



Clinical Insights on Leveraging Kinetics-Based PK/PD Modeling to Drive Degrader Optimization

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7th TPD & Induced Proximity Summit
Oct 29, 2024

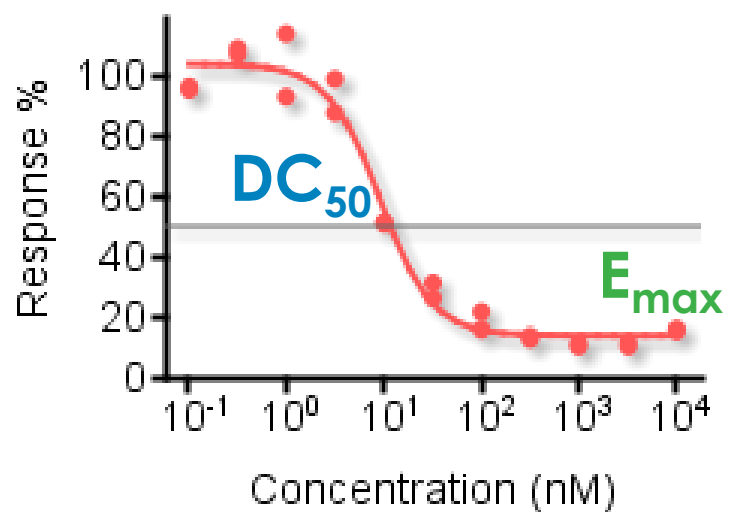


Disclosure Information

- I have the following financial relationships to disclose:
 - Stockholder in: C4 Therapeutics, Inc.
 - Employee of: C4 Therapeutics, Inc.

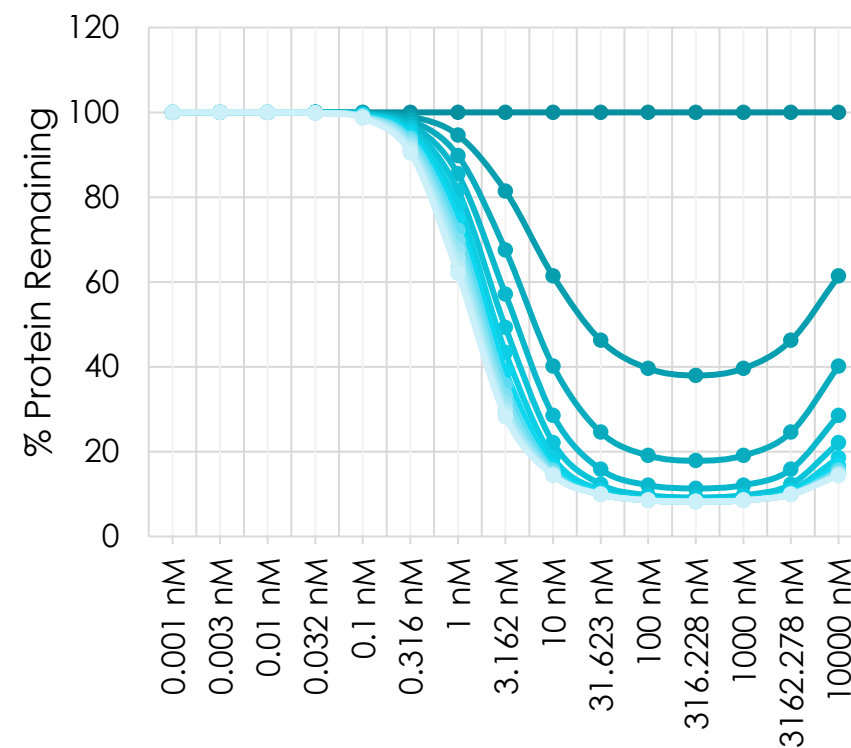
Catalytic Mechanism Requires Assessment of Time Dependence

Static Timepoint

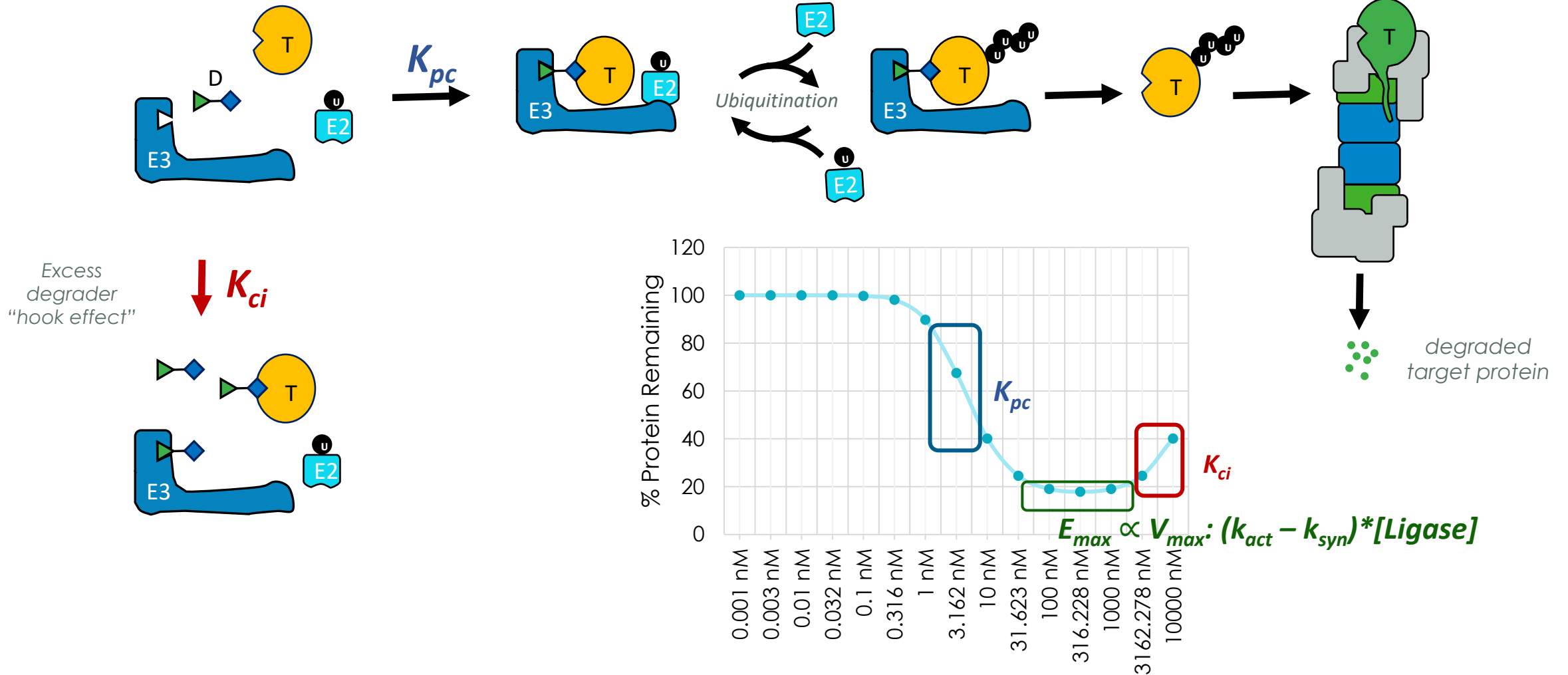


- DC₅₀** – [degrader] for 50% target depletion
(≈ cellular potency)
- E_{max}** – % remaining target @ assay timepoint
(maximal degradation ≈ degradation rate)

Time course

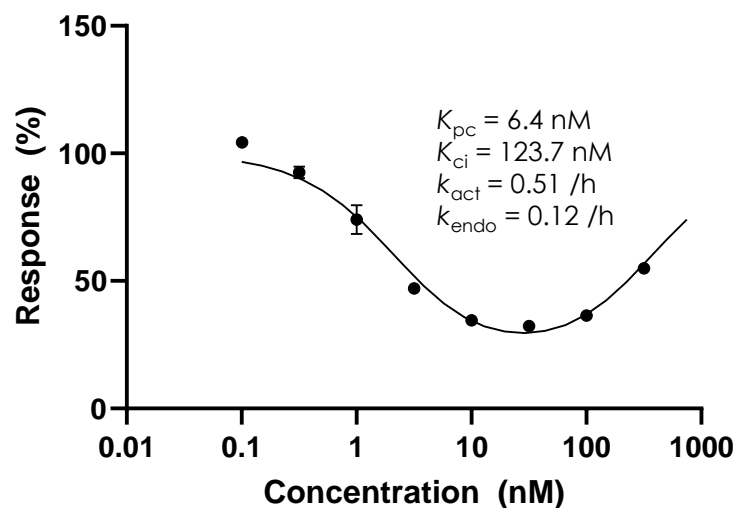


Applying an Enzymology Framework Provides Quantitative Assessments of Degradator Activity



Modeling Degradation Action Requires Tailored Equations

- Change in target concentration after degrader treatment is determined by:



$$\frac{d[T]}{dt} = \underbrace{(100\% \times k_{endo})}_{\text{endogenous synthesis}} - \underbrace{k_{endo} \times [T]}_{\text{endogenous degradation}} - \underbrace{k_{deg} \times [T]}_{\text{degrader-induced degradation}}$$

$$[T](t) = (100\% - E_{dss})e^{-(k_{endo}+k_{deg})t} + E_{dss}$$

$$k_{deg} = \frac{k_{act}}{1 + \frac{K_{pc}}{[D]} + \frac{[D]}{K_{ci}}} \quad E_{dss} = \frac{100\% \times k_{endo}}{k_{endo} + k_{deg}}$$

References:

Flaxman, H., Deibler, R., Conicella, A., Ingham, O. Orsi, D., Sowa, M., Cassidy, K., Pollock, R., Fisher, S. (2023) Applications of Kinetics Modeling in Targeted Protein Degradation [Poster]. *Bioorganic Gordon Research Conference, Andover, NH.*

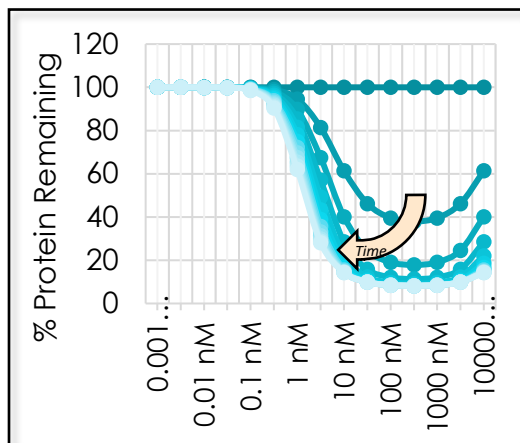
Segel, I. H. (1975). *Enzyme kinetics : behavior and analysis of rapid equilibrium and steady state enzyme systems.* Wiley.

Bartlett, D.W., Gilbert, A.M. (2021) A kinetic proofreading model for bispecific protein degraders. *J Pharmacokinet Pharmacodyn* 48, 149–163. <https://doi.org/10.1007/s10928-020-09722-z>

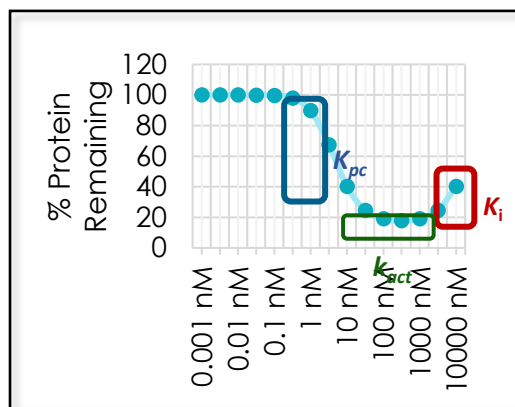
Haid, R.T.U. and Reichel, A. (2024), Transforming the Discovery of Targeted Protein Degradation: The Translational Power of Predictive PK/PD Modeling. *Clin Pharmacol Ther*, 116: 770-781. <https://doi.org/10.1002/cpt.3273>

