

2nd Annual

# Ligase Targeting Drug Development

Hijacking E3 Ligases to Mediate Degradation or Modulation of Undrugged Targets

## Chemically Harnessing Novel E3 Ligase Biology for Next-generation TPD Therapeutics



KYMER A

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**INVENTING NEW MEDICINES**

WITH TARGETED PROTEIN DEGRADATION

April 26<sup>th</sup>, 2022

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# Outline of Presentation

- Kymera's pipeline and platform
- Identifying a small molecule ligand for a novel E3 ligase
- Developing a heterobifunctional degrader for a POC POI\*
- Evaluating pharmacology for cellular POC efforts
- Summary and Outlook

\* POC, proof-of-concept; POI, protein-of-interest

Founded  
2016











Recognition



Partnerships



# Kymera's Pipeline of Novel Protein Degraders

Pathway	Program	Indication(s)	Discovery	IND Enabling	Phase 1	Phases 2/3	Next Milestone	Rights*
IL-1R/TLR	IRAK4	Multiple Immuno-inflammatory Diseases: HS, AD, RA others	<div>KT-474</div> <div>Multiple molecules staged as potential back ups if needed</div>				Patients POB mid-22	 sanofi
	IRAKiMiD (IRAK4, Ikaros, Aiolos)	MYD88 <sup>MT</sup> Tumors	KT-413				POM: 2022	 KYMERA
JAK/STAT	STAT3	Liquid & Solid Tumors	KT-333				POM: 2022	 KYMERA
	STAT3	Autoimmune & Fibrotic Diseases						 KYMERA
p53	MDM2	Liquid & Solid Tumors	KT-253			NEW	IND: 2H22	 KYMERA
Collaboration	Confidential	Confidential						 sanofi
Discovery Pipeline	Several Discovery Programs		Multiple programs in immune-inflammatory and oncology indications to deliver ≥ 1 IND/year				≥ 1 DC: 2H22	 KYMERA
Collaboration	6 Undisclosed Programs		6 targets in 5 disease areas outside of immunology-inflammation and oncology					 VERTEX

● = Oncology ● = Immunology-Inflammation

\*Option to participate equally in the development and commercialization of Sanofi-partnered programs in the US

# We Want to Drug All Target Classes

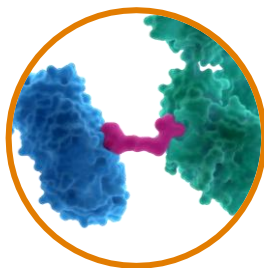
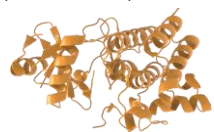


## Expanding the Druggable Proteome with TPD

ID

### Inadequately Drugged Targets with Clear Degradation Advantage

Small molecule binders exist but unable to drug target fully  
e.g., IRAK4, MDM2...



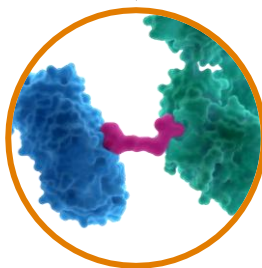
Heterobifunctional Degraders

UD

### Undrugged Targets

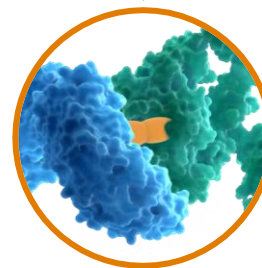
No other technology can drug

Ligandable Proteins  
e.g., STAT3...



Heterobifunctional Degraders

Un-ligandable Proteins  
e.g., other transcription factors



Molecular Glues

TR

### Clinically Validated Targets Enabled by E3 Ligase Tissue Restricted Expression

On-target unwanted pharmacology limits clinical application



Tissue sparing or selective E3 ligases eliminate unwanted toxicity and allow full clinical potential



