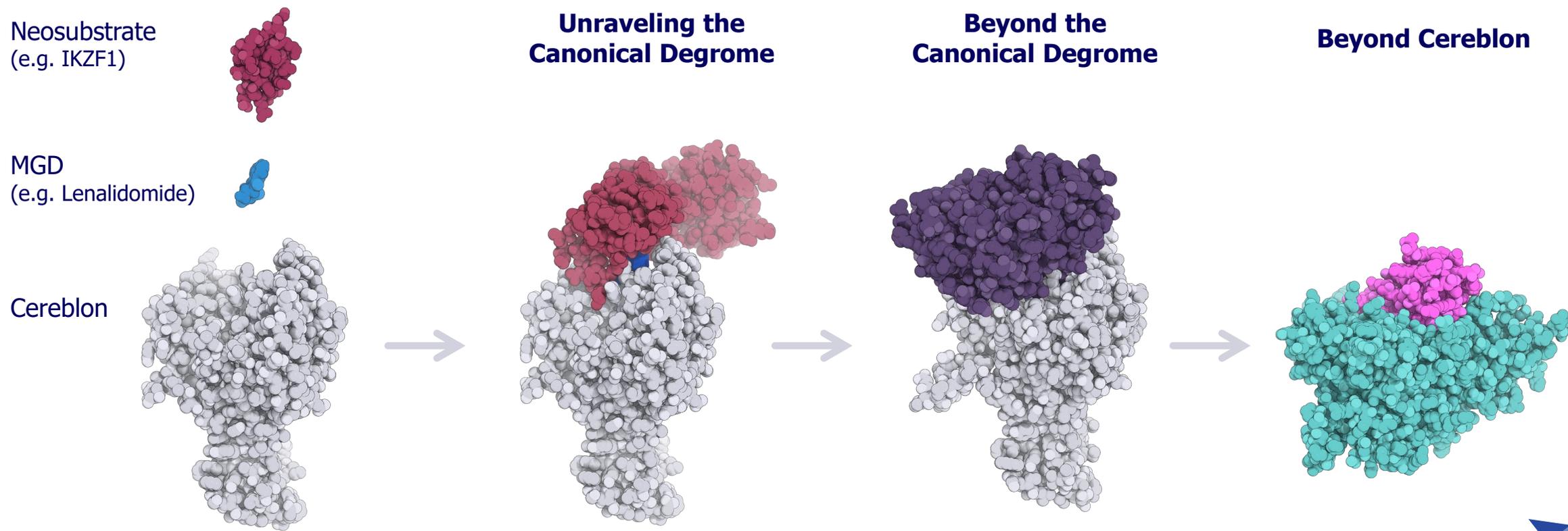


Teaching CRBN New Tricks

Georg Petzold | Keystone Symposia Proximity-Induced Therapeutics | January 23rd, 2024



Our Rational Approach to Unleash the Full Potential of MGDs



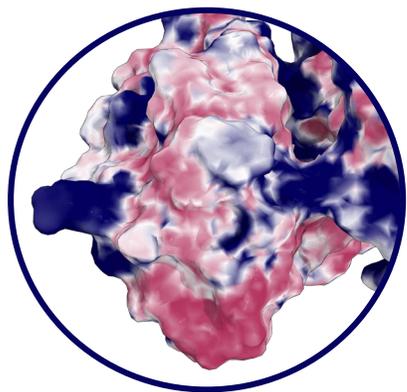
Expanding the Degradable Proteome

Chemical Space

Target Space

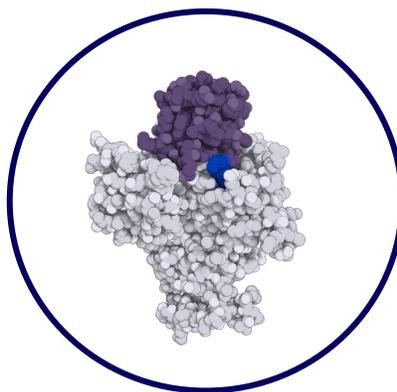


The QuEEN™ Engine – Unique Capabilities for MGD Discovery and Design



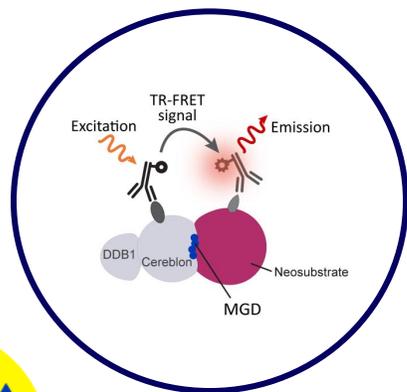
AI/ML

In silico degron & ternary complex discovery using proprietary AI-powered algorithms



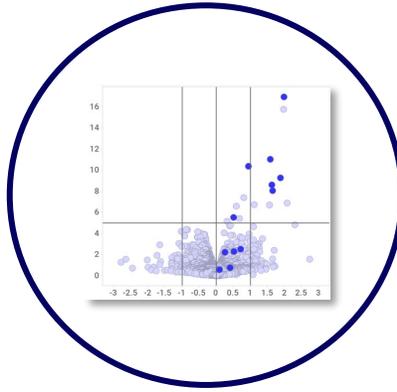
Structure-based Design

Proprietary database of >100 cryo-EM and crystal structures to enable rapid structure-based MGD design



Proximity Screening

Specialized suite of biochemical and cellular assays to assess proximity and degradation in high throughput



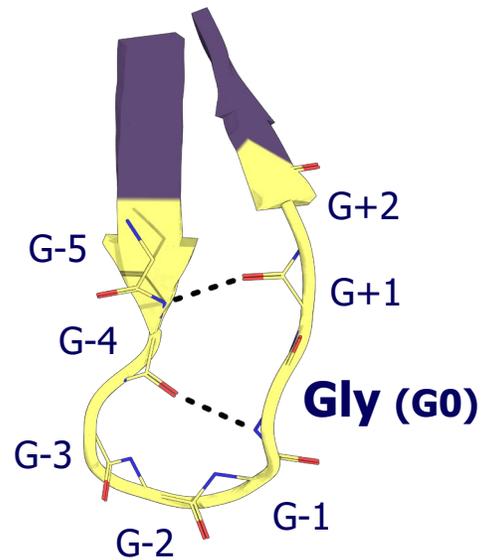
Proteomics

Integrated proteomics engine and database to identify novel targets and to explore cellular complex formation and degradation

Neosubstrates Engage CRBN Through a Shared Structural Motif

The G-loop degron: a β -hairpin α -turn with a conserved glycine

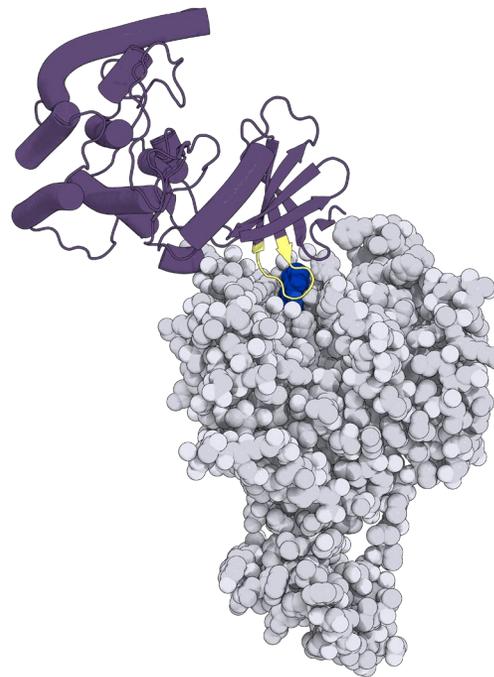
G-loop motif



CK1a	INITN G EE
GSPT1	VDKKS G EK
ZNF692	QCEIC G FT
SALL4	VCSVC G HR
IKZF2	HCNQC G AS

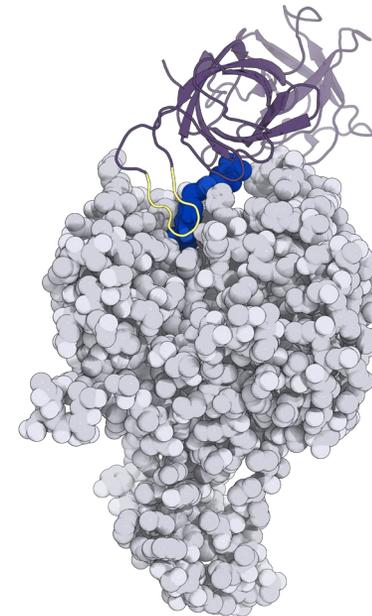
Structurally characterized neosubstrates in the public domain