Degrader Specific PK/PD Models Founded on Enzymology Framework

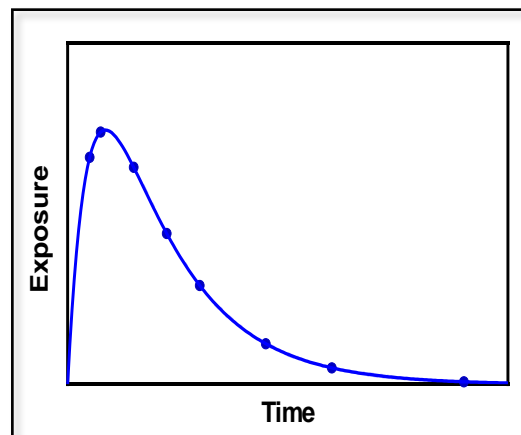
Enzymology Framework



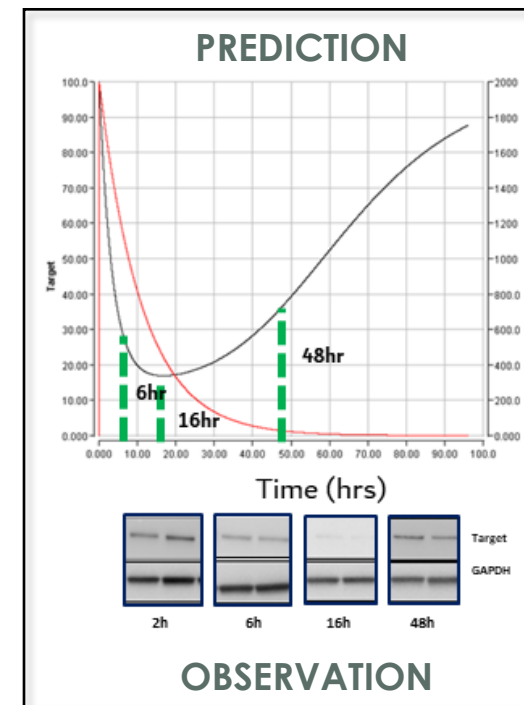
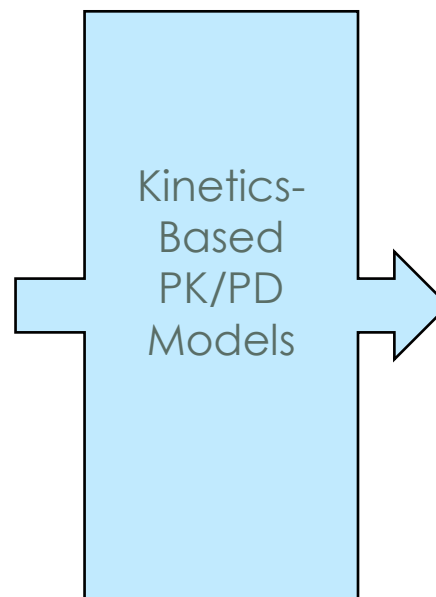
TIME DEPENDENCE



KEY PARAMETERS

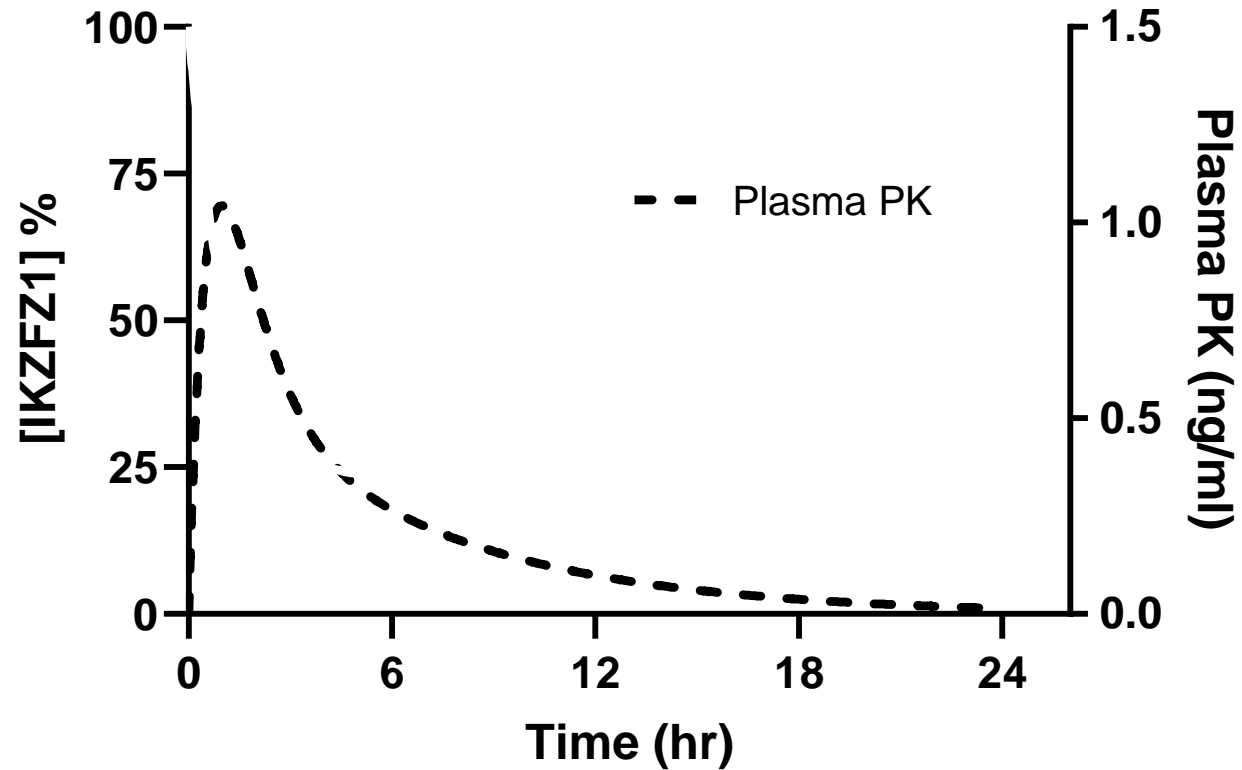


DMPK PROPERTIES



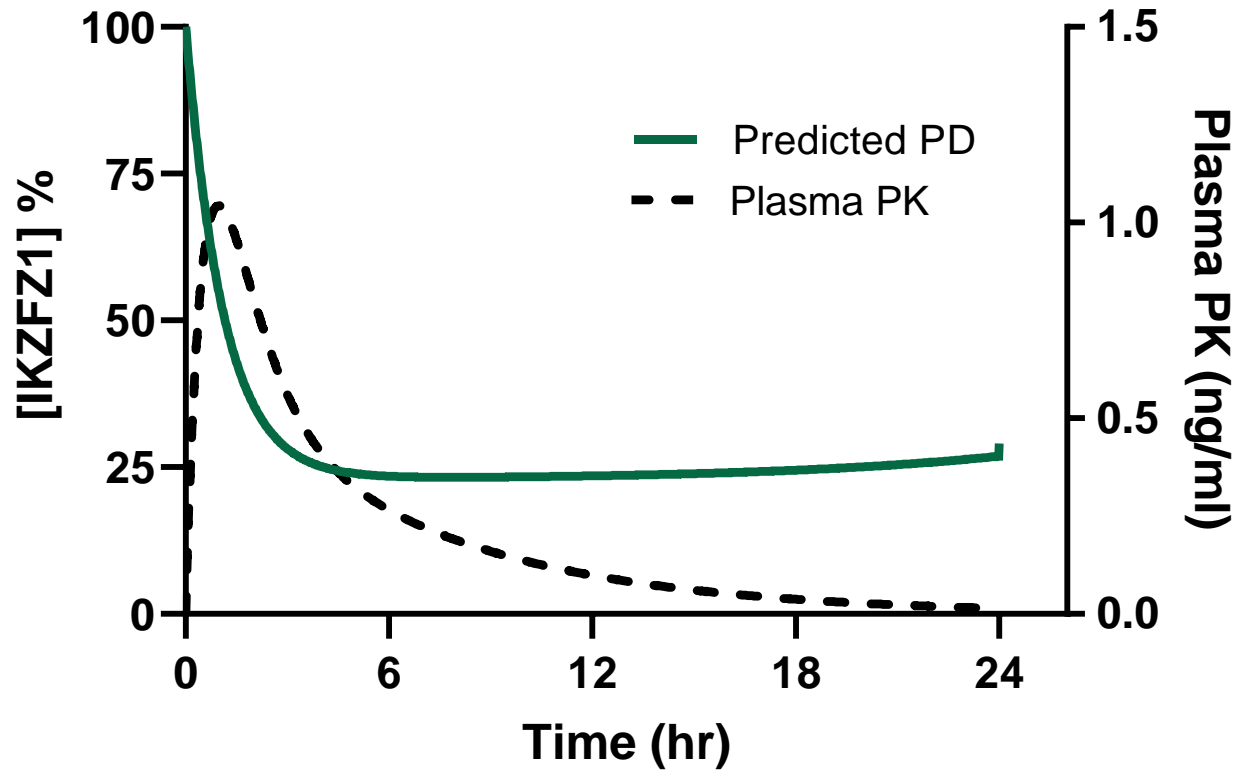
OBSERVATION

Predictive PK/PD Models Drive Efficient Drug Discovery



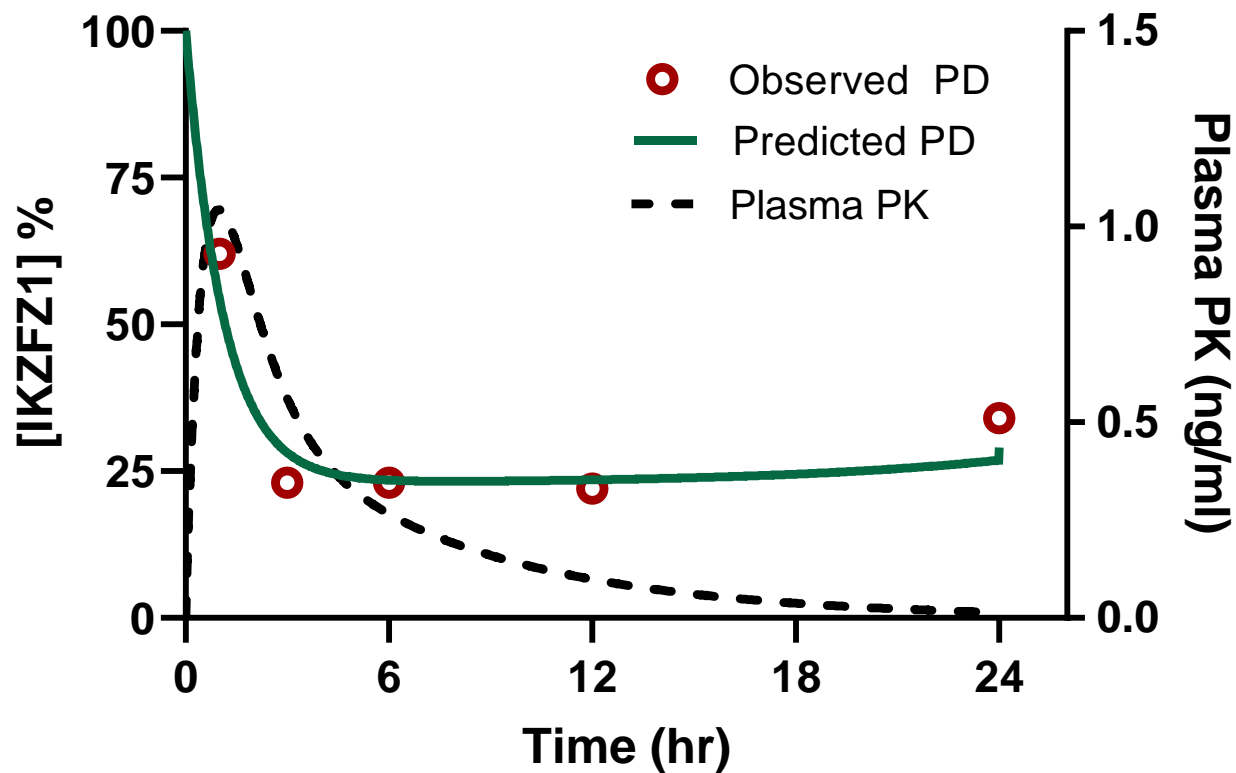
CFT7455, 1 mg/kg dose po, KI-KJ Anaplastic Large Cell Lymphoma model

Predictive PK/PD Models Drive Efficient Drug Discovery



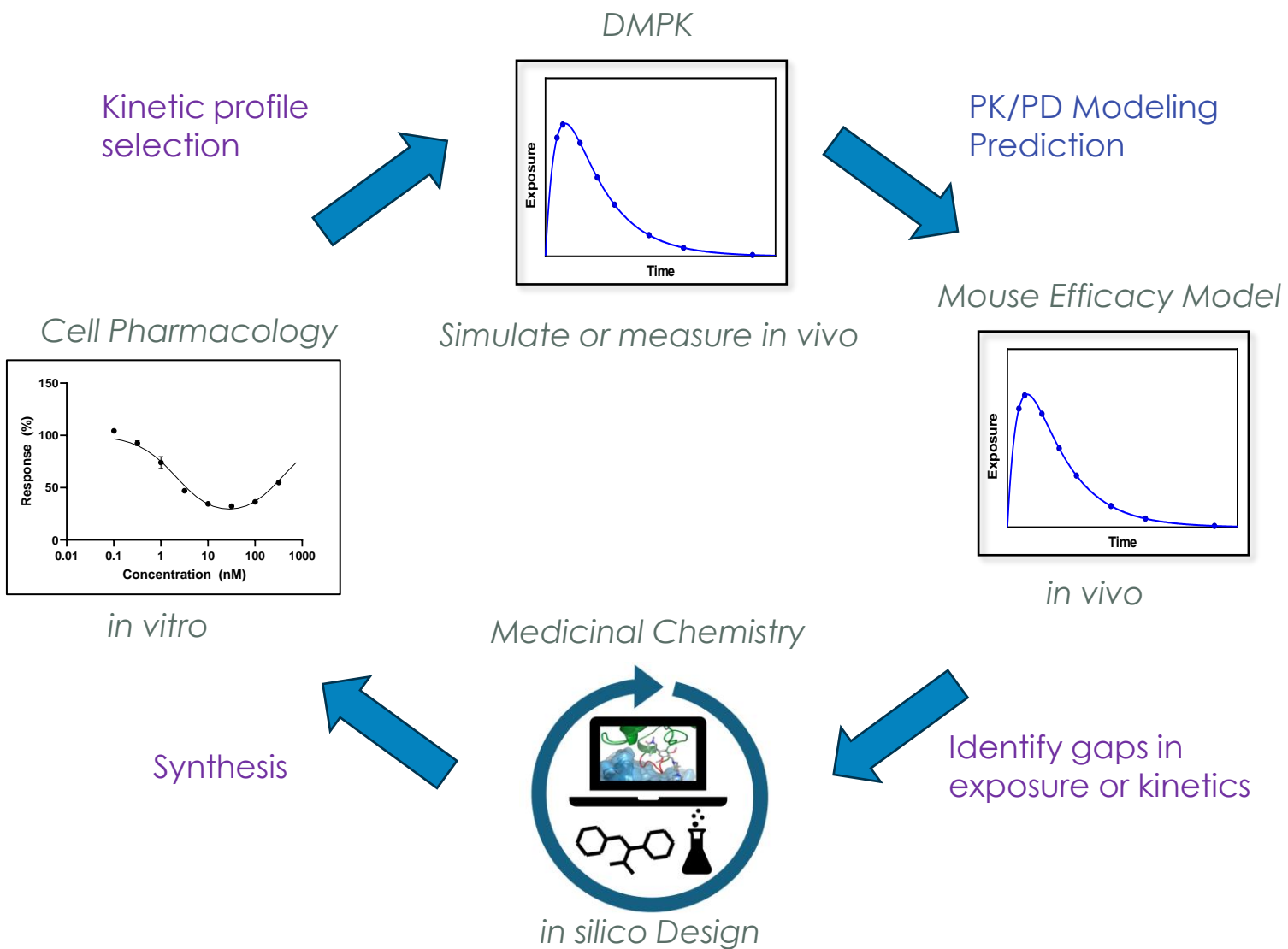
CFT7455, 1 mg/kg dose po, KI-KJ Anaplastic Large Cell Lymphoma model