# Platform for Harnessing Novel E3 Ligase Biology

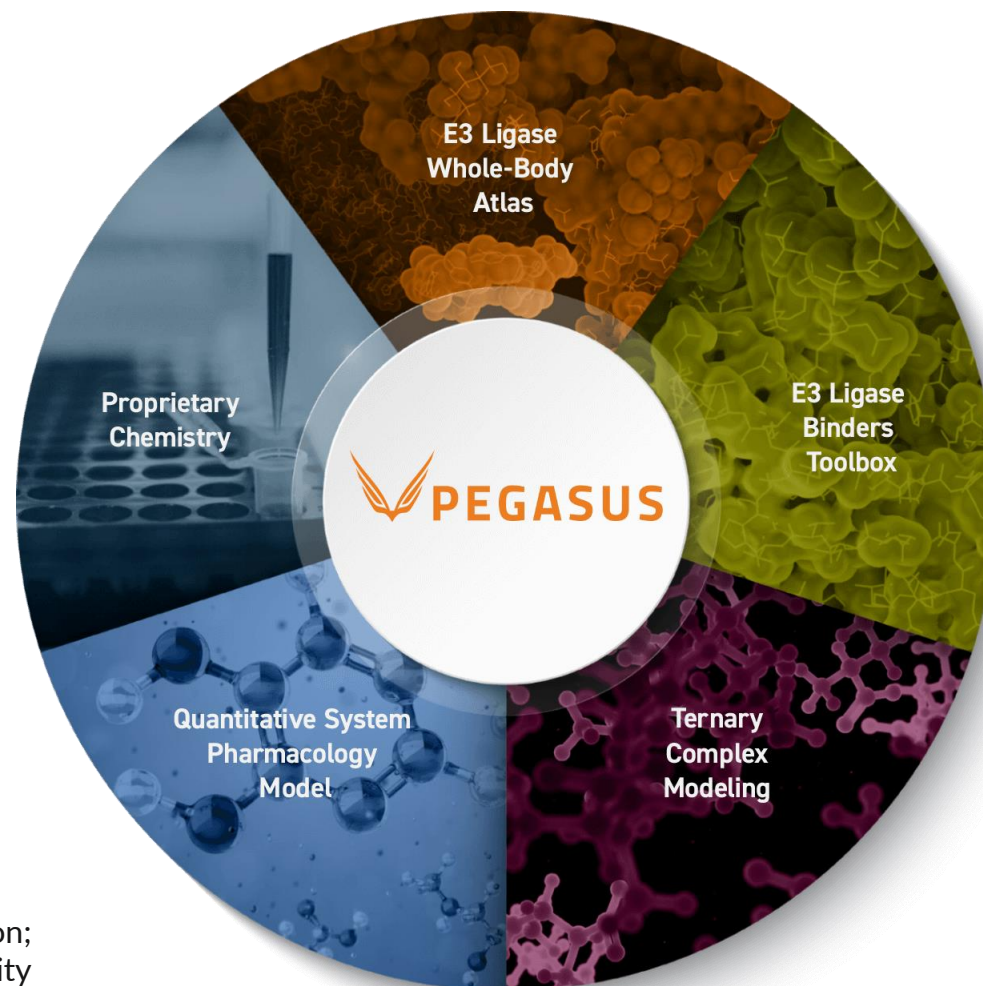
## E3 Ligase Whole-body Atlas

- RNA & protein expression profiles of ~ 600 E3s
- Disease & healthy tissues & cells (tissue distribution, absolute abundance, & subcellular localization)
- Novel E3 & POI pairing based on expression & biology

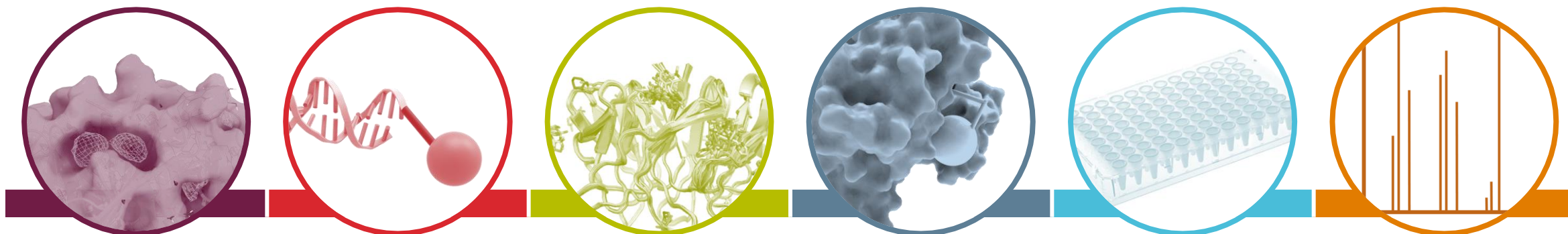
## Proprietary Chemistry

- High-quality ligands for novel E3s
- Innovative degraders for new therapeutic opportunities
- Advanced molecular design principles for improved drug properties (e.g.,  $DC_{50}$ ,  $D_{max}$ ,  $S_{H_2O}$ ,  $P_{app}$ , &  $F_{oral}$ )\*

\*  $DC_{50}$ , concentration at half-maximum degradation;  $D_{max}$ , maximum degradation;  $S_{H_2O}$ , aqueous solubility;  $P_{app}$ , cell permeability;  $F_{oral}$ , oral bioavailability



# Comprehensive Hit Finding Toolbox



## Virtual Screen

### Criteria

- Availability of structure or homology model

### Approaches

- DB ~8 million purchasable cpds
- Cloud enables screen < 24hrs
- AI to improve enrichment

## DEL

### Criteria

- High quality protein
- Ideal QC profile (single-species by SEC; <5% aggregation by DLS)

## Fragment-Based Screen

### Criteria

- Availability of high quality (crystallization-grade) protein
- Robust crystallization system

### Approaches

- SPR, NMR
- X-ray
- LC/MS (covalent)

## Cysteine Covalent Screening

### Criteria

- Proteins have reactive cysteines

### Approaches

- Covalent fragment screening on recombinant protein
- Whole cell covalent fragment screening

## HTS

### Criteria

- Available high-throughput assay format

### Approaches

- Focused library
- Diversity set

## ASMS

### Criteria

- Availability of high-quality protein

# Guiding Principles

## Value-added Portfolio

- Strategic pairing of novel E3s & POIs for targeted diseases
- Judicious balancing of biology & chemistry risks

