

Understanding the Nuances of Targeted Protein Degradation



C4 Therapeutics

Destroying
~~Targeting~~ disease-causing
proteins to deliver hope

Stewart L. Fisher
Webinar

December 10, 2020

Forward-looking Statements and Intellectual Property

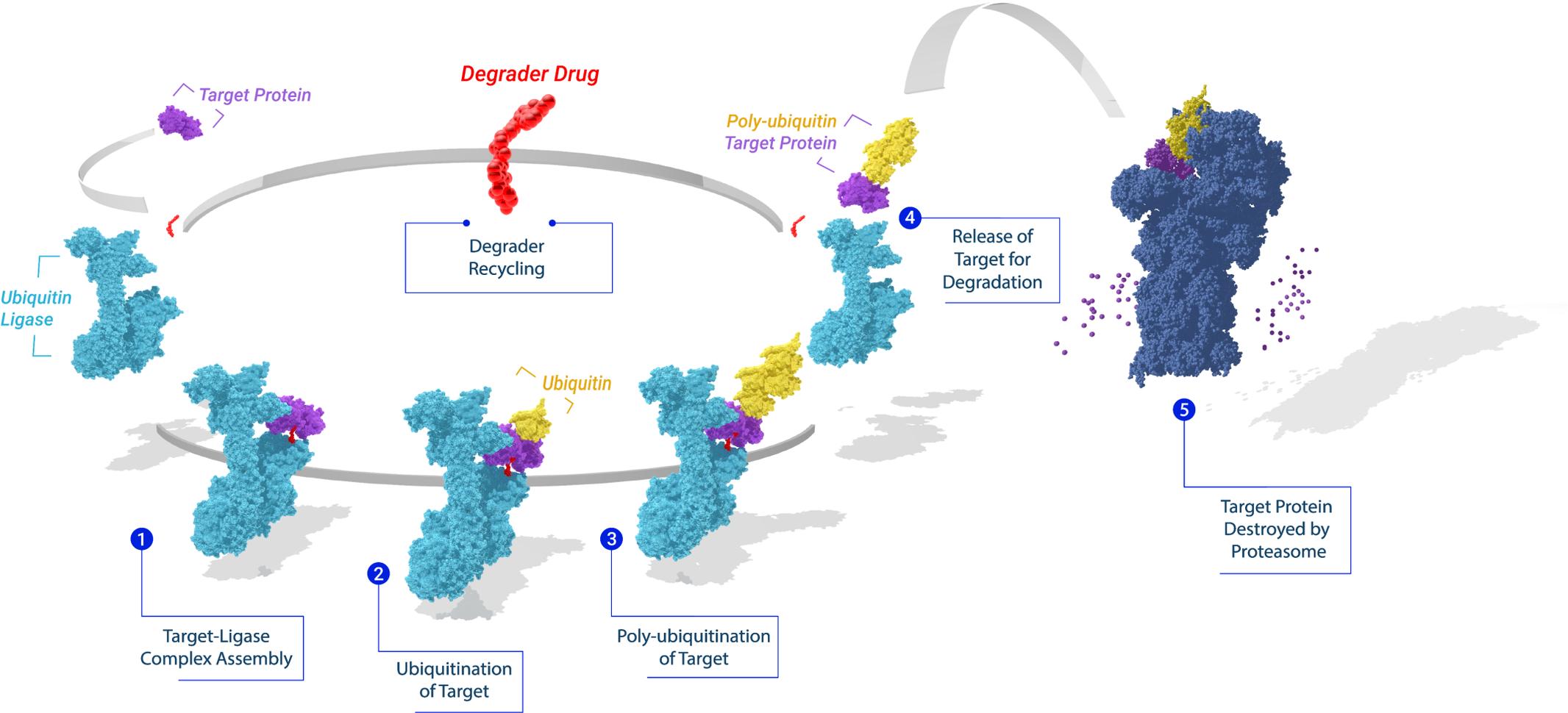
Forward-looking Statements

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Intellectual Property

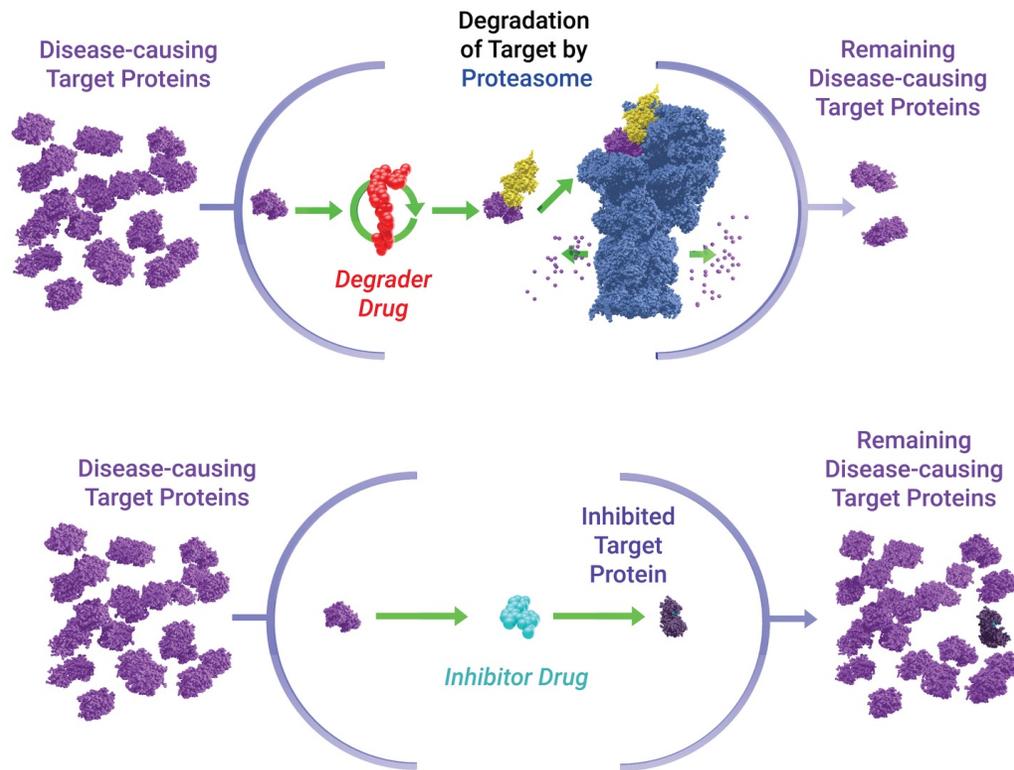
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Degraders Enable a Catalytic Cycle that Destroys Disease-Relevant Proteins



Protein Degradation is Fundamentally Different than Protein Inhibition

Protein degraders allow for a **more potent and durable pharmacological response** at lower overall exposure levels than inhibitors



Key Advantages of Protein Degraders

1. Improved Potency

Degraders are recycled and can engage multiple target proteins, resulting in improved activity against resistant proteins, greater depth of effect, and more durable outcomes

2. Fast Response

Rapid degradation of target leads to strong and prolonged biological response

3. High Selectivity

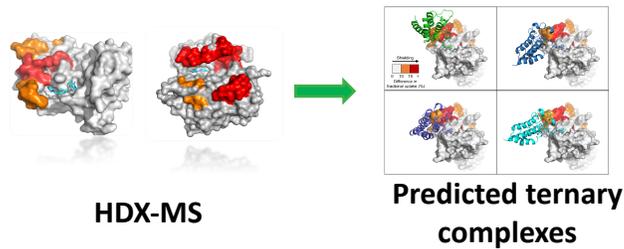
Degraders can leverage multiple layers of selectivity in cellular machinery

4. Expansive Target Landscape

Degraders can be designed to bind to any part of the protein and are not limited to the active site, like most small molecule inhibitors, which means that previously undruggable targets may be degraded

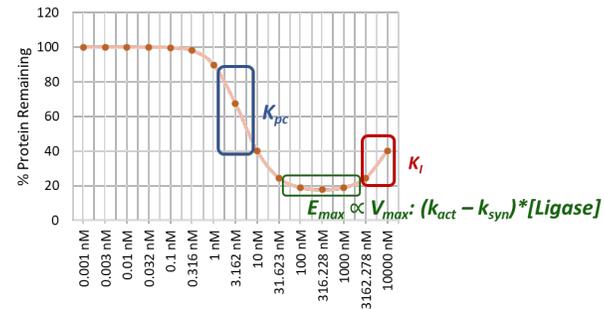
TORPEDO Platform: Robust Drug Discovery and Higher Confidence in Clinical Outcomes

