



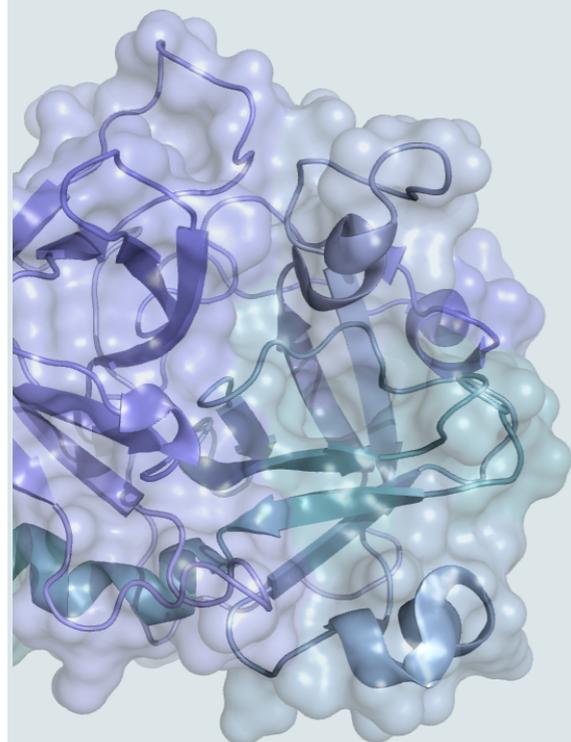
***The “Undruggable” Targets
of Medicinal Chemistry***

Modern Therapeutic Strategies

Literature Group Meeting

May 2nd, 2025

Katherine Burton
MacMillan Lab
Princeton University



Modification Strategies for Undruggable Targets

Targeted Interactors

Part 1

Part 2

*Designer Peptidomimetics and Synthetic
Biologics*

*Exploiting structure-function properties to
access novel therapeutics*

Part 3

***Prions and Multi drug
resistance: The
Looming Plagues***

Investigating Druggability

What defines a target's druggability?



Investigating Druggability

What defines a target's druggability?

*“An ideal small-molecule drug target is **disease modifying**,*



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What defines a target's druggability?

*“An ideal small-molecule drug target is **disease modifying**, capable of binding a **selective, orally bioavailable molecule** at a site that elicits a functional effect*



Investigating Druggability

What defines a target's druggability?

*“An ideal small-molecule drug target is **disease modifying**, capable of binding a **selective, orally bioavailable molecule** at a site that elicits a functional effect, has no **on-target toxicity** and is **expressed in disease-relevant tissue**”*



Druggable Targets – the Human Proteome

Identification of disease-causal targets in the human proteome



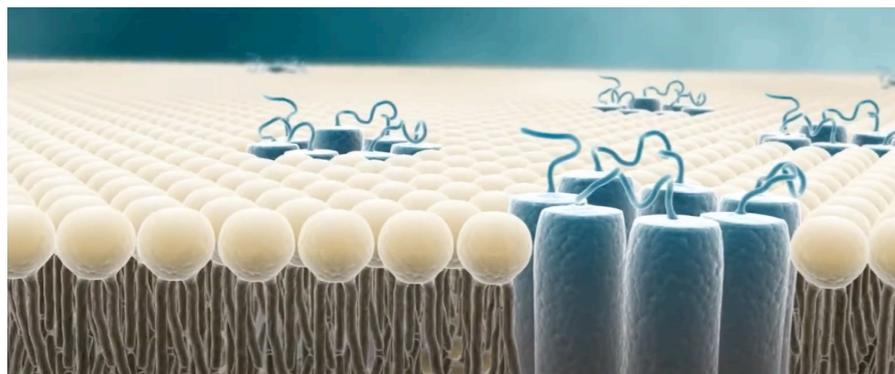
Human proteome (~20,000)

Druggable Targets – the Human Proteome

Identification of disease-causal targets in the human proteome

Conventionally ‘druggable’