Predictive PK/PD Models Drive Efficient Drug Discovery

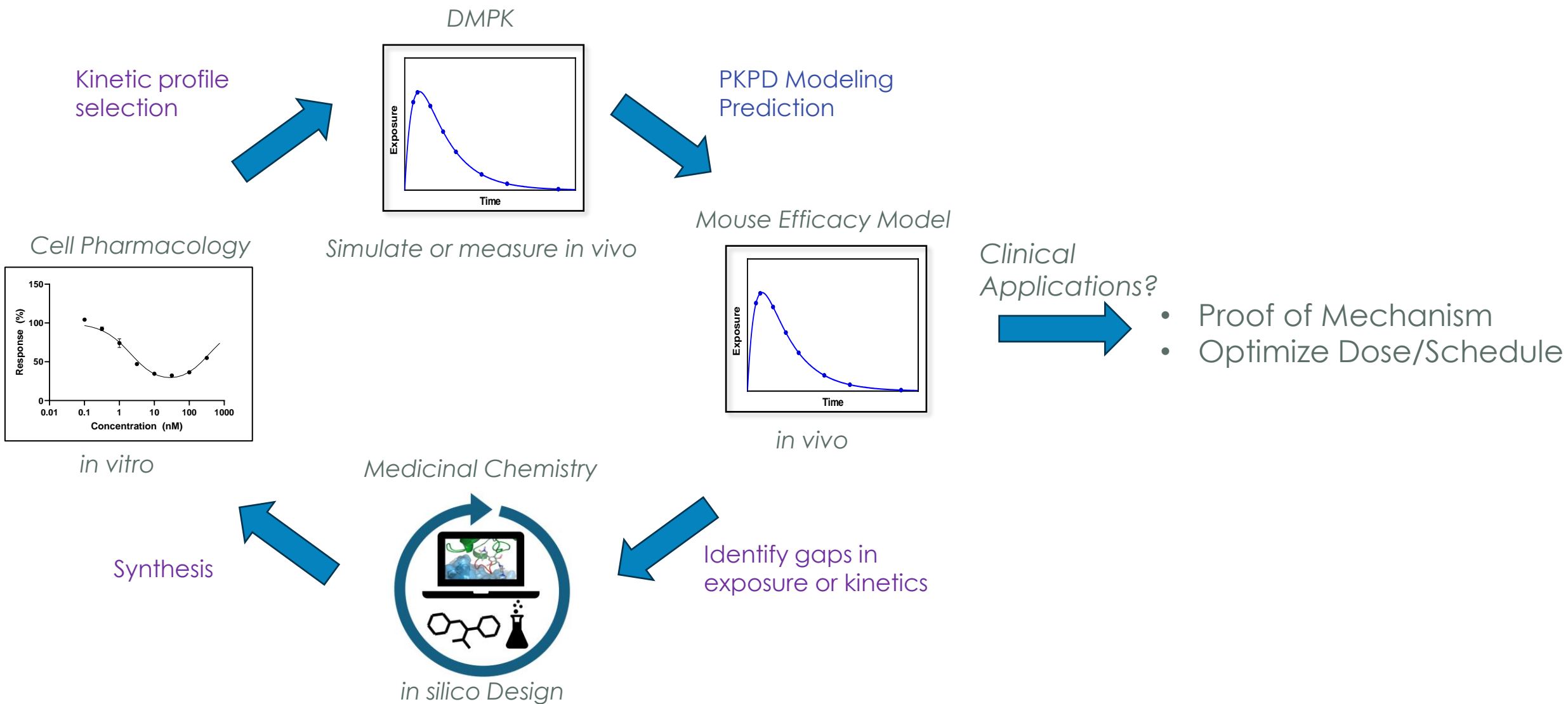


CFT7455, 1 mg/kg dose po, KI-KJ Anaplastic Large Cell Lymphoma model

PK/PD Modeling is Integral to Degradation Optimization



PK/PD Modeling is Integral to Degradator Optimization



Robust Pipeline of Degradable Medicines Pursuing Multiple Targets

Program ³	Target	Indications	Discovery	Preclinical	Early Phase Development	Late Phase Development	Rights
Cemsidomide	IKZF1/3	Multiple Myeloma & Non-Hodgkin's Lymphoma					
CFT1946	BRAF V600 Mutant	V600 Mutant Cancers					
CFT8919 ¹	EGFR L858R	Non-Small Cell Lung Cancer					
Discovery Stage Programs	Various Cancers						
Collaboration Programs	Autoimmune & Cancer		2 targets				
	Cancer		2 targets				Merck KGaA Darmstadt, Germany
	Cancer		1 target				
	Autoimmune & Neurological		2 targets				²

¹License and collaboration agreement with Betta Pharmaceuticals for development and commercialization in Greater China; ²Delivered development candidates to Biogen in Q1 2024 and Q3 2024; ³CFT8634 BRD9 degrader program for synovial sarcoma and SMARCB1-null solid tumors patients was closed in Q4 2023.

BRD9 Previously Considered an Undruggable Target Where Inhibitors Are Ineffective for Synovial Sarcoma

1 Incorporation of SS18-SSX fusion results in eviction of SMARCB1

- cBAF complex compromised
- Oncogenic state

2 Inactivation of SMARCB1 leads to dependency on ncBAF complex

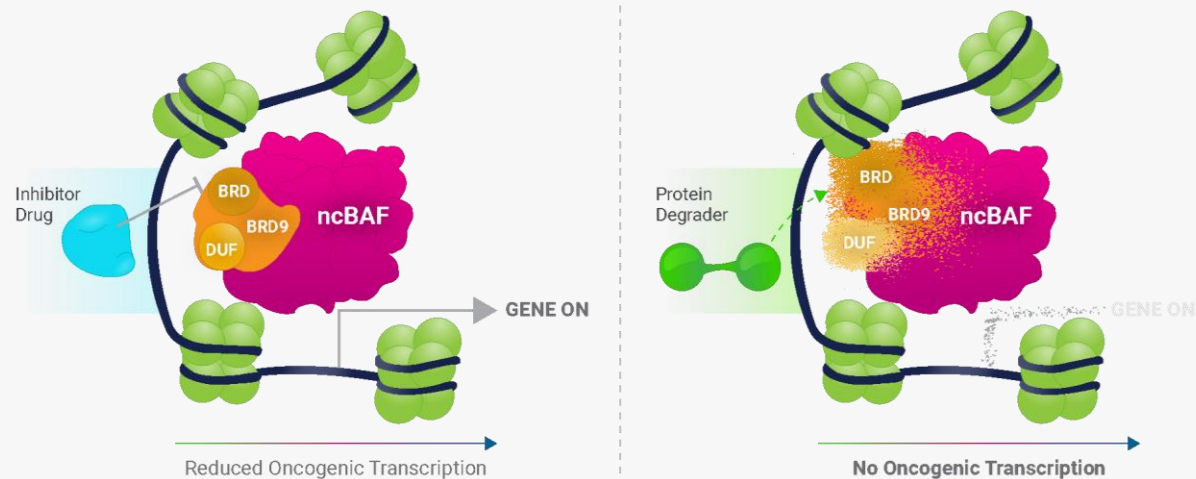
- BRD9 is uniquely present in ncBAF
- **Synthetic lethal dependency on BRD9** in synovial sarcoma and other SMARCB1-deficient cancers

Key Properties of CFT8634

- Orally bioavailable
- Potent
- Selective

Degrader Rationale

Oncogenicity of BRD9 depends on protein function not addressed by traditional inhibitors

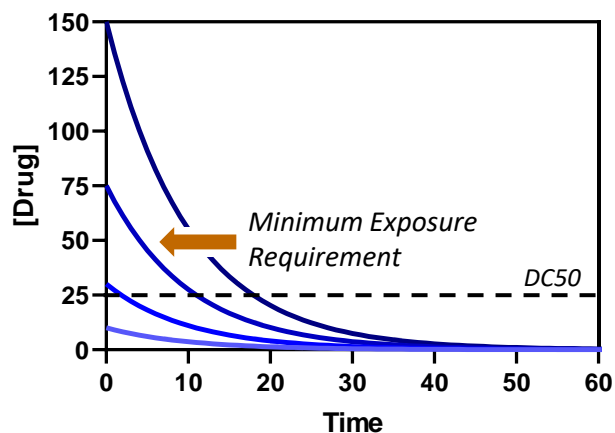


Sources:

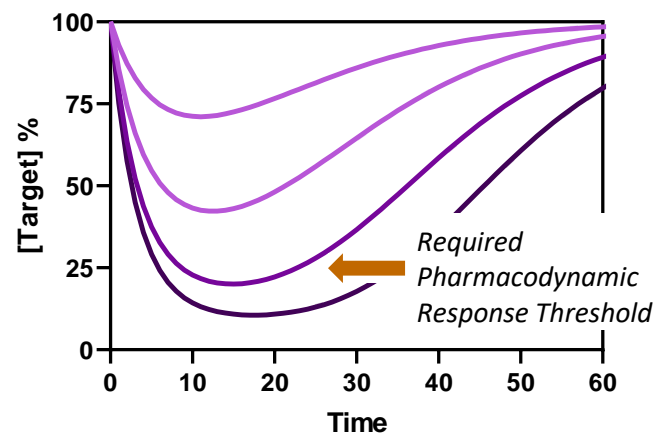
1. Wang BC, et al. *Front Oncol.* 2021;11:76228.
 2. Sleijfer S, et al. *J Clin Oncol.* 2009;27(19):3126-3132.
- Progression Free Survival (PFS)

