



Monofunctional Degradation Activating Compounds: From Platform Development to the Clinic

Discovery on Target – Next Generation Protein Degraders



Forward-looking Statements and Intellectual Property

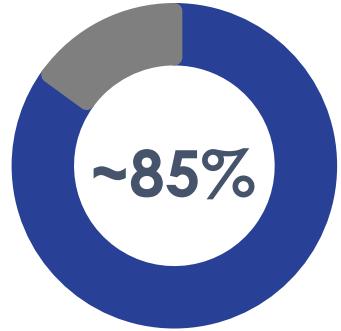
Forward-looking Statements

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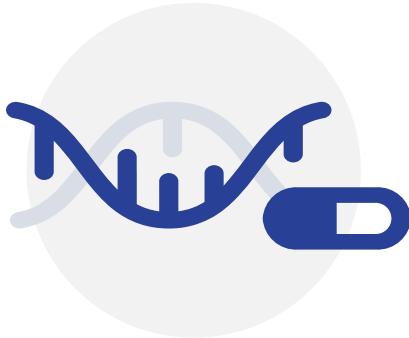
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Targeted Protein Degradation Has the Potential to Transform Treatment of Disease



TPD Has an Expansive Target Landscape

85% of proteins are currently undruggable or poorly drugged



TPD Offers a Powerful Modality

Benefits of genetic knockdown with a small molecule approach

C4T's TORPEDO platform creates therapeutic candidates that have the potential to improve patient care



Overcome Resistance



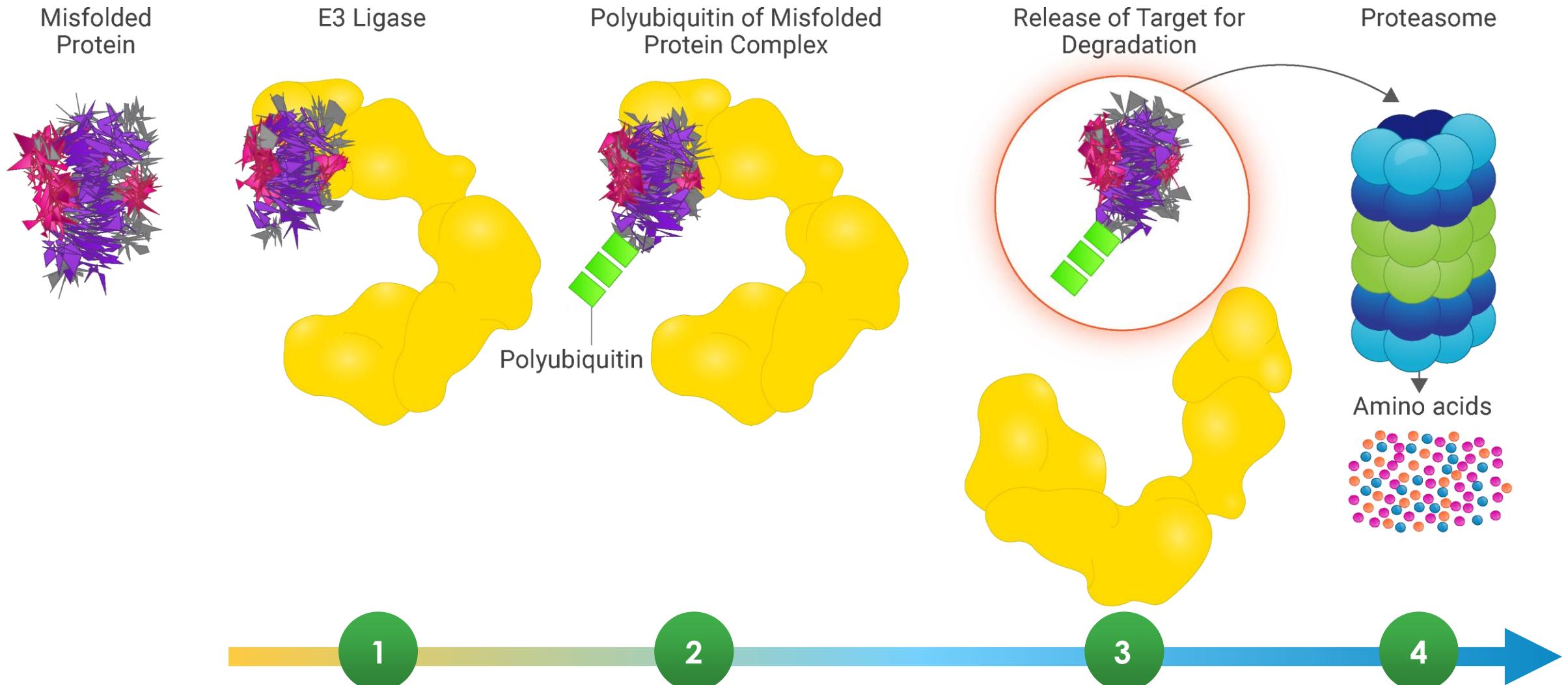
Drug Undruggable Targets



Improve Treatment Options

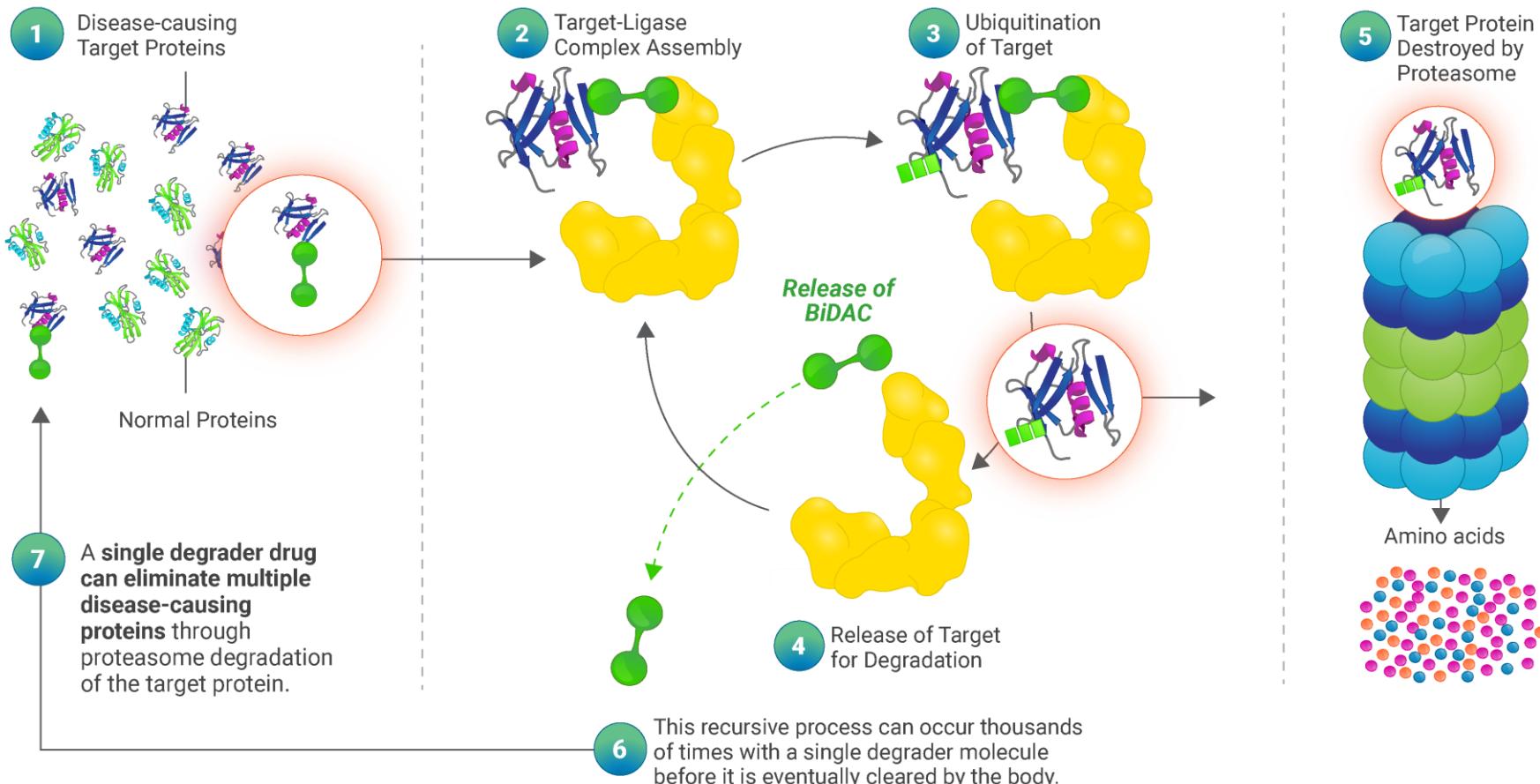
Source: Hopkins, A., Groom, C. The druggable genome. *Nat Rev Drug Discov* 1, 727–730 (2002).

The Human Body Has A Natural Process to Destroy Unwanted Proteins



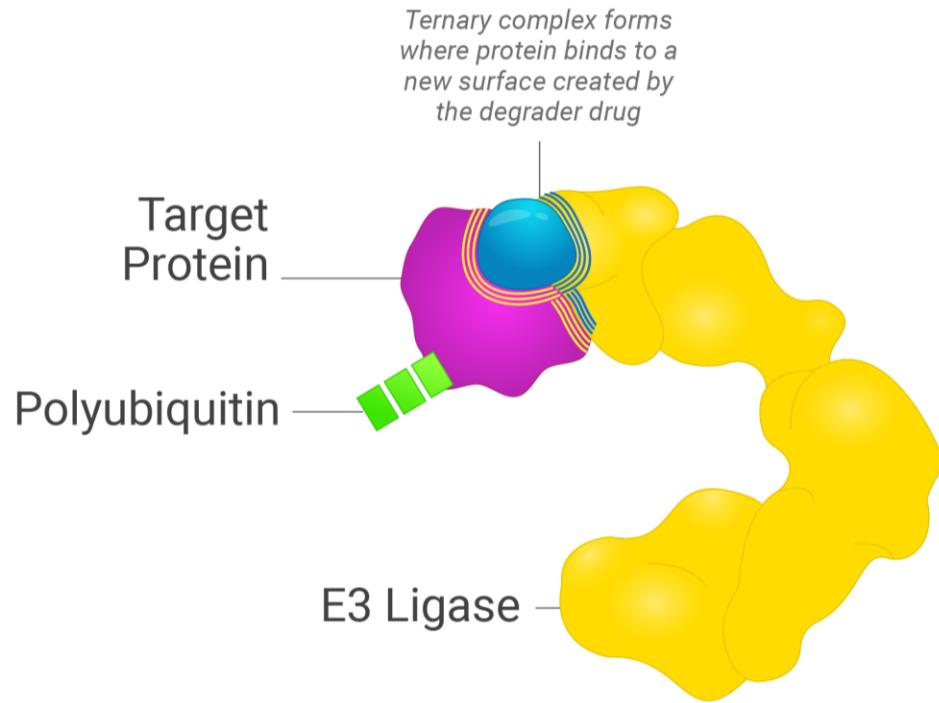
Targeted Protein Degradation Leverages the Body's Natural Process to Destroy Disease-Causing Proteins

