

Ultra-High-Throughput Miniaturized Cell-Based Assays to Discover CDK2 Molecular Glue Degraders

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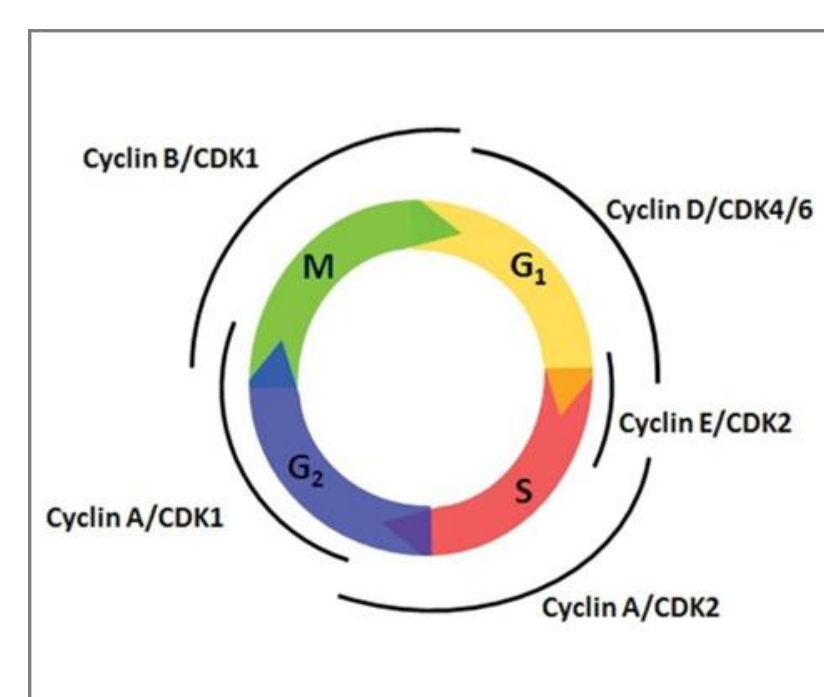
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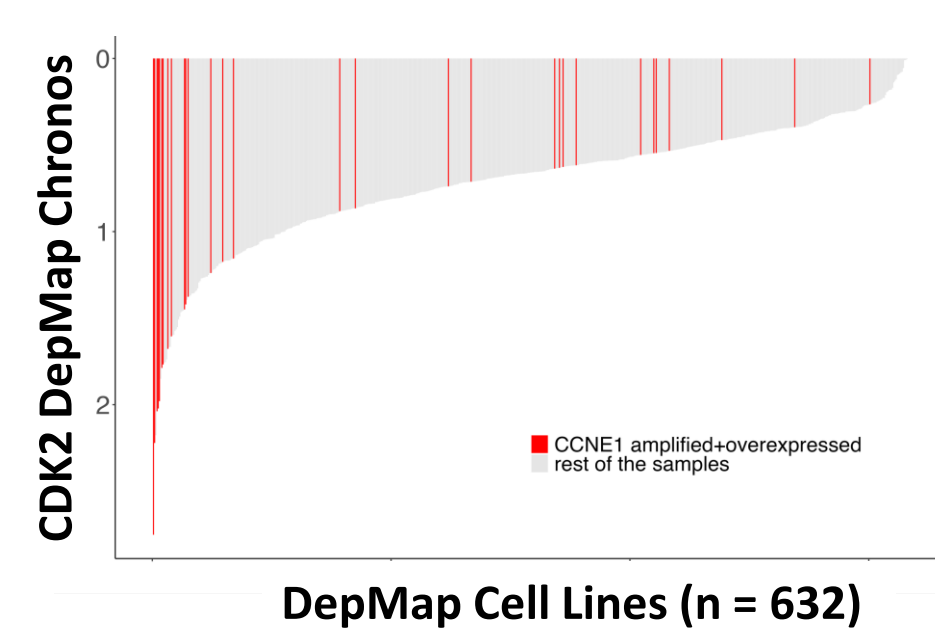
Introduction

- CDK2 associates with cyclin E (CCNE1) to regulate cell cycle progression. Aberrant Cyclin E levels activate CDK2 and correlate with poor survival (subset of Ovarian and Breast)
- Tumor cell lines with CCNE1 amplifications are sensitive to loss of CDK2
- CDK2 degrader has potential for superiority over inhibitors by (1) selectivity degrading CDK2 without modulating other CDKs and (2) disrupting CDK2 complexes
- Human cancers with cyclin E overexpression/amplification may be sensitive to loss of CDK2. Patients on CDK4/6 inhibitors for ER+HER- breast cancer develop resistance which can be driven by cyclin E overexpression

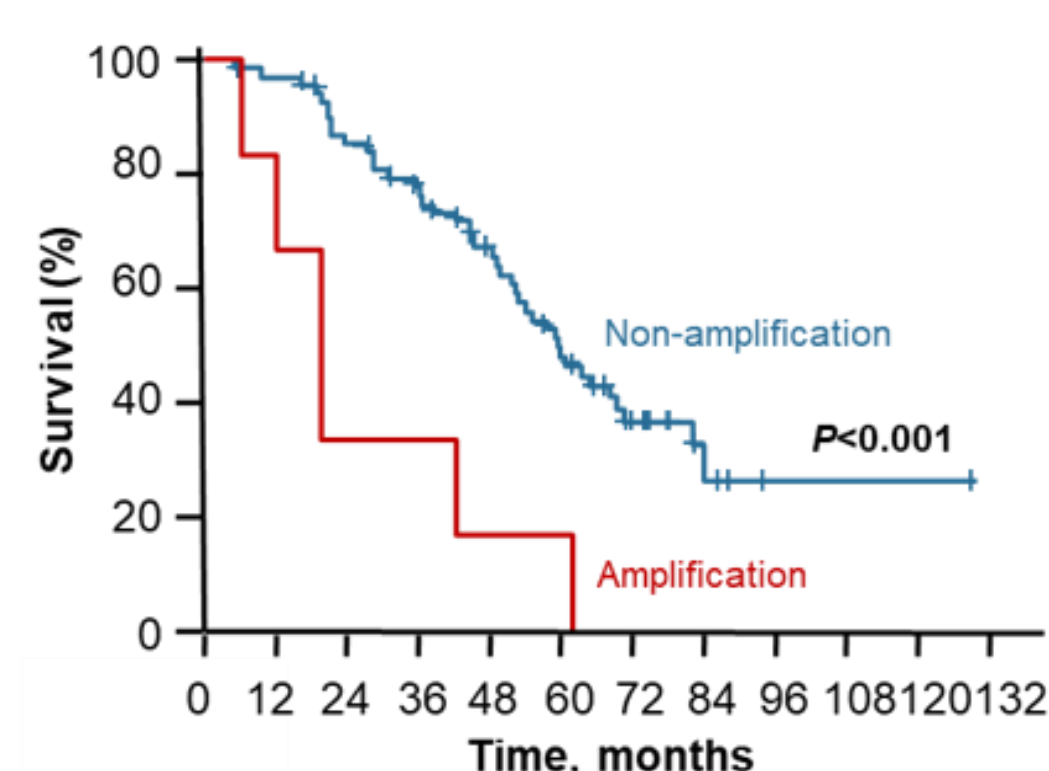
CDK2 Regulates G1/S Cell Cycle Transition