Clinical PK/PD Modeling Requires Pharmacodynamic Threshold Identification

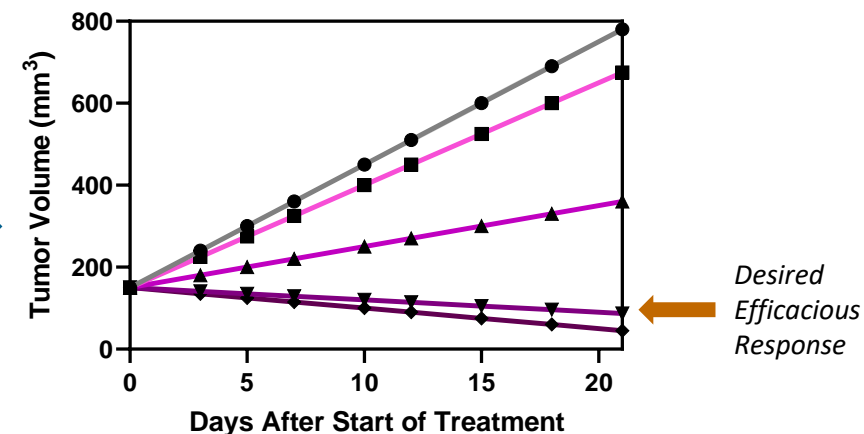
Ascending Dose PK



Pharmacodynamic Response



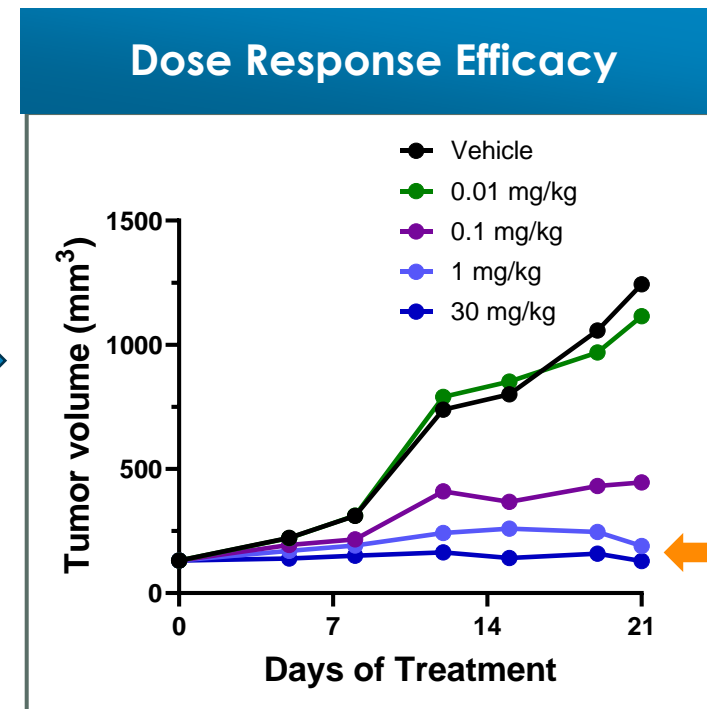
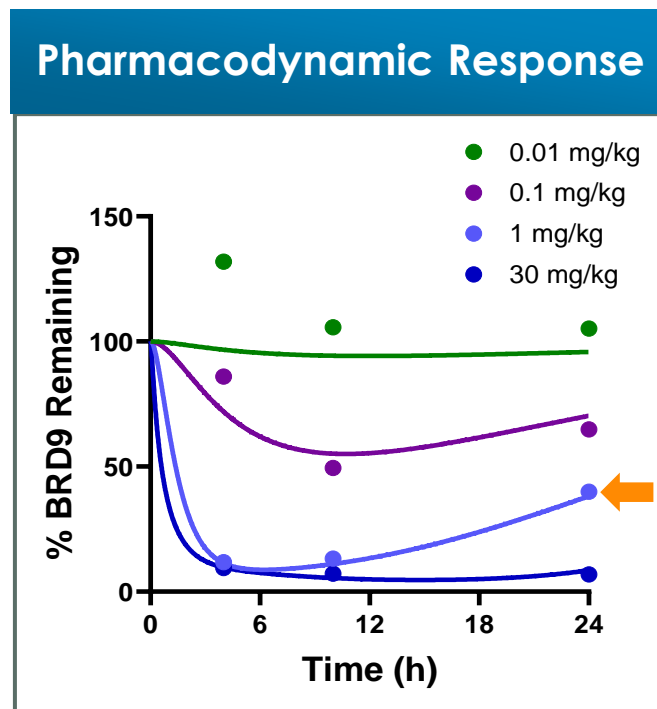
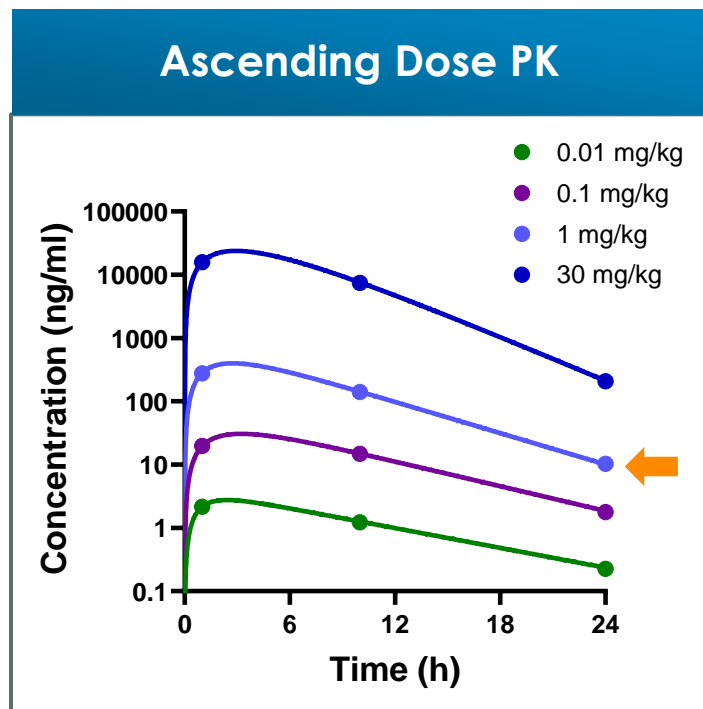
Dose Response Efficacy



Pharmacodynamic threshold required for desired efficacious response

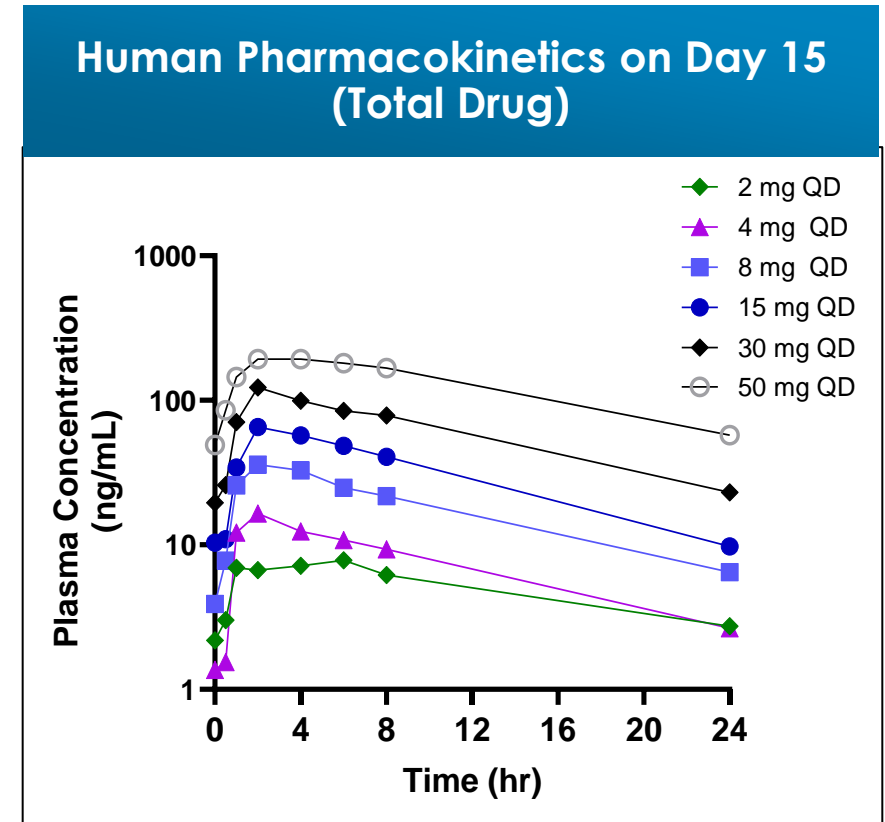
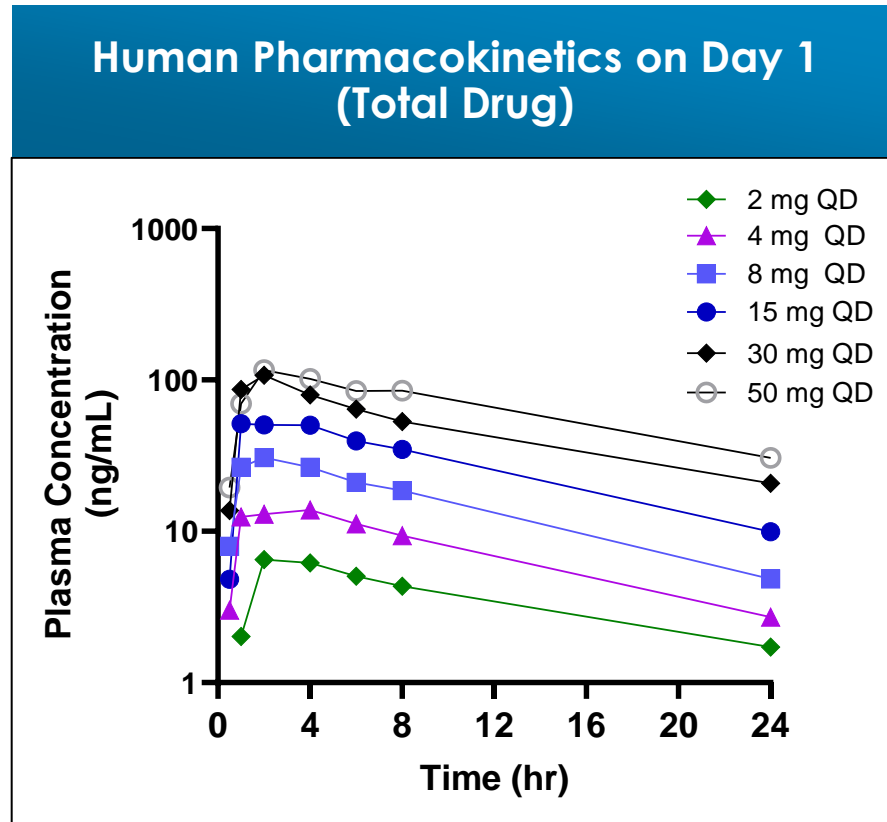
- Function of target engagement/degradation and exposure
- Dependent on target biology and tumor; not dependent on drug modality

PK/PD Modeling of CFT8634 in a Mouse Synovial Sarcoma PDX Model



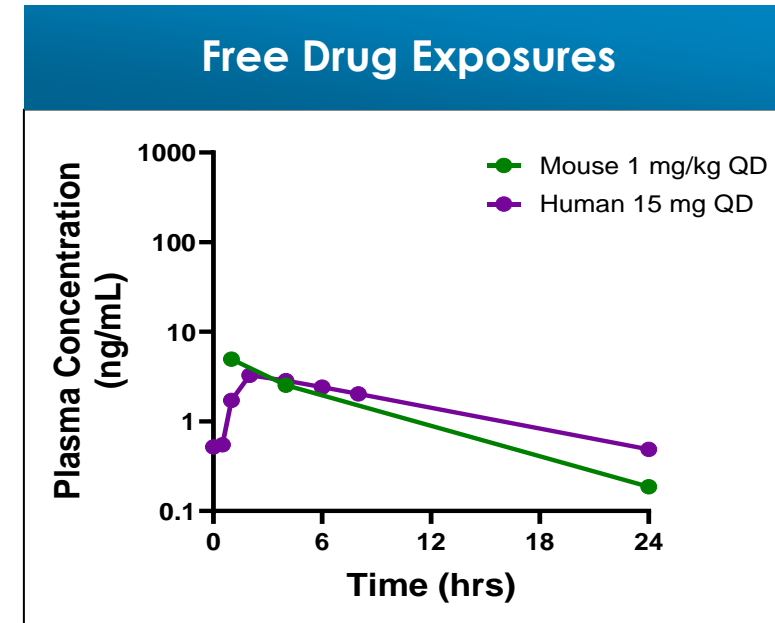
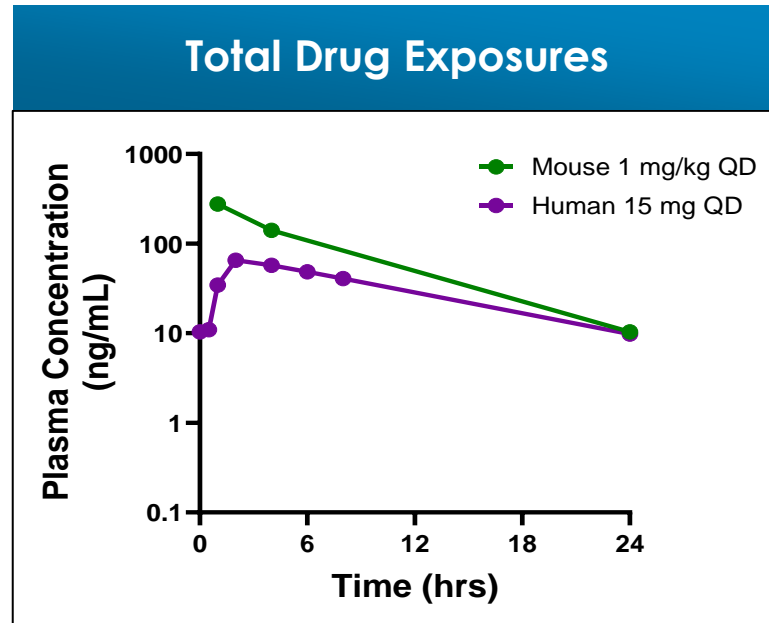
Dose response efficacy indicates that the 1 mg/kg dose should be used to set the pharmacodynamic threshold for PK/PD modeling

Clinical Pharmacokinetics of CFT8634 in Patients with Synovial Sarcoma and SMARCB1-null Tumors



Clinical PK is linear and dose proportional over the entire dose range
minimal accumulation observed at steady state