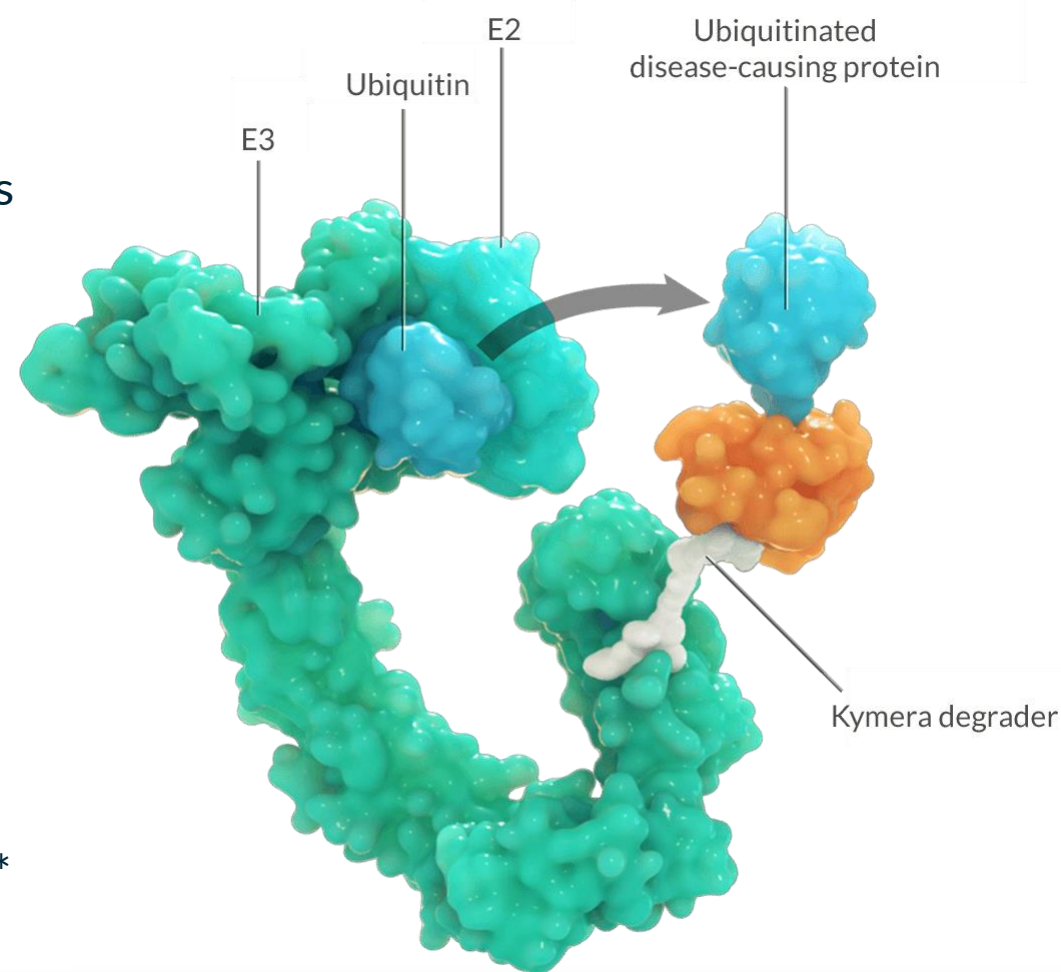
## Qualified Biology

- Holistic assessment of novel E3s (“LED” qualification)
- LED: ligandability, expression profile, & degradative activity

## Enabled Chemistry

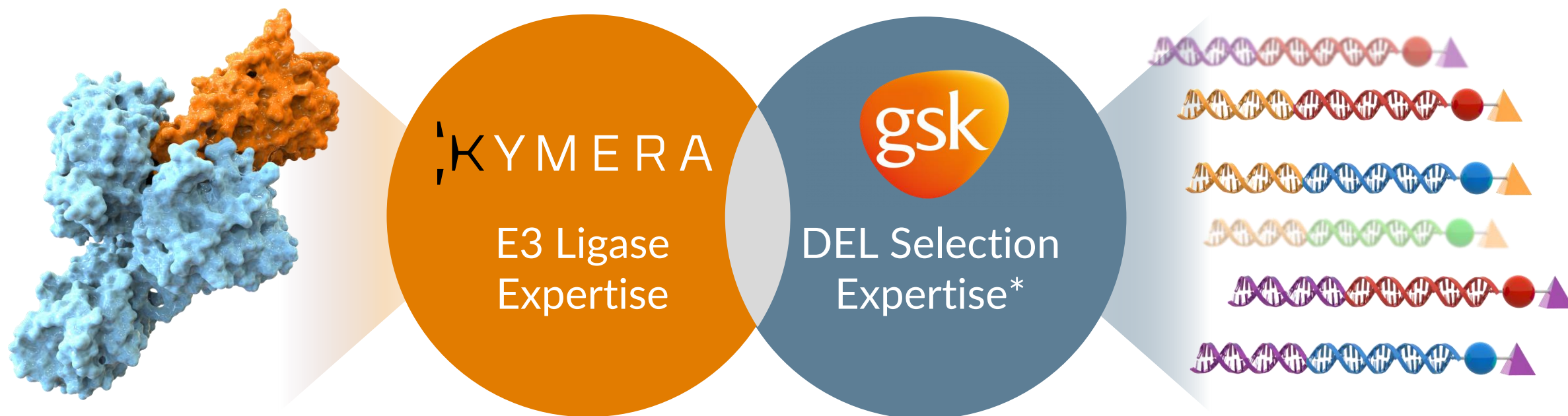
- Strategic tailoring of hit-finding: binding sites & ligand types
- X-ray crystal structures: ligandability, hit finding, & SBDD\*

\* SBDD, structure-based drug design





# Kymera-GSK Partnership



\* DEL, DNA-encoded library

# Novel E3 Ligase X (E3LX): Value Proposition

## Current E3 Ligases are Limited

- All are ubiquitous: cereblon, VHL, MDM2, IAP, etc.
- Each has chemistry, biology, or safety challenges