Tumor Cell Lines with CCNE1^{amp} Sensitive to CDK2



CCNE1^{amp} Correlates with Poor Survival (ovarian)



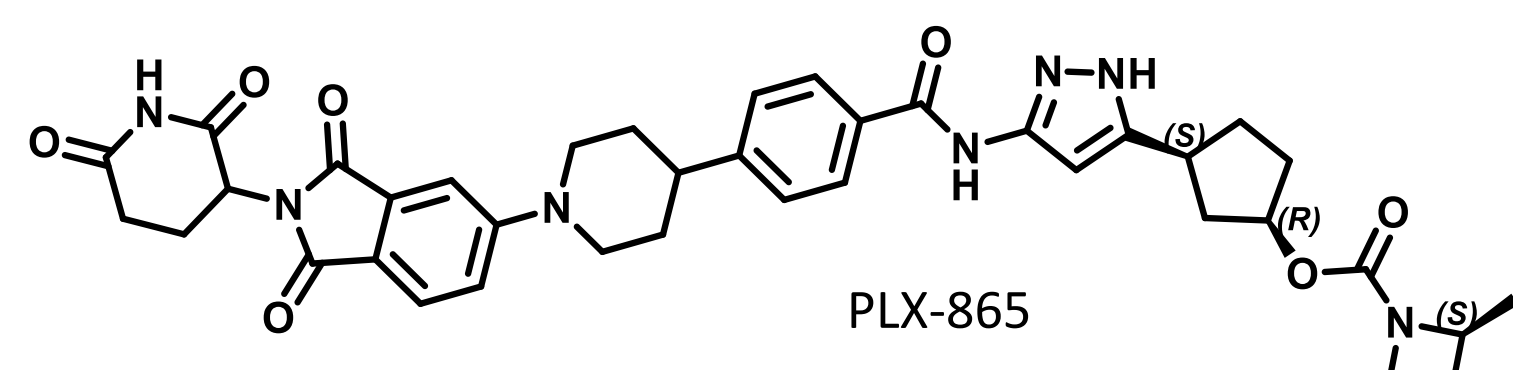
Tumor Type	CCNE1 ^{amp} Frequency*
Uterine	40%
Ovarian	19%
Gastric	11%
Esophageal	8%
Endometrial	8%
Sarcoma	8%
Bladder	6%
NSCLC	5%

*cBioPortal frequency of CCNE1 amplification

Benefits of a CDK2 degrader:

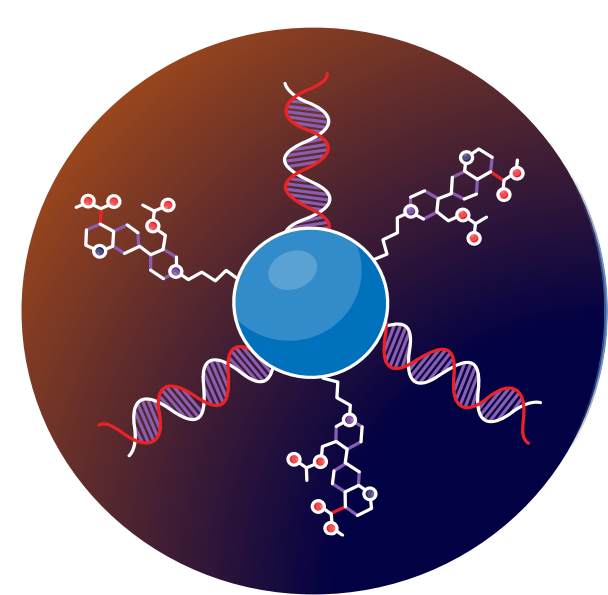
- Increase selectivity
- Improve efficacy from reducing CDK2 levels to drive deeper pRb suppression
- Address potential future resistance mechanisms

Identification of Selective CRBN-based CDK2 PROTAC

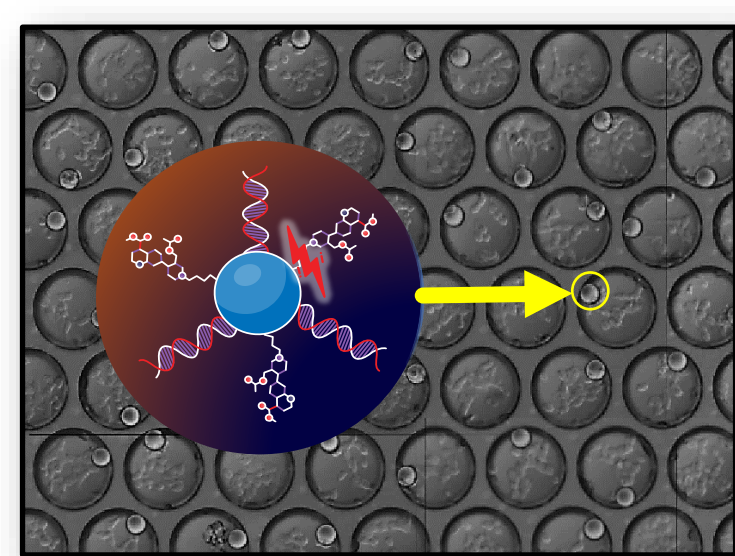


- Potent CDK2 degrader
- in vivo* CDK2 modulation in tumor model (IP dosing)
- Suboptimal selectivity (CDK1 inhibition/degradation)
- Highly lipophilic (LipE < 3) with limited oral exposure