Focus on Overall Catalytic Degradation

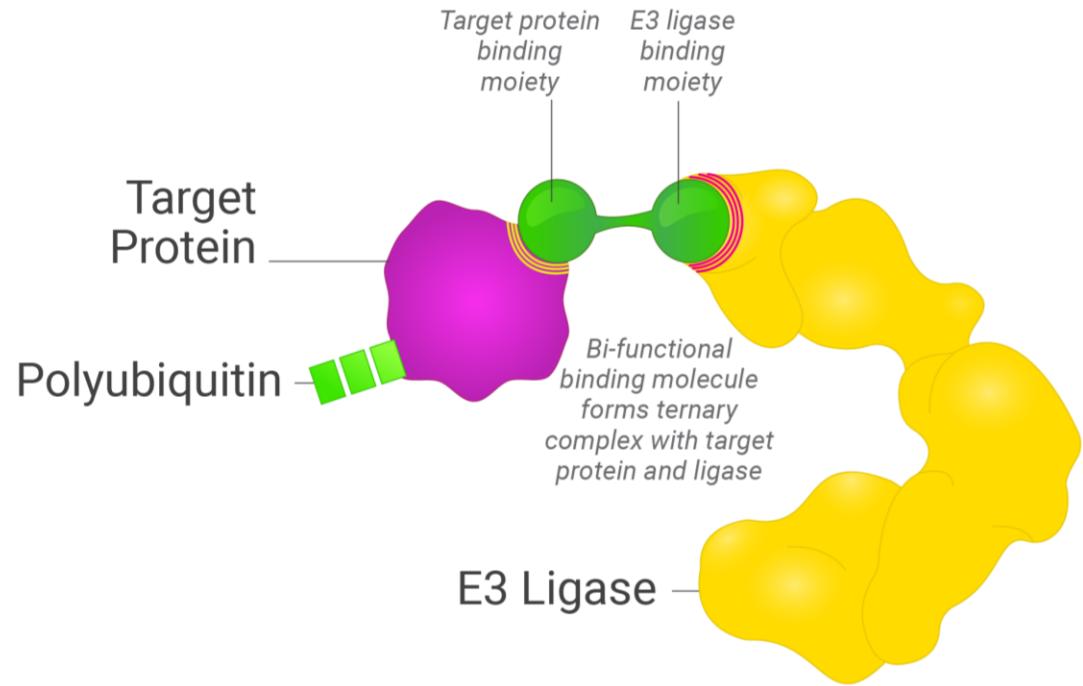


TORPEDO Platform Offers Flexibility to Design MonoDAC and BiDAC Degraders

MonoDAC Degrader

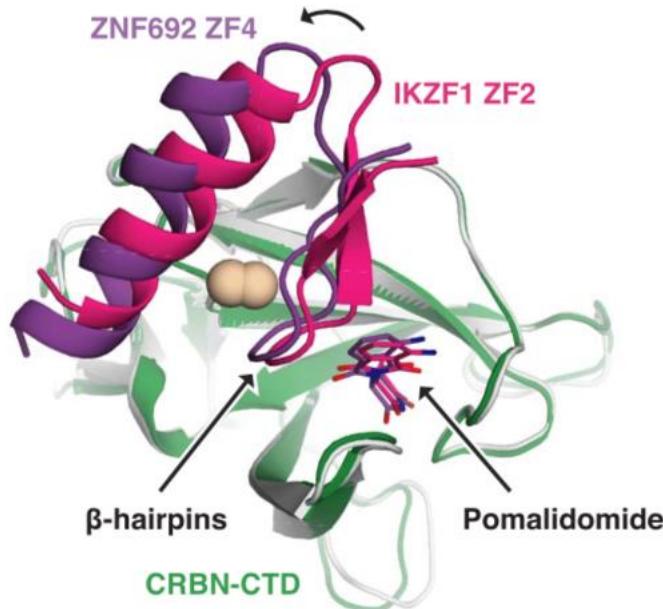


BiDAC Degrader

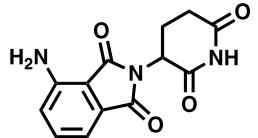


Flexibility to Address Different Targets with Tailored Approach

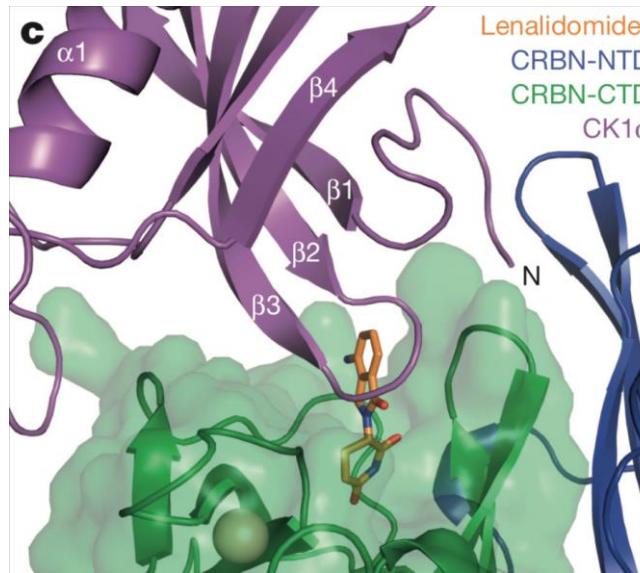
Molecular Glue Degraders (MGDs) in the Literature



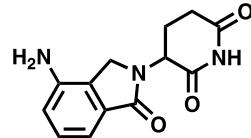
Thalidomide-related Zinc Finger degraders



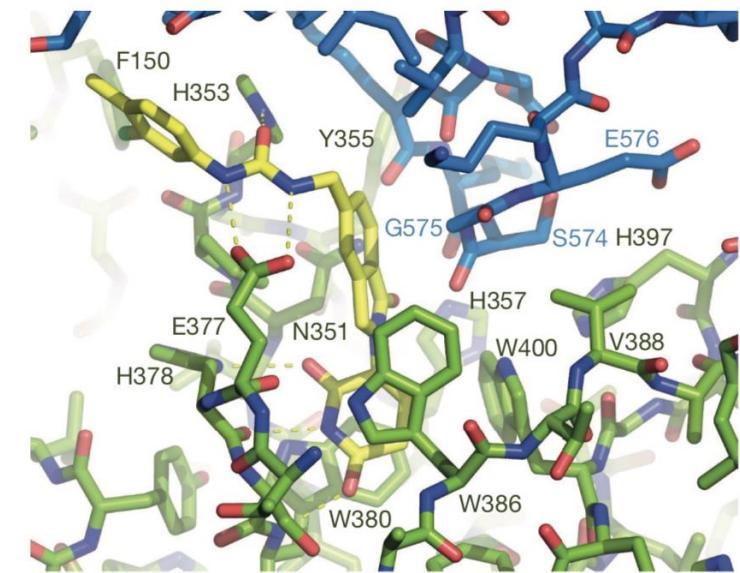
Science 2018, 362(6414), eaat0572



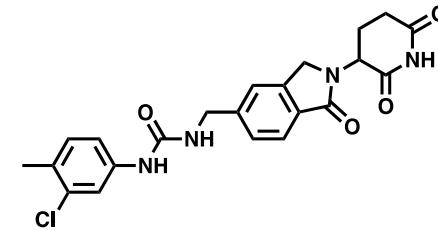
Lenalidomide, CK1- α degrader



Nature 2016, 532(7597), 127

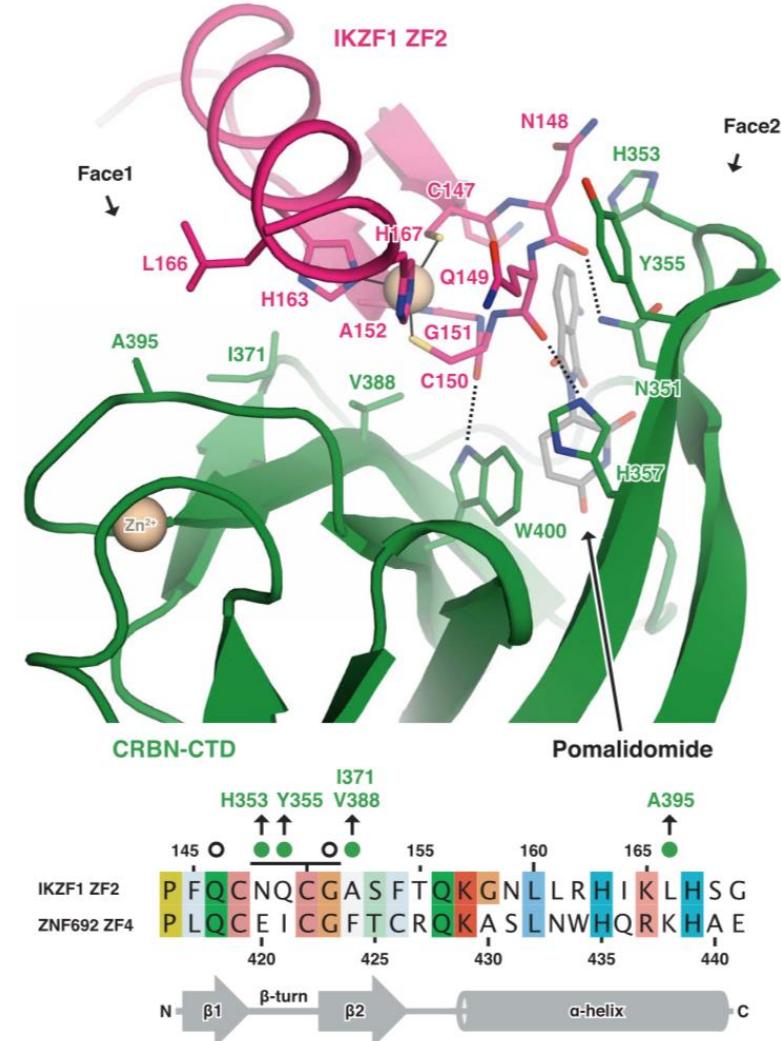
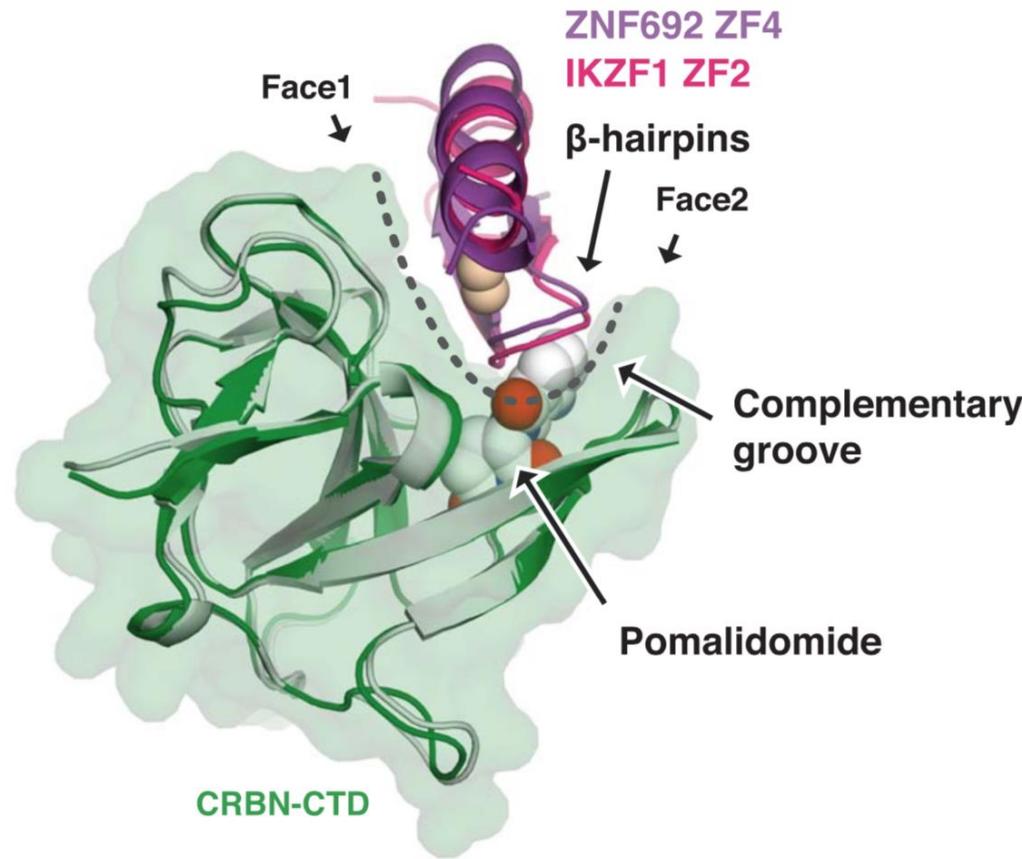


CC-885/90009 GSPT1 degraders



Nature 2016, 535(7611), 252

MGDs in the Literature



β-turn is the primary recognition element, 2nd interactions play a role in activity and selectivity

Science 2018, 362(6414), eaat0572

Why MonoDAC Degraders and Molecular Glue Degraders?