CK1 α



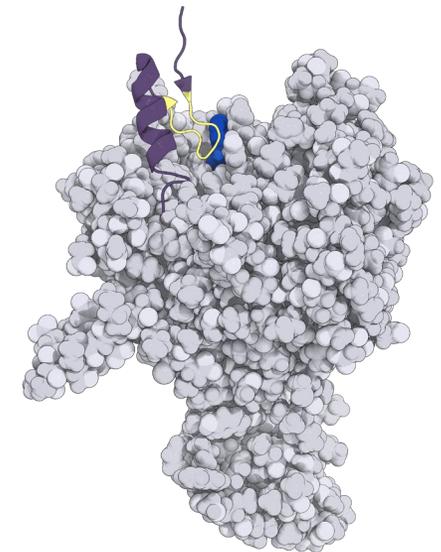
Petzold et al. 2016

GSPT1



Matyskiela et al. 2016

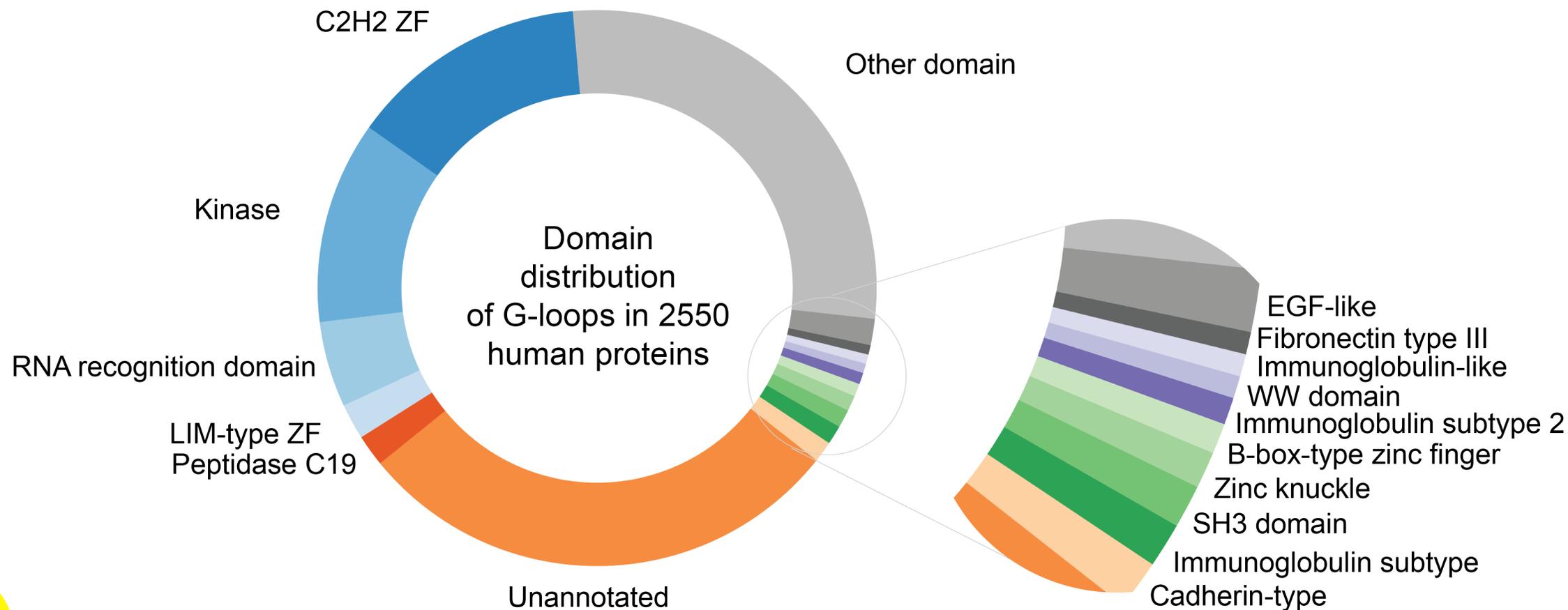
C2H2 ZFs



Sievers/Petzold et al. 2018

Mining the Human Proteome for Canonical G-loop Degrons

Over 2,500 human proteins contain a G-loop-like motif, many in undruggable domains

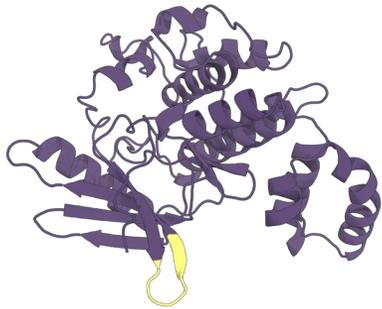


* Based on AlphaFold2 structures



The G-loop Degron Recruits Different Domain Types to CRBN

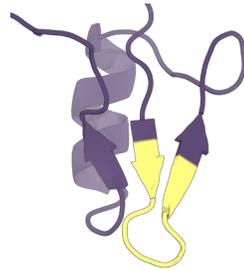
Mined G-loops validate in proximity readouts (NanoBRET, TurboID, ...)



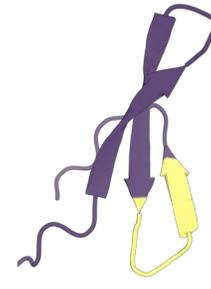
Kinases (beyond CK1α)



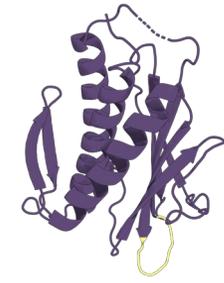
RNA-recognition domain



BRK domain



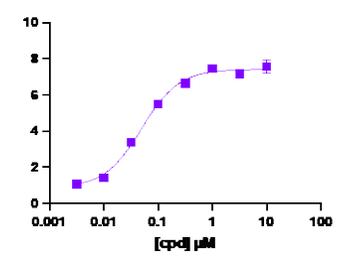
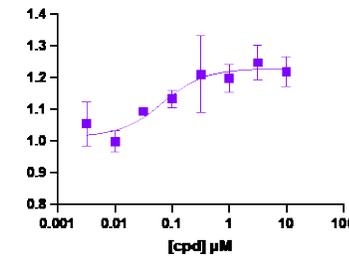
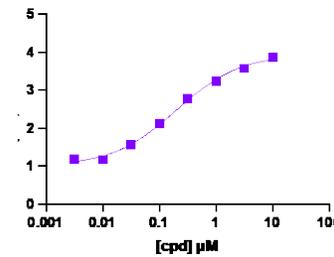
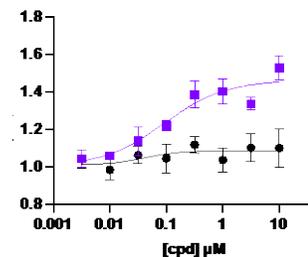
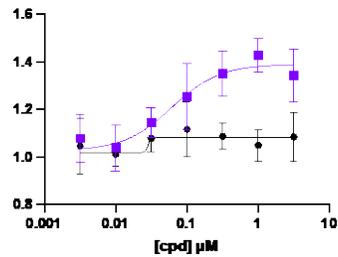
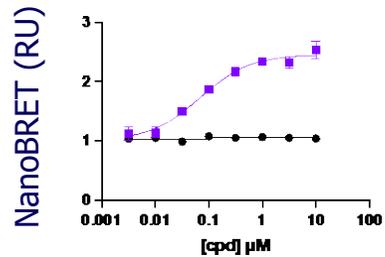
WW domain