Design



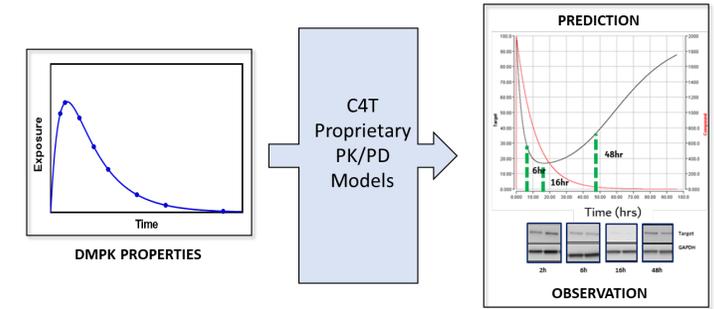
- **Computational method** incorporates experimental data to identify top models
- **Atomic-level degrader design** utilized to improve selectivity and exquisite potency

Analyze



- **Cellular degradation data** fitted using an enzymology framework
- **Key parameters** describe intrinsic degradation activity

Predict

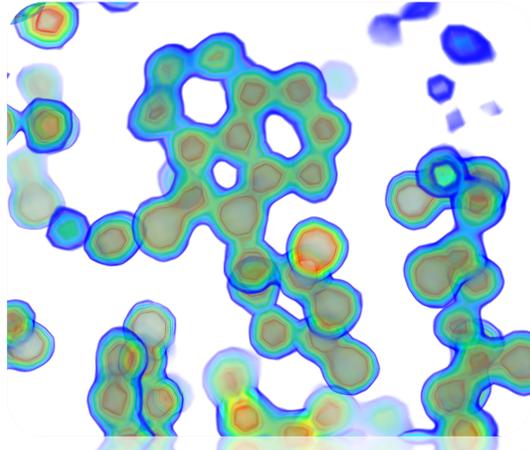
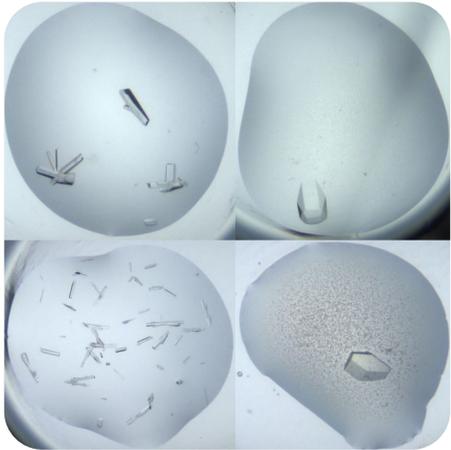


- **Universal modeling framework** merges degradation activity with degrader exposure
- **Robust predictions** of depth and duration of *in vivo* target degradation at any dose

Rapid delivery of potent drug candidates through informed and efficient drug discovery

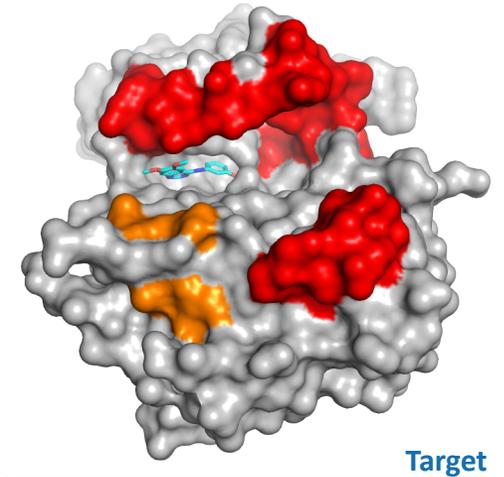
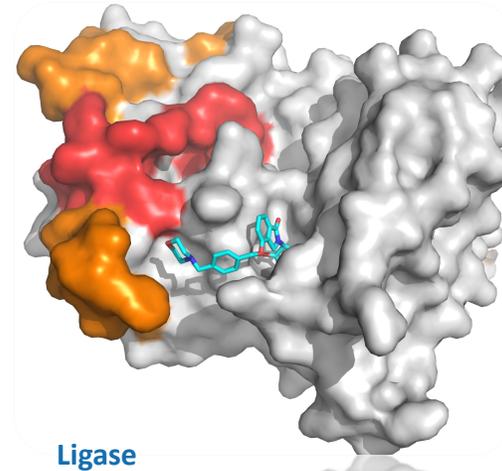
The TORPEDO Platform Employs Cutting Edge Structure-based Design

X-RAY CRYSTALLOGRAPHY



- *>70 proprietary X-ray structures solved*
- *Coverage includes key E3 ligases, ~70% of targets*
- *Supports rapid degrader chemical optimization*

HYDROGEN-DEUTERIUM EXCHANGE MASS SPEC (HDX-MS)

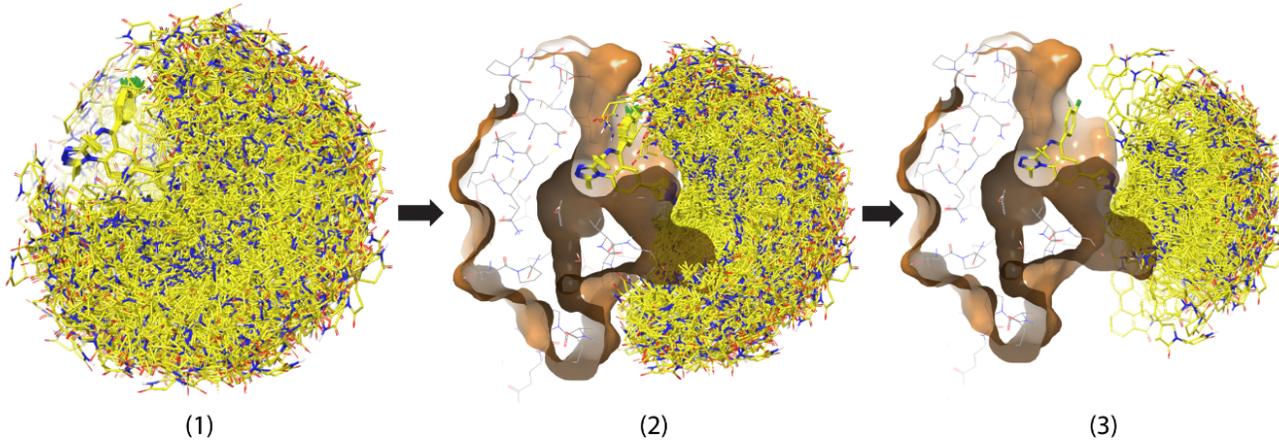


- *Established in 2018 via open access labs at UMass Amherst*
- *Allows in solution mapping of degrader promoted complexes*
- *Enables C4T proprietary ternary complex prediction pipeline*

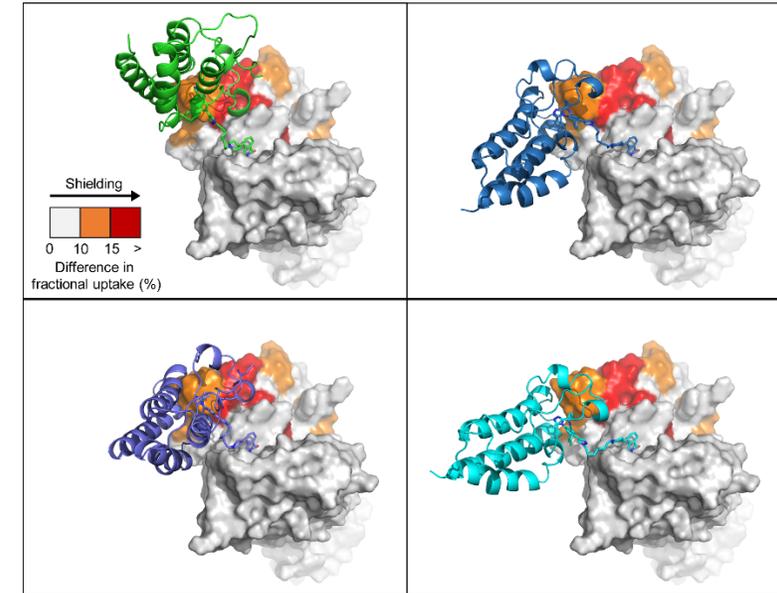
Incorporation of Solution State Data is Critical for Predictive Ternary Complex Models