Disease Target and Potential for New Medicines

- Access to Undruggable/or Unligandable Targets
- MonoDAC degraders and MGDs exhibit degradation-only pharmacology

Drug Properties and Performance

- Access to degrader drug candidates within more traditional Rule of 5 physicochemical property space

MonoDAC Degraders and MGDs should be aligned to the right target and clinical opportunities



C4 Therapeutics

Identification and Characterization of MonoDAC CFT7455

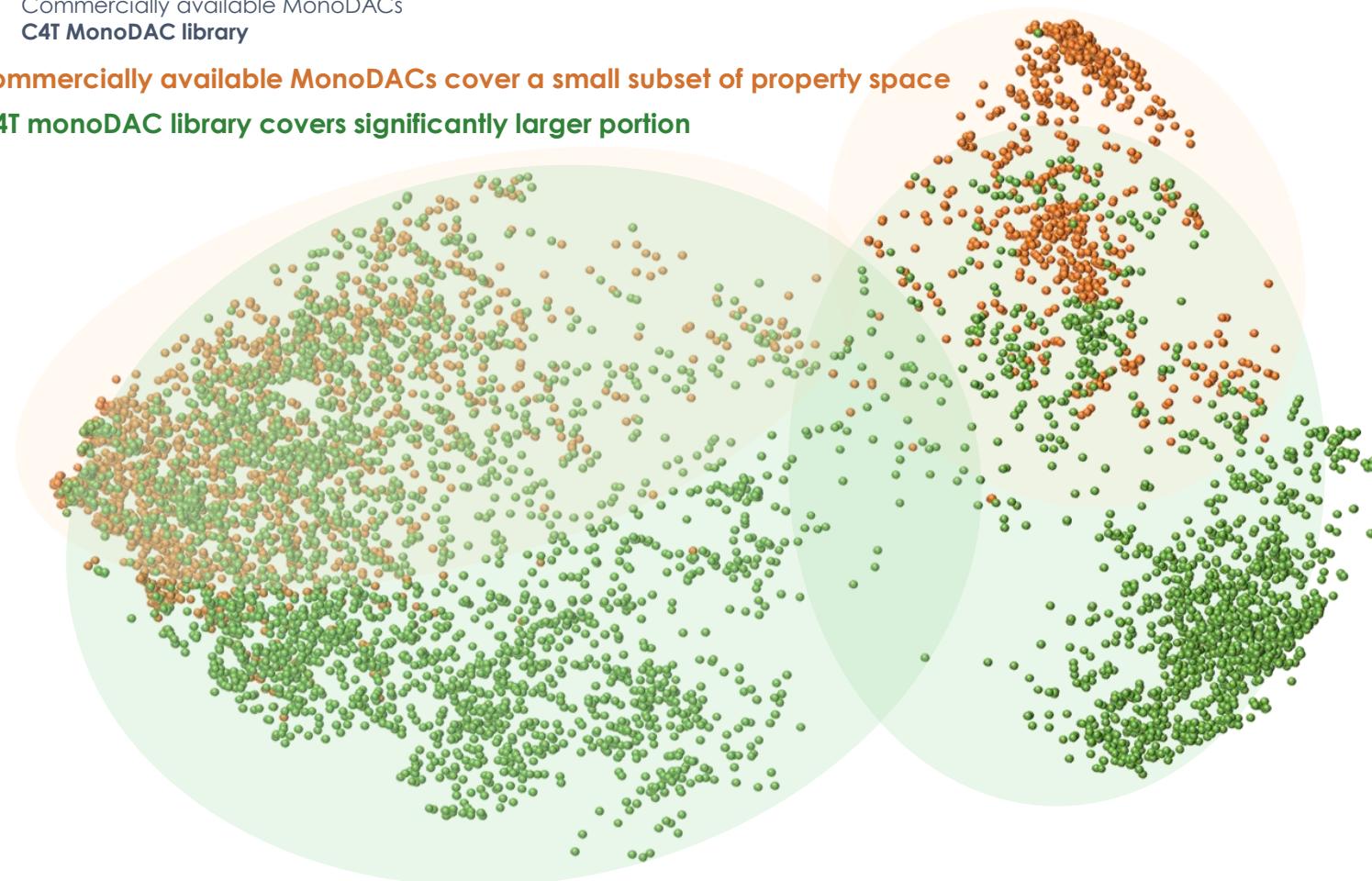


C4T MonoDAC Library: Expanding the Cereblon Toolbox

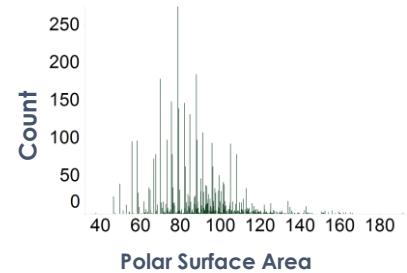
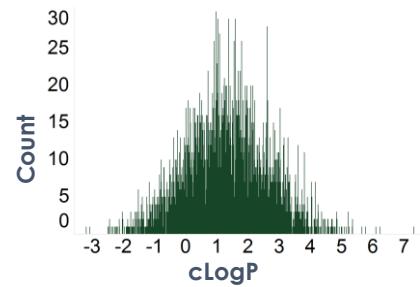
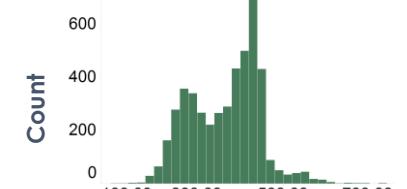
- Commercially available MonoDacs
- C4T MonoDAC library

Commercially available MonoDacs cover a small subset of property space

C4T monoDAC library covers significantly larger portion



Drug-like property space



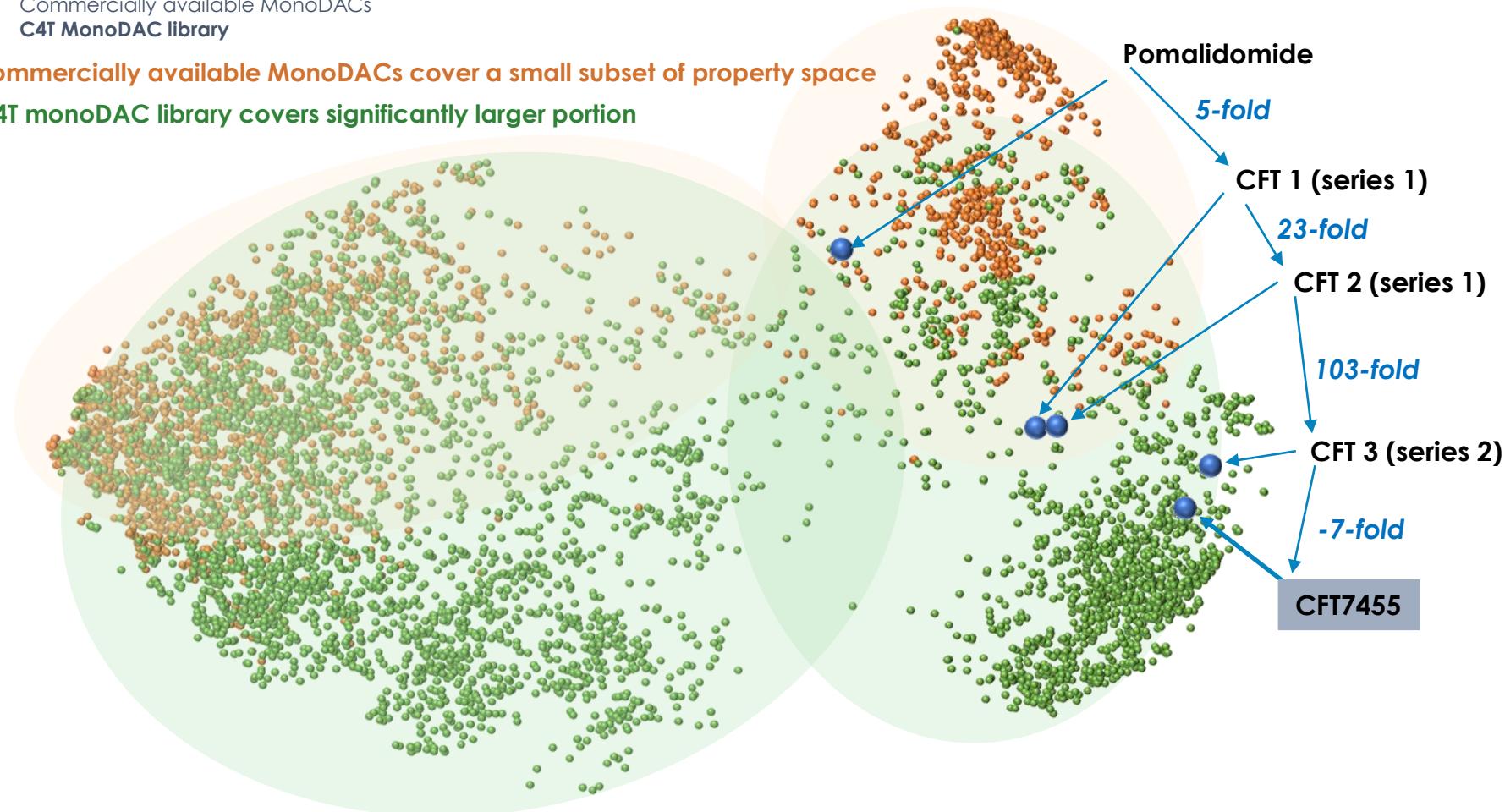
>5,000 membered library constructed from >200 unique scaffolds to maximize MonoDAC structural diversity and CRBN surface remodeling

C4T MonoDAC Library in Action

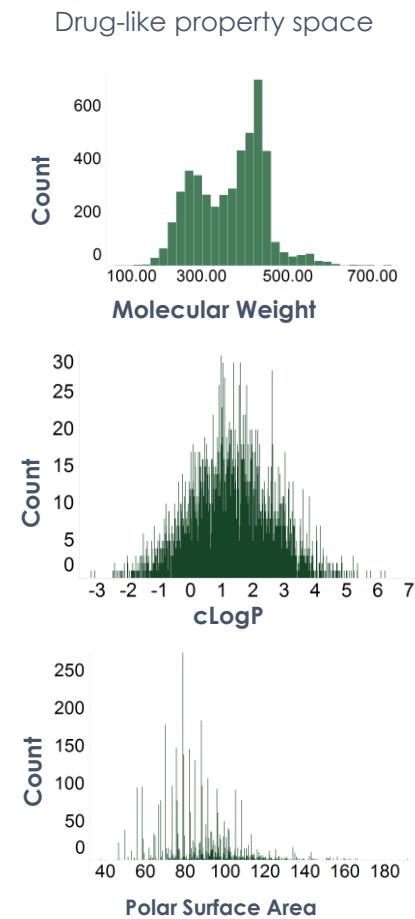
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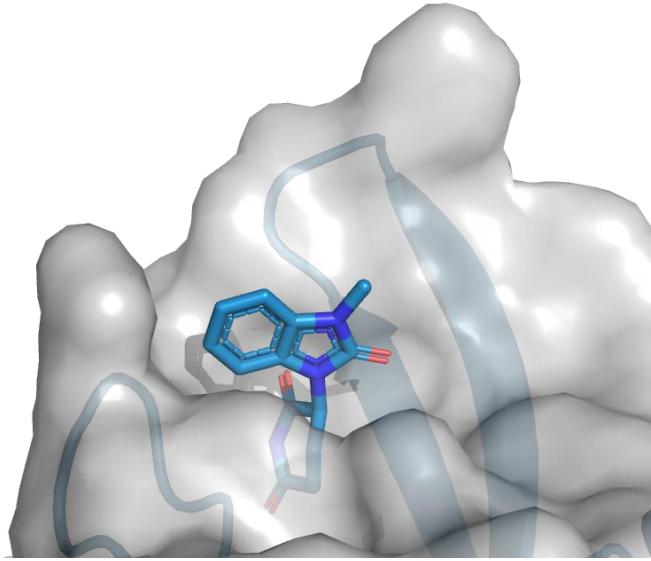
C4T MonoDAC Library has produced hits to novel MonoDAC Targets and a development candidate