Comparison of Mouse and Human Pharmacokinetic Profiles

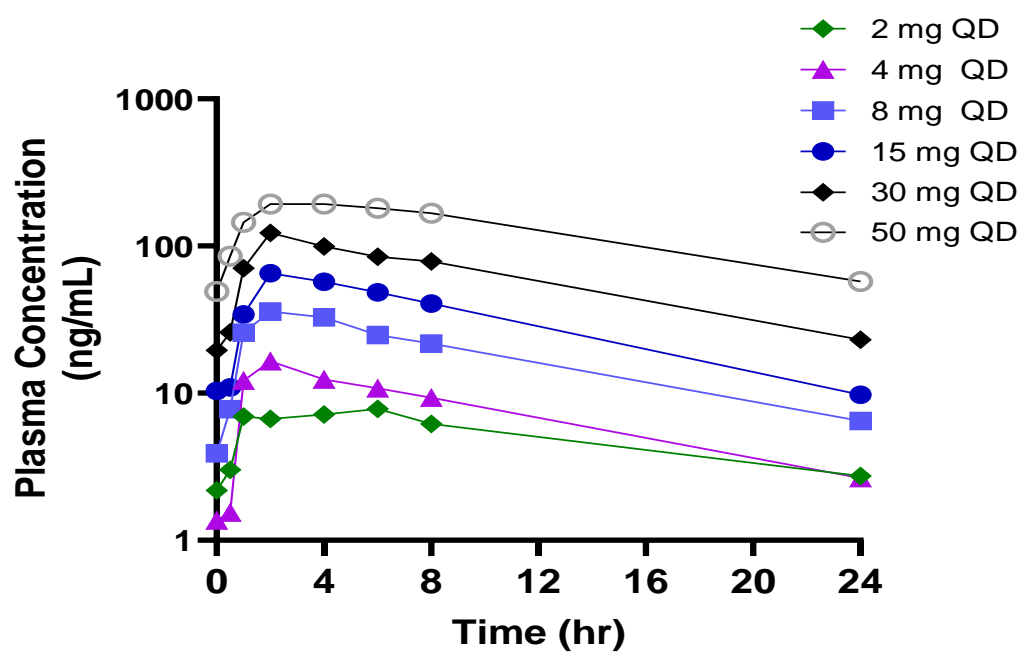


Human PPB Free Fraction: 0.05
Mouse PPB Free Fraction: 0.018

Mouse and human exposures are highly similar at equivalent doses, particularly with free fraction correction

Simulated PD Using Clinical Pharmacokinetics of CFT8634

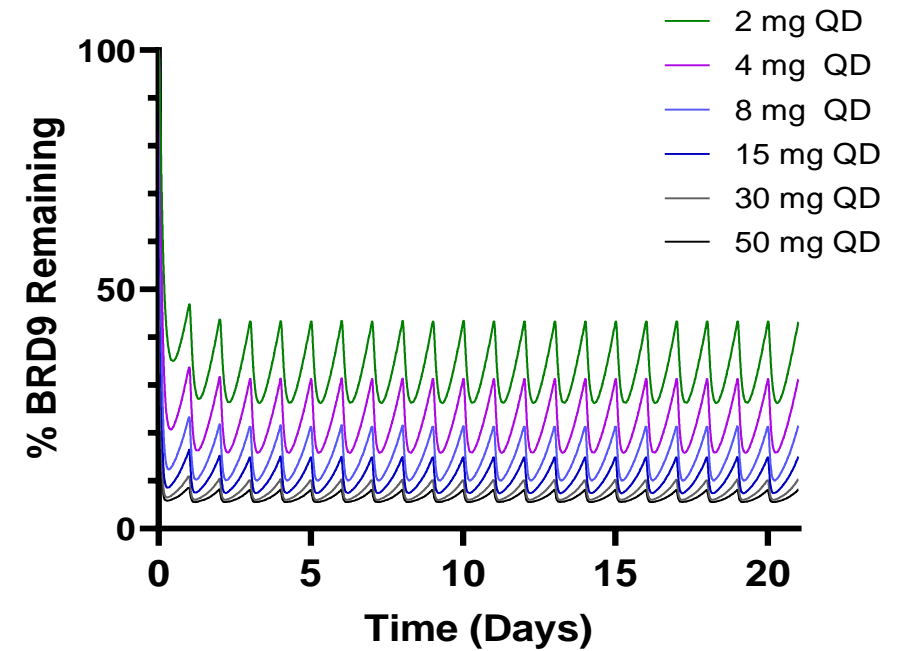
Human PK (Day 15, Steady State)



Utilize kinetic degradation parameters from mouse PDX model

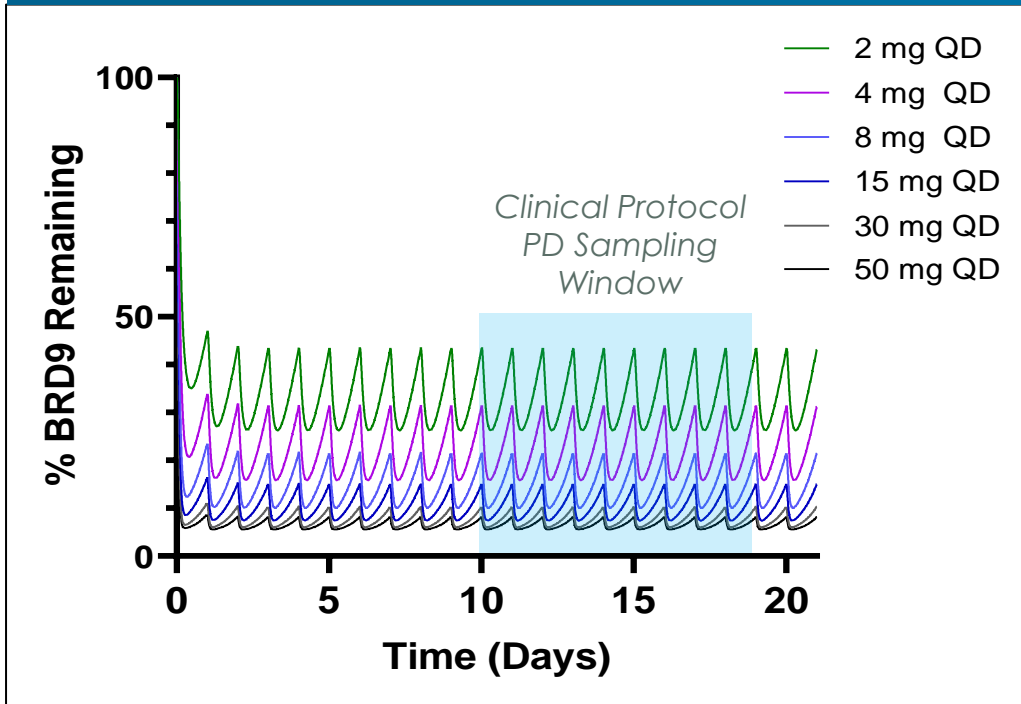


Predicted Human PD Response



Predicted vs Observed PD in Patients

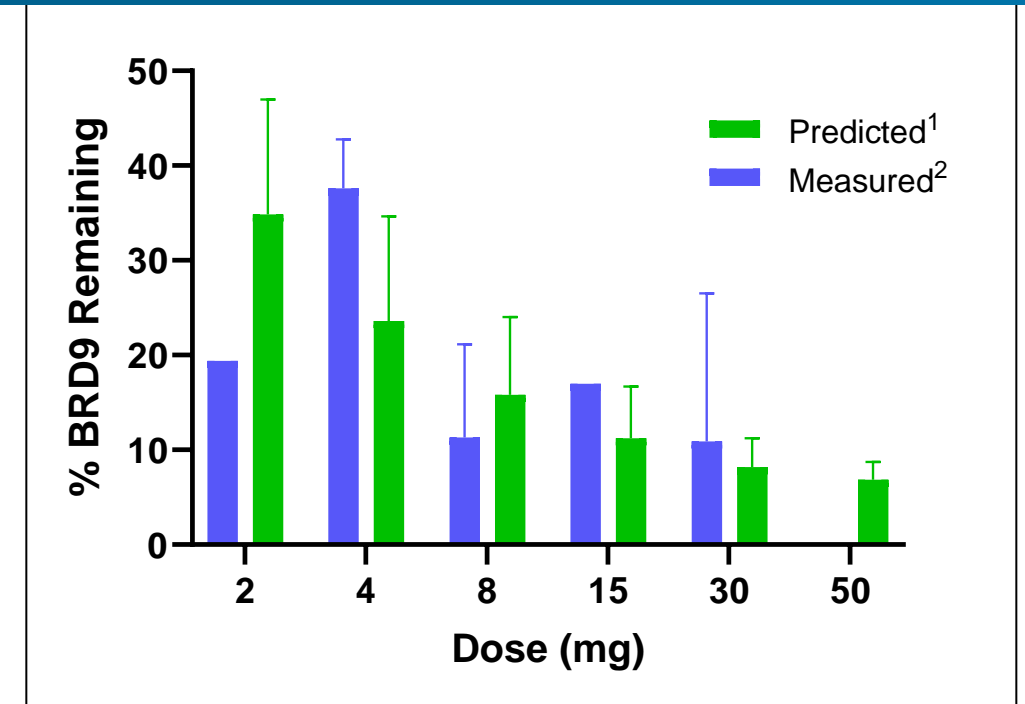
Predicted Human PD Response (Steady State)



Predict PD response range per dose



Predicted Human PD Response (Clinical Protocol Sampling Window)



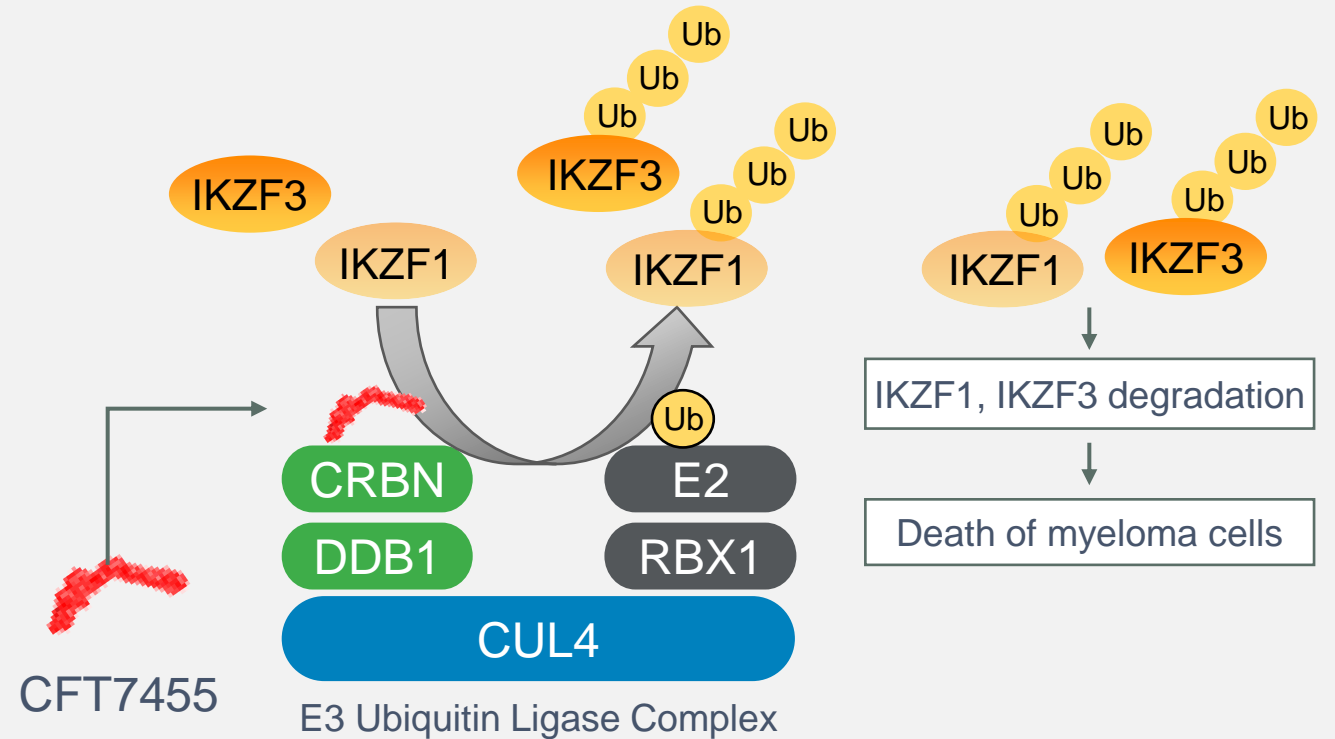
1. Error bars represent predicted range of response over 24 h
2. PD data were measured on tumor tissue by BRD9 IHC via H-score and normalized to the average H-score from all samples at baseline. Average of H-score and SD at all dose levels are reported on the graph.