in silico modeling of BRD4 degraders

Ternary complex ranking using HDX-MS Data



Utilize HDX-MS Surface Mapping as Constraints



Degrader Only
>10,000 Conformations

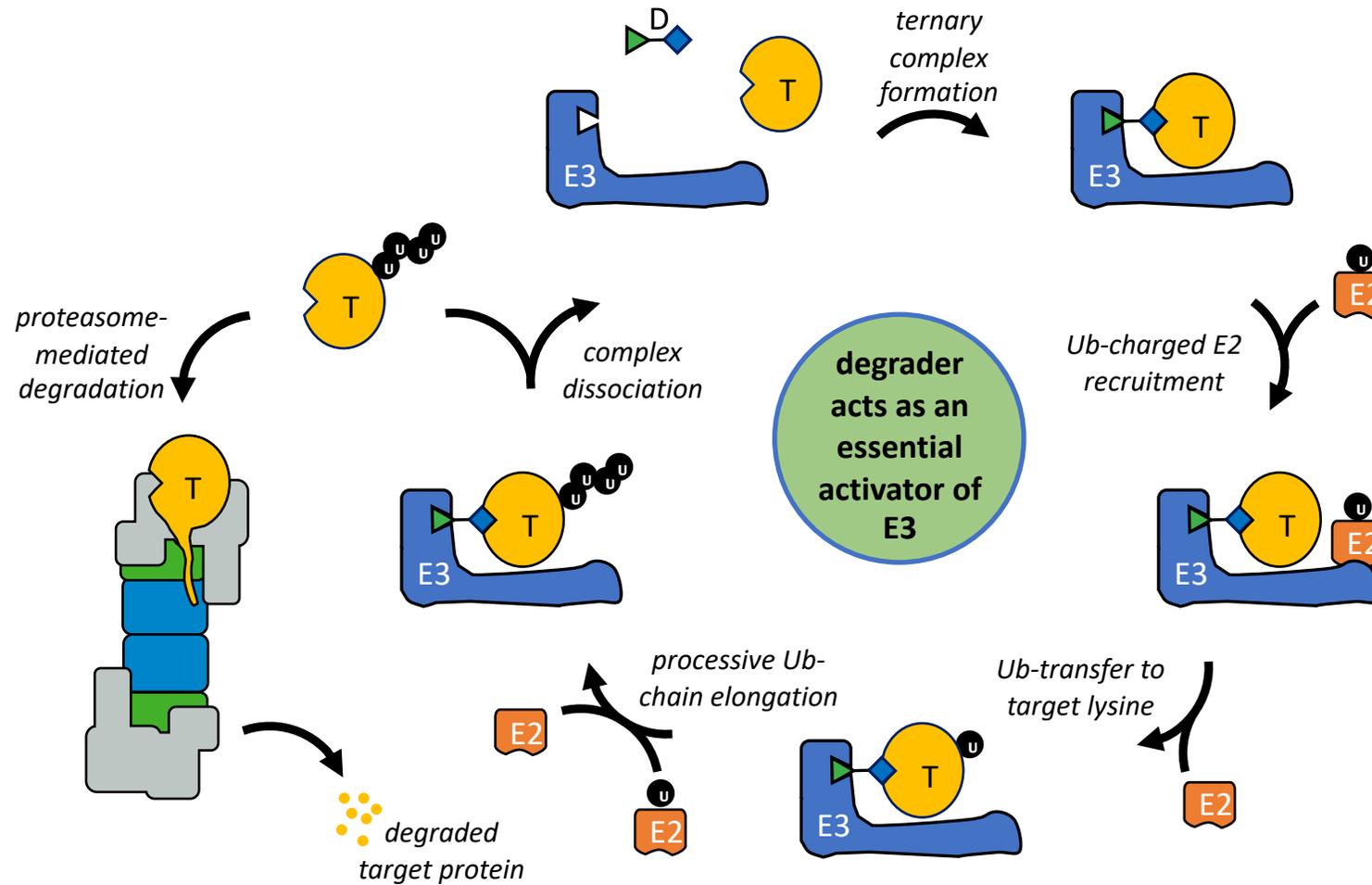
Remove BRD4 Steric Clashes
~3,200 Conformations

Virtual Docking with CRBN
~430 Conformations

Rank Conformers on HDX Constraints
4 Conformations

Ternary Complex Modeling Approach Validated using CRBN-based BRD4 Degraders

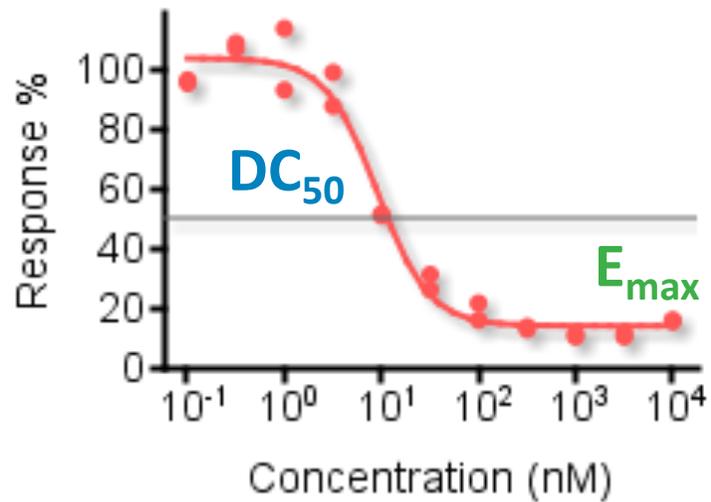
Degraders are Essential Catalytic Activators