Deep Structural Design Expertise of MonoDAC Degraders

Benzoimidazolone

C4T unpublished
1.17 Å

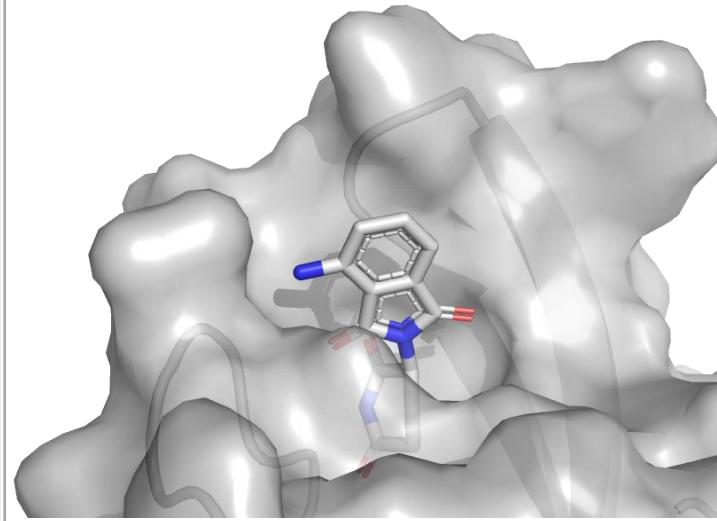


Compound 4
CRBN FP K_D = 830 nM



Pomalidomide

PDB 6h0f



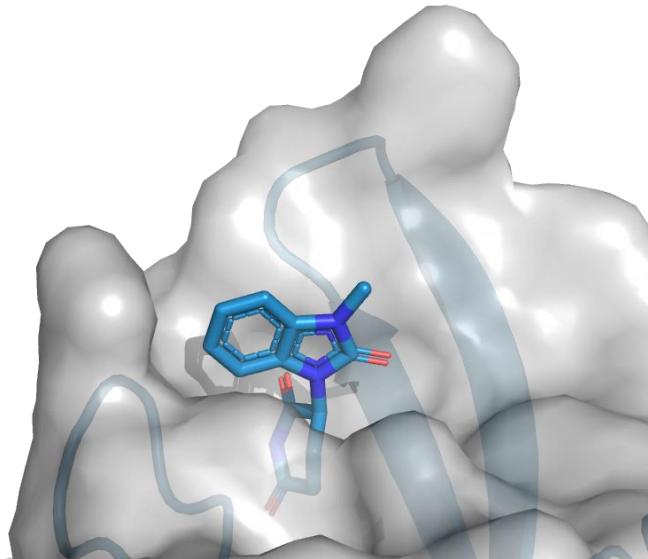
Pomalidomide
 K_D = 1600 nM



Deep Structural Design Expertise of MonoDAC Degraders

Benzoimidazolone

C4T unpublished
1.17 Å



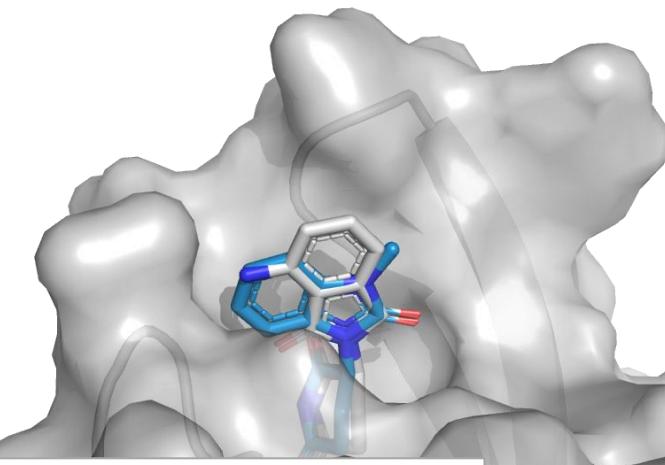
Compound 4
CRBN FP K_D = 830 nM



CRBN, cereblon; FP, fluorescence polarization; IKZF1, Ikaros family zinc finger protein 1.

Pomalidomide

PDB 6h0f



Overlay with Compound 4

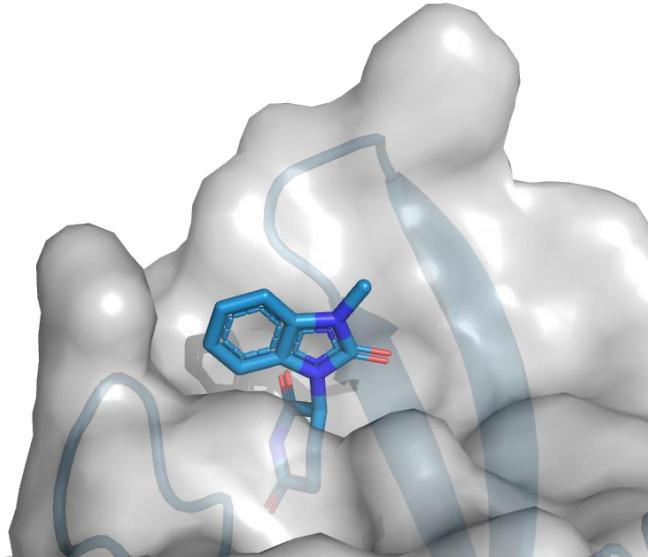
Pomalidomide
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Deep Structural Design Expertise of MonoDAC Degraders

Benzoimidazolone

C4T unpublished
1.17 Å



Compound 4
CRBN FP K_D = 830 nM

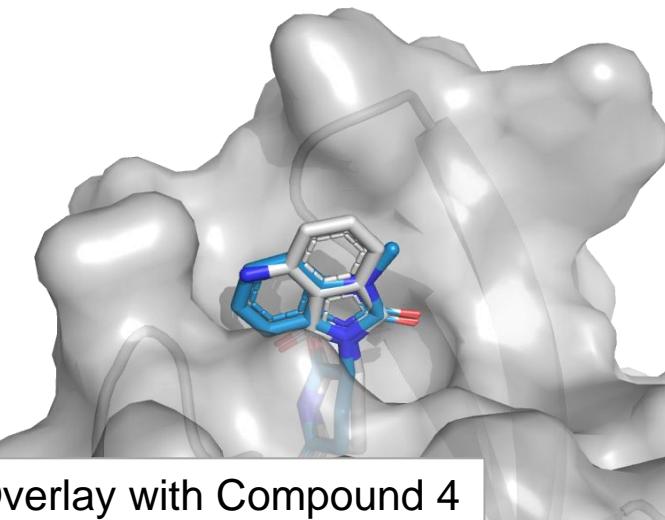


CRBN, cereblon; FP, fluorescence polarization; IKZF1, Ikaros family zinc finger protein 1.