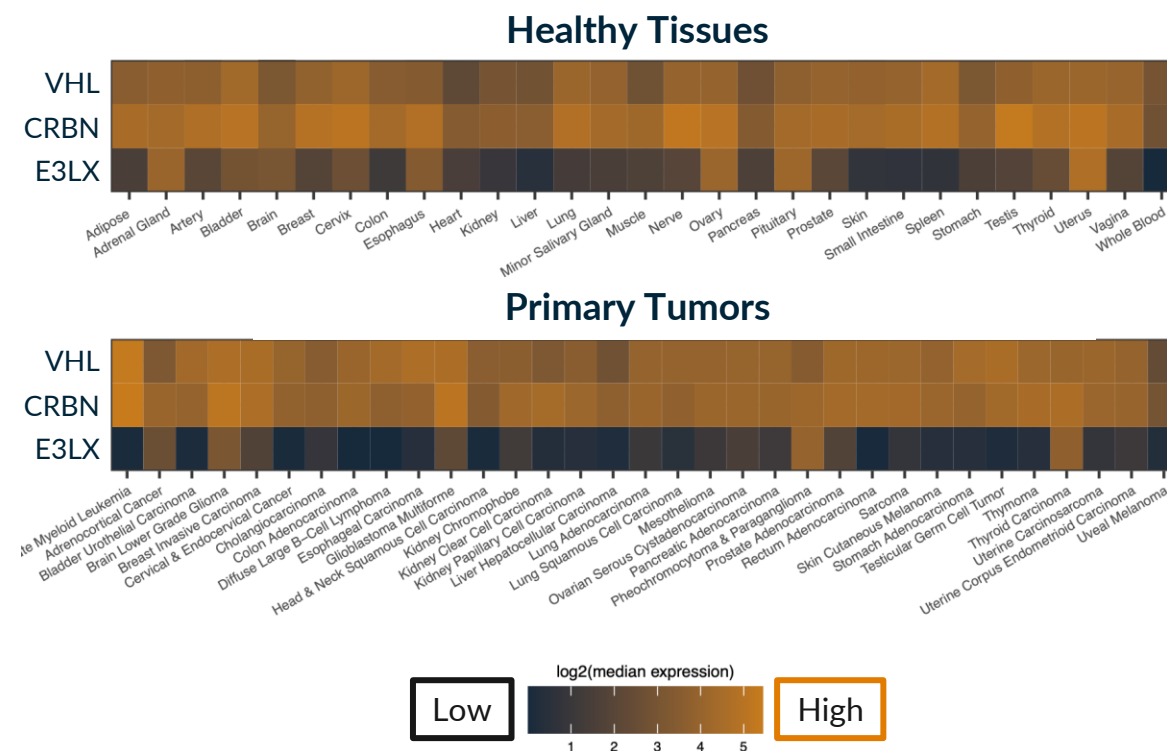
## Improved Ubiquitous E3s Needed

- Novel E3-based degraders that allow improved oral bioavailability, increased neo-substrate scope, and fewer safety challenges

## Tissue-selective E3s Most Valued\*

- Including tissue-restricted or tissue-sparing
- Potential for improved efficacy and safety

## E3LX Expression Profile by RNA-Seq<sup>#</sup>



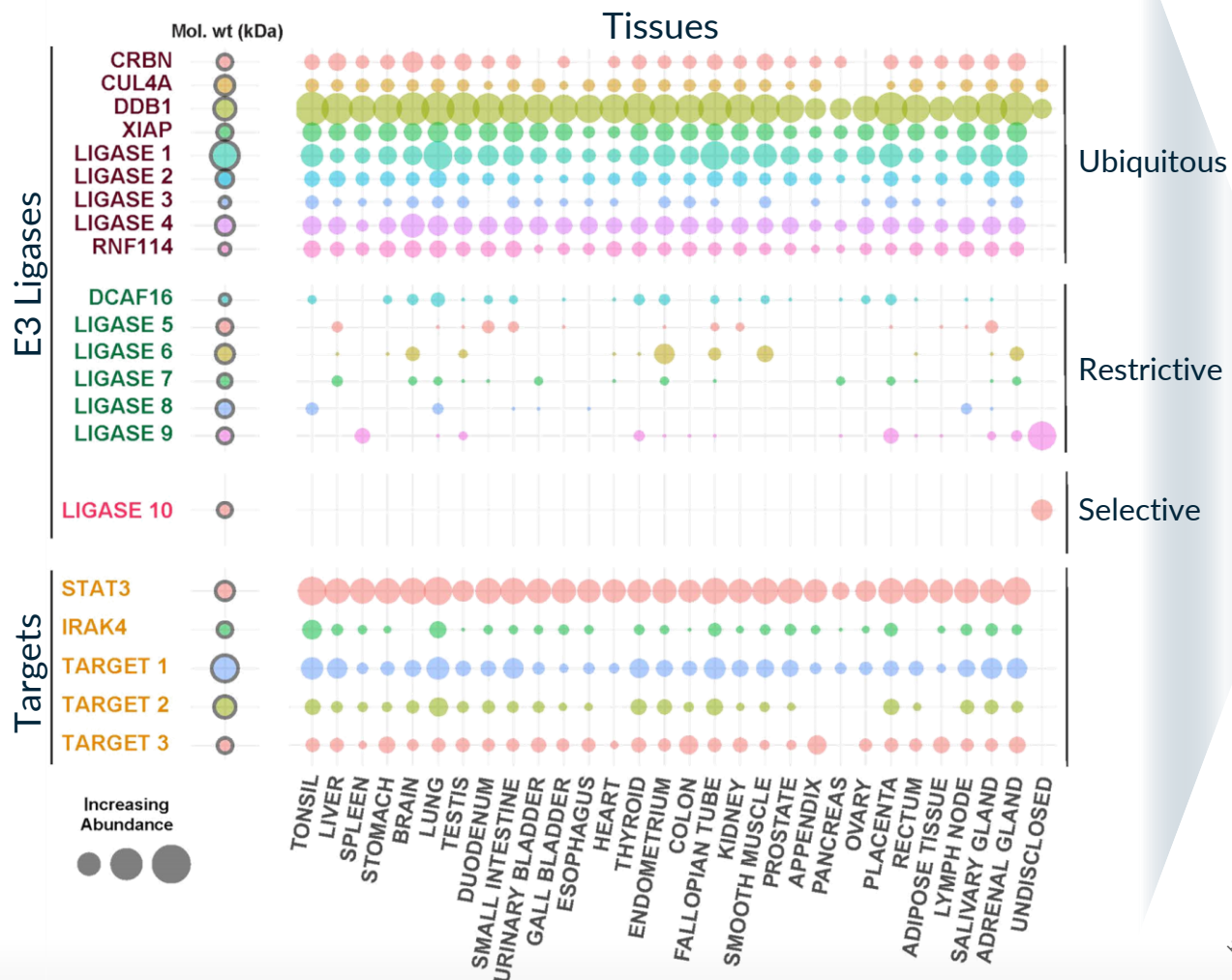
E3LX: low expression in most healthy tissues  
E3LX: high expression in select primary tumors

\* Békés, M.; Langley, D. R.; Crews, C. M. *Nat. Rev. Drug Discov.* **2022**, *21*, 181-200.