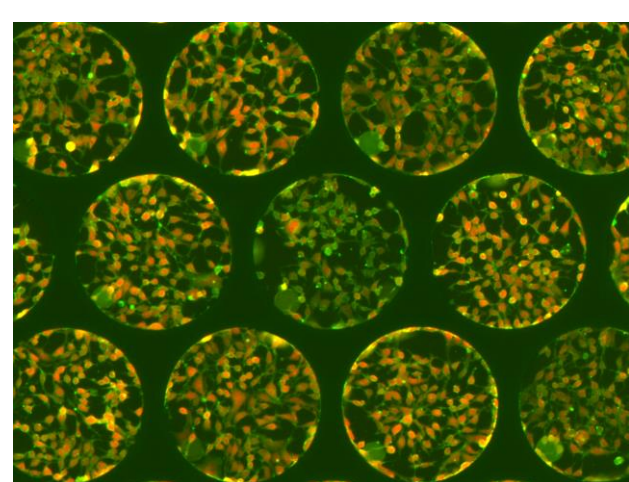
Picowell Platform



88,000 Picowell Device



1 Bead / 1 Compound Per Well

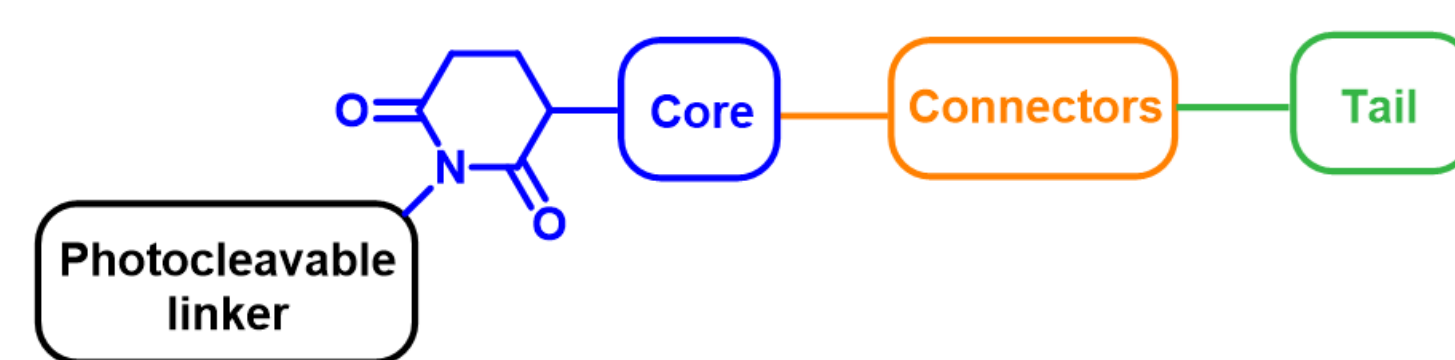


Protein of Interest Depletion



Decoding – Compound identification

Cereblon-based Compound Library



Library distribution

Property	Mean
logD	2.5
logP	2.8
MW	486.7
HBD	1.4
HBA	7.8
TPSA	94.1
Rotatable Bonds	8.7
Fraction sp3	0.36

Cereblon binder / Core

- Literature and proprietary scaffolds

Connector

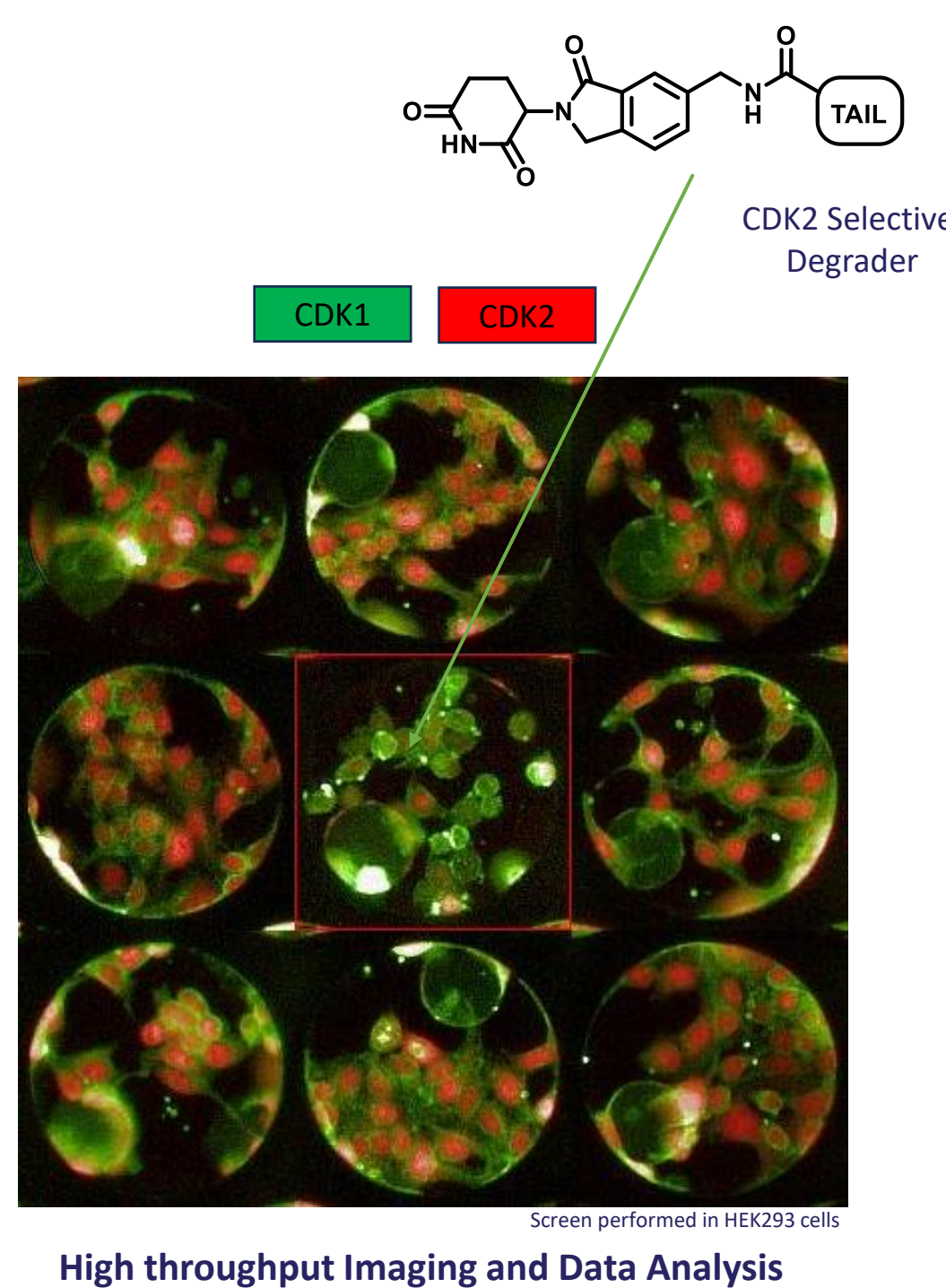
- Allow for flexible chemistry and installation of broad diversity in the tail region