Pomalidomide

PDB 6h0f

Overlay with Compound 4



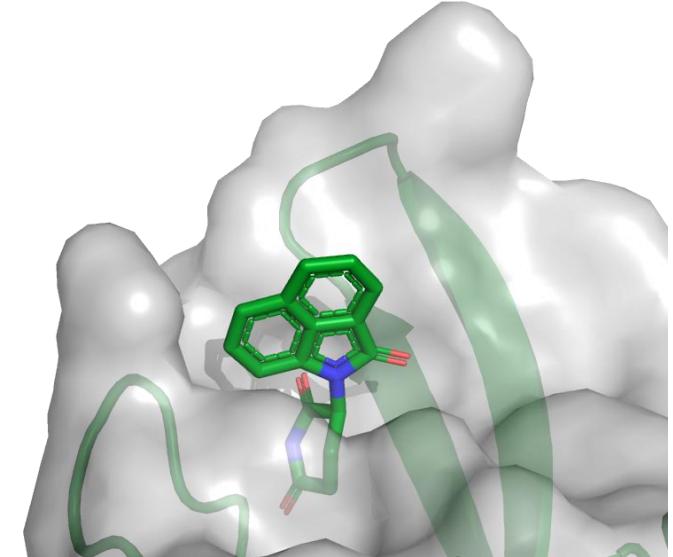
Pomalidomide
 K_D = 1600 nM



50-fold
affinity
increase

Benzoisoindolinone

C4T unpublished
1.06 Å

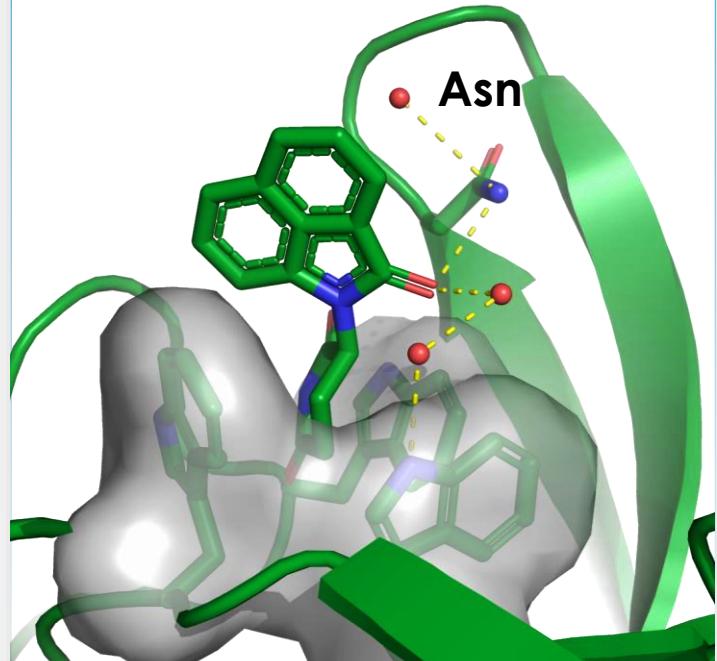


Compound 5
 K_D = 34 nM

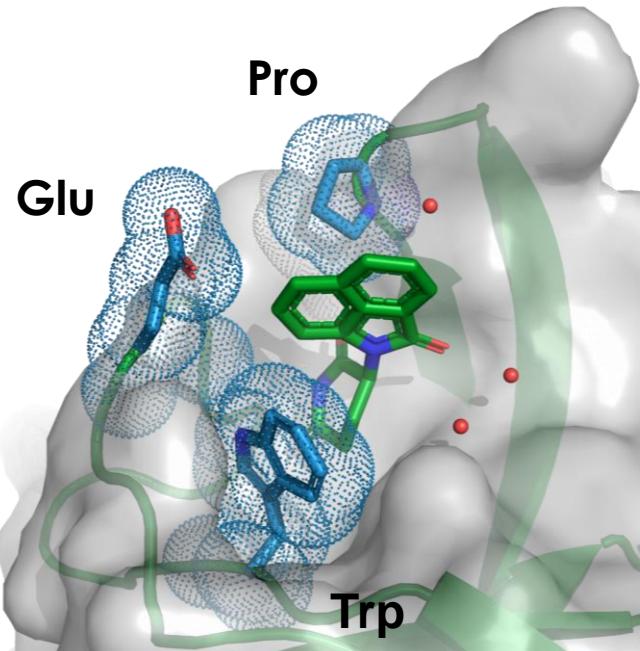


Exploring CRBN Interactions with the Potent Tricyclic Core

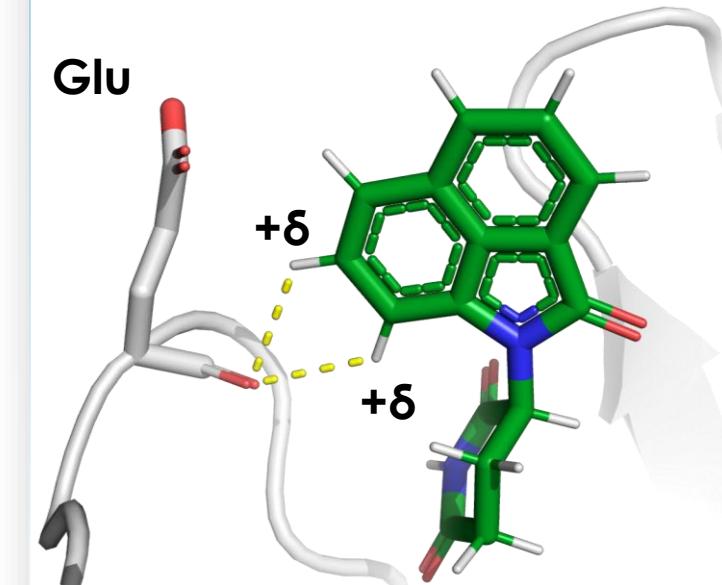
Tri-Trp Pocket Interactions



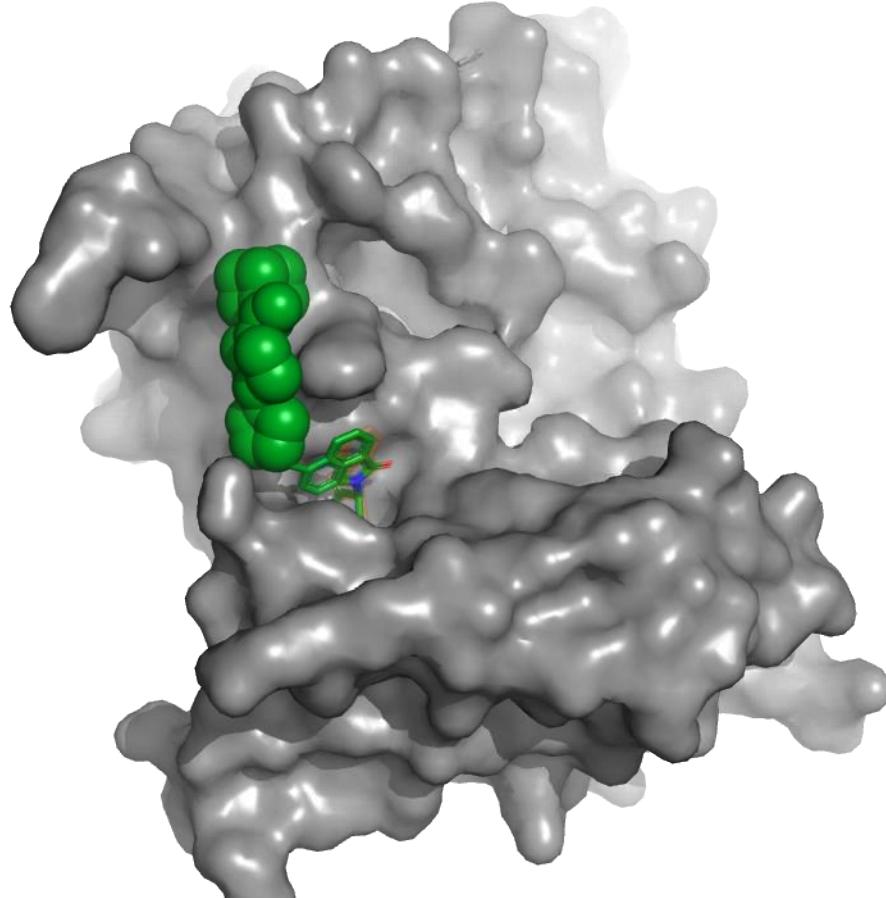
Increased Hydrophobic Contacts with CRBN



+δ Aromatic C-H Interactions with Backbone Carbonyl

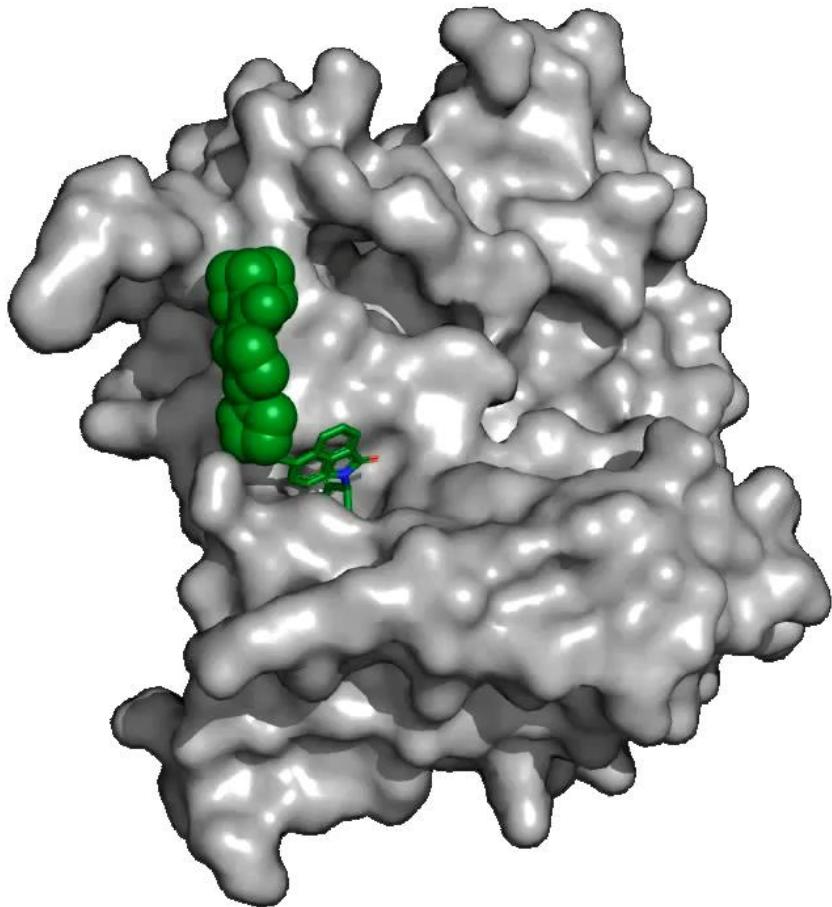


Design Beyond the Tricyclic Core - Crystallography and Ternary Complex Models

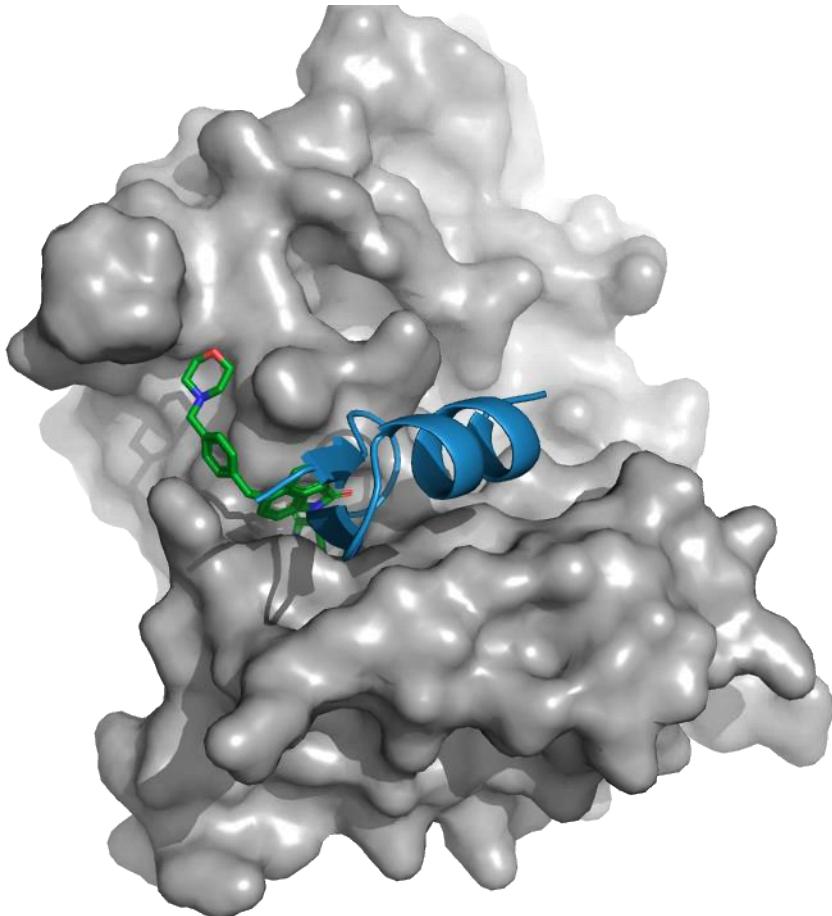


PDB 4tz4

Design Beyond the Tricyclic Core - Crystallography and Ternary Complex Models



Design Beyond the Tricyclic Core - Crystallography and Ternary Complex Models



C4T unpublished structure
Blue cartoon = IKZF1 model

Summary: Deep structural understanding of CRBN was critical in developing CFT7455

- MonoDAC library provides coverage of diverse chemical space
- Structural understanding of CRBN binding yielded potent tricycle core
- Further designs extend beyond the Tri-Trp pocket; alter CRBN surface
- Result of the chemistry campaign was CFT7455 – a potent CRBN binder with fast, selective degradation of IKZF1/3 that has made it to the clinic



Finding MonoDAC Hits
to Novel Neosubstrates



Strategic Approach to MonoDAC Hit Identification

In Silico Ternary Complex Design

- Identify G-loop containing proteins across the proteome
- Generate ternary complex models that inspire new monoDAC design
- Approach does not necessarily identify productive degraders

Ternary Complex Identification

- Develop high-throughput biochemical methods to identify ternary complex formation
- Develop high-throughput cellular assay methods to identify ternary complex formation
- Approaches do not identify productive degraders