- **Ion channels + GPCRs**



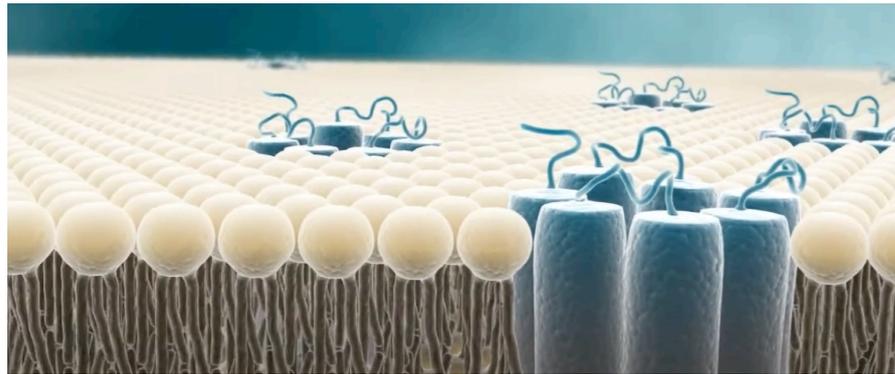
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**~30% of all drugs on the
market act by binding
GPCRs**

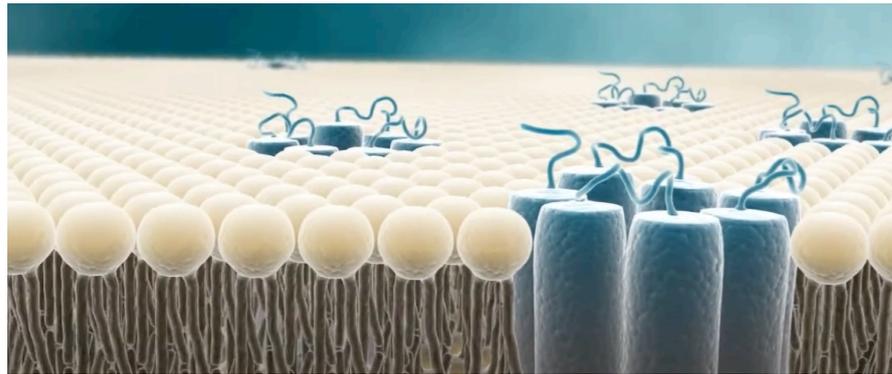
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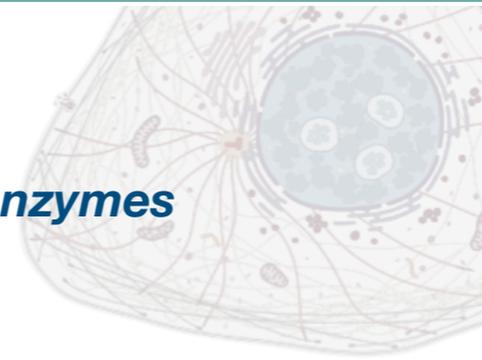
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- Intracellular enzymes



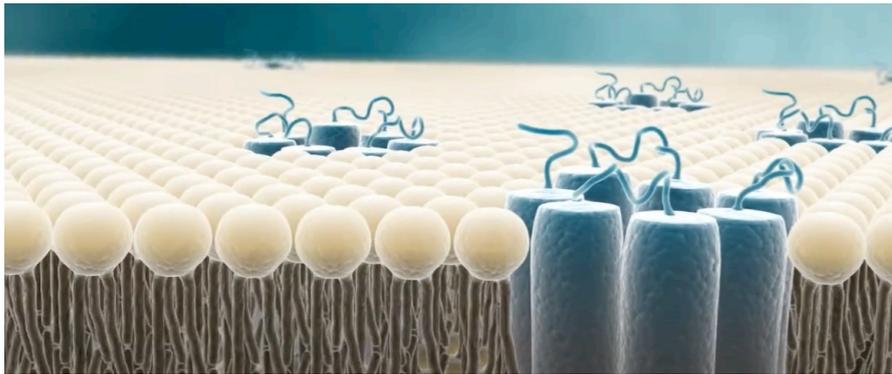
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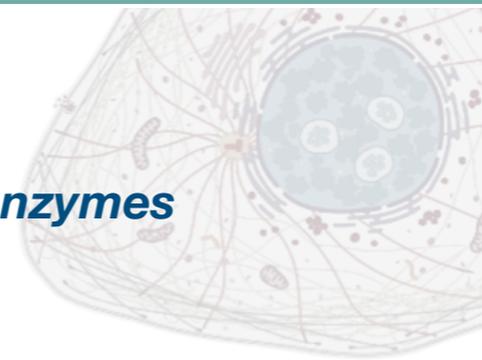
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- ligand binding sites
- other hydrophobic pockets