Tail

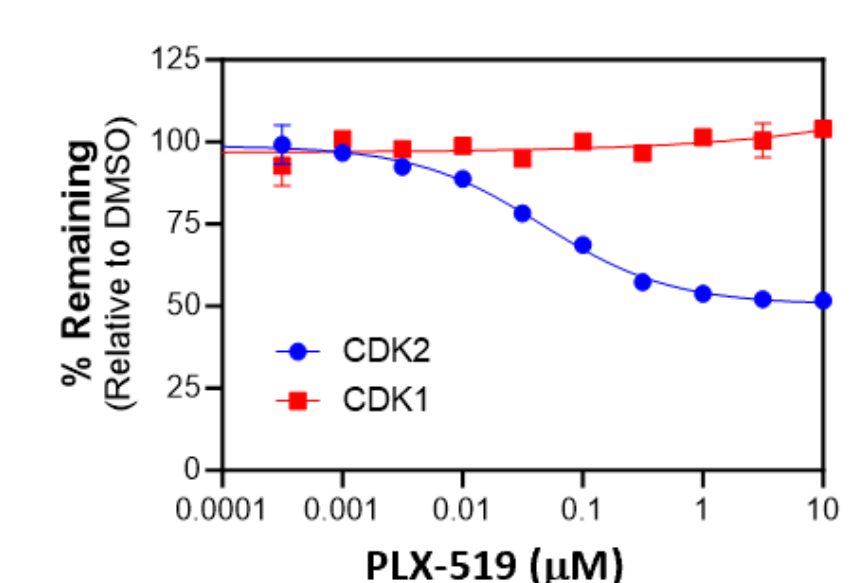
- Interacting group that reaches out to interact with the protein of interest
- Consists of broad diversity, or specific groups based on targets of interest to Plexium

Our CRBN bead library has reached one million compounds

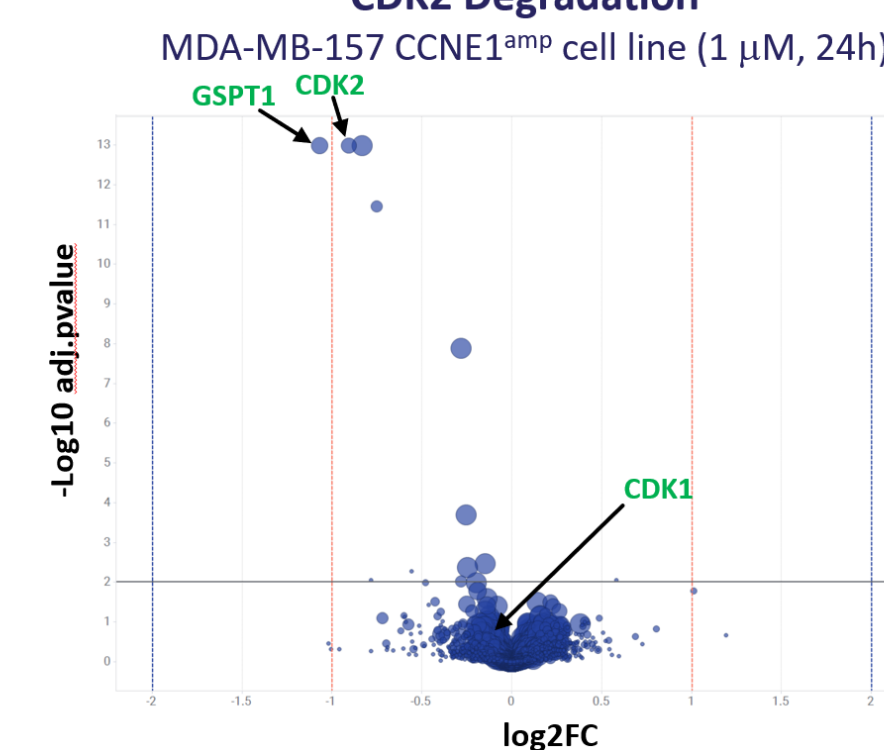
Hit Identification – PLX-519



Selective Degradation HiBiT cell line (24 hrs)



