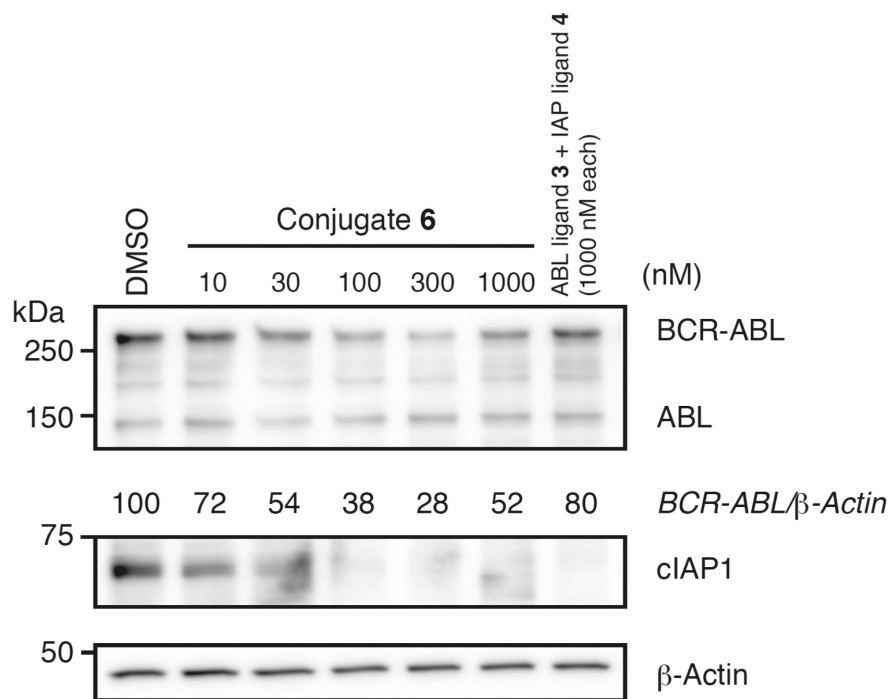
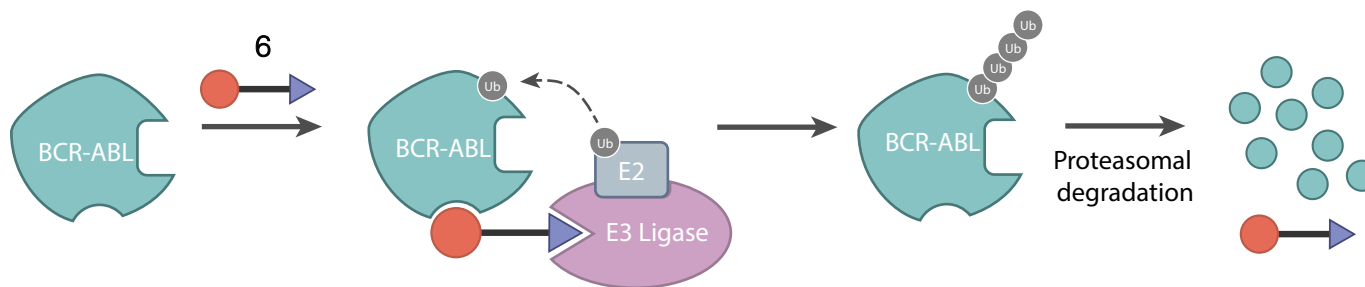


Table 1. Results of TR-FRET Based Binding Assay for ABL1 (Allosteric Site), cIAP1/2, and XIAP^a