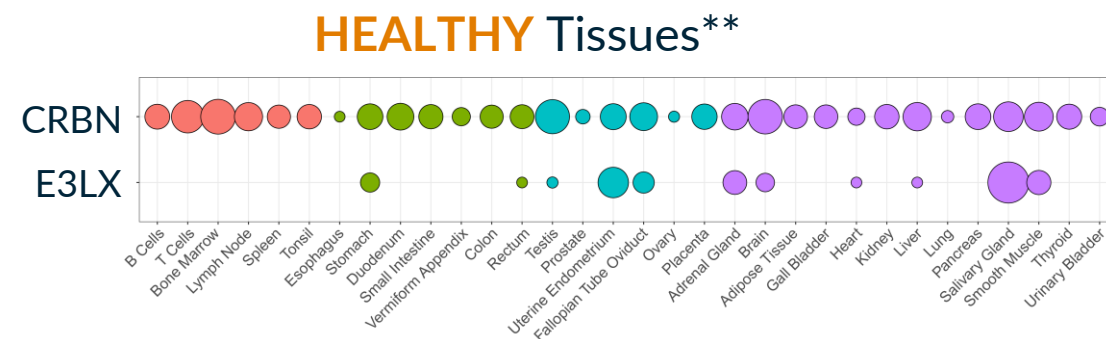
<sup>#</sup> RNA-Seq, RNA sequencing; GTEx, TCGA data

# E3LX Expression Profile Substantiated by Proteomics

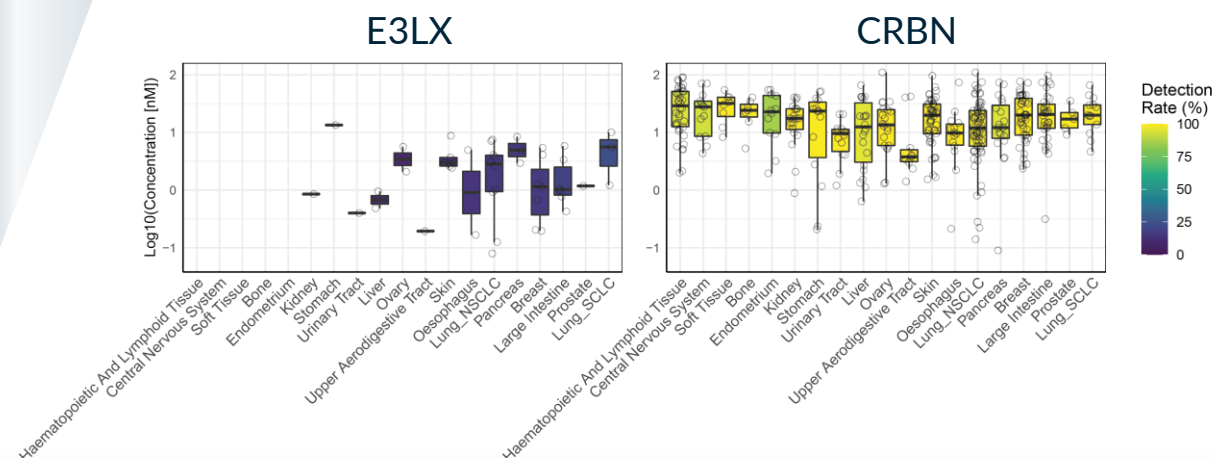
## E3 Ligase Whole-body Atlas



## E3LX Protein Expression Profile



## CANCER Cell Lines\*\*\*



\*\* Wang et al., Mol Syst Biol 2019, reprocessed and supplemented with internally acquired data.

\*\*\* Nusinov et al., Cell 2020, reprocessed

# E3LX: Qualified Biology

## Expression Profile

- RNA & protein show favorable healthy & disease profile for tissue-selective degradation; cytosolic & nuclear localization of protein

## Degradative Activity

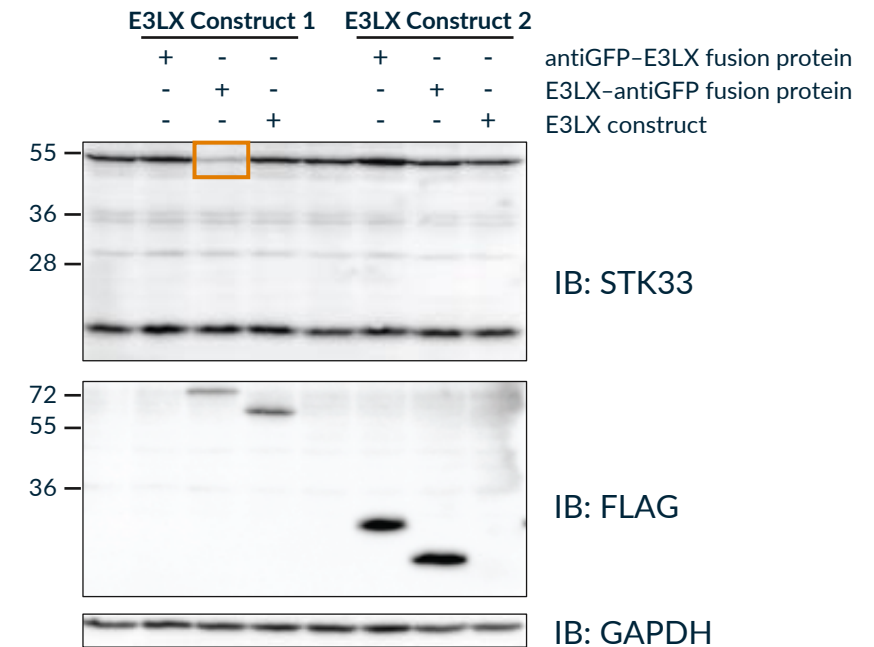
- Endogenous: no known substrate → no known degron
- Induced: STK33 is neo-substrate using AdPROM system

## Ligandability

- RING E3 ligase (family includes MDM2, cIAP1, etc.)\*
- No reported X-ray crystal structures or SM ligands

## E3LX Degradative Activity by AdPROM<sup>#</sup>

### A549 Cells Stably Expressing GFP-STK33 Fusion Protein



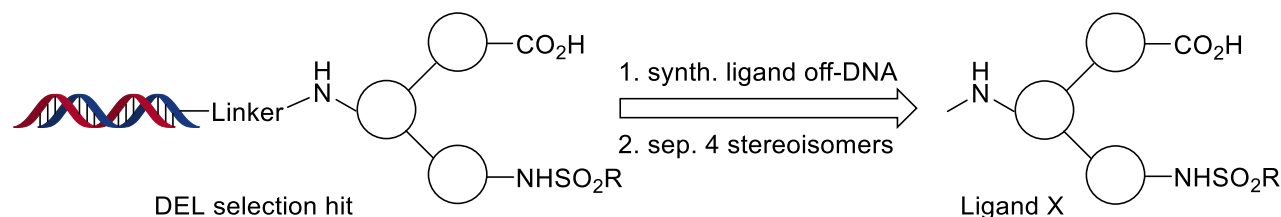
\* Jevtić, P.; Haakonsen, D. L.; Rapé, M. *Cell Chem. Biol.* **2021**, *28*, 1000-1013.