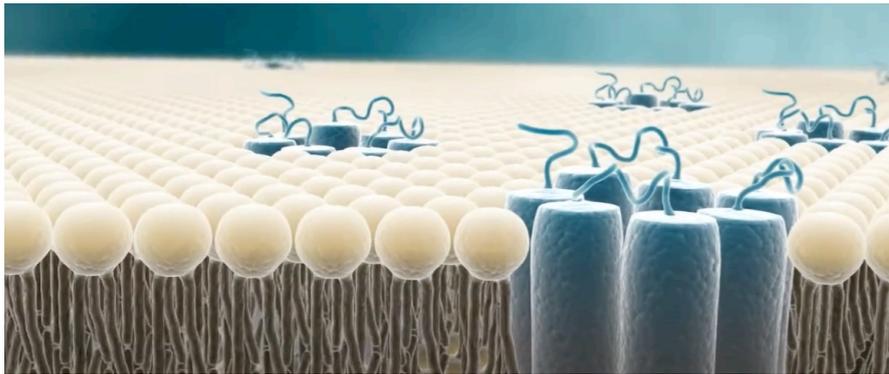
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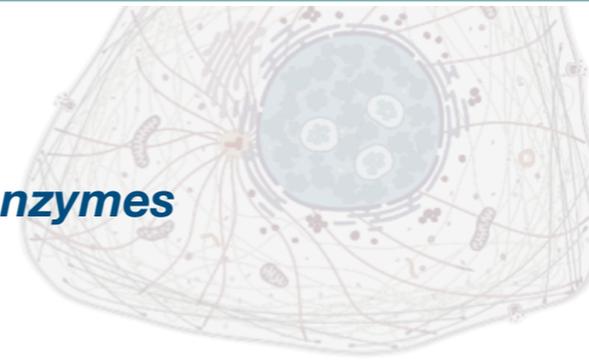
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- *Ion channels + GPCRs*



- *Intracellular enzymes*



- *Transcription factors*

- *ligand binding sites*
- *other hydrophobic pockets*



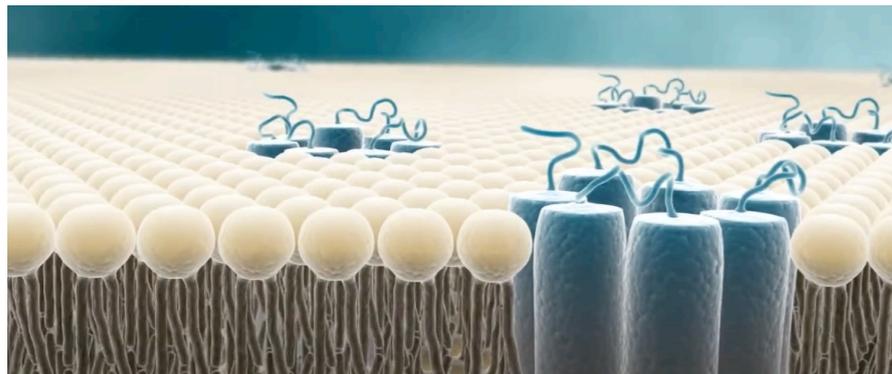
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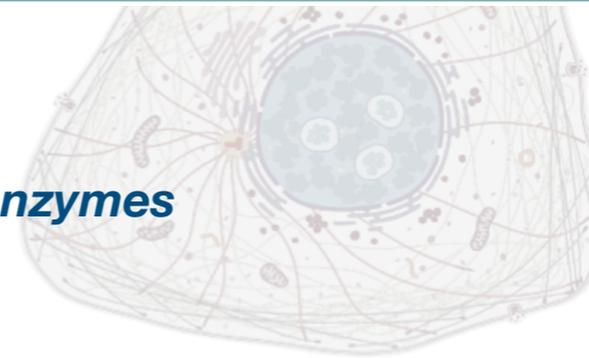
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- **Transcription factors**

p53

Myc

Estrogen receptor (ER)

Androgen receptor (AR)