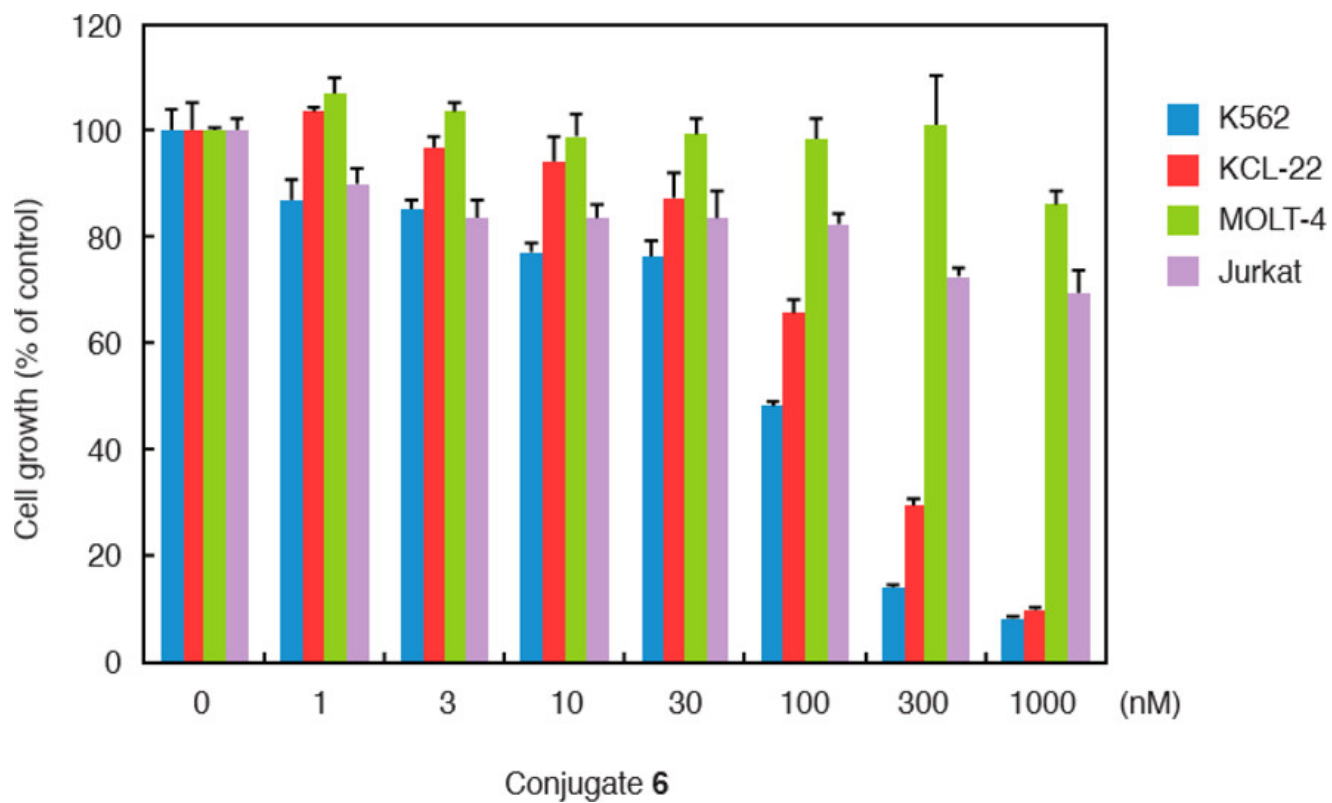
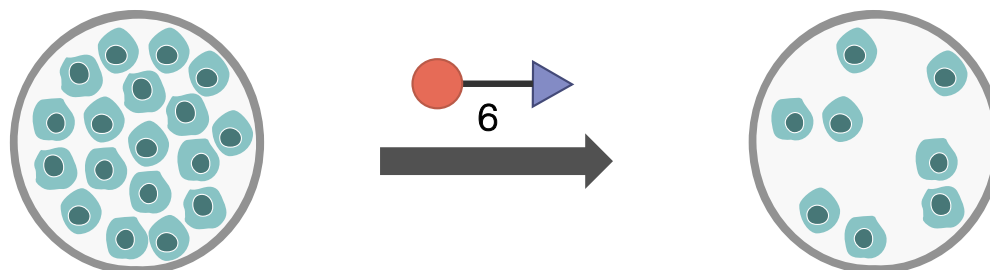
compd	ABL1 IC ₅₀ (nM)	cIAP1 IC ₅₀ (nM)	cIAP2 IC ₅₀ (nM)	XIAP IC ₅₀ (nM)
1 (GNF-2)	2800 (2000–4000)	n.d.	n.d.	n.d.
2 (GNF-5)	2000 (1400–2900)	n.d.	n.d.	n.d.
3 (ABL001 derivative)	35 (27–45)	n.d.	n.d.	n.d.
4 (LCL-161 derivative)	n.d.	4.8 (4.3–5.4)	5.7 (4.3–7.5)	67 (49–96)
5 (SNIPER(ABL)-21)	2000 (1200–3300)	220 (180–280)	330 (220–500)	94 (70–130)
6 (SNIPER(ABL)-62)	360 (220–590)	86 (78–94)	140 (120–160)	120 (99–140)
7 (SNIPER(ABL)-64)	340 (210–570)	>1000	>1000	>1000

^aThe inhibitory activity of the test compounds at several concentrations were examined as described in [Supporting Information](#). IC₅₀ values and 95% confidence intervals were calculated by nonlinear regression analysis of percent inhibition data ($n \geq 3$). n.d.: not determined.