<sup>#</sup> AdPROM, affinity-directed PROtein Missile

# E3LX: Enabled Chemistry

## Hit Finding Strategy

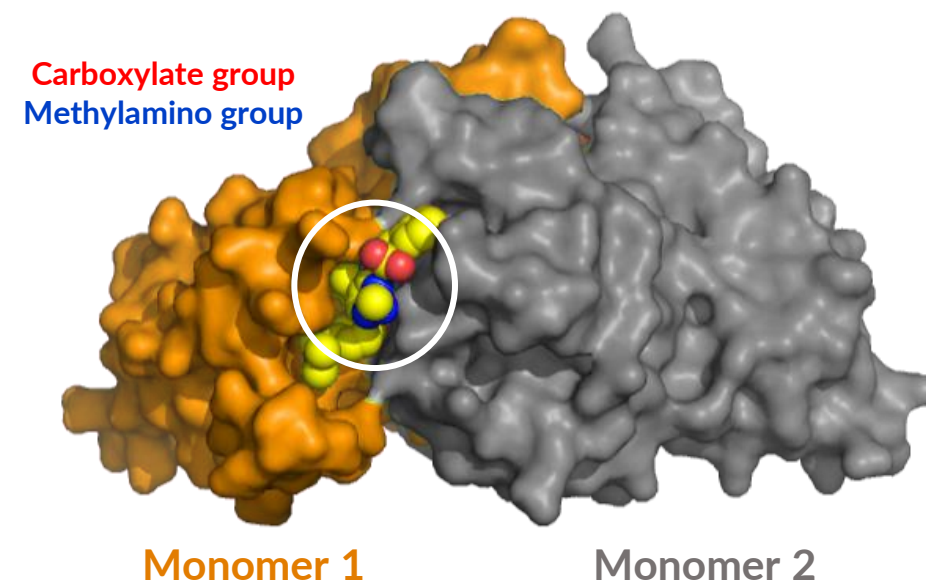
- Binding sites unknown at time of DEL selection
- DEL selection done at GSK (~ 100 unique DELs)
- Diverse, 2-4 cycle library; billions of compounds



## X-ray Crystal Structure

- Ligandability validated (Ligand X  $K_d = 0.20 \mu\text{M}$ )
- Enables structure-based virtual screening
- Allows SBDD for binding affinity & exit vectors

## E3LX-Ligand X Complex Structure by X-ray Crystallography (3.3 Å)

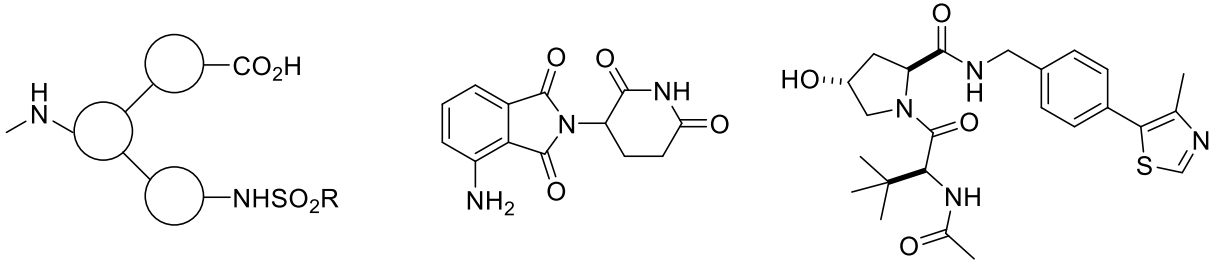


Ligand X binds at the interface of dimeric C-terminal domain of E3LX



# Ligand X: Key Properties

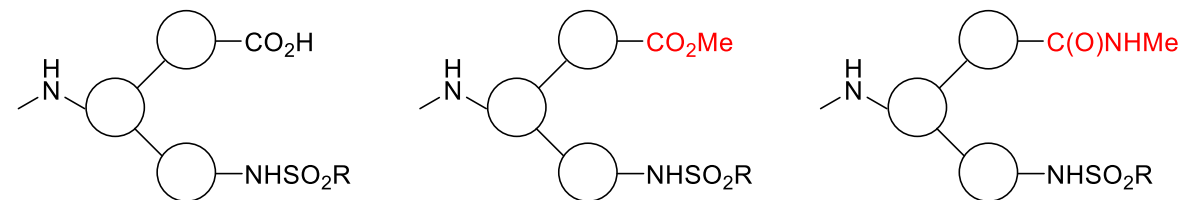
## Improved Properties Needed



Molecular, Physicochemical, & Pharmacological Properties	E3LX, Ligand X	CRBN, Pomalidomide	VHL, VH032
Binding affinity, $K_d$ ( $\mu\text{M}$ )	0.20	1.2	0.60
Molecular weight, MW (Da)	623	273	473
Topological polar surface area, TPSA ( $\text{\AA}^2$ )	128	110	111
Lipophilicity, cLogP	3.8	-0.20	0.70
Kinetic aqueous solubility, PBS at pH 7.4 ( $\mu\text{M}$ )	15	258	284
Passive permeability, WT-MDCK $P_{\text{app}}$ A $\rightarrow$ B ( $\times 10^{-6}$ cm/s)	0.30	30	0.60