Cemsidomide: Potent Small Molecule IKZF1/3 Degradator with Enhanced Catalytic & Pharmacologic Properties

- IKZF1/3 are transcription factors required for cancer cell growth and survival in multiple myeloma (MM)
- Approved IKZF1/3 degraders (lenalidomide, pomalidomide) are widely used in MM treatment
- Relapsed/refractory MM remains a high unmet medical need

Goal: Develop an IKZF1/3 MonoDAC™ Degradator with these properties:

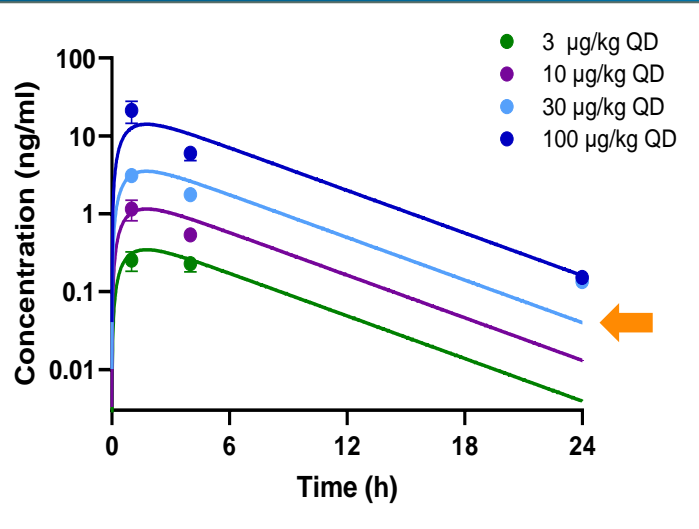
- Class-leading catalytic activity to enable potent, rapid, and deep target degradation
- High binding affinity to overcome resistance to lenalidomide and pomalidomide
- Selective to reduce off-target liabilities
- Pharmacologic profile that enables sustained IKZF1/3 degradation



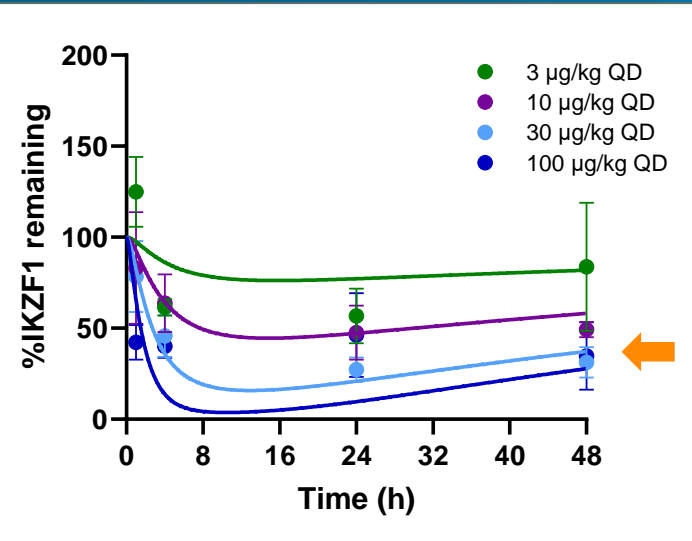
CRBN, cereblon; CUL4, cullin 4; DDB1, DNA damage-binding protein 1; IKZF1/3, Ikaros family zinc finger proteins 1 and 3; MonoDAC, monofunctional degradation activating compound; MM, multiple myeloma; RBX1, ring box protein 1; Ub, ubiquitin.

PK/PD Modeling of Cemsidomide in Multiple Myeloma Mouse CDX Model

Ascending Dose PK

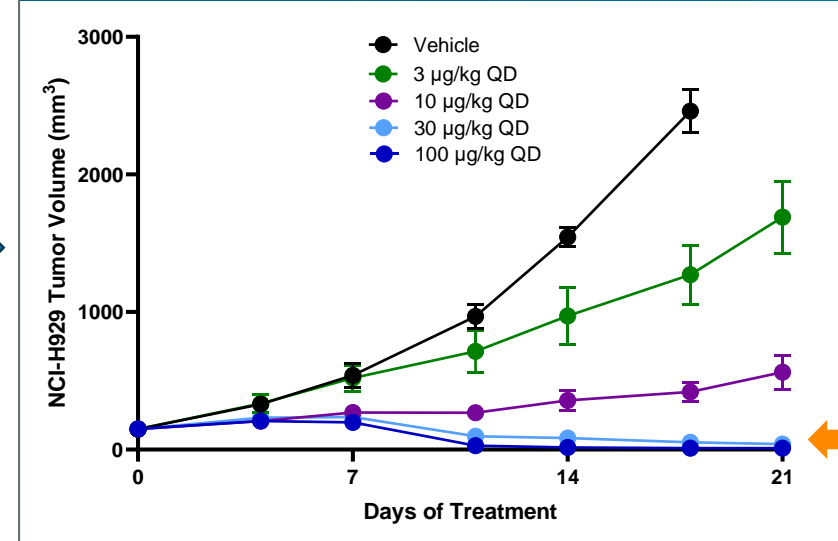


Pharmacodynamic Response¹



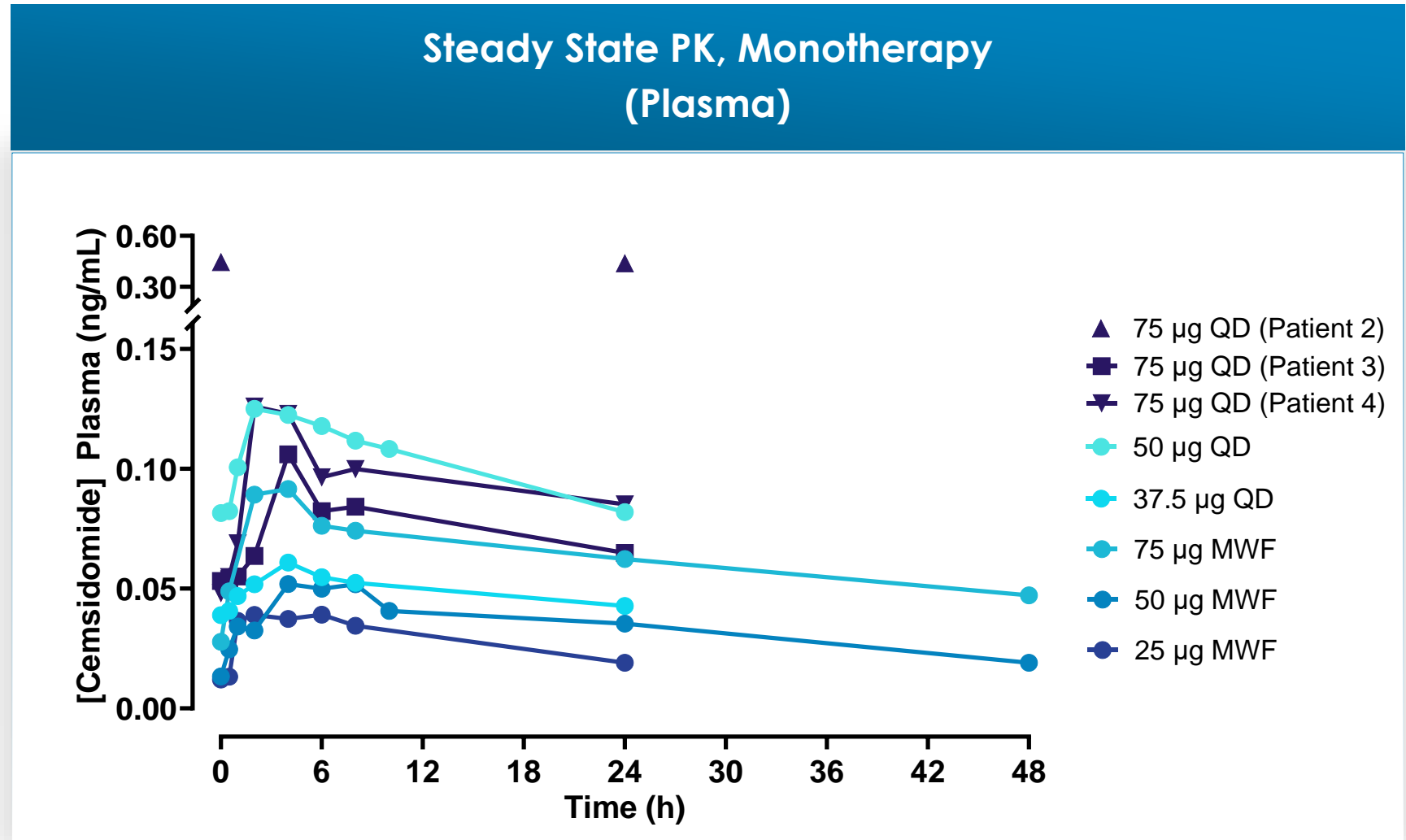
1. Similar response profile observed for IKZF3

Dose Response Efficacy



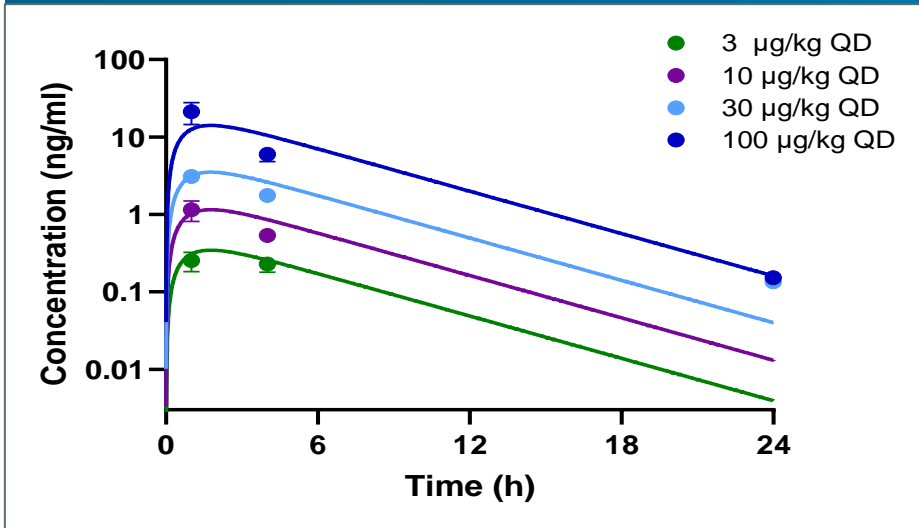
Dose response efficacy indicated that the 30 µg/kg dose should be used to set the pharmacodynamic threshold for PKPD modeling

Proportional Plasma Exposure Increase Observed with Cumulative Dose



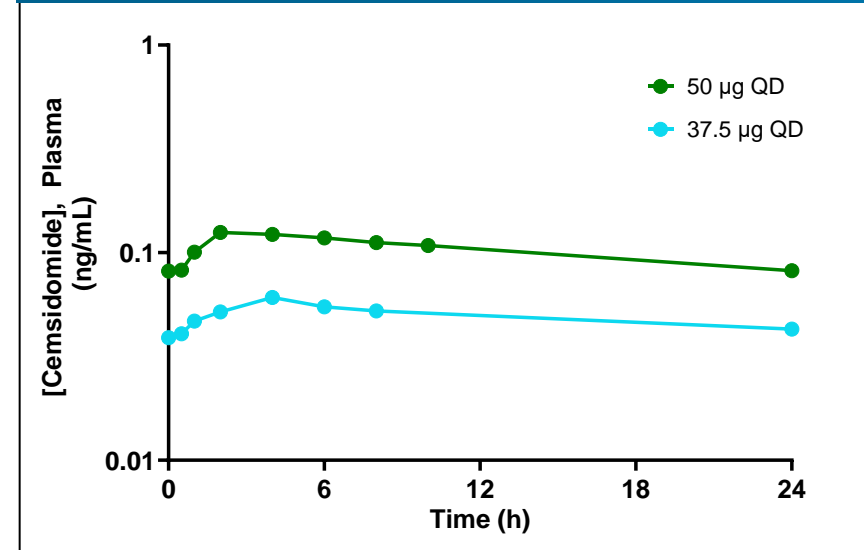
Clinical PK Exhibits a Significant Disconnect from Mouse PK

Mouse Pharmacokinetics (Single Dose, Plasma)



$T_{1/2} \approx 3$ h
No accumulation observed upon multi-day dosing

Steady State Human Pharmacokinetics (Day 14, Plasma)



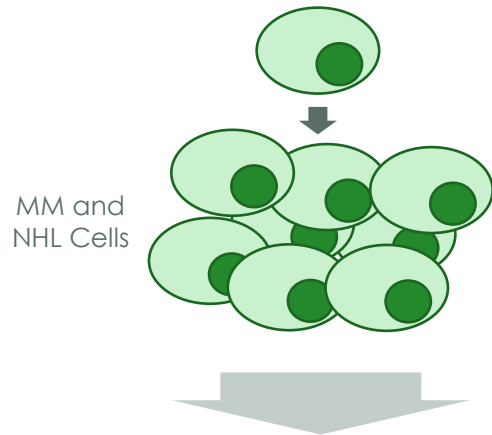
$T_{1/2} \approx 48$ h
Significant accumulation observed (≈ 3.5 -fold)

Combined effect of 3-fold accumulation and much longer half-life results in
 ~ 10 -fold higher overall efficacious exposure in human than in mouse

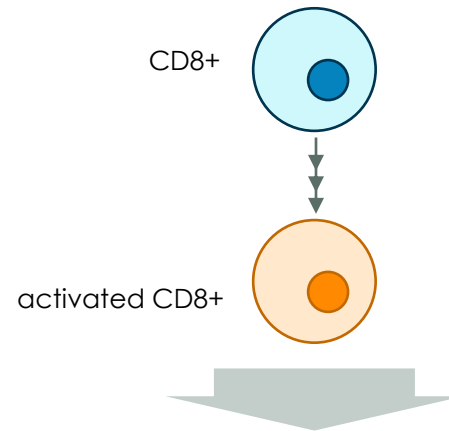
IKZF1/3 Degradation Drives Three Distinct Areas of Hematopoietic Biology; Degradating IKZF1/3 is a Validated Therapeutic Strategy in MM and NHL