Fisher and Phillips, *Curr Opin Chem Biol.* **2018**, 44, 47

Cellular Degradation is Time Dependent

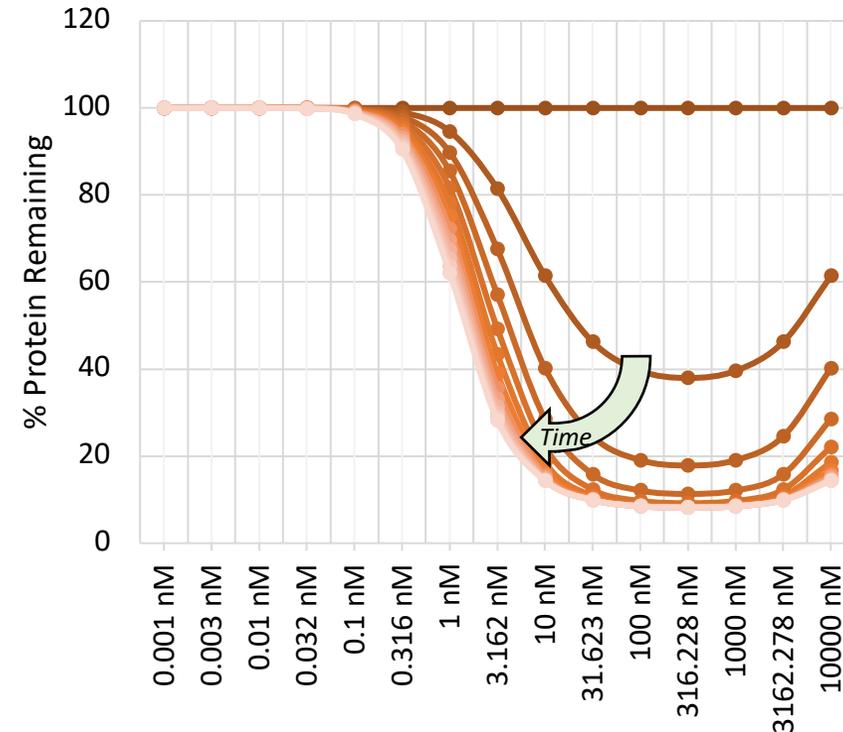
Single Timepoint



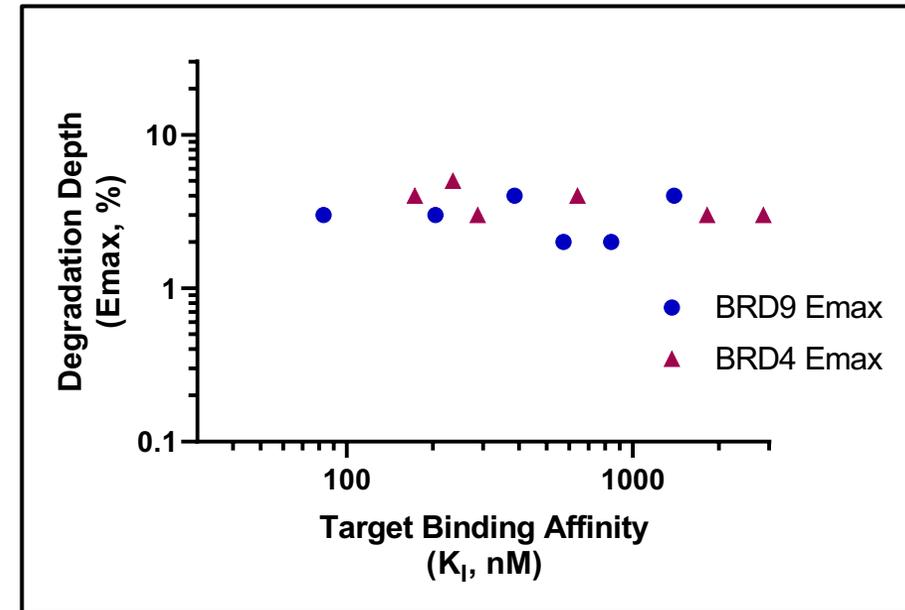
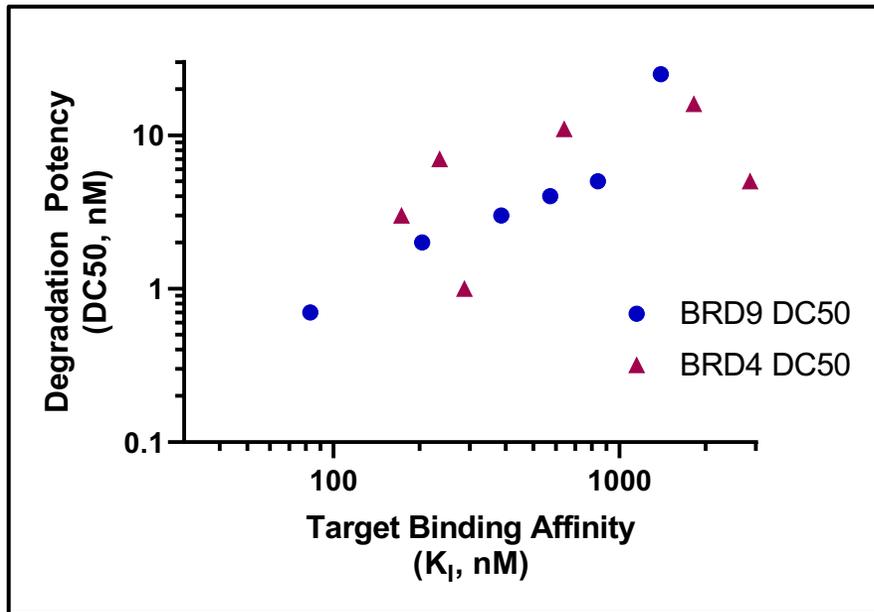
DC_{50} – [degrader] for 50% target depletion
(\approx cellular potency)

E_{max} – % remaining target @ assay timepoint
(maximal degradation \approx degradation rate)

Time Course

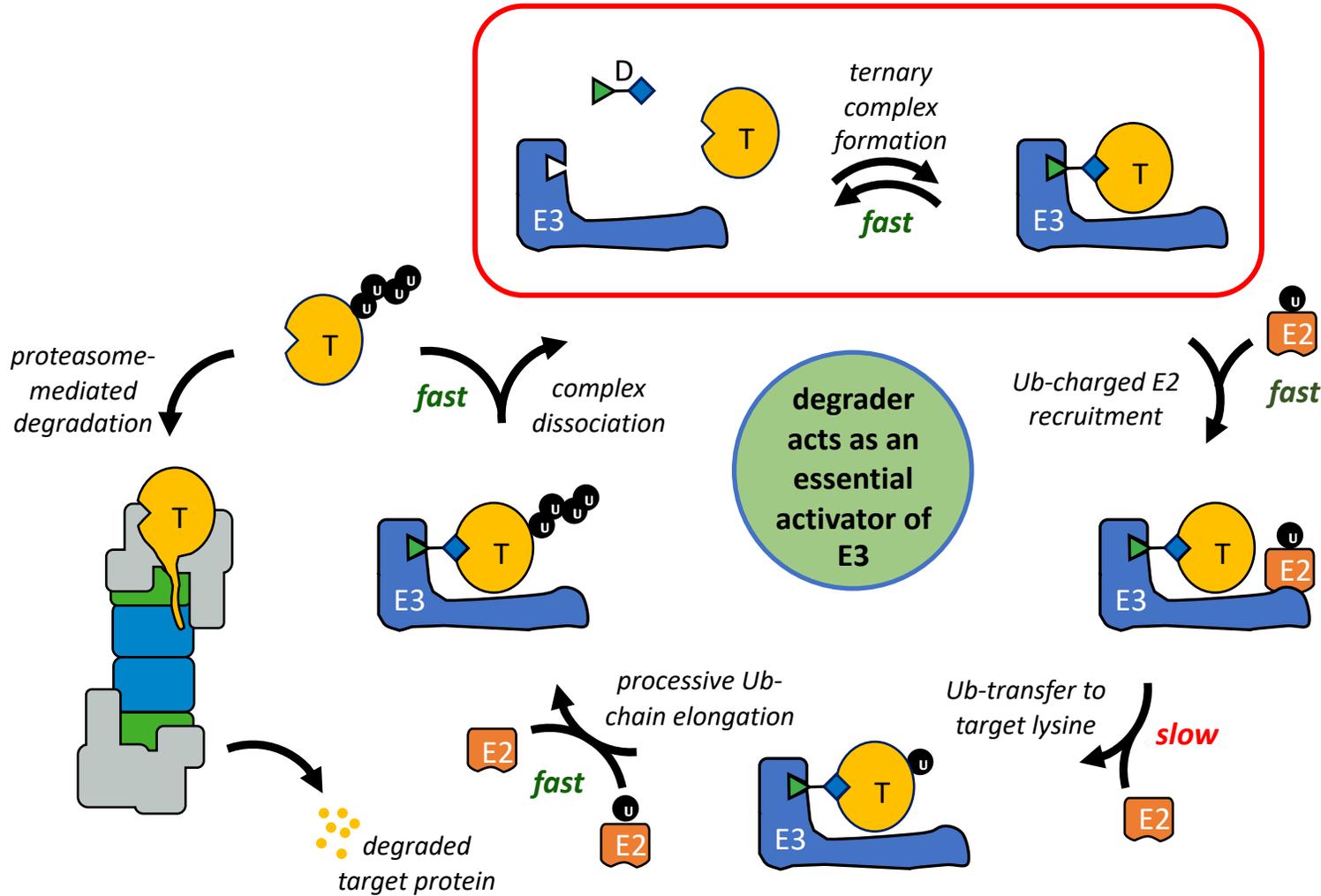


BiDAC Degradation Activity is Not Strictly Dependent on Target Binding Affinity



- Excellent degradation observed with reduced (weak) target binding affinity
- Can be leveraged to obtain coverage of clinically-relevant, secondary resistance mutations to inhibitor therapies

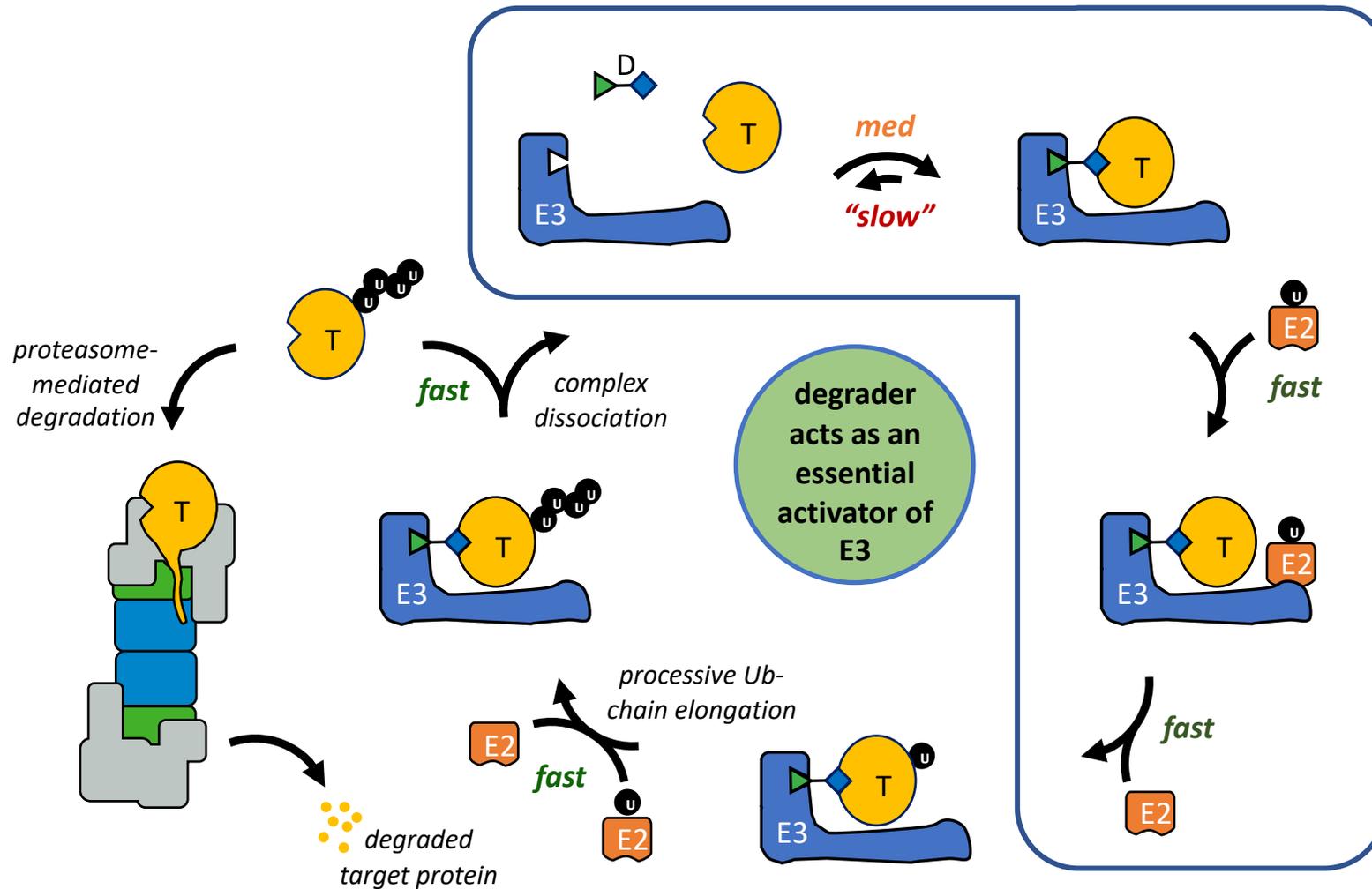
Prevailing Assumption: Ternary Complex Formation Drives Potency