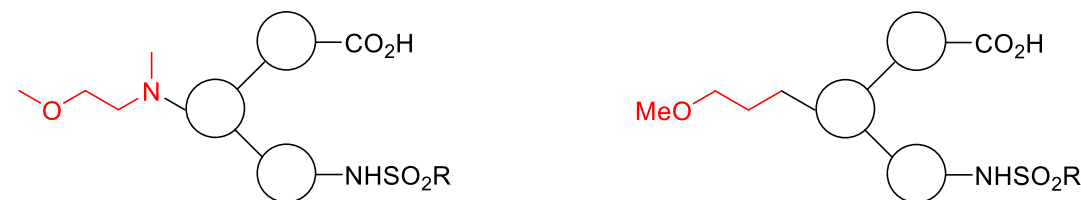
# Ligand X: Exploratory Binding SAR

## Carboxylic Acid is Important



Binding Affinity	Ligand X	Analogue 1	Analogue 2
E3LX SPR $K_d$ ( $\mu$ M)	0.20	9.5	46

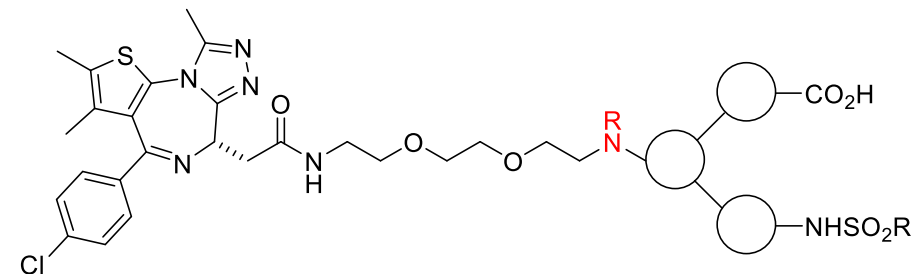
## DNA Exit Vector is Favorable



Binding Affinity	Analogue 3	Analogue 4
E3LX SPR $K_d$ ( $\mu$ M)	0.16	0.14

# Degrader X: Exploratory Binding SAR

## Degraders Have Lower Affinity



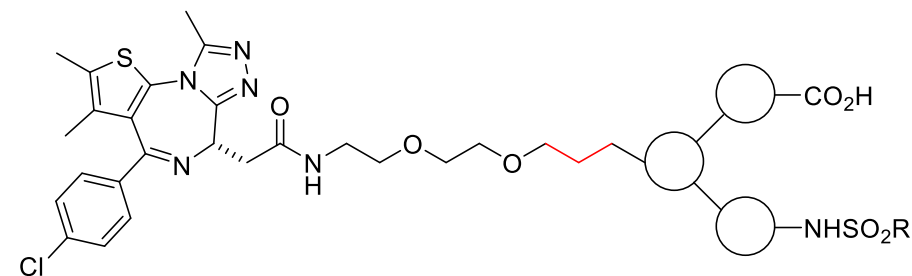
### Binding Affinity

### Degrader X (R = H) and Analogue 1 (R = Me)

E3LX SPR  $K_d$  ( $\mu$ M)

Degrader X = 1.6; Analogue 1 = 6.3

## Methylene Linker Similar to Amine



### Binding Affinity

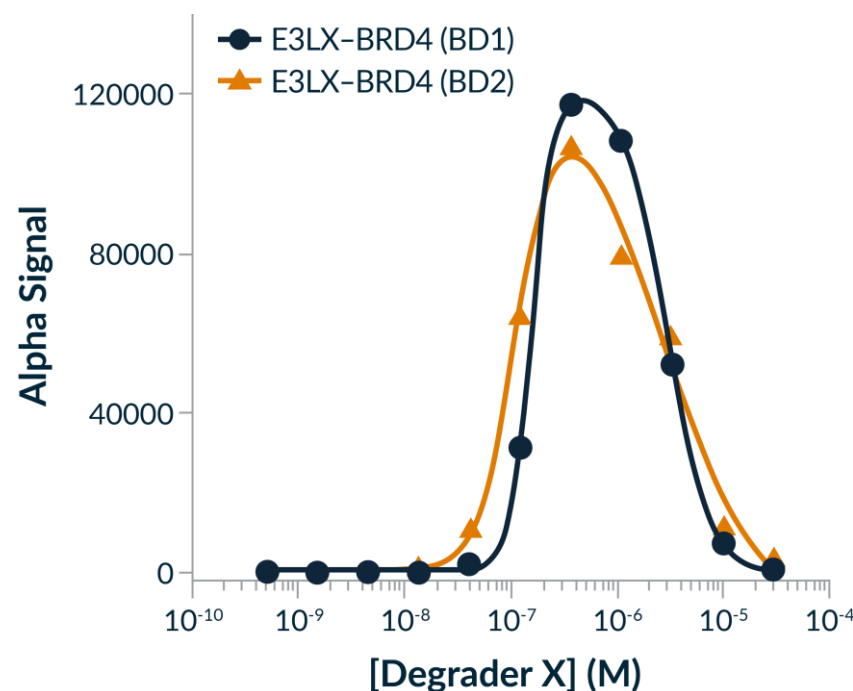
### Analogue 2

E3LX SPR  $K_d$  ( $\mu$ M)