IKZF1 / IKZF3 Transcription Factors

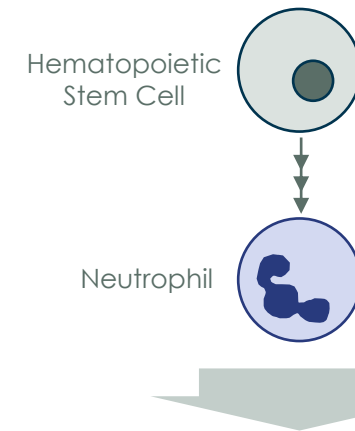
Drive MM and NHL Cell Growth and Survival



Activate Fully Differentiated T-cells



Regulate Hematopoietic Stem Cell Differentiation



Consequences of IKZF1/3 Degradation:

- MM and NHL Cell Death

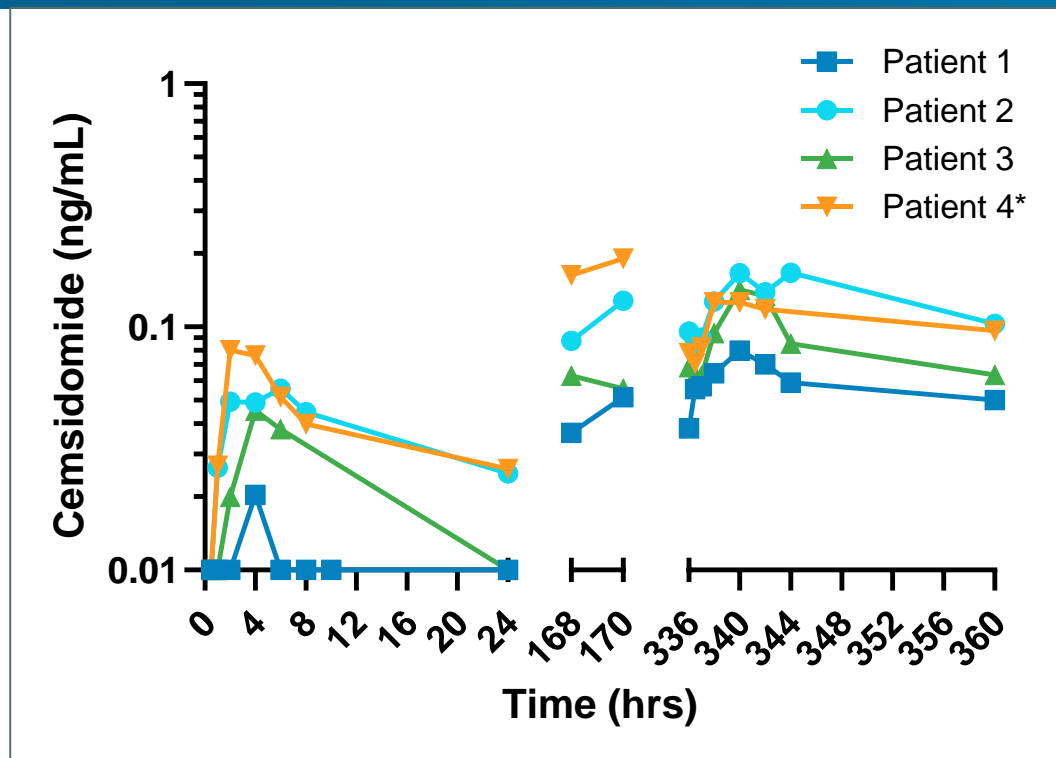
- T-cell Activation

- On-target Neutropenia

Ikaros Family Zinc Finger proteins 1 and 3 (IKZF1/3); Multiple Myeloma (MM); Non-Hodgkin's Lymphoma (NHL).

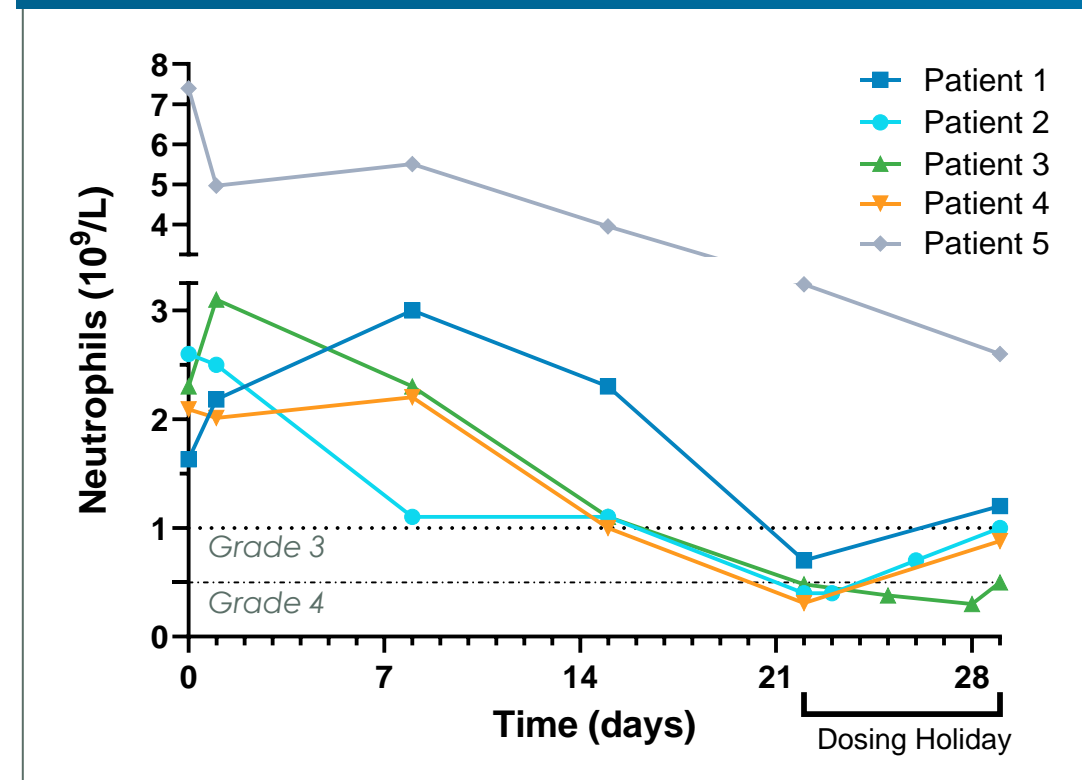
Prolonged Steady State Exposure Is Associated With Clinical Neutropenia

Cohort A, Cycle 1 Pharmacokinetics 21 Days on/7 Days off Schedule



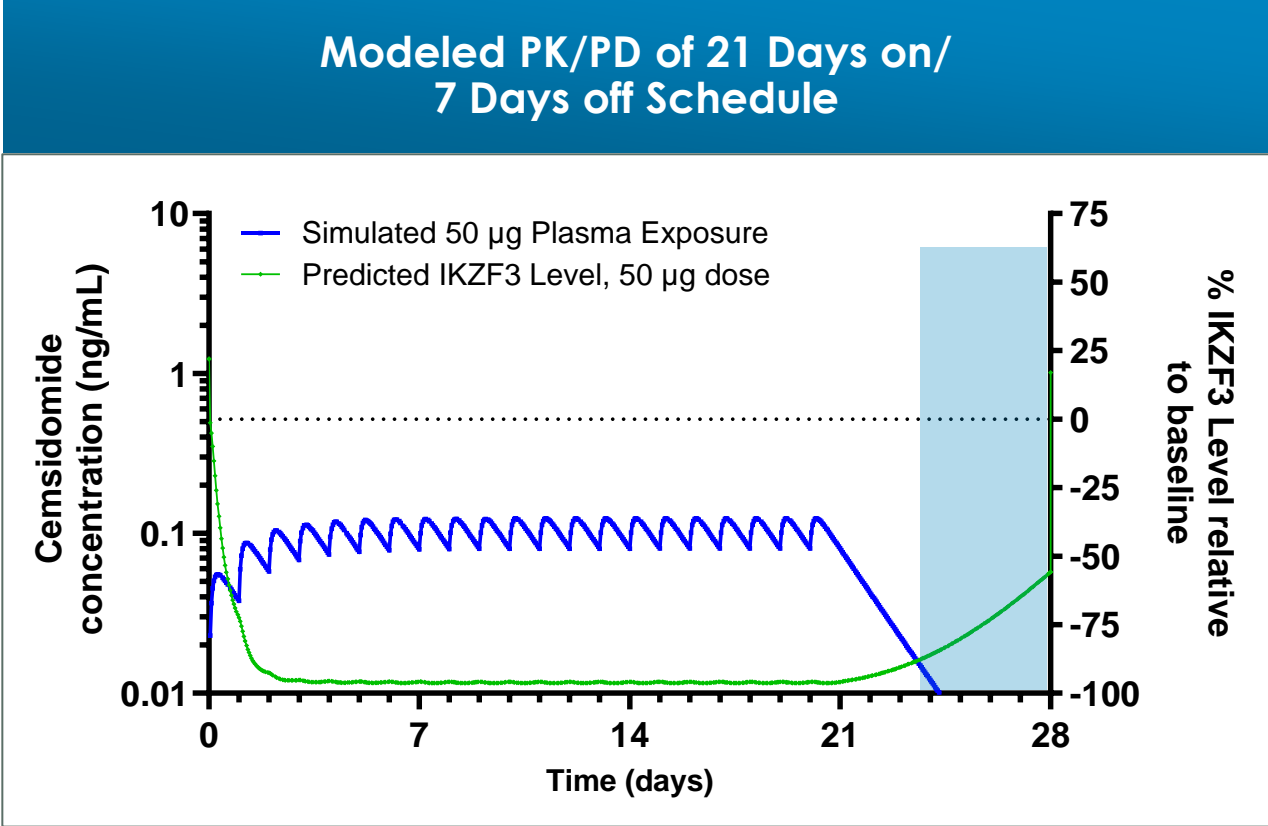
*Patient 4 received 50 µg for 8 days followed by 25 µg for 13 days followed by the regular 7- day rest period in cycle 1, subsequent cycles continued at 25 µg 21 days on and 7 days off in a 28 -day cycle
Data not shown for Patient 5 who received 25 µg Dose
BQL (below quantification limit) results are shown at 0.01 for display only

Cohort A, Cycle 1 Neutrophil Counts 21 Days on/7 Days off Schedule



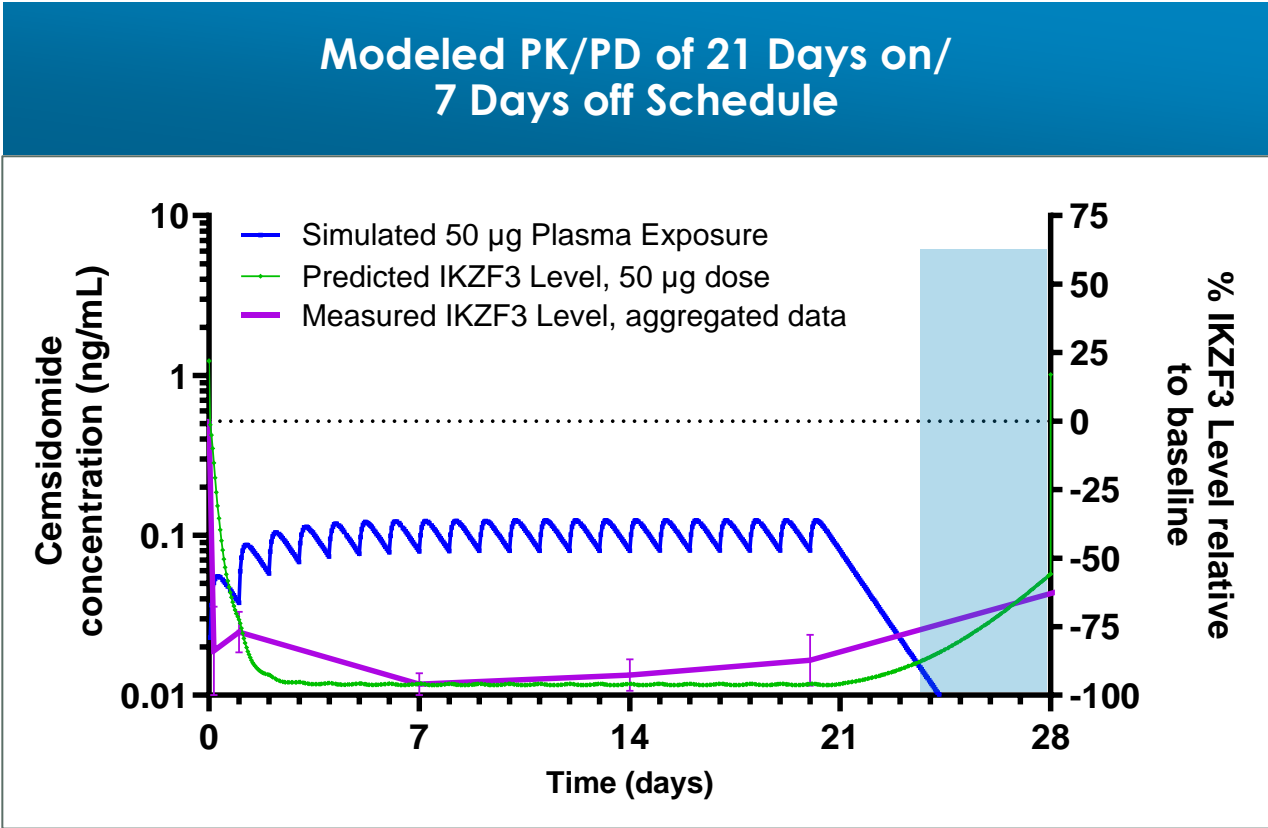
Patient 4 received 50 µg for 8 days followed by 25 µg
Patient 5 received 25 µg Dose