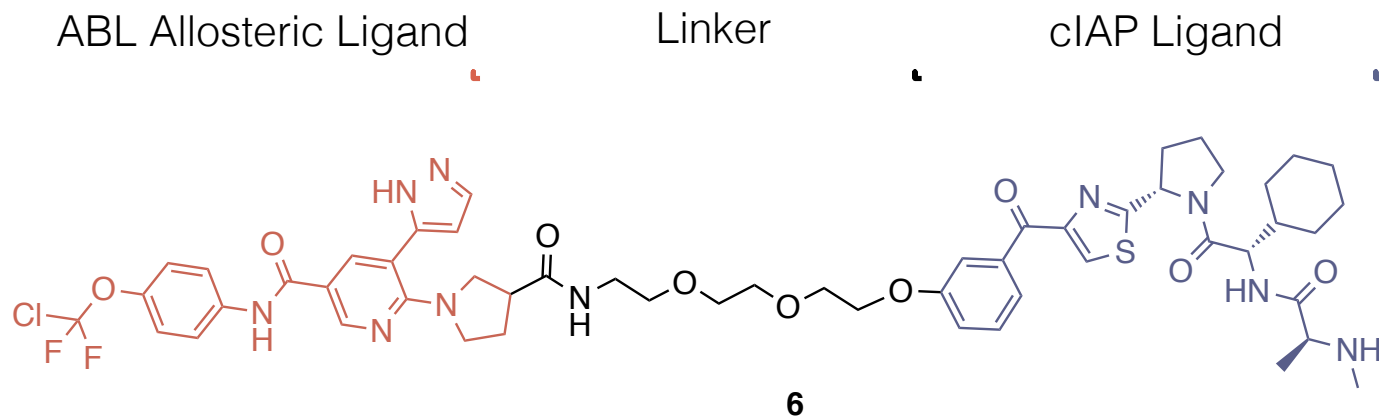
Compound 6-induced BCR-ABL Protein Degradation



Compound 6 Effect on Cell Proliferation



Summary



- Designed and developed an allosteric BCR-ABL PROTAC that potently induces BCR-ABL protein degradation in cell assays.

Half-maximal degradation concentration (DC_{50}): ~30 nM

Maximum degradation efficacy (D_{max}): ~70% between 100-300 nM

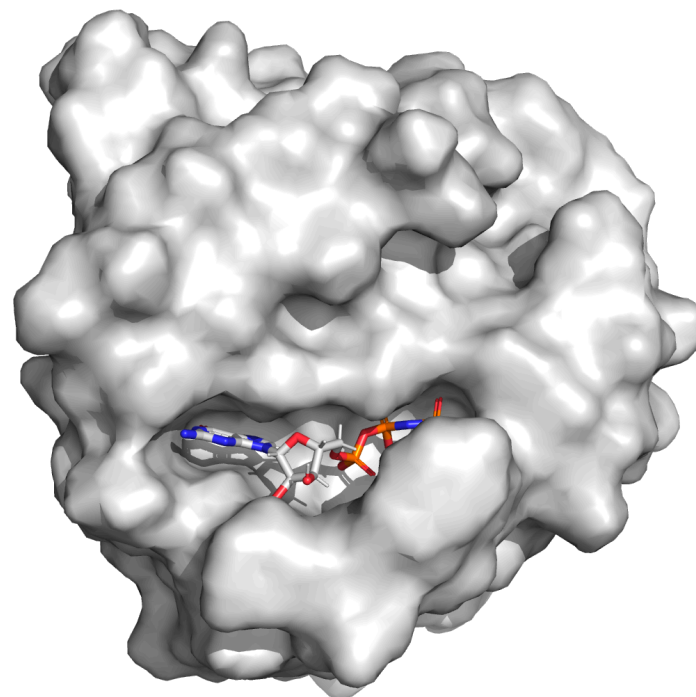
Further developments:

- LCL161 derivative **4** induces auto-ubiquitination leading to IAP protein degradation
- Evaluation of compound **6** in *in-vivo* models

Drugging the “Undruggable”

- The RAS genes constitute the most frequently mutated oncogene family in cancer.
- Approximately ~25% of human tumors have a RAS mutation.
- Despite more than 30 years of effort to develop a pharmacologic inhibitor of RAS, a clinically effective anti-RAS therapy does not exist.
- What approach will prove to be the most effective RAS modulator? Which approach will produce the first clinical anti-RAS agent?

Perhaps an allosteric RAS PROTAC to induce RAS protein degradation?



Science 2017, 355, 1158.