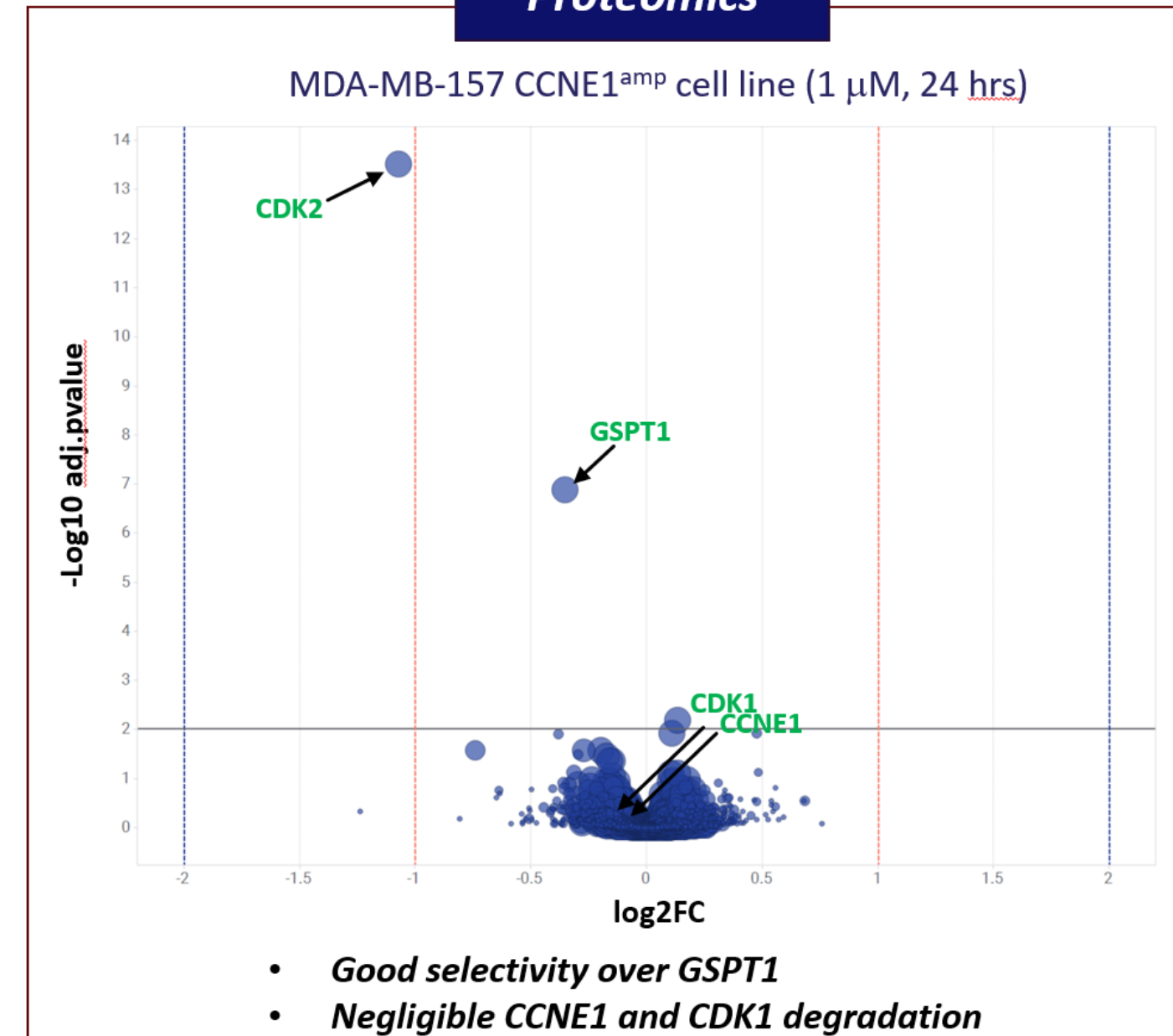
CDK2 Degradation



Hit Optimization – PLX-322

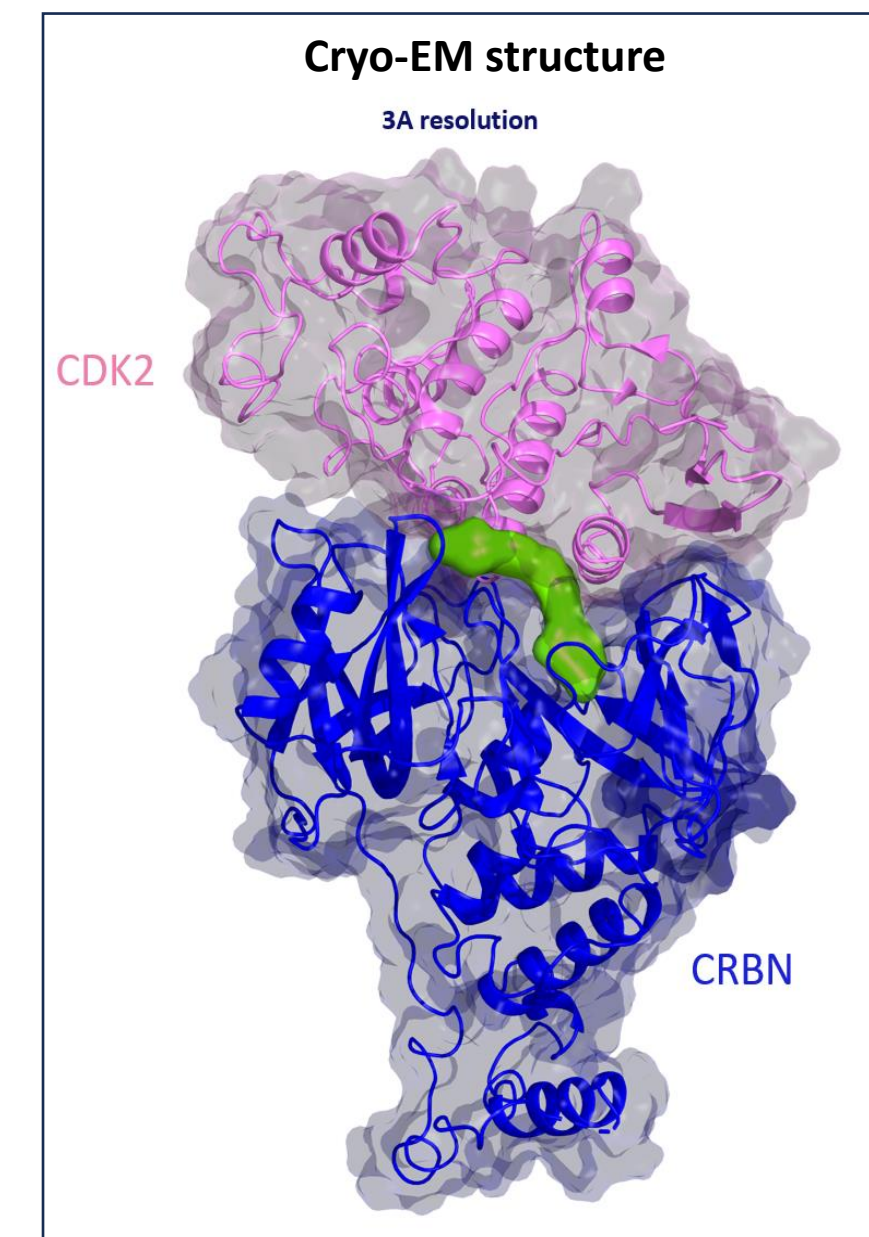
	PLX-519	PLX-581	Novel Scaffold PLX-322
CDK2 HiBit DC ₅₀ , D _{max} , CDP	79 nM, 46%, 4.1	18 nM, 68%, 6.6	61 nM, 61%, 5.5
CDK1 / GSPT1	GSPT1 degradation	>10 μM	>10 μM
CRBN HTRF EC50	1.6 μM	0.84 μM	0.58 μM
HLM CL (mL/min/kg)	< 8.6	13.1	<8.6
Kin Solubility 7.4	44 μM	<2 μM	64 μM
Mouse PK	NA	NA	Good exposure