Clinical PD Confirms Sustained Suppression of IKZF1/3 With 21/7 Schedule



21/7 Schedule Does Not Provide Sufficient Time for Drug Clearance for Neutrophil Recovery

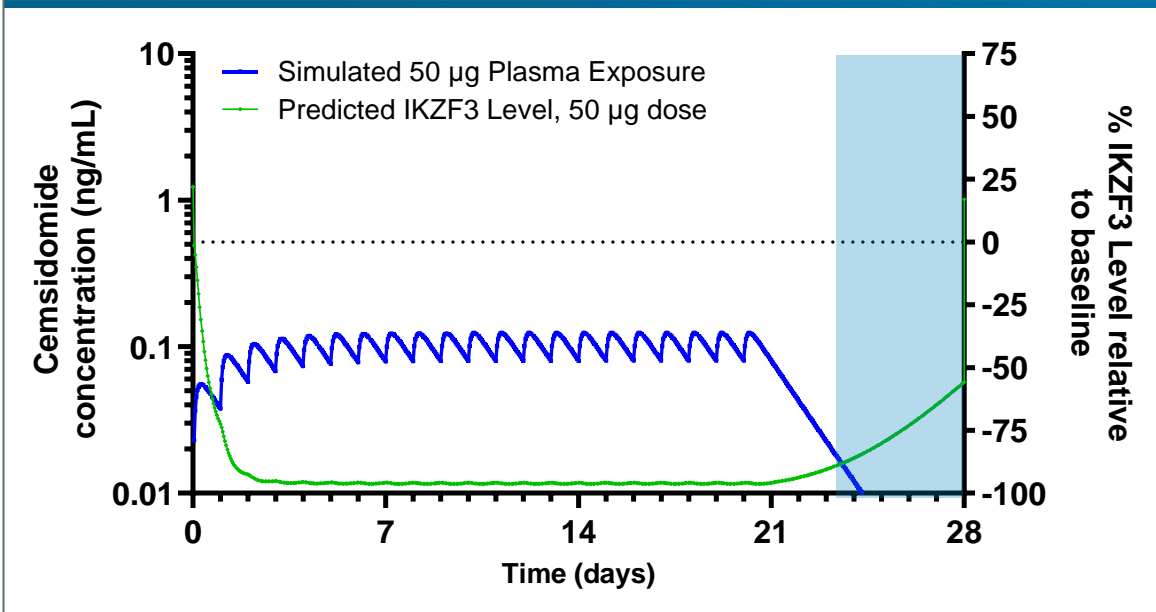
Clinical PD Confirms Sustained Suppression of IKZF1/3 With 21/7 Schedule



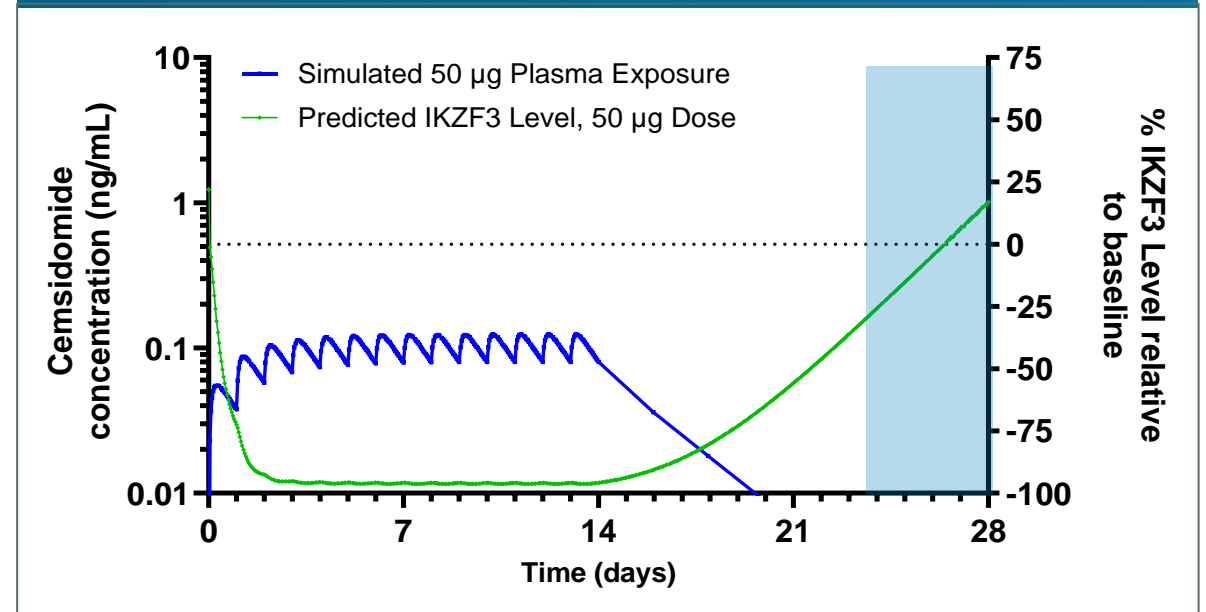
21/7 Schedule Does Not Provide Sufficient Time for Drug Clearance for Neutrophil Recovery

PK/PD Modeling Supports 14 Days on/14 Days off Schedule as it Provides a Sufficient IKZF1/3 Degradation Holiday

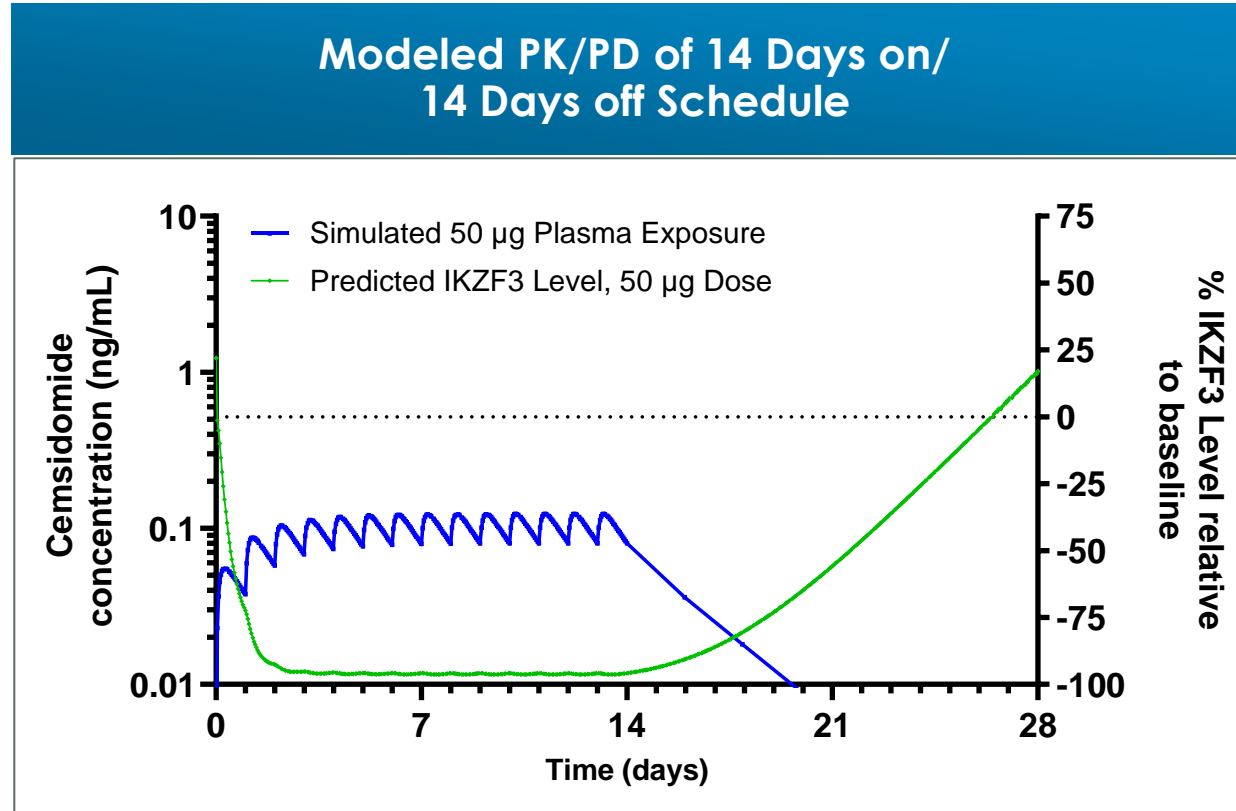
Modeled PK/PD of 21 Days on/7 Days off Schedule



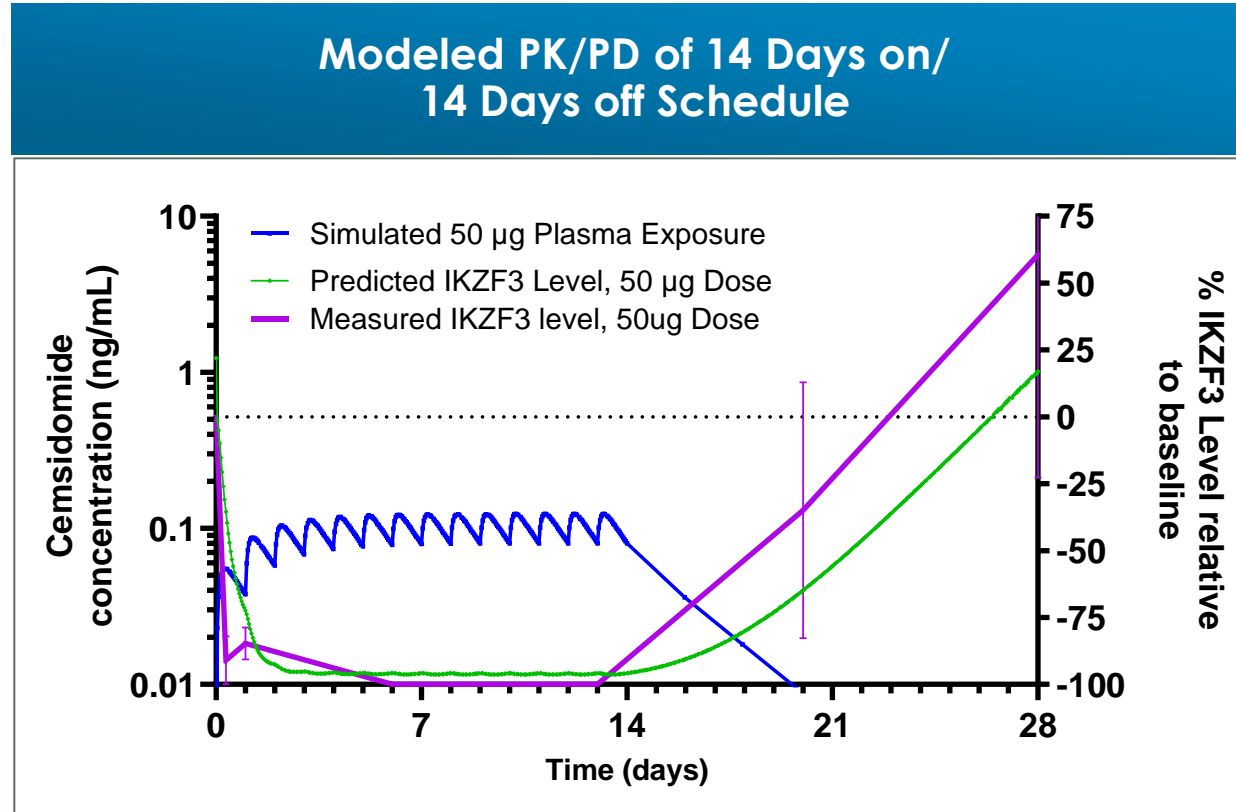
Modeled PK/PD of 14 Days on/14 Days off Schedule



Emerging Clinical Data is Consistent with PK/PD Modeling Prediction for 14 Days on / 14 Days off Schedule



Emerging Clinical Data is Consistent with PK/PD Modeling Prediction for 14 Days on / 14 Days off Schedule



Conclusions

- Semi-mechanistic PK/PD models that incorporate degradation kinetics parameters can be highly predictive of clinical PD response
 - Applicable to both heterobifunctional and monofunctional degraders
 - Demonstrated with different target classes
- In general, kinetic parameters determined from *in vitro* systems or fitting to *in vivo* models translate well to the clinic for oncology (CDX, PDX systems)
- Key factors that influence the predictions include pharmacokinetic differences between preclinical species and human exposure profiles
 - Plasma protein binding free fraction differences
 - Differences in tissue penetration or intrinsic clearance rates

Acknowledgements

- We thank the patients and their families for participating in our clinical trials
- We thank all the investigators and their staff
- We thank the C4T employees, past and present, who contributed to the discovery and development of Cemsidomide and CFT8634, and the PK/PD modeling platform