Implications:

- Ternary complex $K_{tf} = K_M$
- Ternary Complex Max Fraction $\propto V_{max}$
- Positive binding cooperativity $\propto V_{max}$

What about Kinetically-driven Systems?



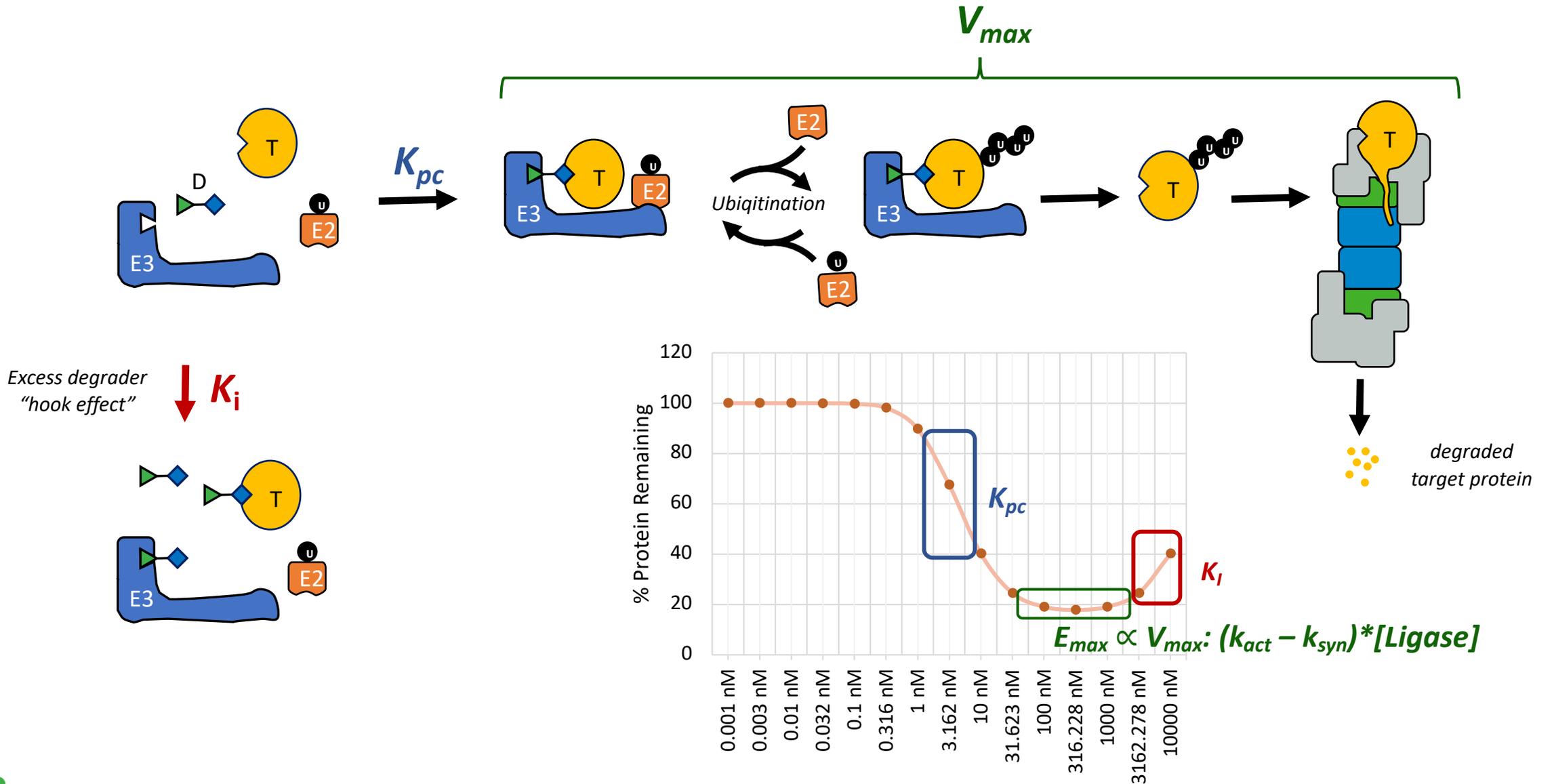
Implications:

- **No correlations** between ternary complex formation and catalysis
- Negative binding cooperativity **tolerated**

“Optimal catalysis does not necessarily result from a high affinity for the substrate”

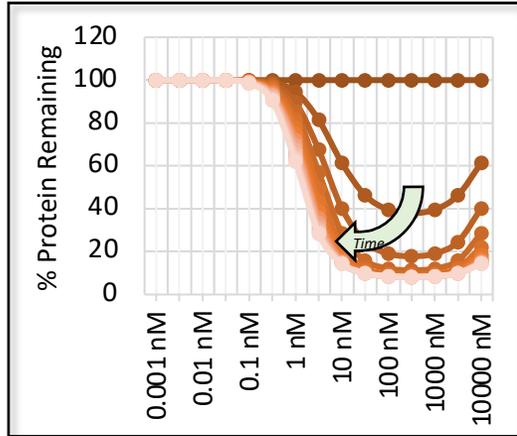
– William P. Jencks, 1997

Applying an Enzymology Framework Provides Quantitative Assessments of Degradator Activity