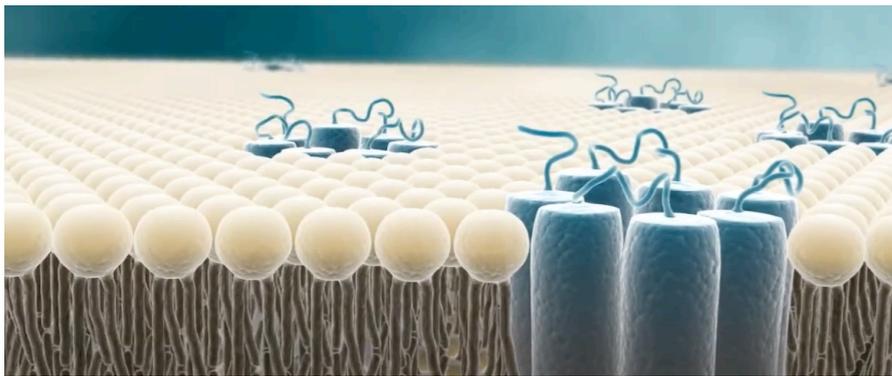
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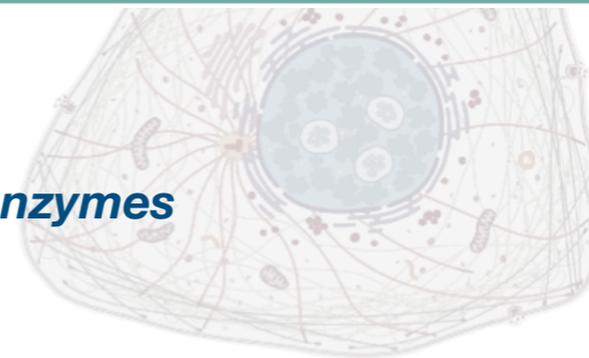
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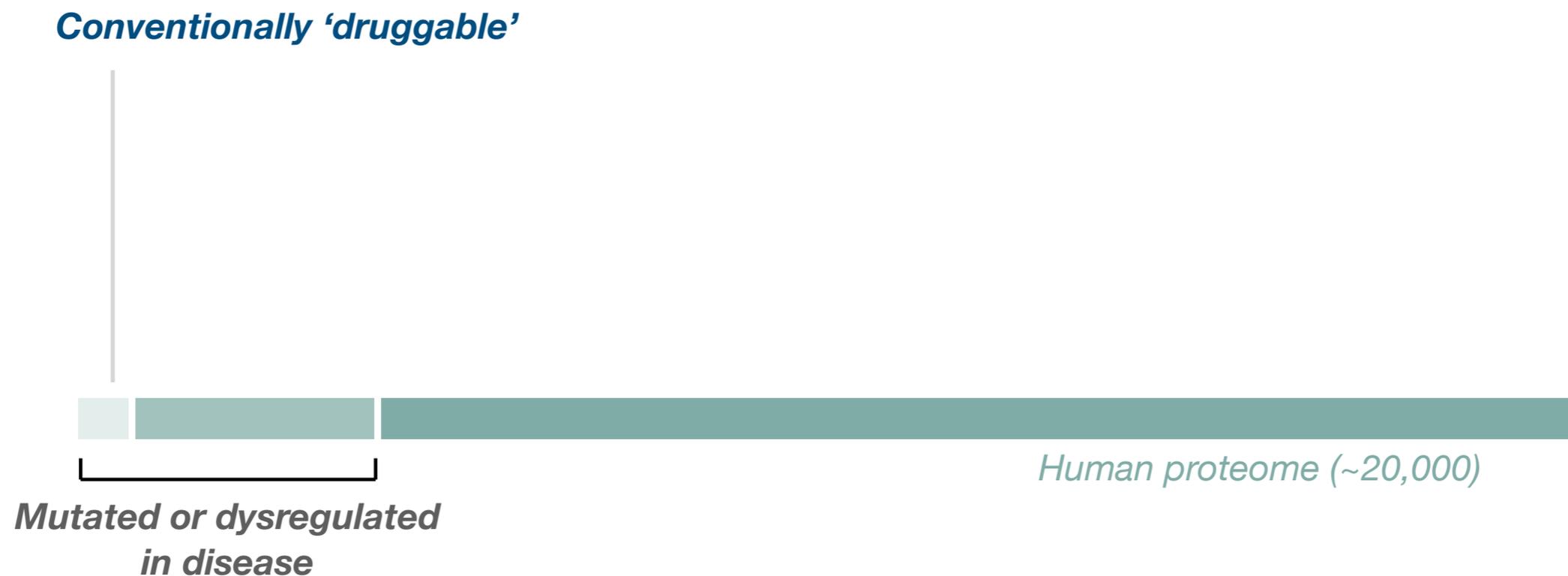
- *Structural heterogeneity*
- *few tractable binding sites*