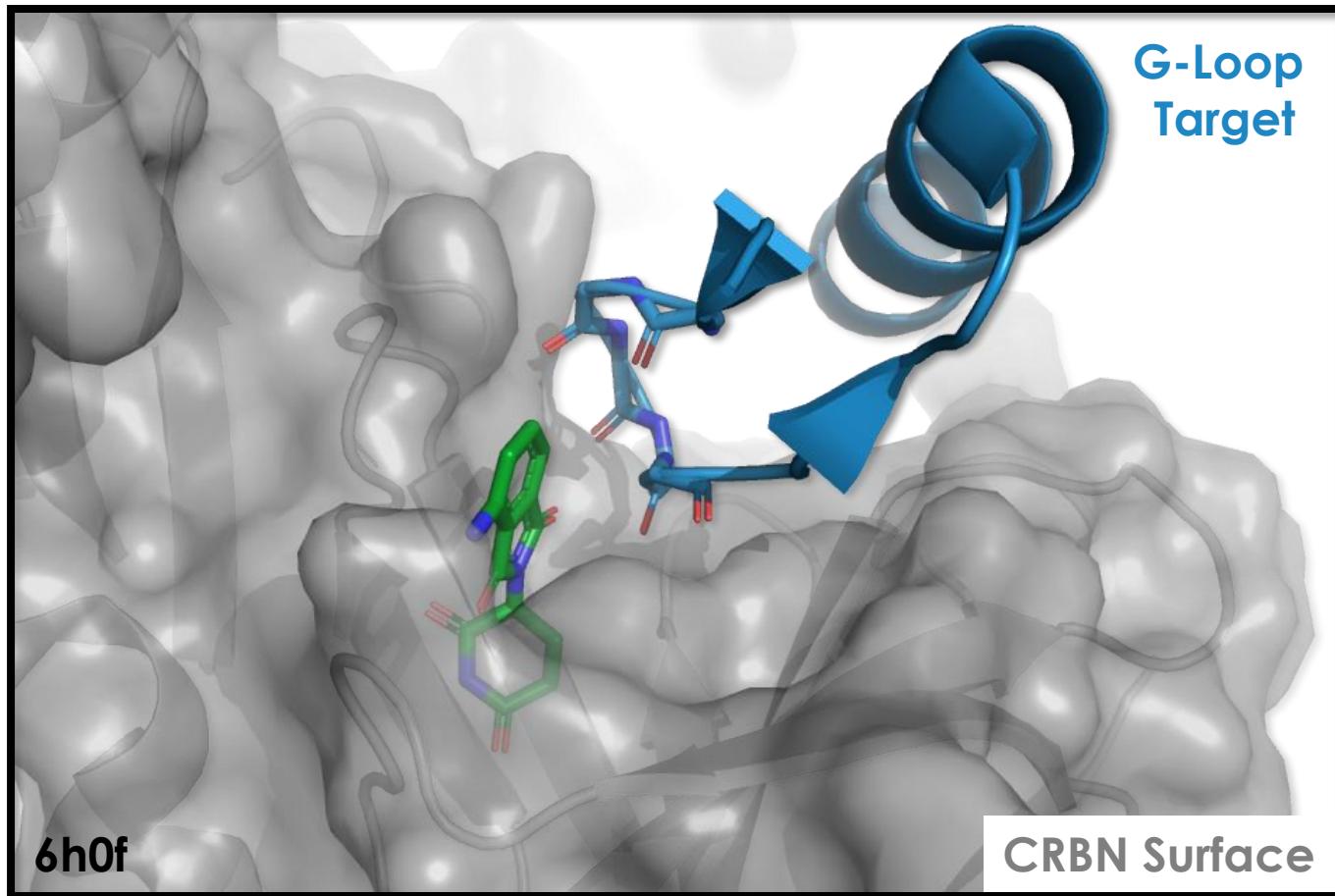
Cellular Degradation

- HiBiT assay – mechanism-informed reduction of target protein levels
- Off-target/off-mechanism and off-target/on-mechanism activity could confound hit identification

A comprehensive approach that will also identify and expand MonoDAC degrons

In Silico: Canonical G-Loop Protein MonoDAC Design

1. Model G-Loop

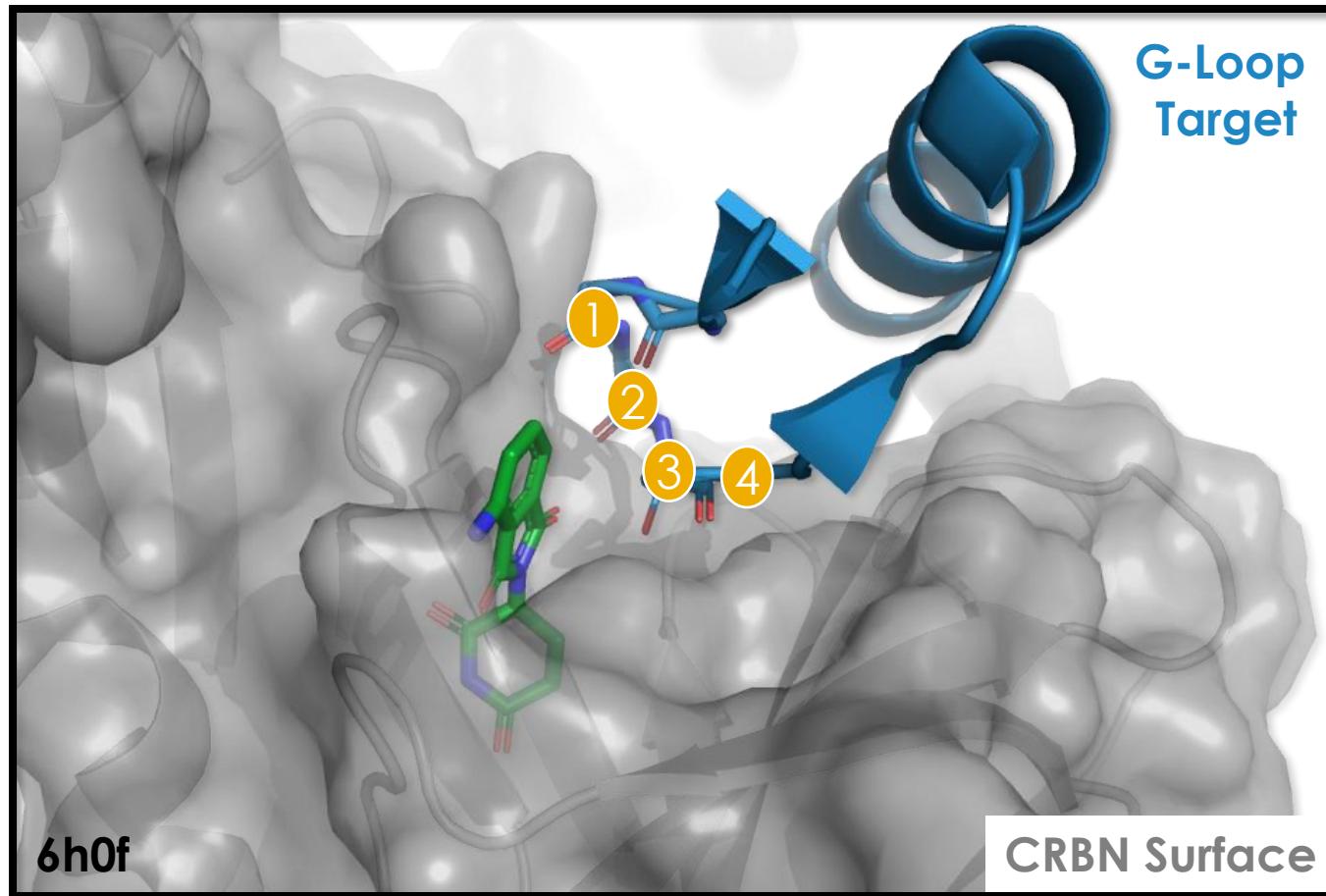


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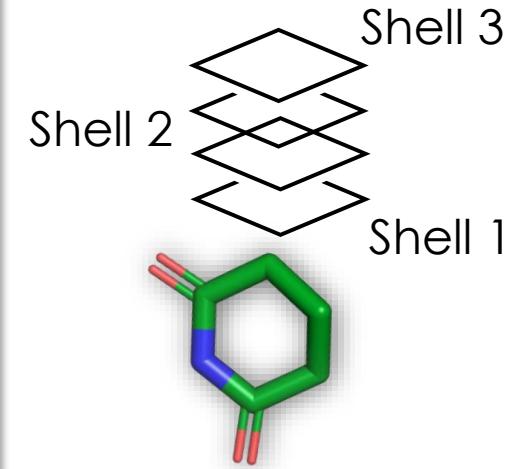
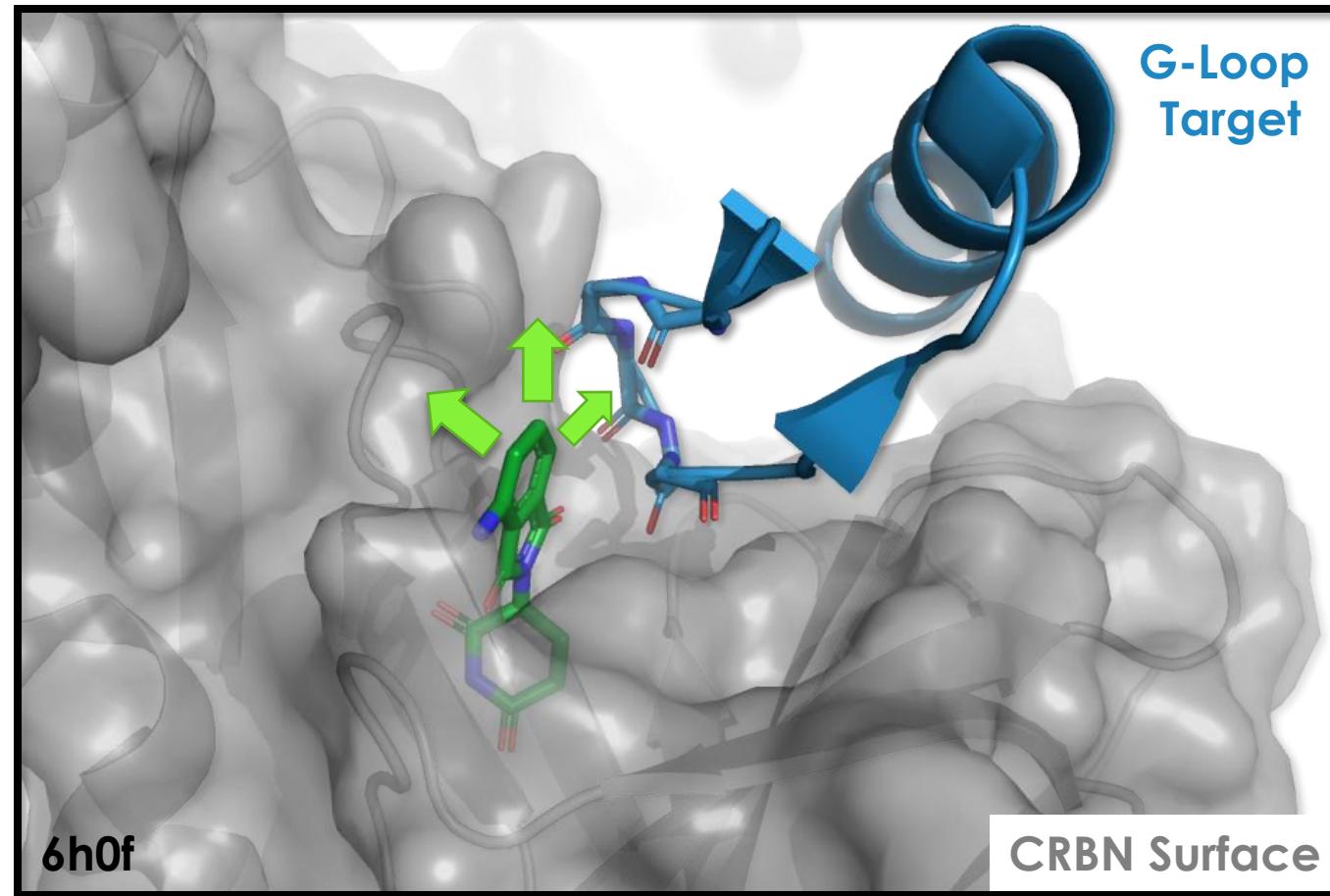