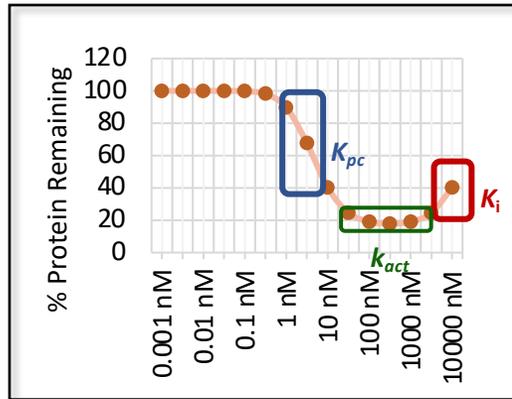


Proprietary PK/PD Models Founded on Degradation Enzymology Framework

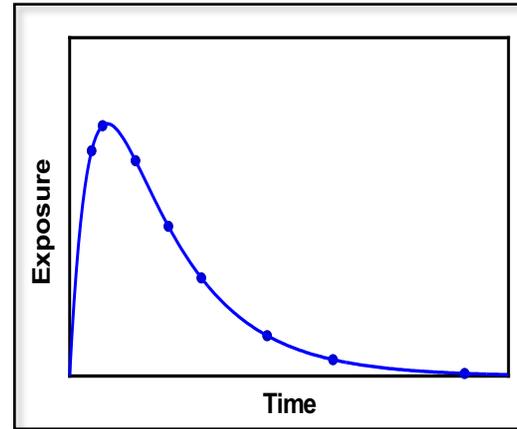
Enzymology Framework



TIME DEPENDENCE

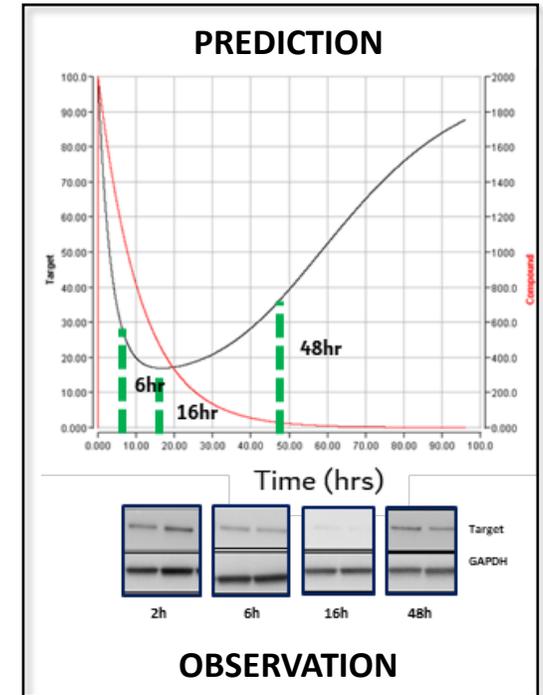


KEY PARAMETERS

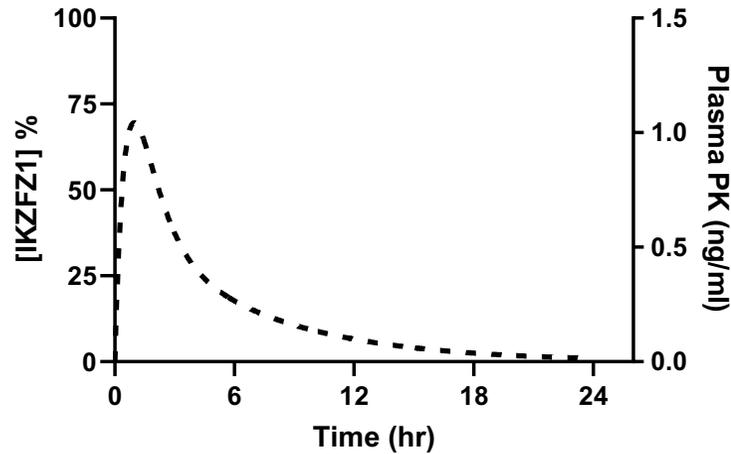


DMPK PROPERTIES

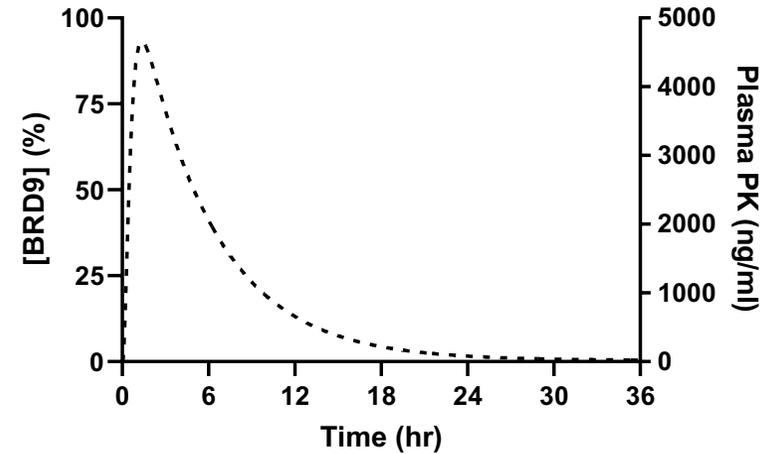
C4T
Proprietary
PK/PD
Models



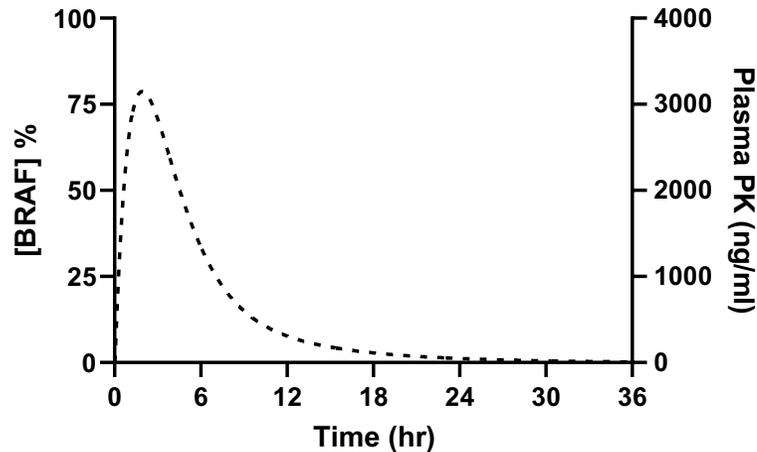
PK/PD Models Provide Robust Predictions Across the Diverse Targets and Degradable Classes



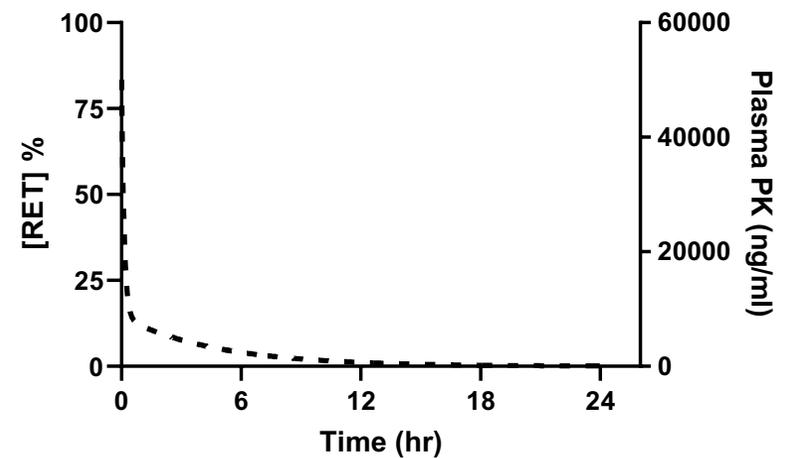
CFT7455, 1 mg/kg dose po, KI-KJ Anaplastic Large Cell Lymphoma model



CFT7503, 10 mg/kg dose po, Yamato Synovial Sarcoma model

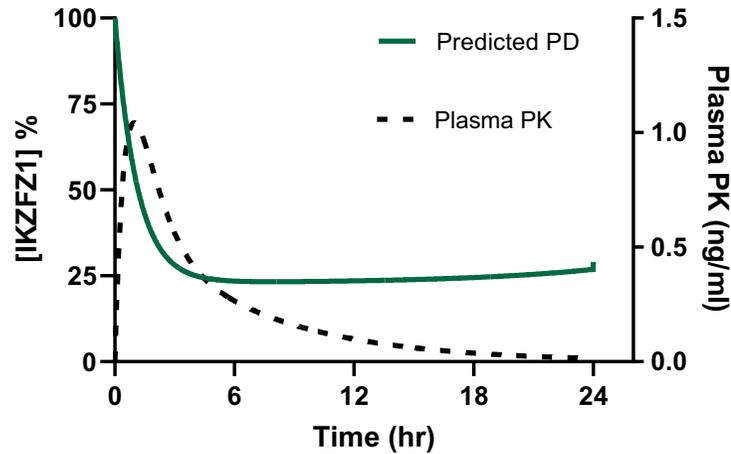


CFT-17977, 30 mg/kg dose po, A375 model

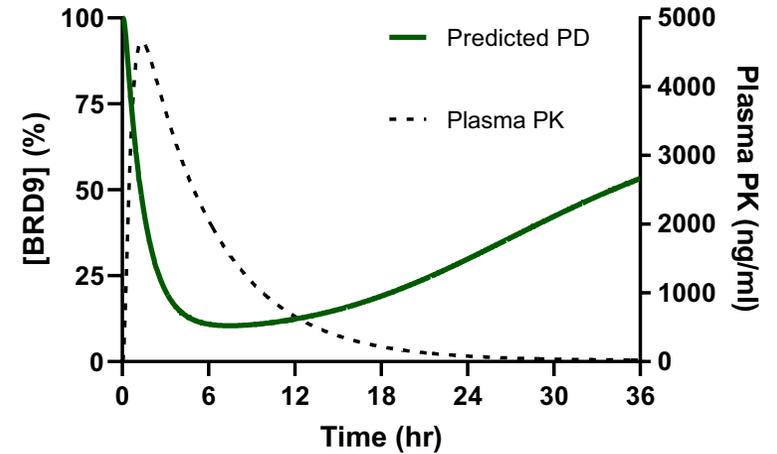


CFT-12521, 30 mg/kg dose iv, KIF-5B:RET Fusion model

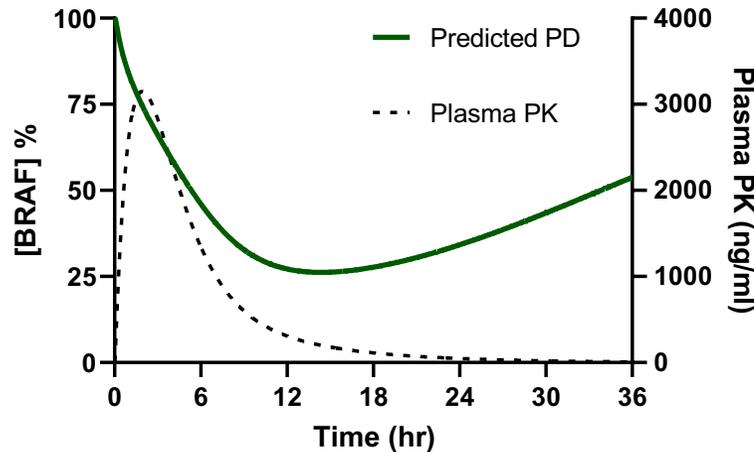
PK/PD Models Provide Robust Predictions Across the Diverse Targets and Degradable Classes