Horma domain



HUP domain

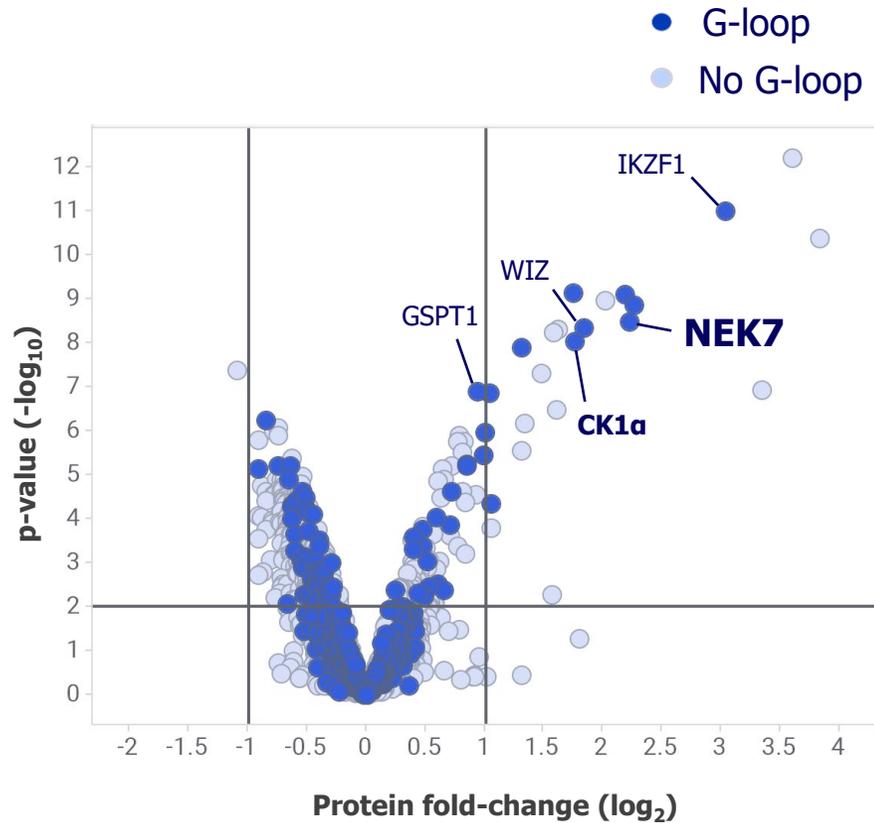


■ WT
● G/N mutant

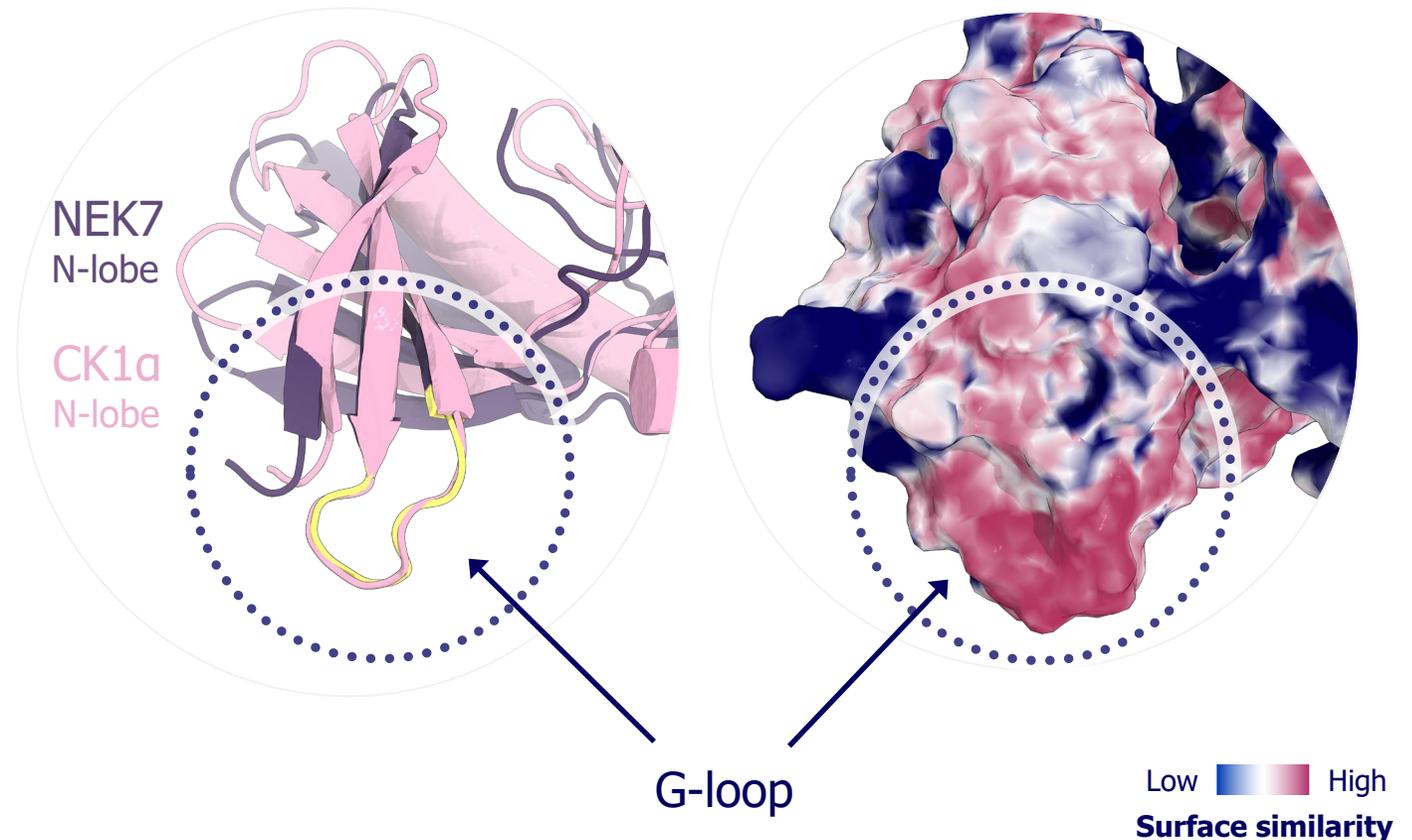
Engineering Selective MGDs for G-loop Targets – Exemplified by NEK7