2. Examine amino acid sidechains



In Silico: Canonical G-Loop Protein MonoDAC Design

1. Model G-Loop
2. Examine amino acid sidechains
3. Grow CRBN ligands from novel scaffolds

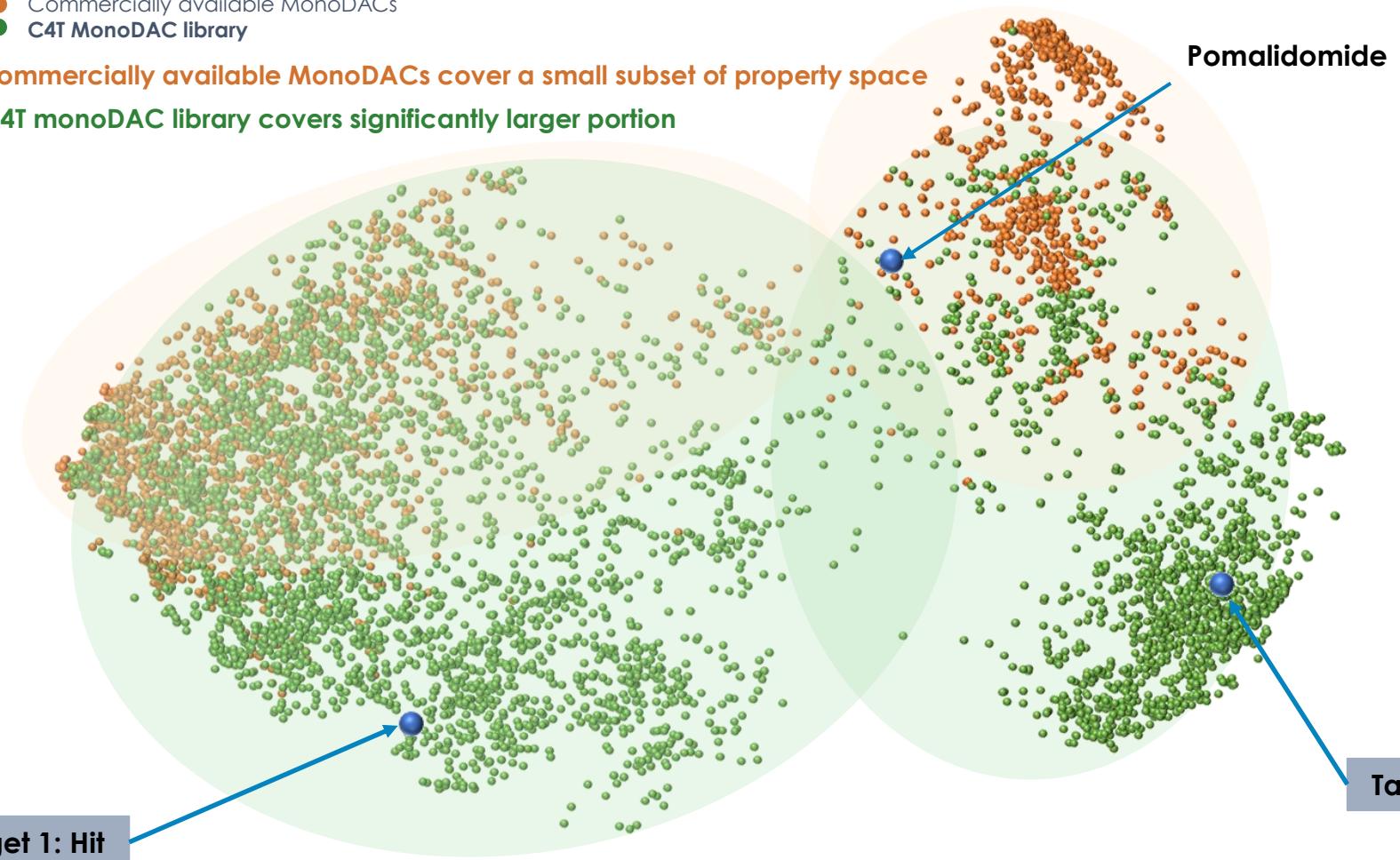


C4T MonoDAC Library in Action – In Silico Ternary Complex Design

- Commercially available MonoDacs
- C4T MonoDAC library

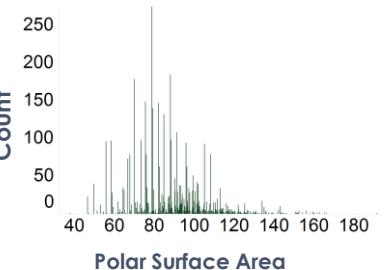
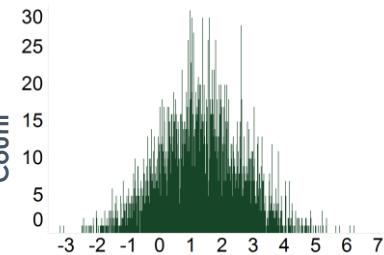
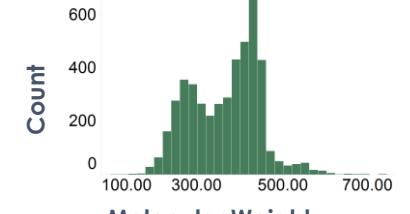
Commercially available MonoDacs cover a small subset of property space

C4T monoDAC library covers significantly larger portion



C4T MonoDAC Library has produced hits to novel MonoDAC Targets and a development candidate

Drug-like property space



In Silico: Test Designed MonoDACs Against Canonical G-Loop Protein

Funnel Assessing *In Silico* Designs

38

Designed compounds to accommodate G-loop of target protein

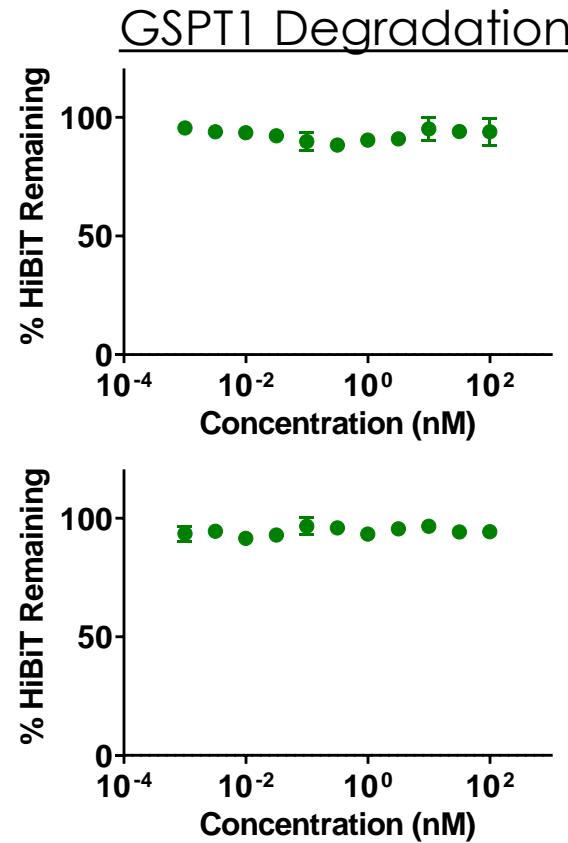
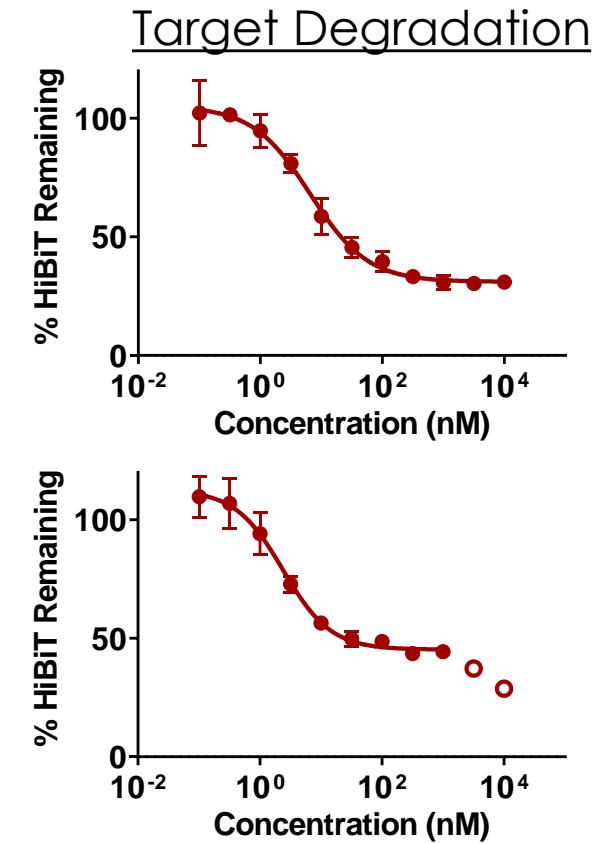
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Hits showing degradation less than 80% E_{max}