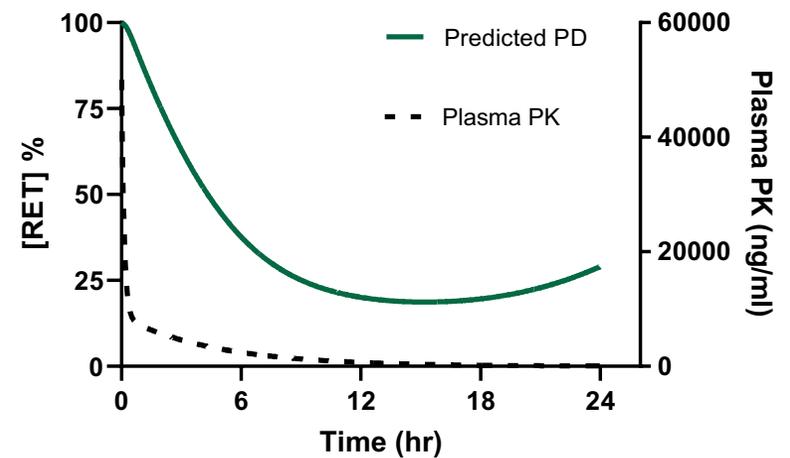
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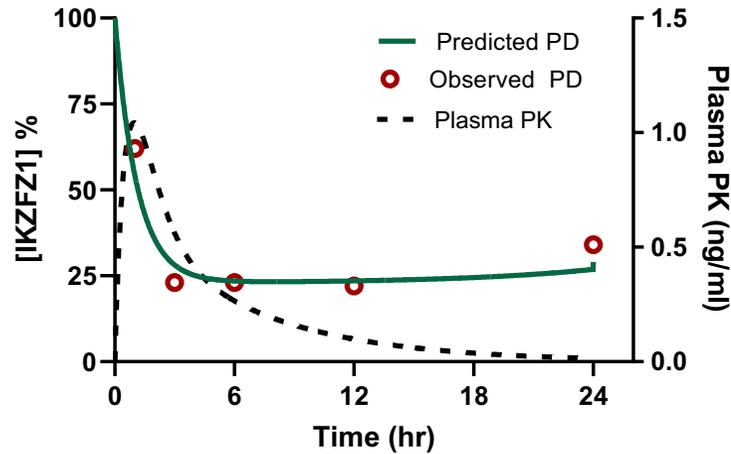


CFT-17977, 30 mg/kg dose po, A375 model

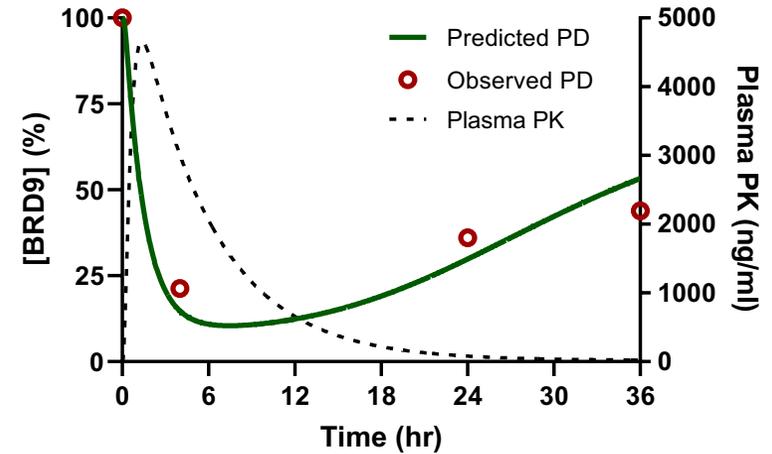


CFT-12521, 30 mg/kg dose iv, KIF-5B:RET Fusion model

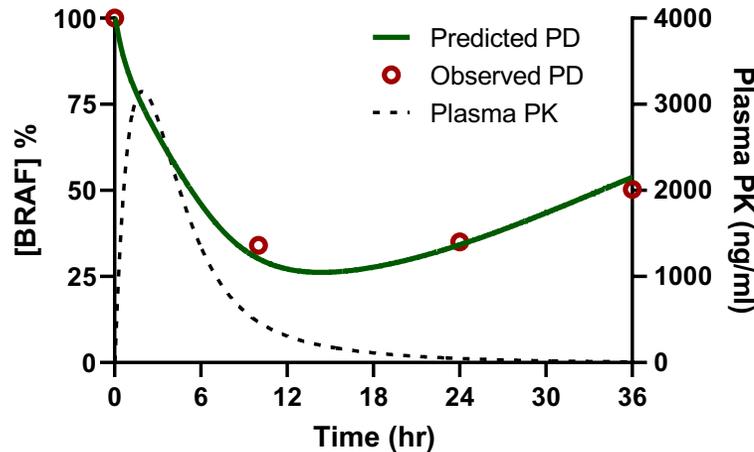
PK/PD Models Provide Robust Predictions Across the Diverse Targets and Degradator Classes



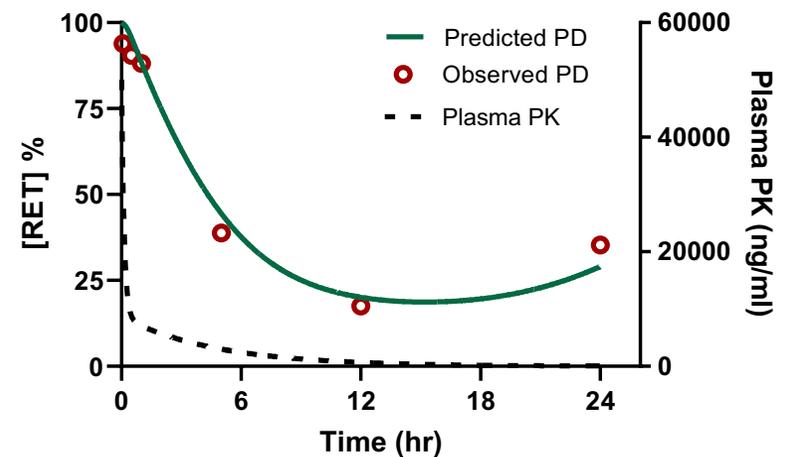
CFT7455, 1 mg/kg dose po, KI-KJ Anaplastic Large Cell Lymphoma model