NEK7 and CK1α show high degree of G-loop surface similarity

Promiscuous MGDs induce proximity of multiple G-loop targets to CRBN

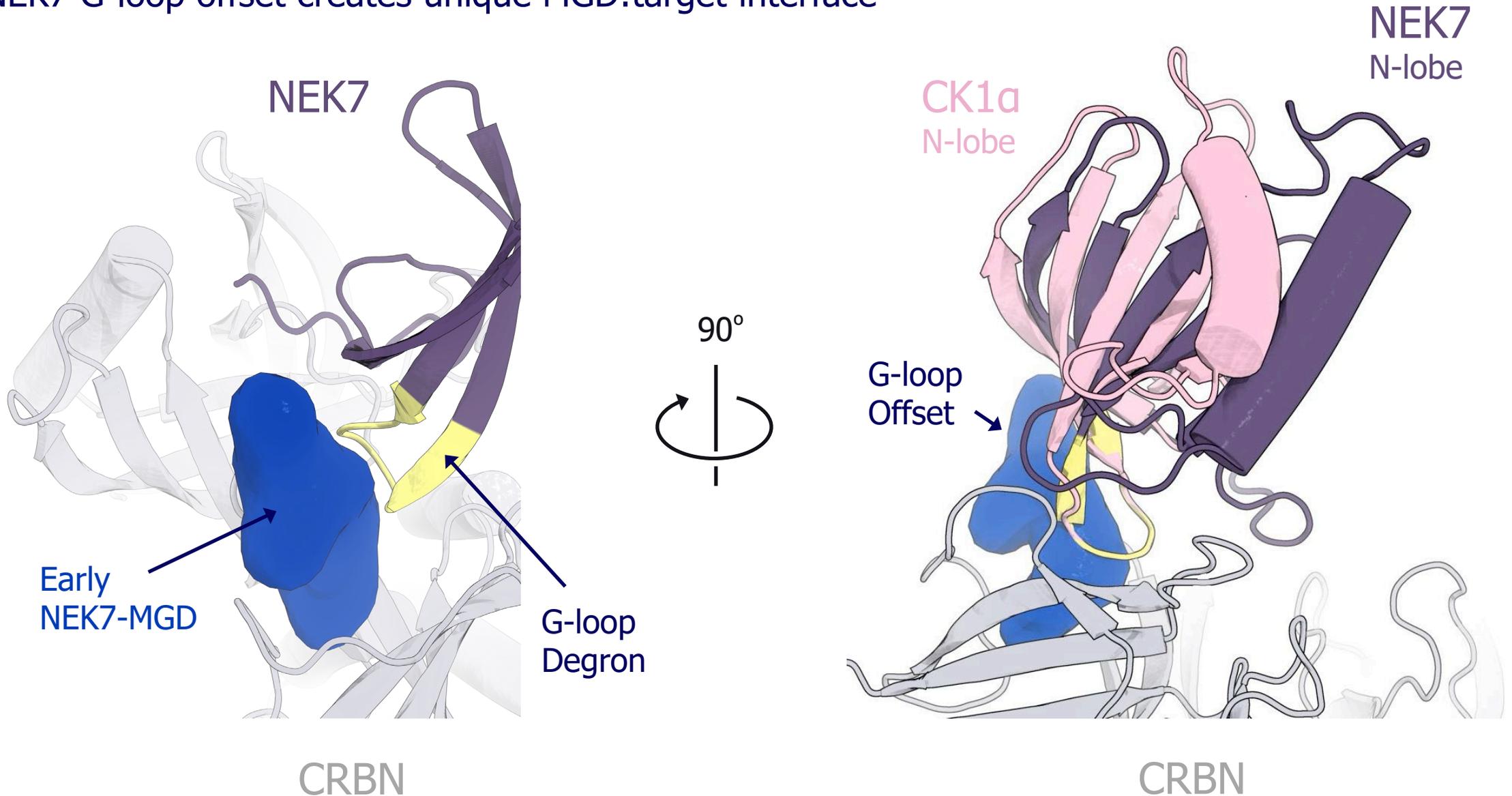


NEK7 and CK1α share high G-loop surface similarity



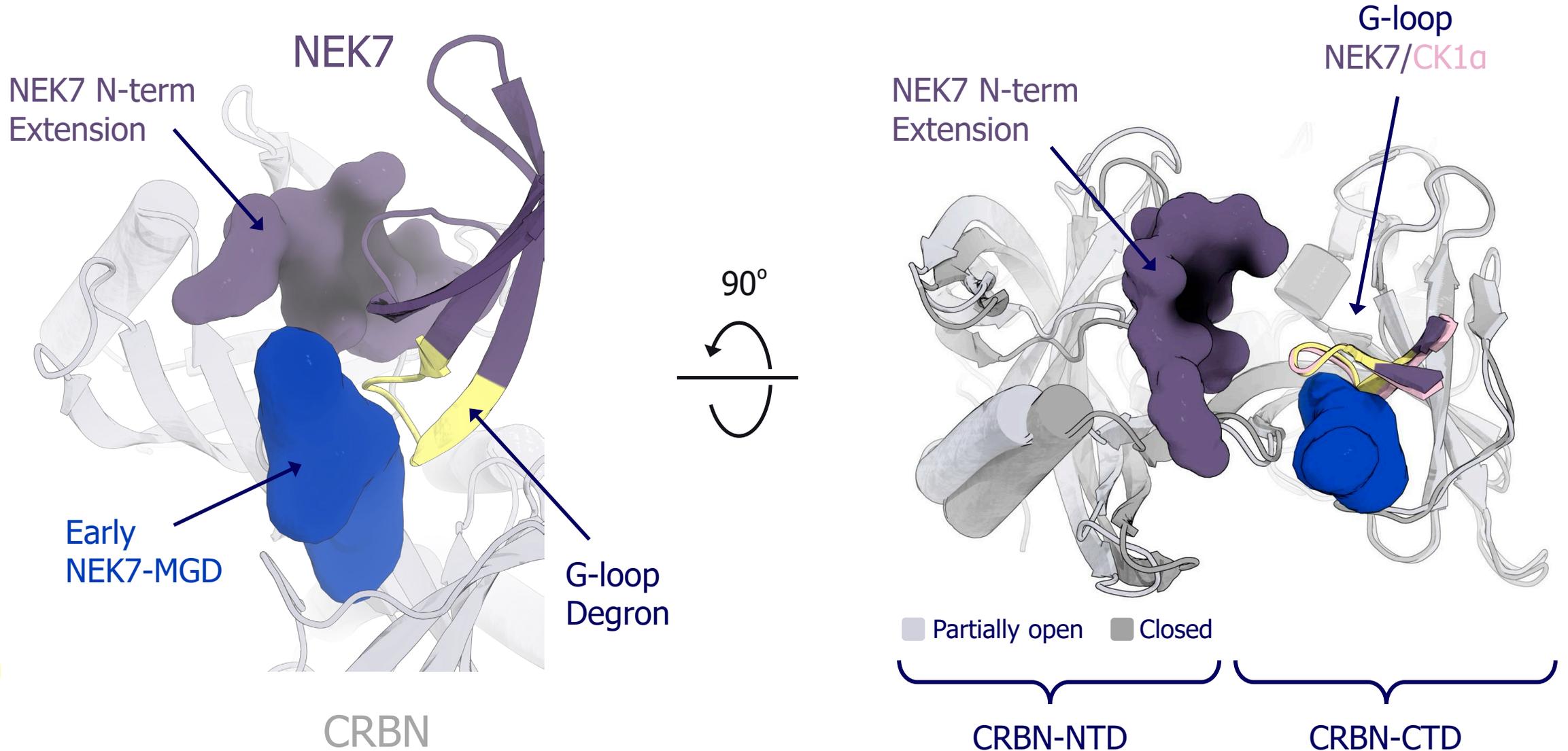
Early Structural Insights into NEK7 Binding Enabled Rational MGD Design

NEK7 G-loop offset creates unique MGD:target interface



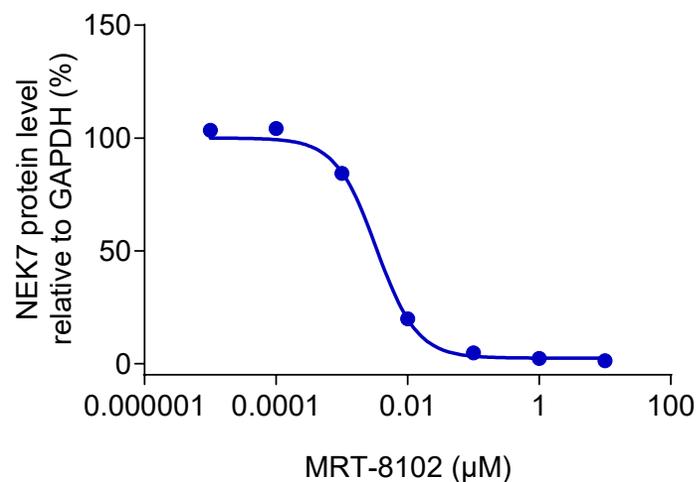
NEK7 Engages CRBN in a Partially Open Conformation

A larger spectrum of CRBN conformations are accessible for TPD



MRT-8102 is a Potent and Selective NEK7-directed MGD

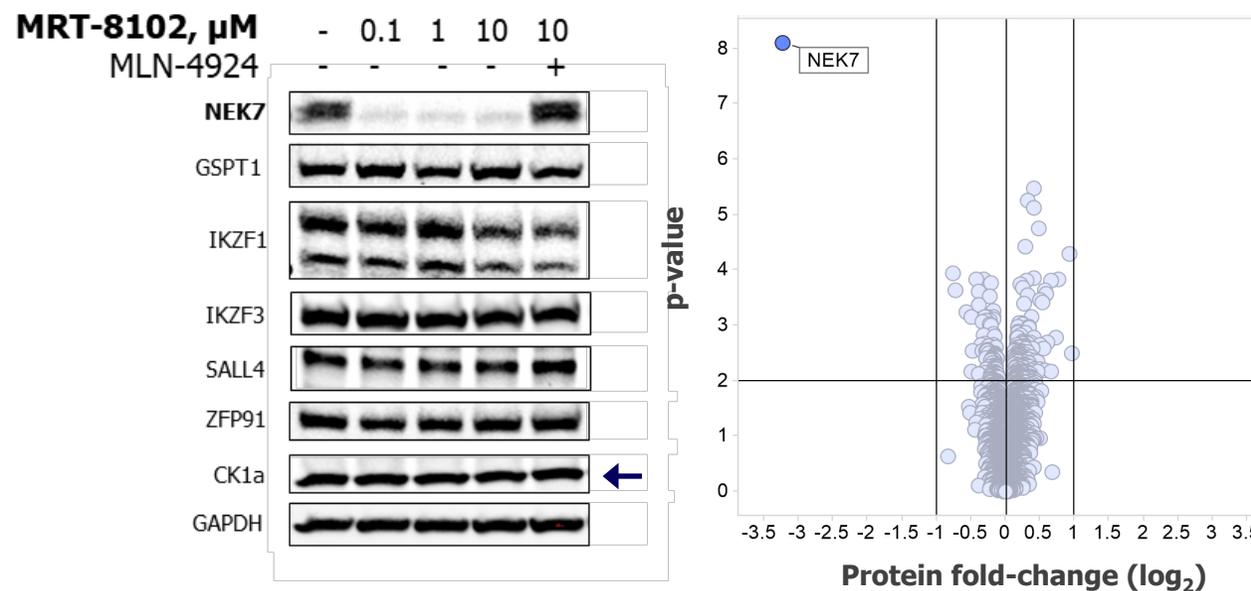
MRT-8102 is a potent NEK7-directed MGD



in vitro data

CRBN binding, IC ₅₀	200 nM
Degradation, DC ₅₀ / D _{max} (hPBMC; 24hr)	10 nM / 89 %

MRT-8102 induces selective NEK7 degradation and has favorable ADME/DMPK properties

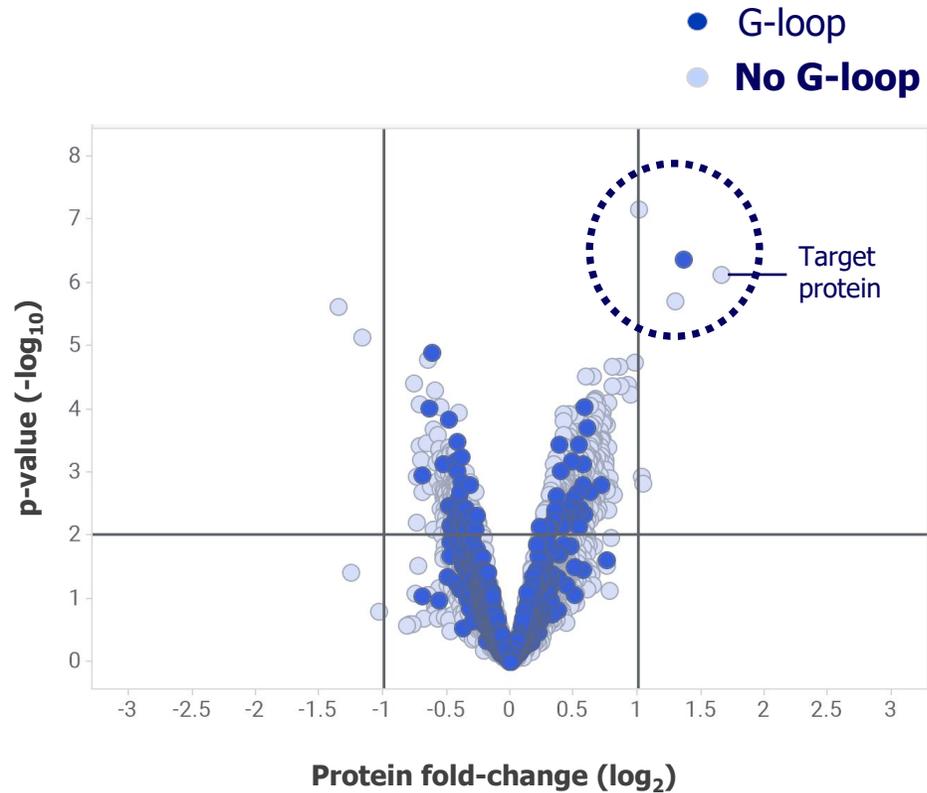


ADMET profile

CEREP panel	No inhibition
hERG inhibition patch clamp	EC ₅₀ > 30 μM
Oral bioavailability	Yes