Proteomics



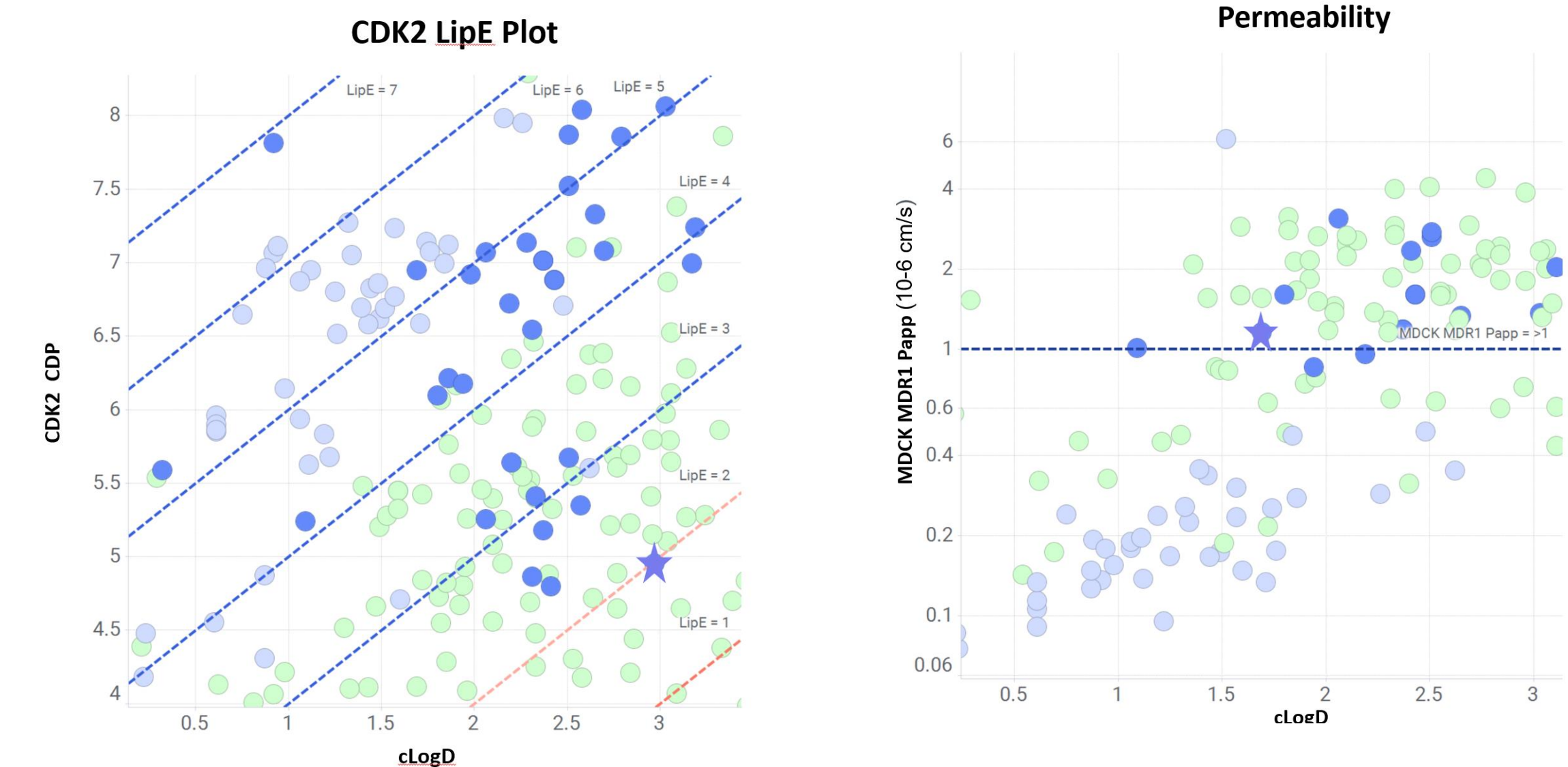
- Good selectivity over GSPT1
- Negligible CCNE1 and CDK1 degradation