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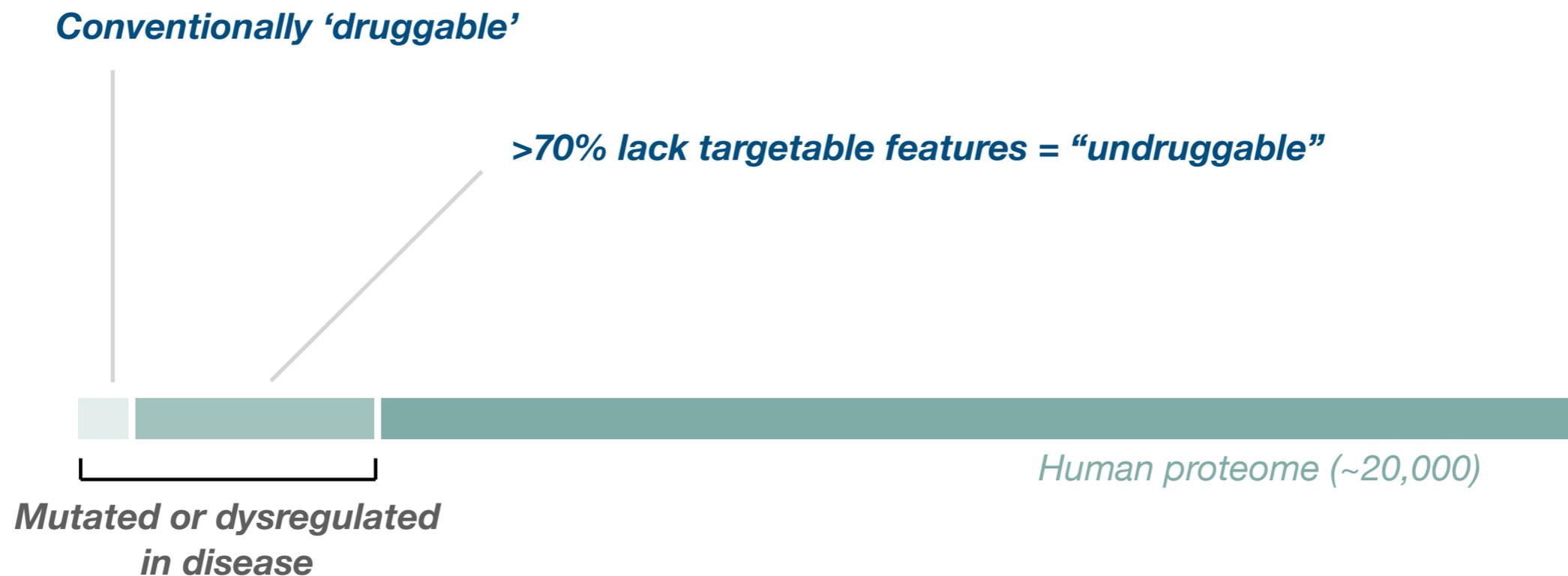
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The **majority** of disease drivers **lack structural features** conventionally targeted by small molecules or antibodies



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Investigating Druggability

3 key factors to “Undruggability”:

■ *Disordered Structures*

■ *Dynamic surfaces*

■ *Undefined binding pockets*

Investigating Druggability

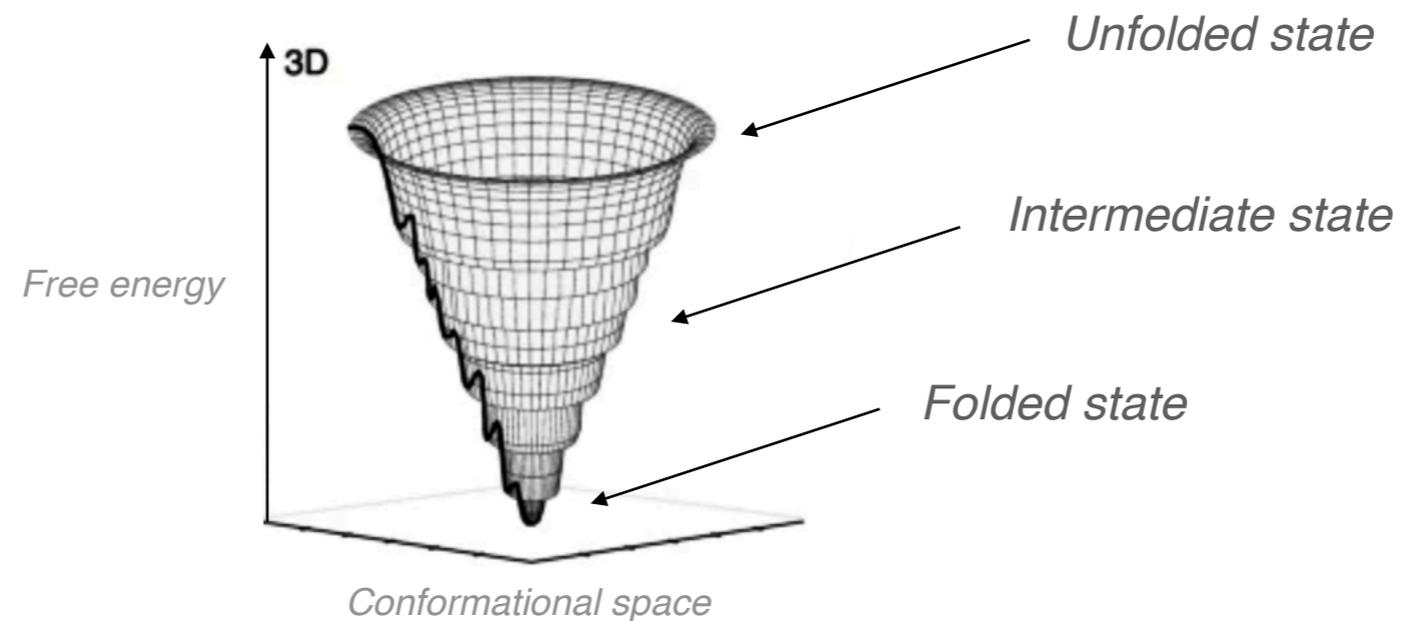
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Folding funnel diagram – energy landscape