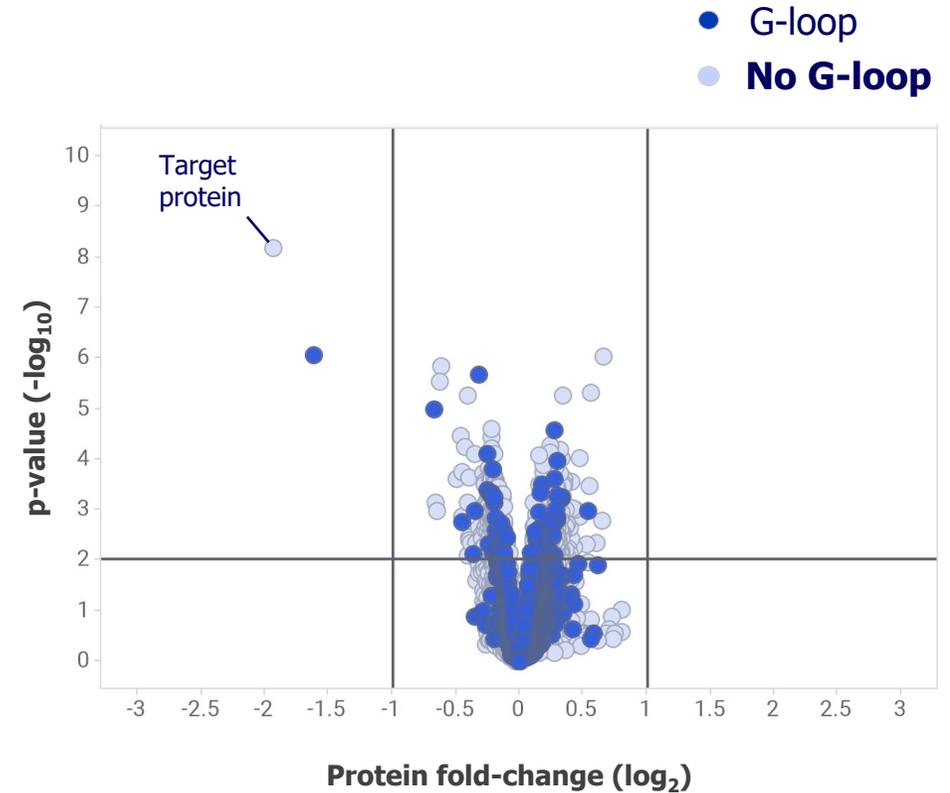
Non-G-loop Targets can be Recruited to CRBN and Degraded

Enrichment of non-G-loop proteins in CRBN proximity-ligation



TurboID-CRBN (CAL51)

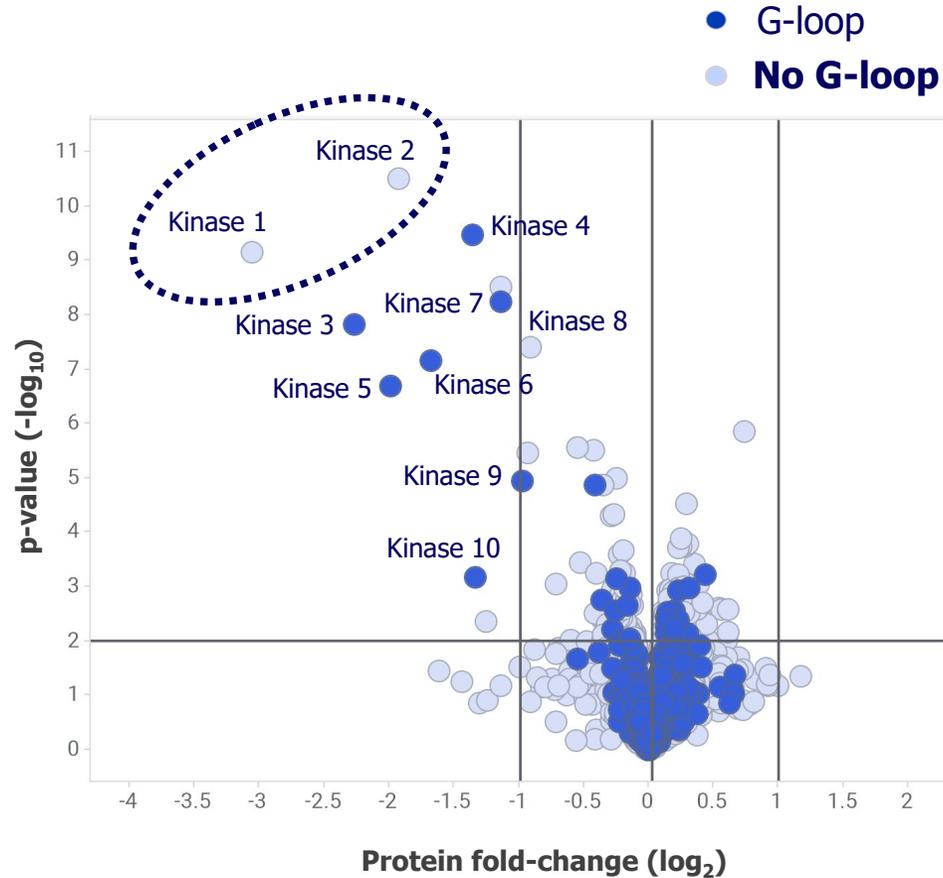
Degradation of a non-G-loop target in TMT-proteomics



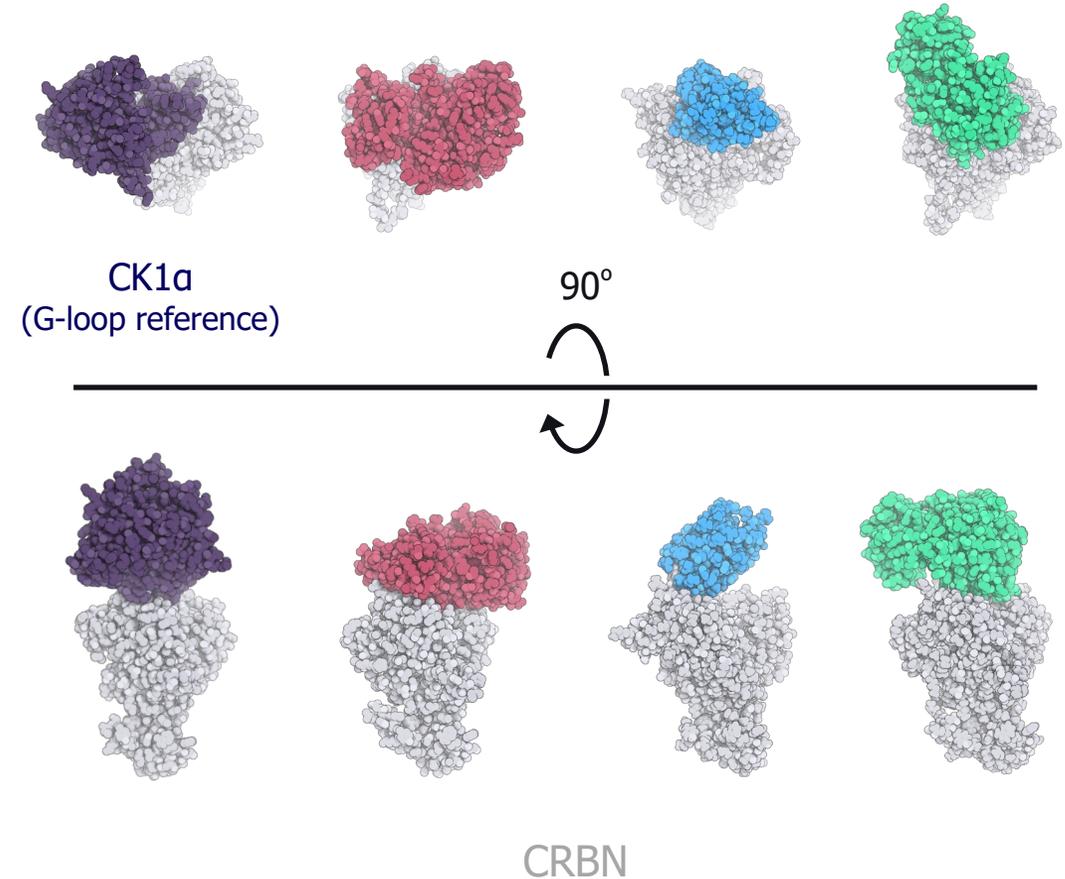
TMT-Proteomics (Jurkat)