CFT7503, 10 mg/kg dose po, Yamato Synovial Sarcoma model

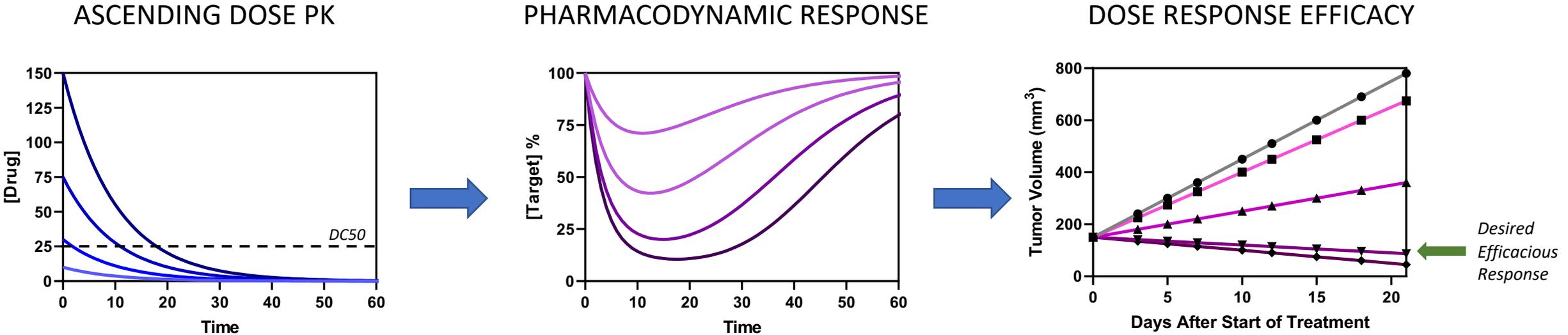


CFT-17977, 30 mg/kg dose po, A375 model



CFT-12521, 30 mg/kg dose iv, KIF-5B:RET Fusion model

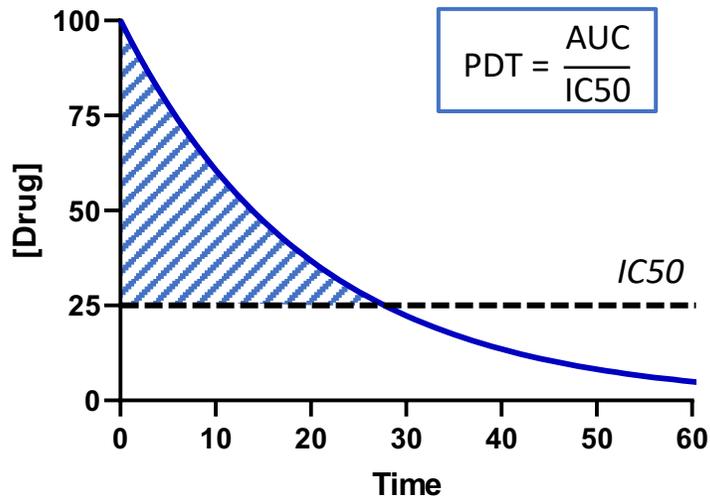
Pharmacodynamic Threshold: Linking Pharmacodynamics to Efficacy



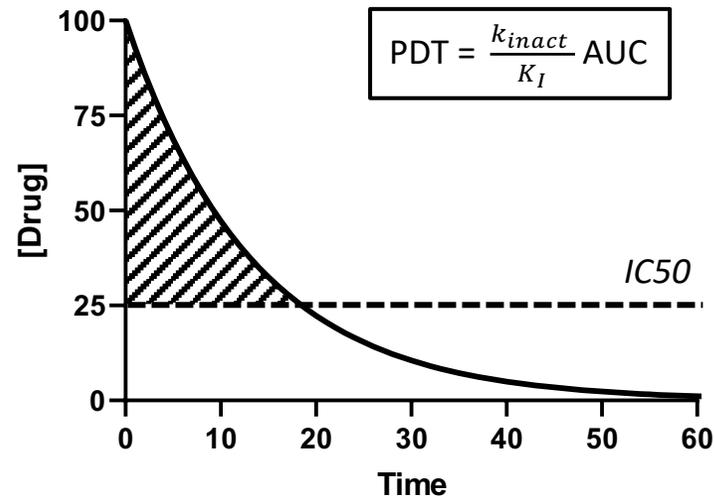
- PDT = Pharmacodynamic threshold required for *desired efficacious response*
 - Function of target engagement/degradation and exposure
 - Dependent on target biology and tumor; not dependent on drug modality

Degrader Catalytic Activity Drives Pharmacology: Lower Exposures Required

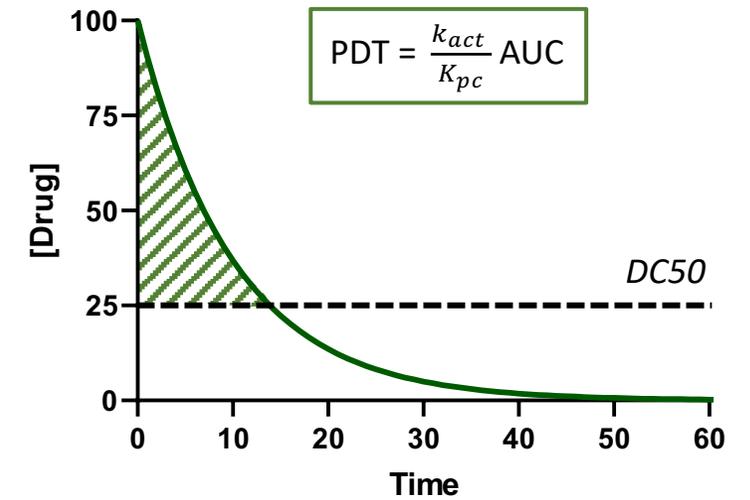
REVERSIBLE INHIBITOR



COVALENT INHIBITOR



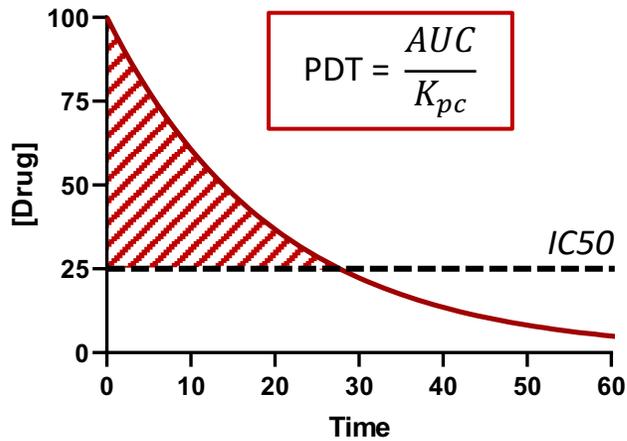
DEGRADER



$\text{AUC}_{\text{Degrader}} < \text{AUC}_{\text{Inhibitor}}$ to Achieve Equivalent Target Efficacious Response

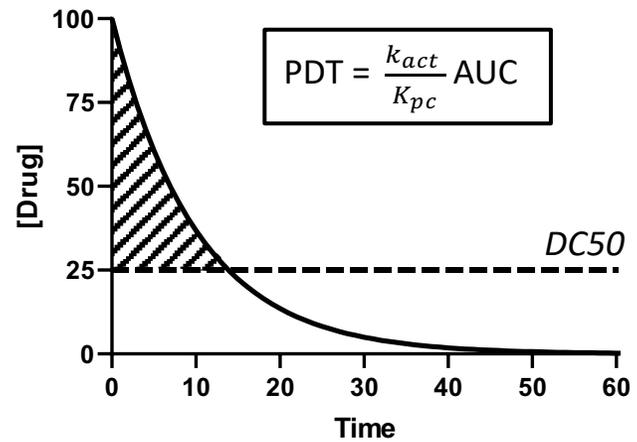
Degrader Pharmacodynamic Driver Landscape

POOR DEGRADER



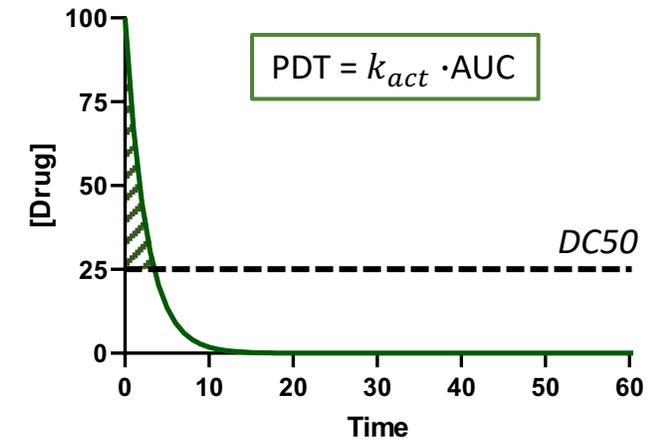
$k_{act} \ll K_{pc}$

GOOD DEGRADER



$k_{act} \gg K_{pc}$

EXCELLENT DEGRADER



- Low catalytic activity
- Pharmacological effect driven by binding/inhibition
- High AUC required to maintain target engagement

- High catalytic activity
- Rapid target degradation drives effect
- No threshold required

Potential Advantages of Degraders over Inhibitors

- PDT analysis assumes equivalent pharmacological response for degraders and inhibitors
- Degraders are expected to exhibit one or more of the following attributes over inhibitors (target dependent):
 - Prolonged activity duration due to target resynthesis requirement (PK/PD hysteresis)
 - Amplified activity against requisite dimers
 - Activity against scaffolding functions
 - Enhanced selectivity
 - Activity against secondary mutations

Degraders \neq Inhibitors

Degraders are expected to have *enhanced* pharmacological response over inhibitors

The C4 Therapeutics Team