Cryo-EM structure

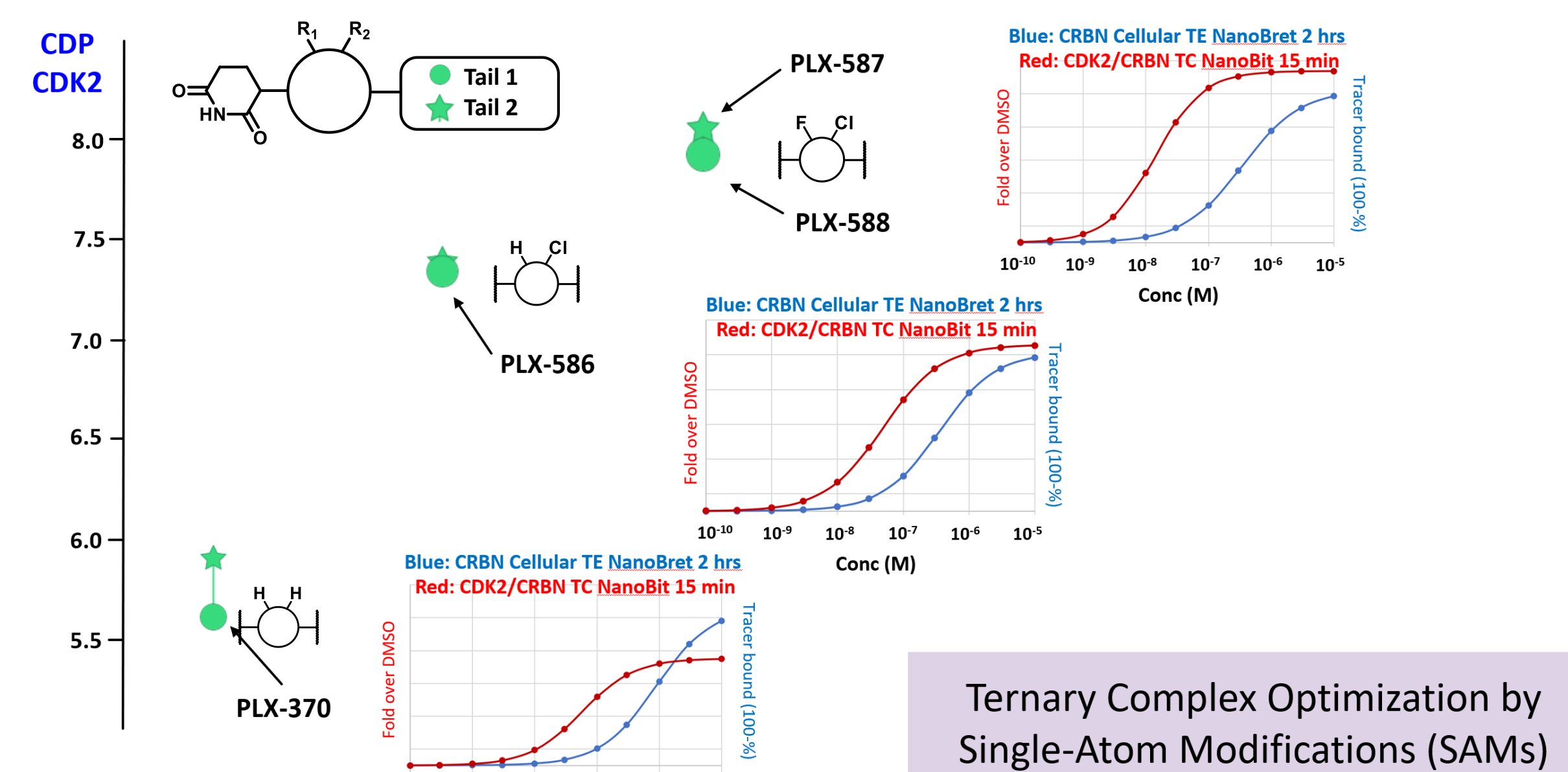


Suboptimal potency observed for 62322 in CCNE1^{amp} cell lines

Identification of a more drug-like series



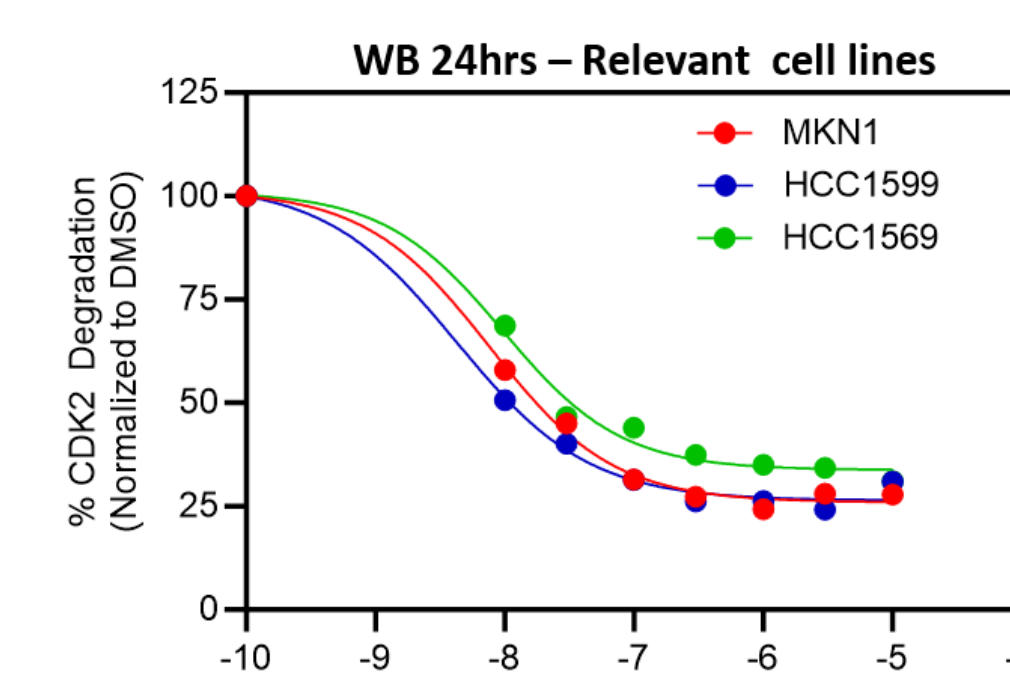
Cell Ternary Complex Formation



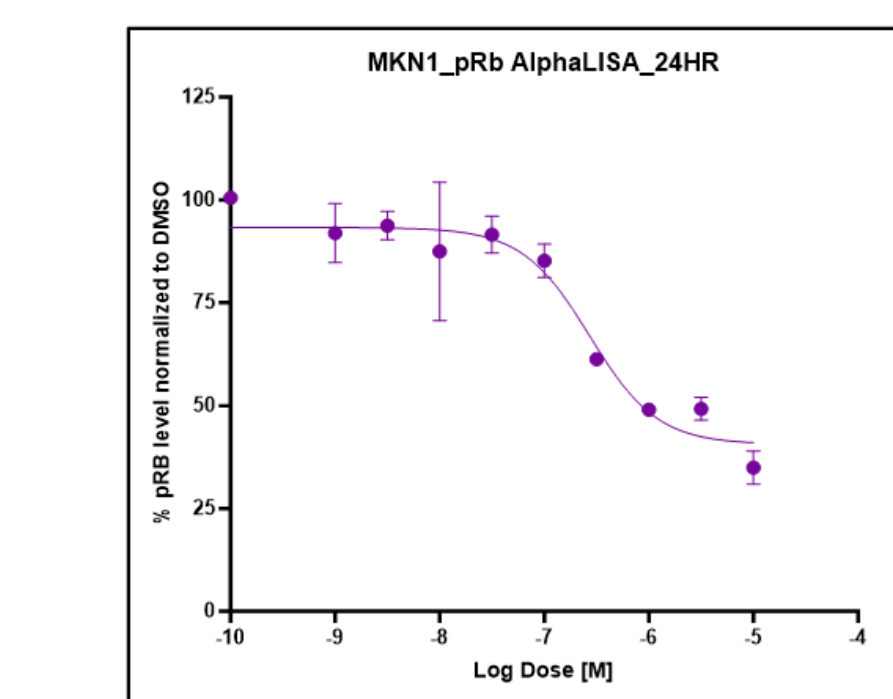
Ternary Complex Optimization by Single-Atom Modifications (SAMs)