Non-G-loop Targets can be Recruited to CRBN and Degraded

Promiscuous kinase degrader



Kinases engage CRBN through canonical and non-canonical binding modes



Novel Binding Modes Employ Otherwise Undruggable Surface Patches

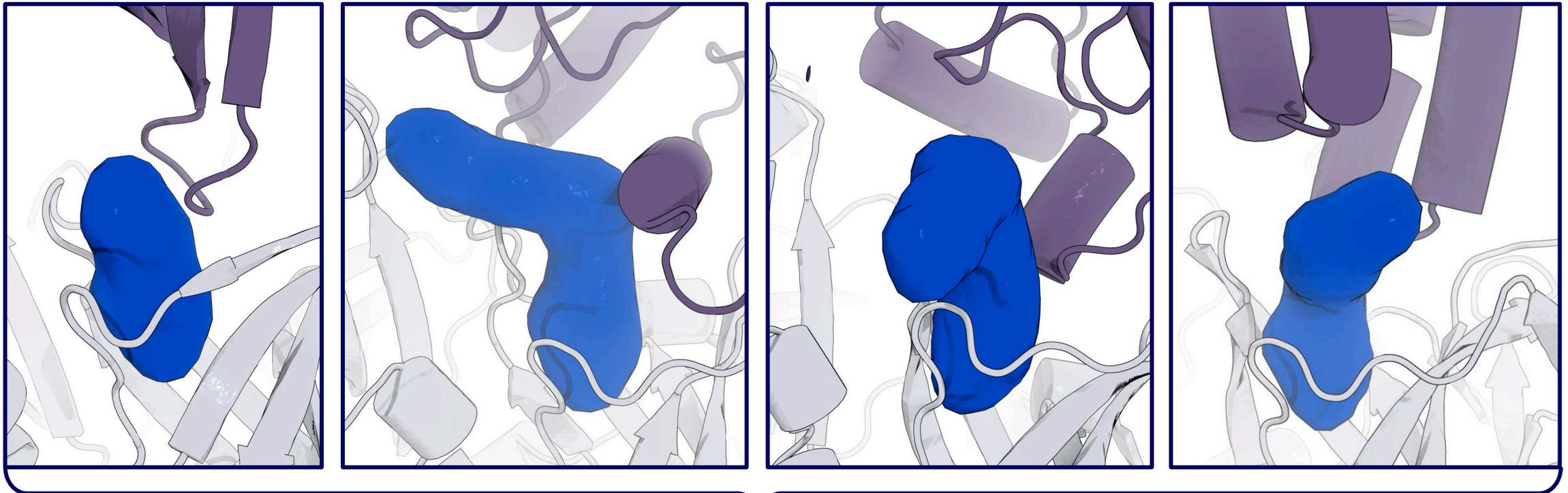
Surface complementarity with CRBN:MGD drives target engagement

Canonical
G-loop degron

Novel binding mode
Type 1

Novel binding mode
Type 2

Novel binding mode
Type 3

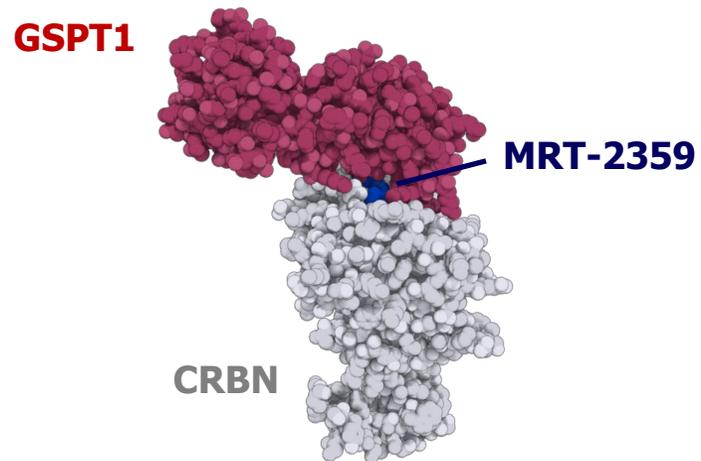


CRBN:MGD

QuEEN™ AI Finds Degrons Using Surfaces

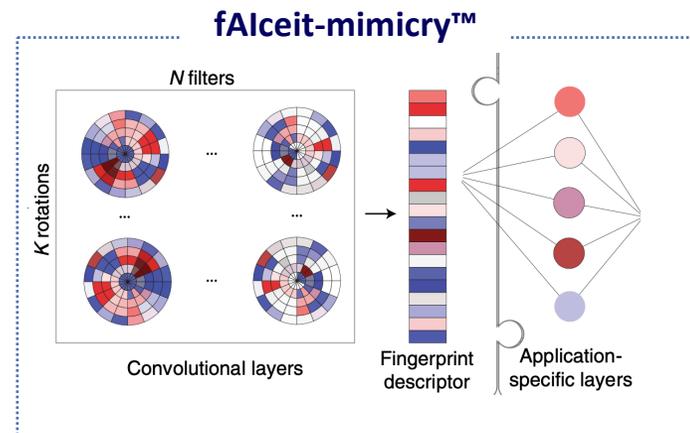
Leverage knowledge of ternary complex structures

Proprietary ternary complexes
X-ray & cryoEM



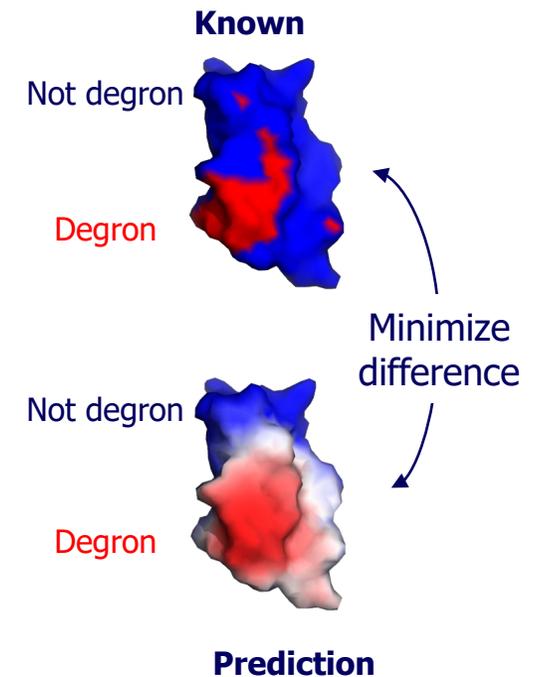
Algorithms tailored to degron discovery

Ultra-fast fingerprint search for surfaces that mimic known degron surfaces



Expand analysis across the proteome

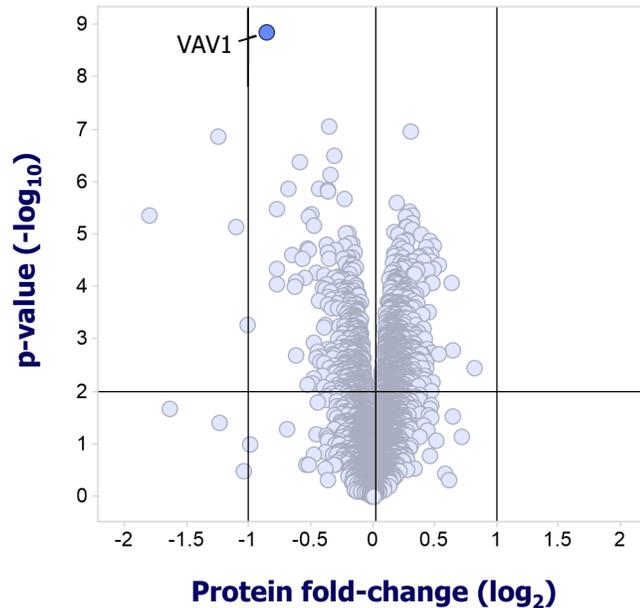
Identify surface patches that match known degron interfaces



A Patch on VAV1 Shows Surface-similarity to the GSPT1 G-loop Degron

VAV1 identified from cell-based whole proteome screening

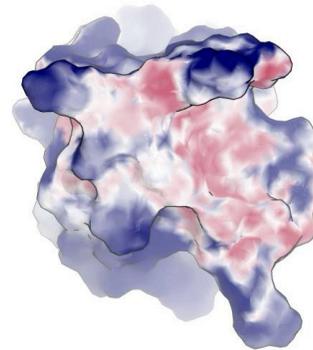
VAV1 shows surface similarity to the G-loop degron of GSPT1



TMT-Proteomics (MOLM13)