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Wolynes, P.G., Onuchic, J.N., Thirumalai, D. *Science*, **1995**, 267, 1619–1620.

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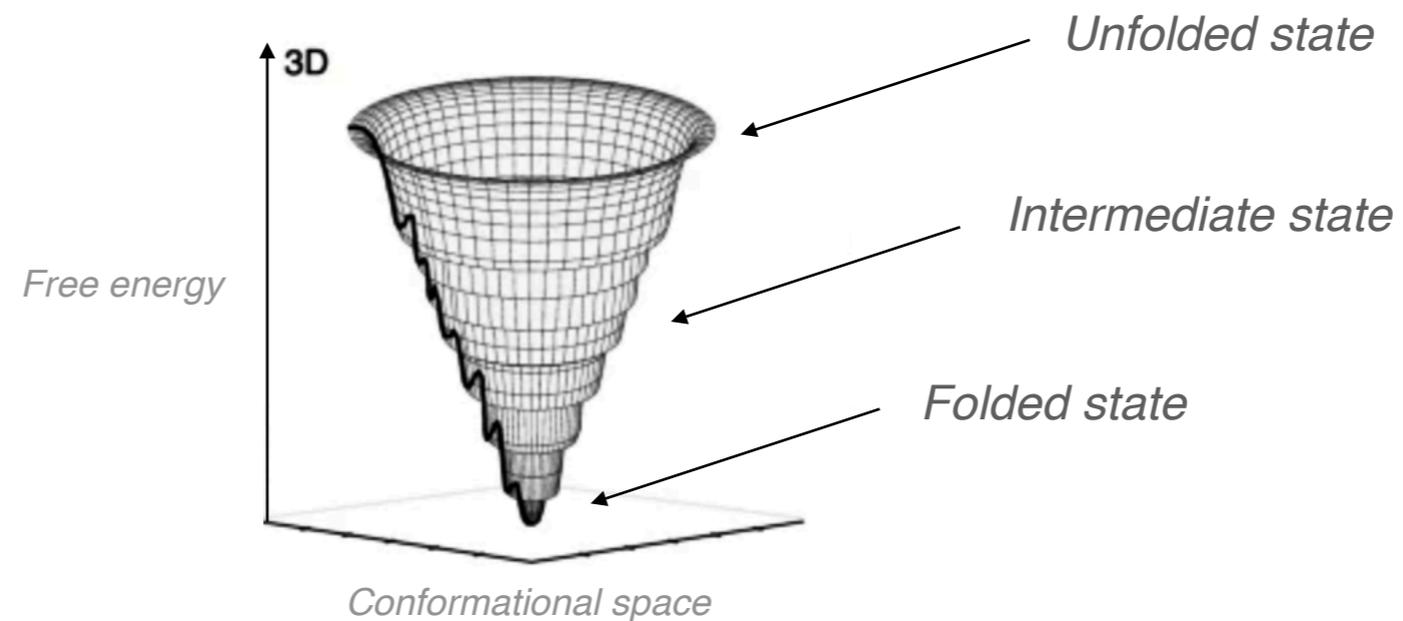
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“The extent of a protein energy landscape is huge. Before folding, each residue can take on about 10 different conformations. Thus, a 60-residue protein can be in any of 10^{60} states.”