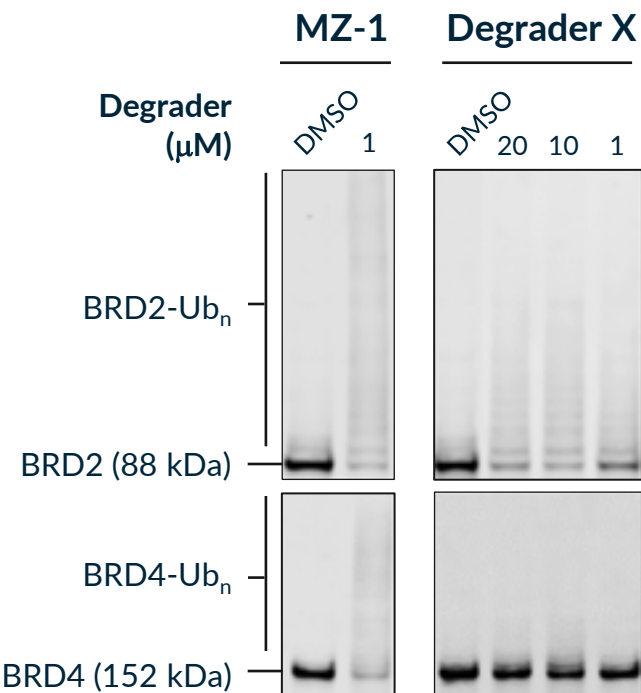
0.89

# Degrader X: Exploratory Cell-free Assays Toward Rapidly Assessing Inducible Degradative Activity

## Ternary Complex Formation by AlphaLISA



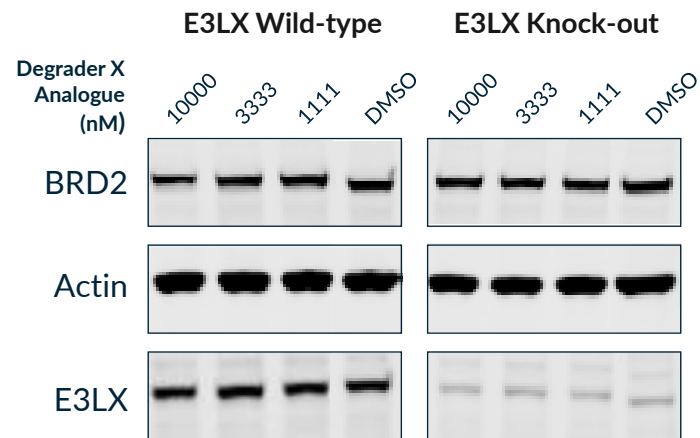
## Cell-free Ubiquitination by Western Blot (WB)\*



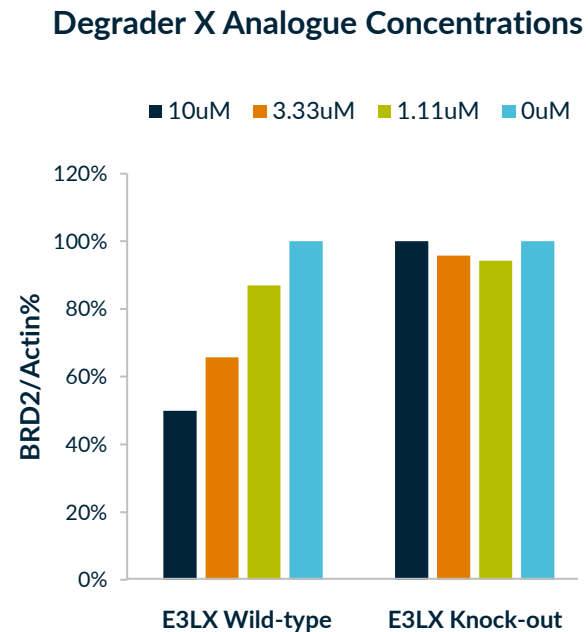
\* Cell lysate derived from OCI-LY10 cells

# Degrader X Analogue: Exploratory Cell-based Assays Toward Rapidly Assessing Inducible Degradative Activity

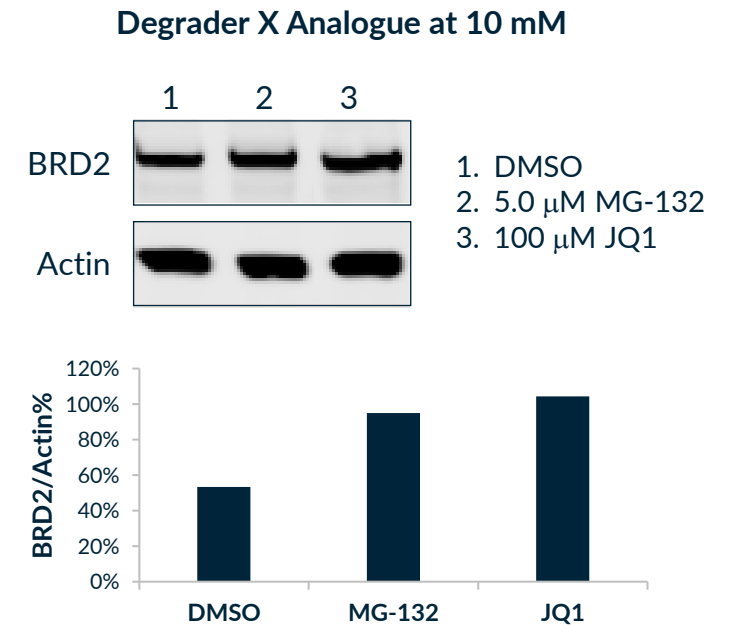
## Cell-based Degradation by WB



## Cell-based Degradation by HiBiT



## Cell-based Degradation Rescue



HEK293 cells used throughout



# Summary and Outlook

- **E3LX**: favorable tissue-selective expression profile was identified by the E3 ligase whole-body atlas at Kymera
- The first SM ligand for E3LX, Ligand X, was identified by DEL selection at GSK
- The first E3LX–Ligand X complex structure by X-ray solved at Kymera
- The first E3LX-based exploratory tool degraders exhibit UPS-mediated degradation
- Improvement of physicochemical and pharmacological properties of new E3LX ligands and E3LX-based degraders needed to further harness this novel E3 ligase

THANK YOU

Q & A

The bottom section of the slide features a wide banner. On the left, the KYMERA logo is displayed, with a stylized orange 'K' icon followed by the word 'YMER A' in white. The background of the banner is a composite image: the left side shows abstract, glowing blue and purple lines, while the right side shows a dark night sky with stars and a constellation of lines, with a silhouette of a forested mountain range at the bottom.

KYMER A