VAV1

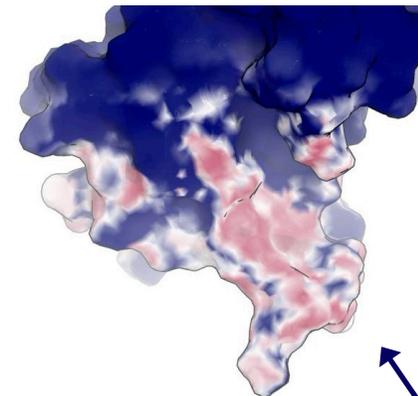
Surface similarity to GSPT1 degron



Low High
Surface similarity

GSPT1

Surface similarity to VAV1 degron



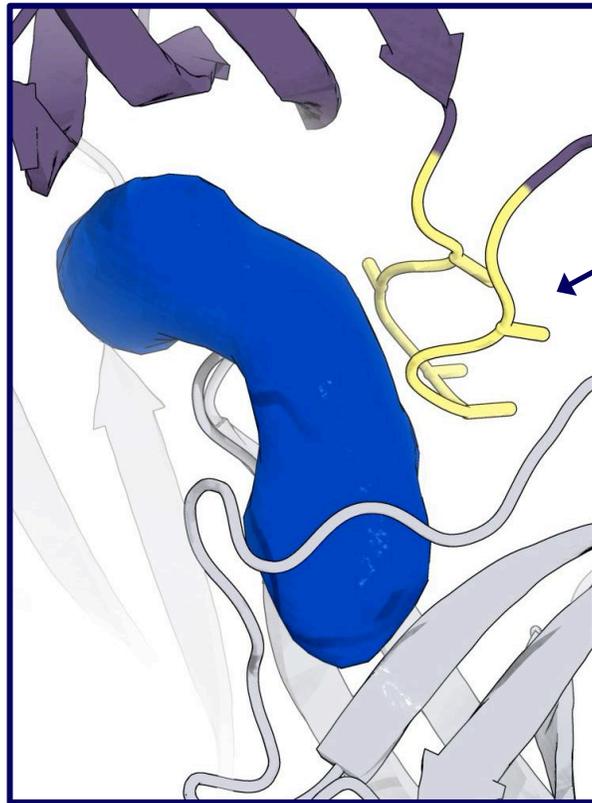
GSPT1 G-loop degron



G-loop Degron

Novel Binding Mode for VAV1 Despite Surface-similarities to GSPT1

GSPT1
Canonical G-loop
degron

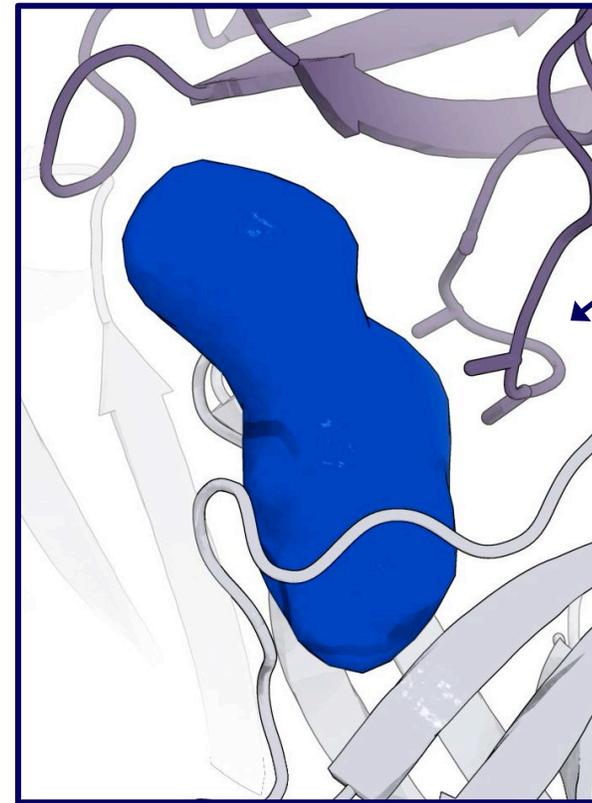


MGD:GSPT1
interactions

**Backbone-
driven**

CRBN:MGD

VAV1
Novel binding mode
Type 4



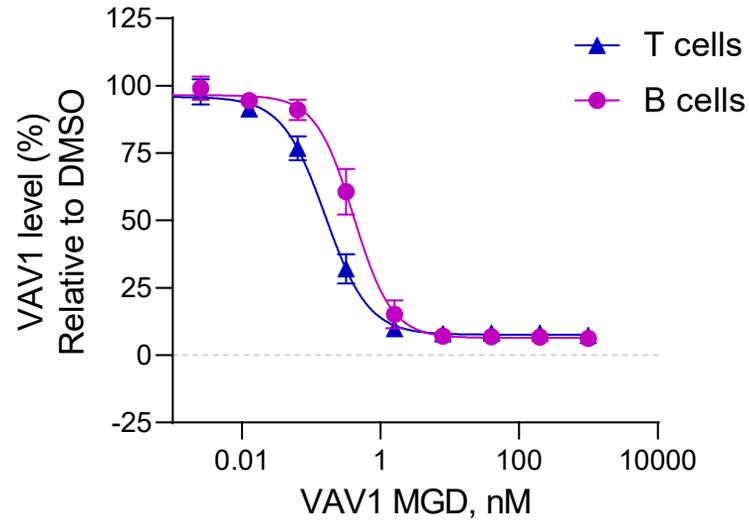
MGD:VAV1
interactions

**Side chain-
driven**

CRBN:MGD

MRT-6160 is a Potent and Selective VAV1-directed MGD

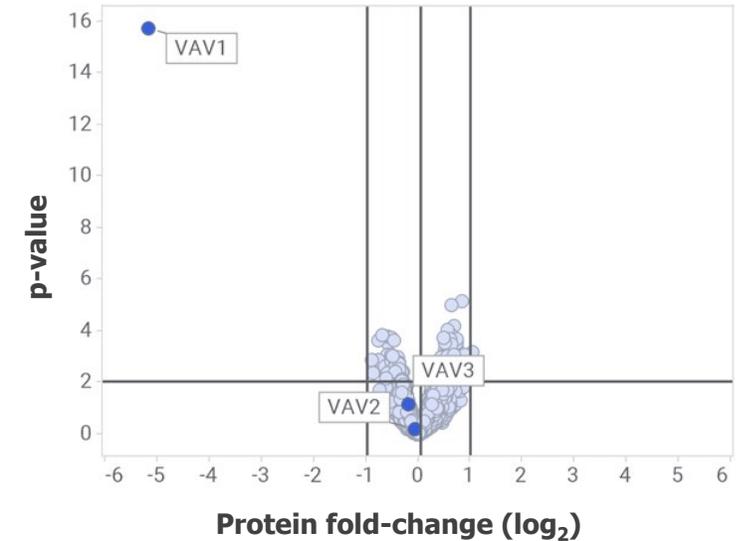
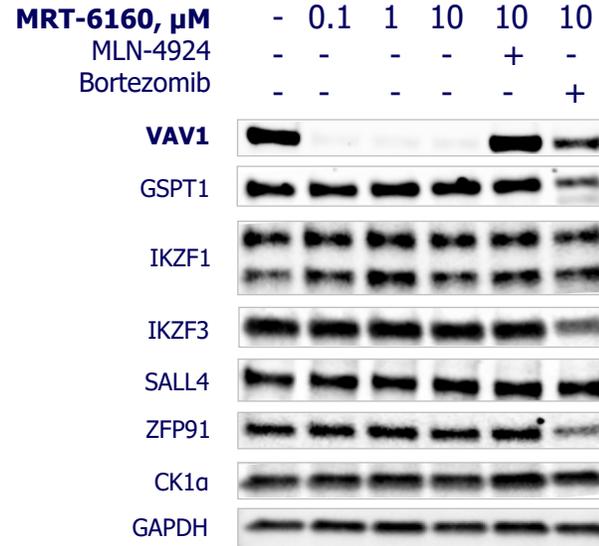
MRT-6160 is a potent VAV1-directed MGD



in vitro data

CRBN binding, IC ₅₀	670 nM
Ternary complex, EC ₅₀	11 nM
Degradation, DC ₅₀ /D _{max} (Jurkat)	7 nM / 97 %

MRT-6160 induces selective VAV1 degradation and has a favorable ADME/DMPK profile

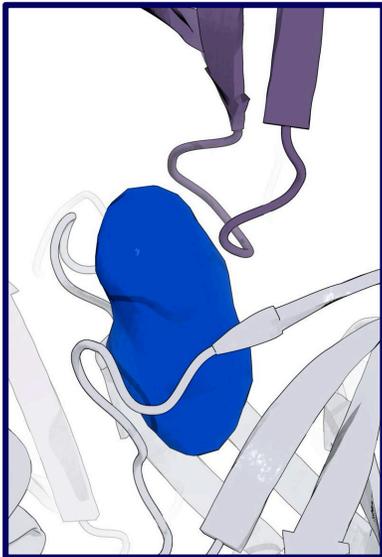


ADMET profile

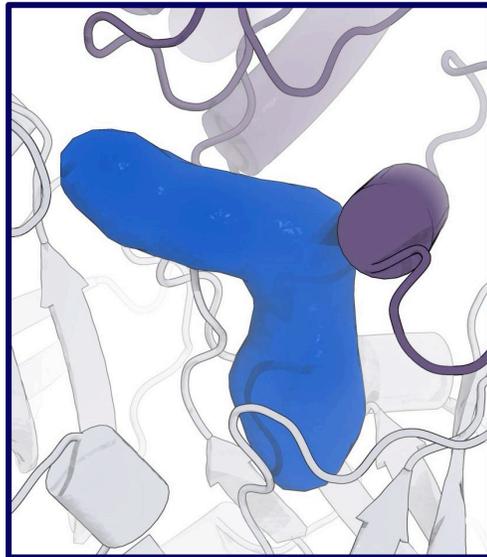
CYP DDIs	IC ₅₀ > 30 μ M
hERG inhibition patch clamp	EC ₅₀ > 30 μ M
Oral bioavailability all species	> 50%