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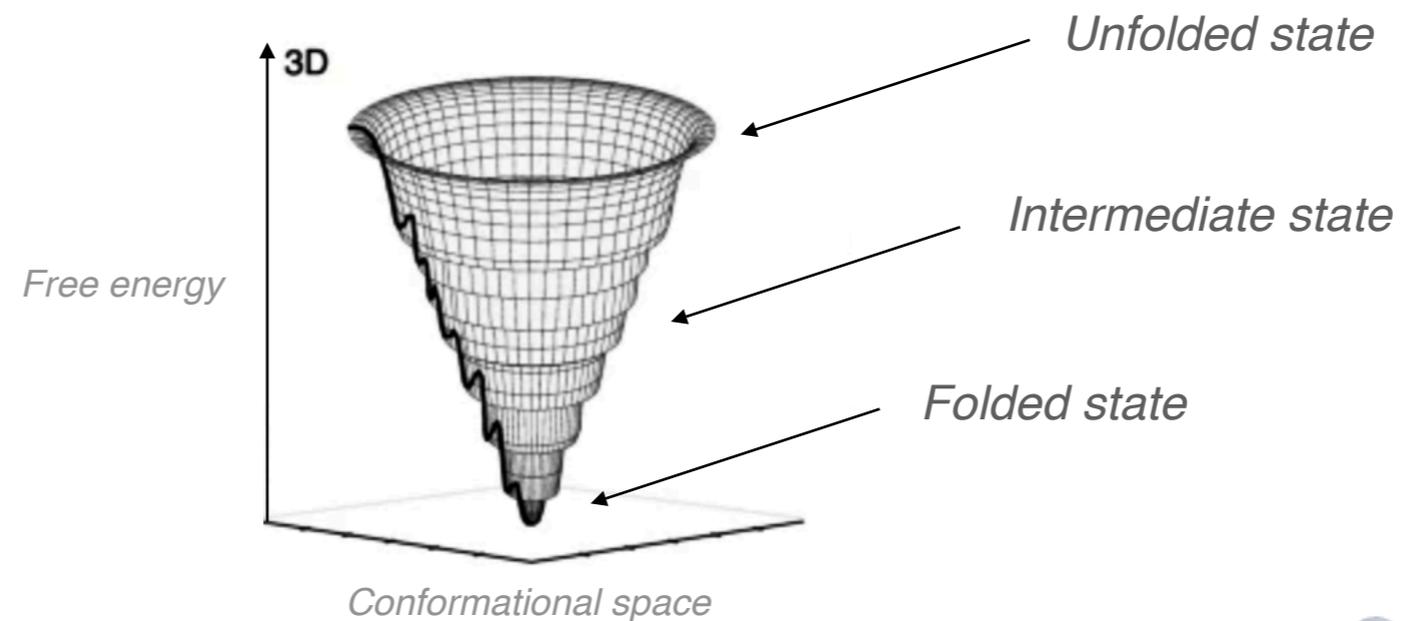
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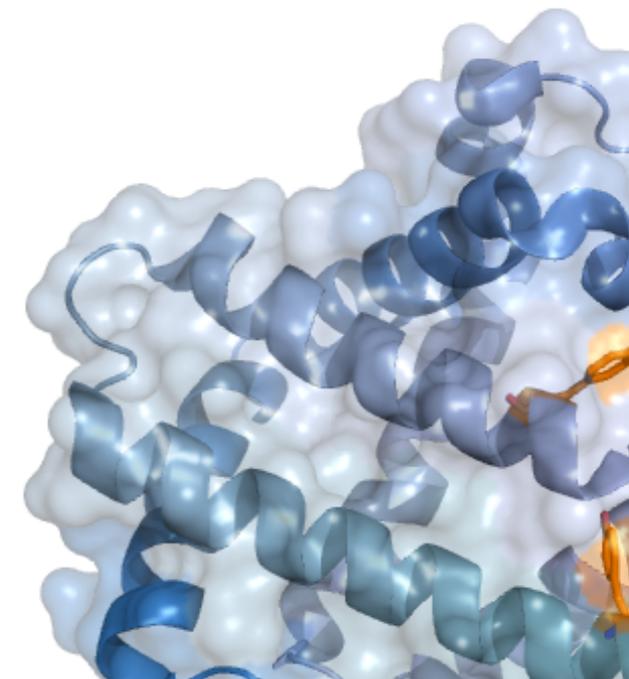
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Folding funnel diagram