Identification of PLX-587

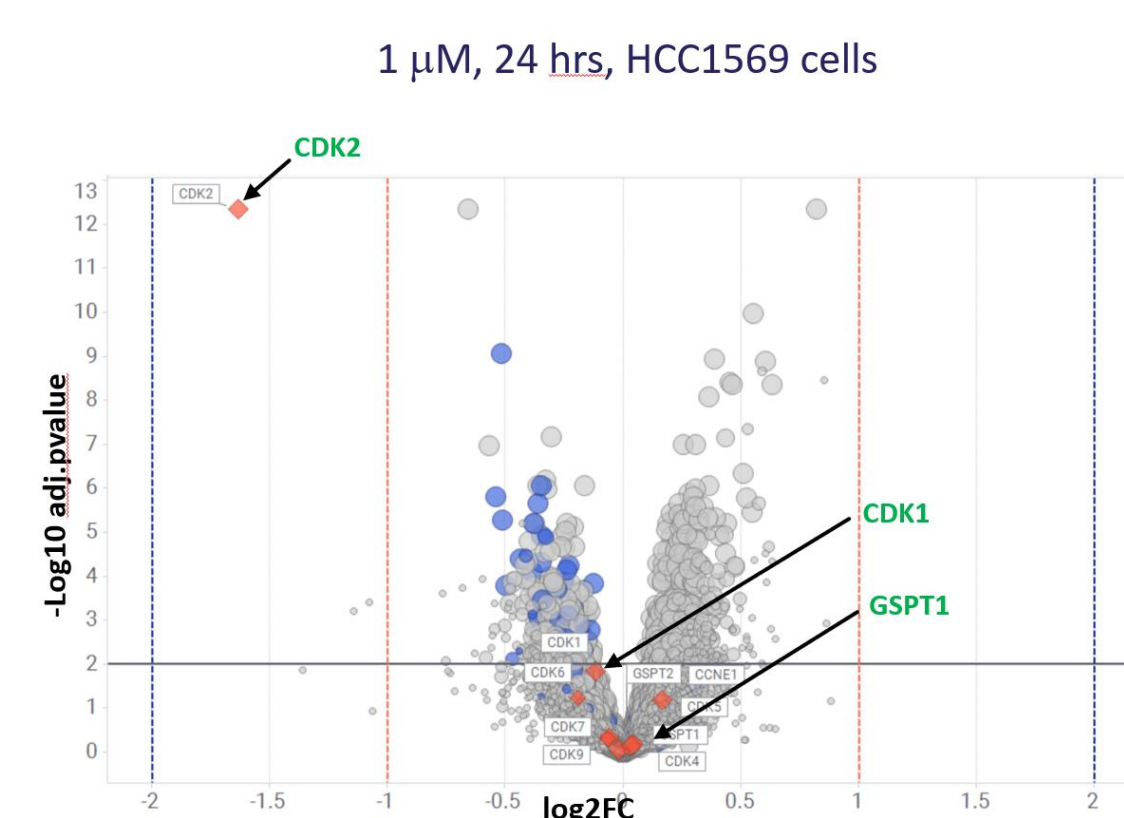
	MW	<550
CRBN HTRF	0.361 μM	
CDK2 HiBit 24h DC ₅₀ , D _{max} , CDP	0.008 μM, 80%, 8.0	
GSPT1 HiBit 24h DC ₅₀ , D _{max}	>10 μM, 26%	
<i>In vitro</i> ADME	Good	
Mouse PO 10 mpk	Good	



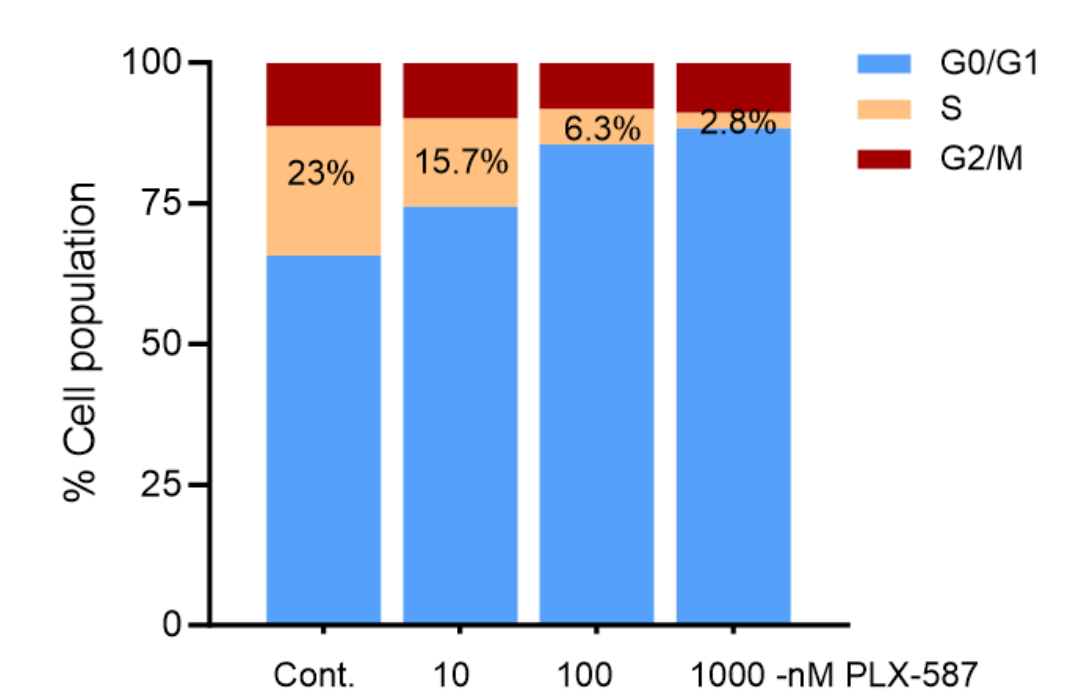
CDK2 24h DC₅₀, D_{max} = 5-10 nM, 70-75%



pRb 24h IC₅₀, I_{max} = 271.5 nM, 65%



MKN1_48HRS treatment



PLX-587 is currently being evaluated in different *in vivo* models

Conclusions

- Ultra high-throughput miniaturized picowell screen provided multiple starting points for developing a CDK2 CRBN molecular glue.
- Established a medicinal chemistry path leading to PLX-587 that demonstrates an efficient and orally bioavailable selective CDK2 degrader.
- TGI studies CCNE1^{amp} breast cancer xenograft are ongoing (single agent/combo).