Novel Binding Modes are Highly Diverse in Structure, Sequence and MGD

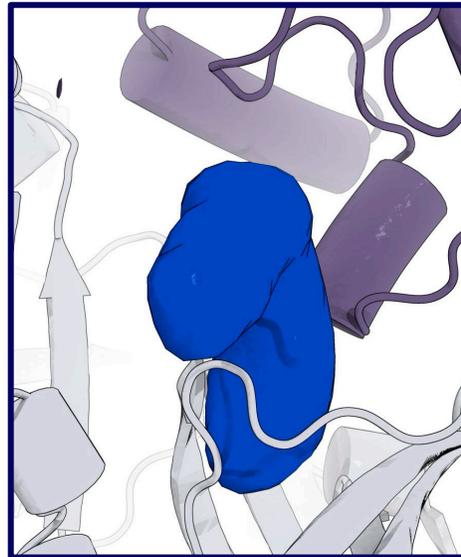
Canonical
G-loop



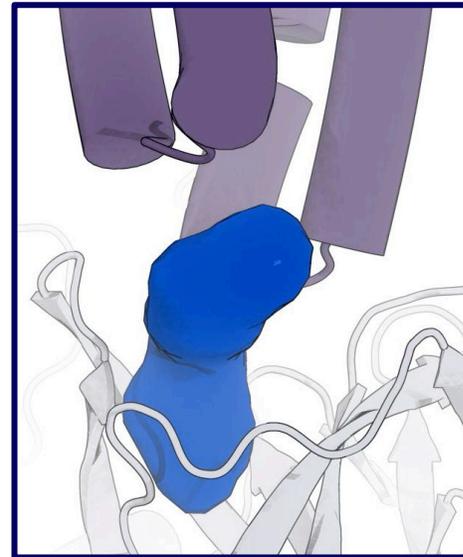
Novel Mode
Type 1



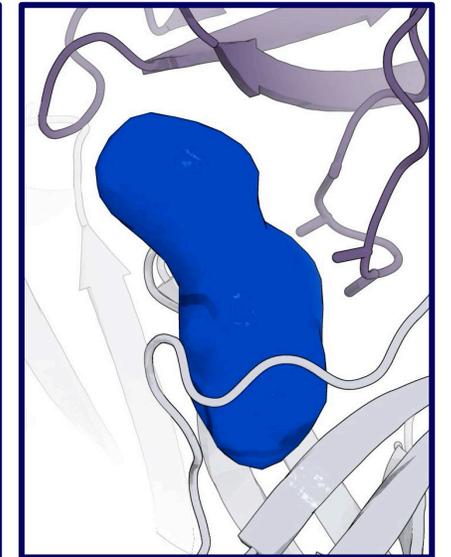
Novel Mode
Type 2



Novel Mode
Type 3



Novel Mode
Type 4



- Novel binding modes broaden target space
- Potential benefits for selective MGD design

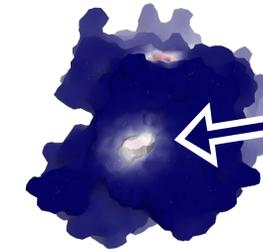
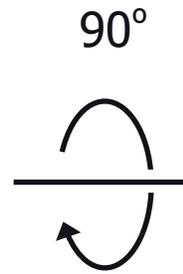
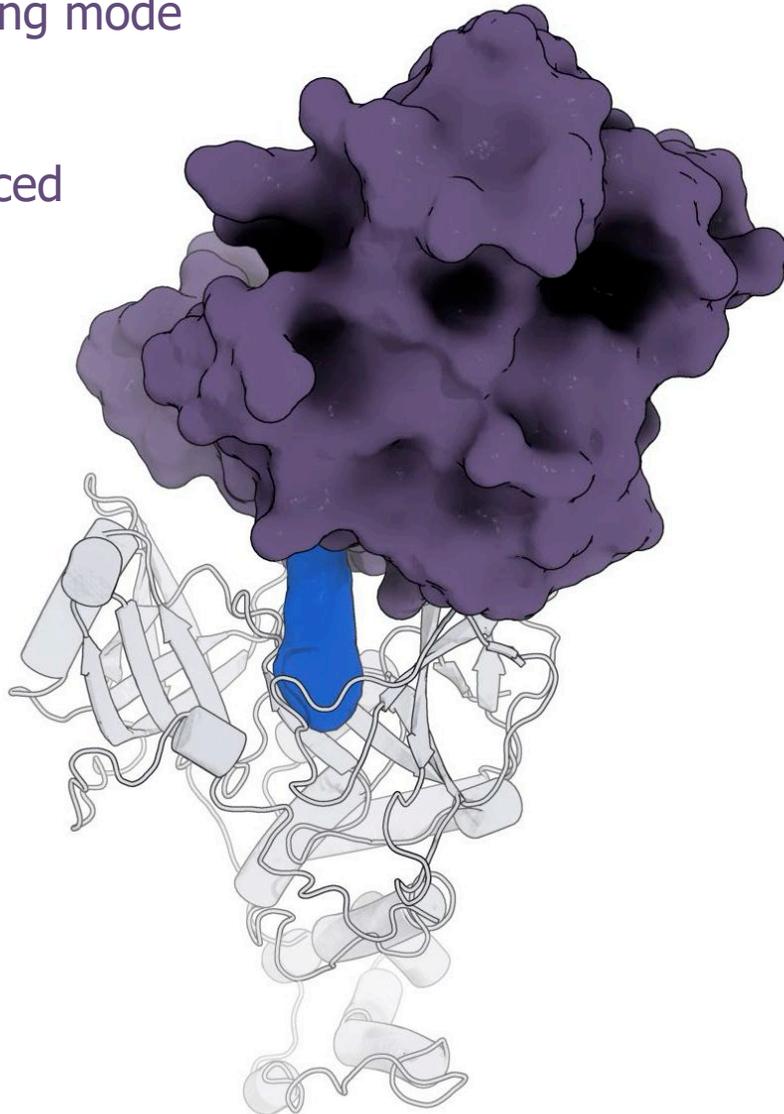
Example of an MGD Engaging a Cryptic Pocket at the Target Interface

Novel binding mode
Type 5

(MGD-induced
pocket)

MGD

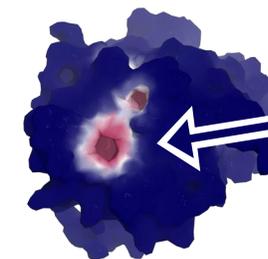
CRBN



Shallow
cavity

Apo-state
(starting frame)

+ CRBN:MGD



Pocket carved
by the MGD

MGD-engaged
(end frame)

Low  High

Pocket propensity

Our Rational Approach to Unleash the Full Potential of MGDs

Neosubstrate
(e.g. IKZF1)



MGD
(e.g. Lenalidomide)



Cereblon



**Unraveling the
Canonical Degrome**

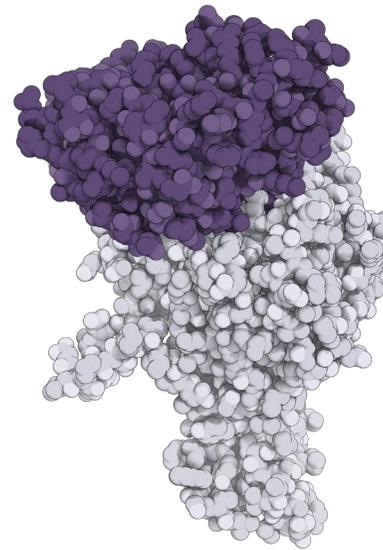


>2,500 G-loop
proteins



**>120 G-loops
validated**

**Beyond the
Canonical Degrome**

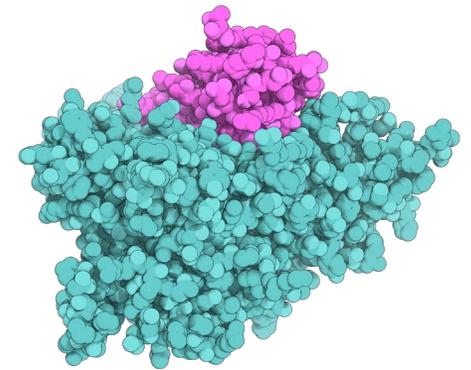


fAIceit-mimicry™
and screening

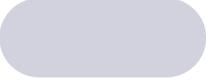


**>10 novel binding
modes identified**

Beyond Cereblon



Monte Rosa Pipeline

Program/ Target	Indication(s)	Discovery	IND-Enabling	Clinical	Next Anticipated Milestone	Ownership
MRT-2359 (GSPT1)	NSCLC, SCLC and other MYC-driven Malignancies				RP2D in Q2 2024	
MRT-6160 (VAV1)	Autoimmune Disease				IND in 1H 2024	
NEK7	Inflammatory Diseases				Development candidate in Q1 2024	
CDK2	Ovarian Cancer, Breast Cancer				Development candidate in 2024	
Discovery Targets	Multiple				Lead optimization	
Discovery Targets	Oncology and Neurological Diseases				Undisclosed	

Oncology
 Immunology
 Inflammation
 Various

Acknowledgments – It's a HUGE Team Effort!