14

Pass the GSPT1 filter

Example: Two Hits From Screen Degrade Target 1 & Spare GSPT1

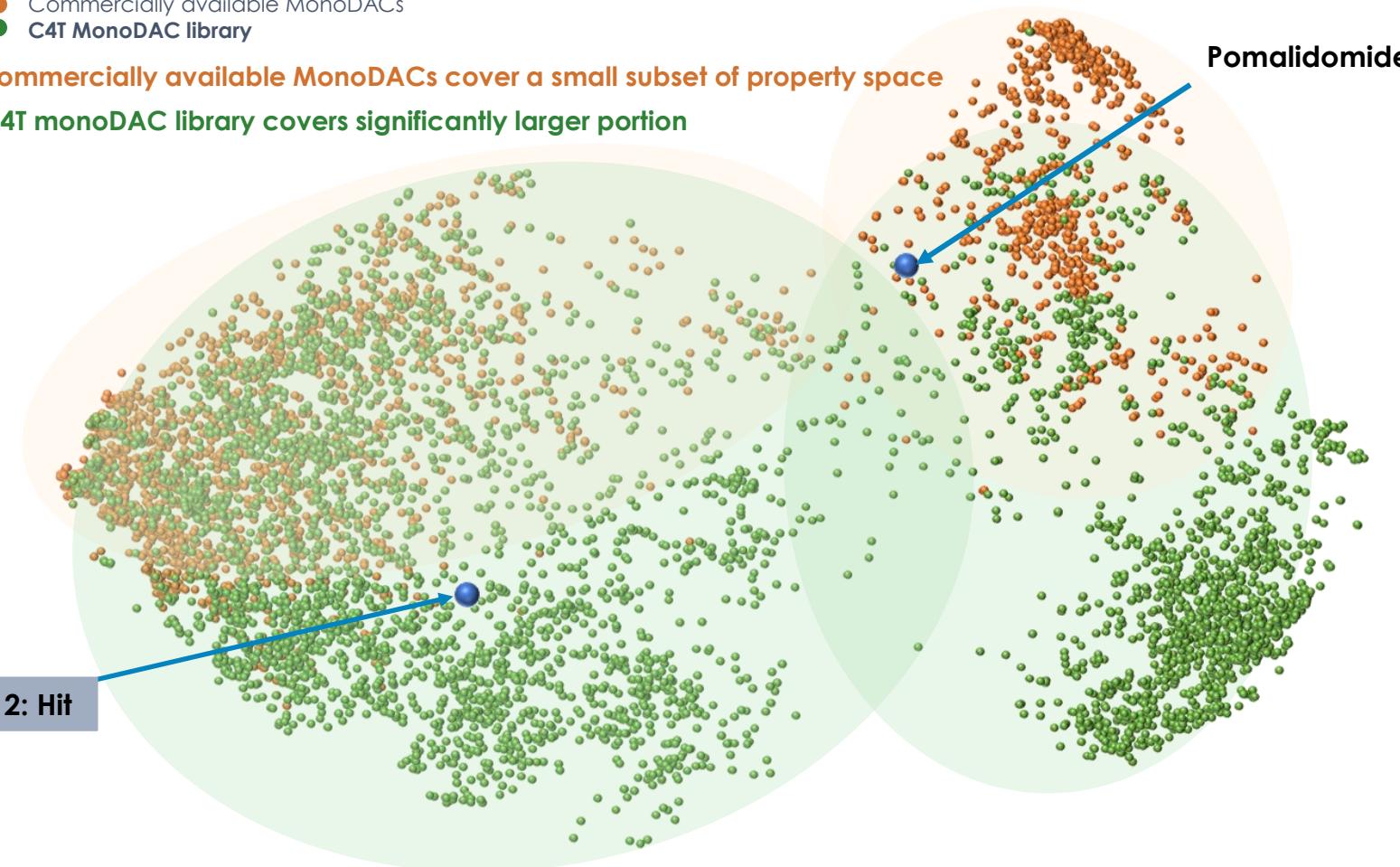


C4T MonoDAC Library in Action – Cellular Degradation of Specific Target

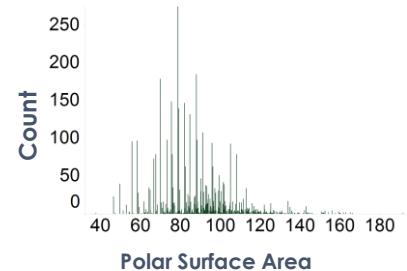
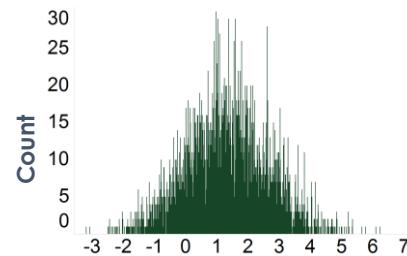
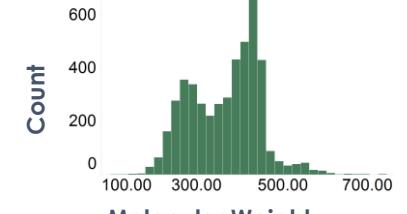
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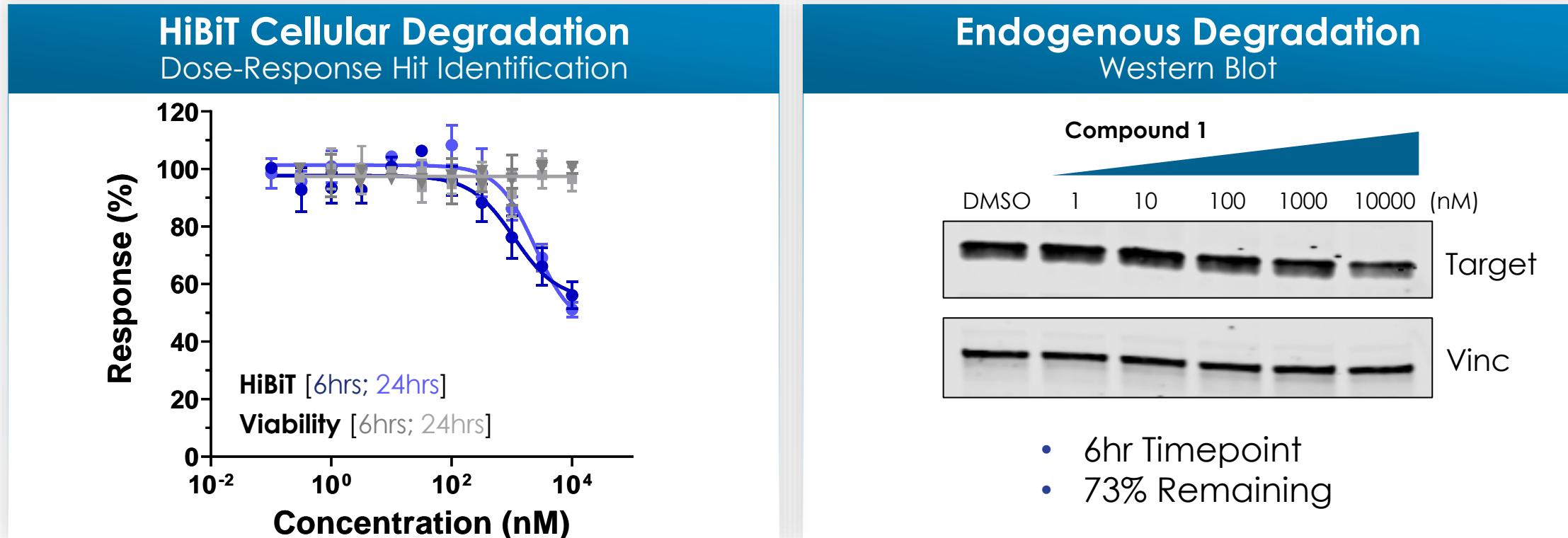


Drug-like property space



C4T MonoDAC Library has produced hits to novel MonoDAC Targets and a development candidate

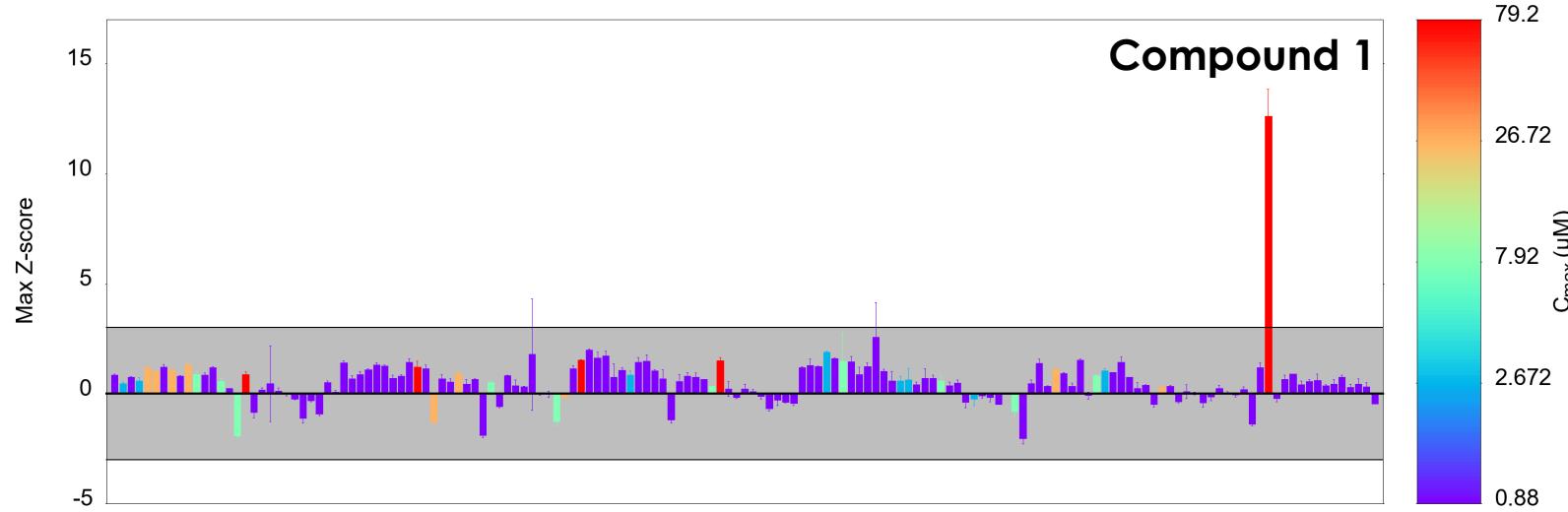
C4T MonoDAC Library in Action – Cellular Degradation of Target 2



Identified hit reduces tagged and endogenous Target 2 protein levels

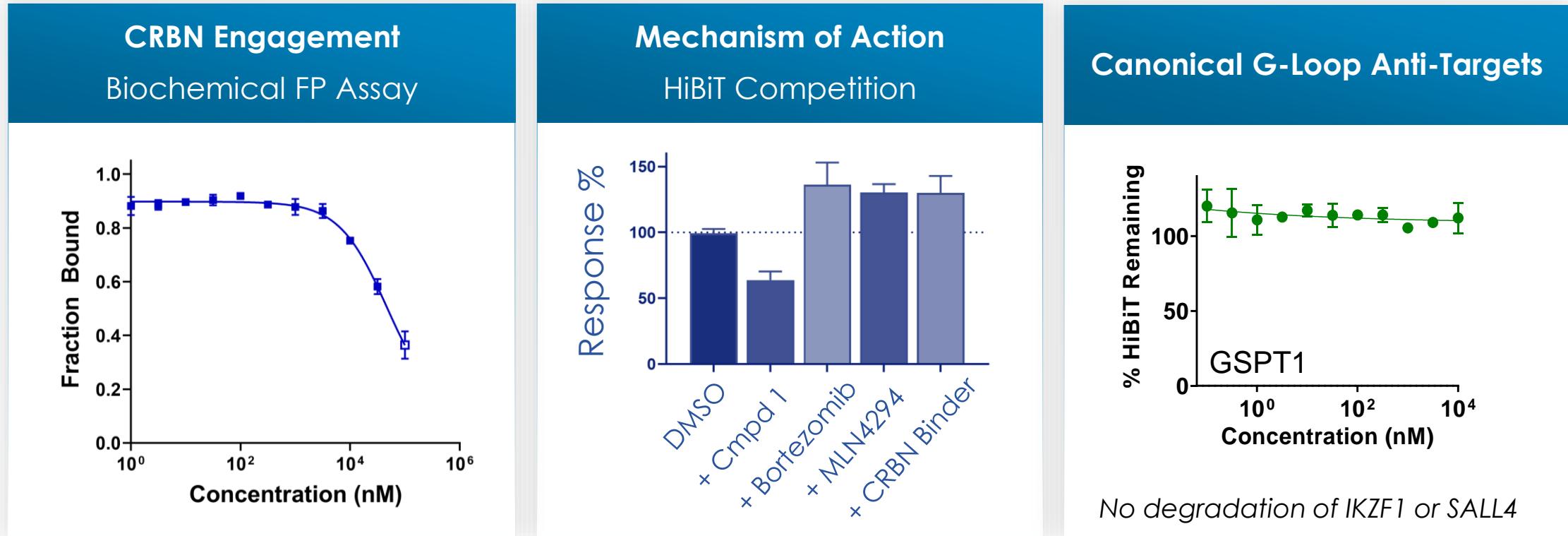
C4T MonoDAC Library in Action – Biochemical Ternary Complex

- AlphaLISA assay format
- Ternary complex between Target 2 and CCRN-DDB1
- Analysis of library subset shown



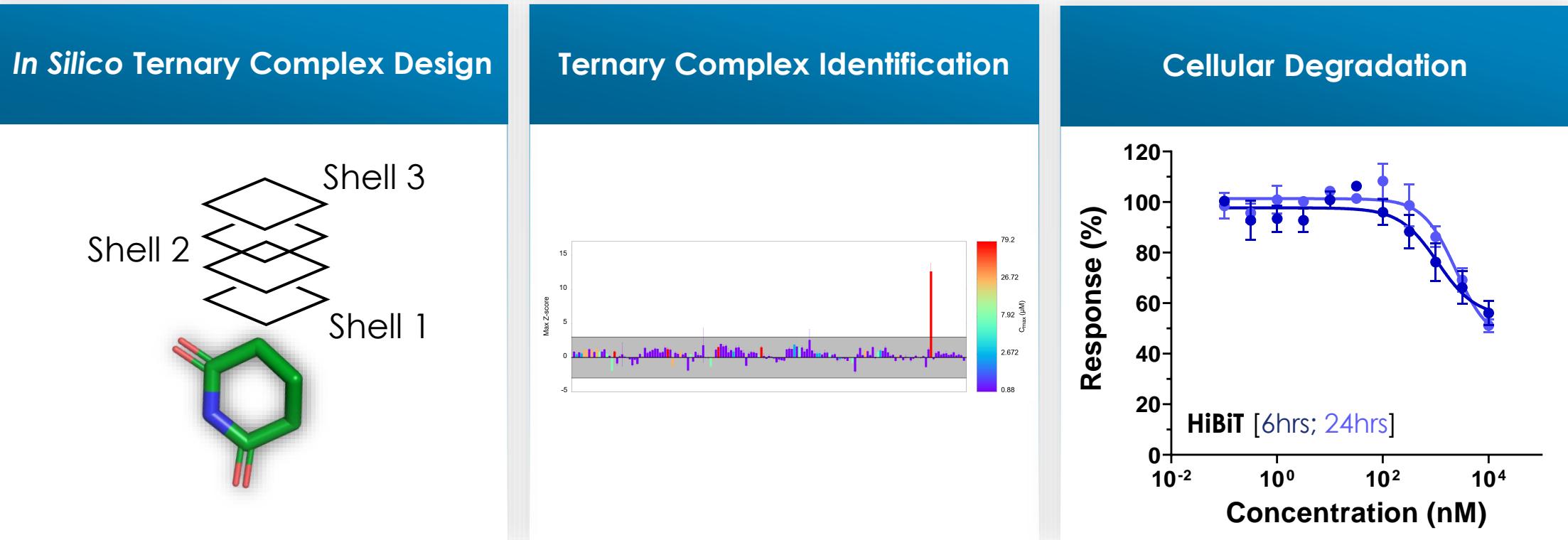
Biochemical screen of the MonoDAC library identifies the same hit compound

C4T MonoDAC Library – Hit Validation for Compound 1



Compound 1 demonstrates selective on-target, on-mechanism degradation of Target 2

Strategic Approach to MonoDAC Screening



A comprehensive approach to identify and expand MonoDAC degrons

Thank You C4T Team