Folded proteins exhibit a deep minimum



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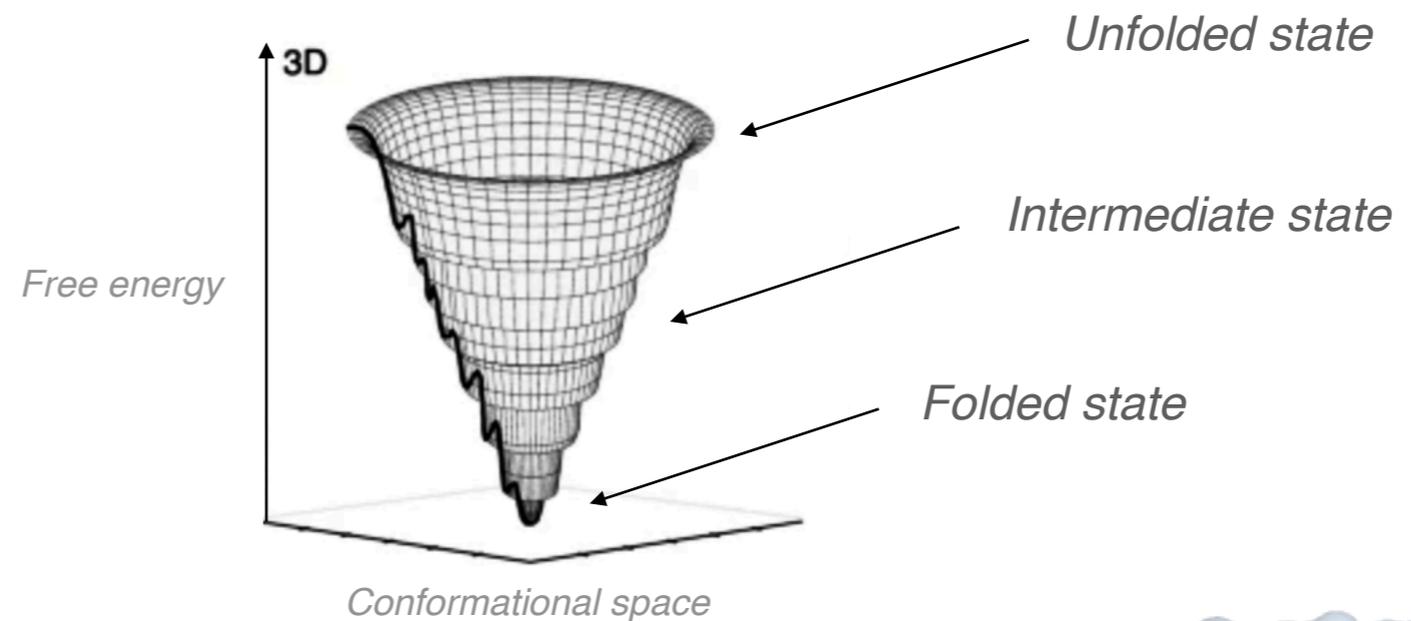
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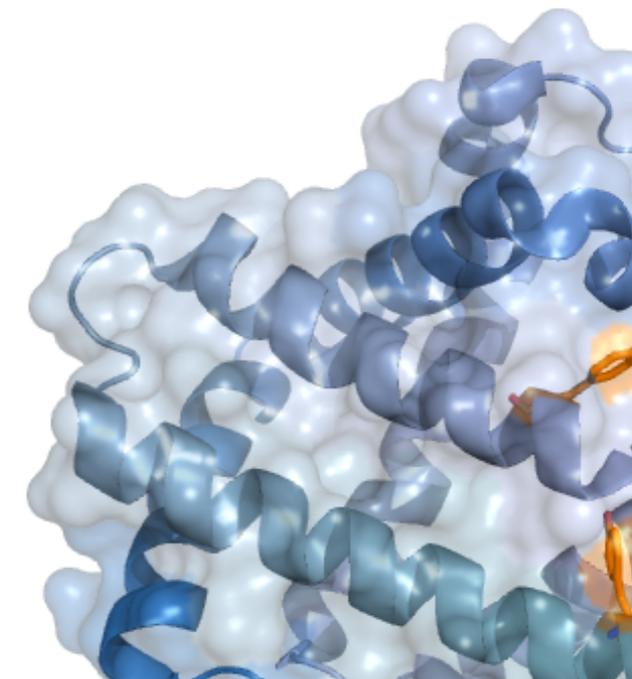
Intrinsically disordered proteins (IDPs)

- *Lack well-defined structure*

Folding funnel diagram



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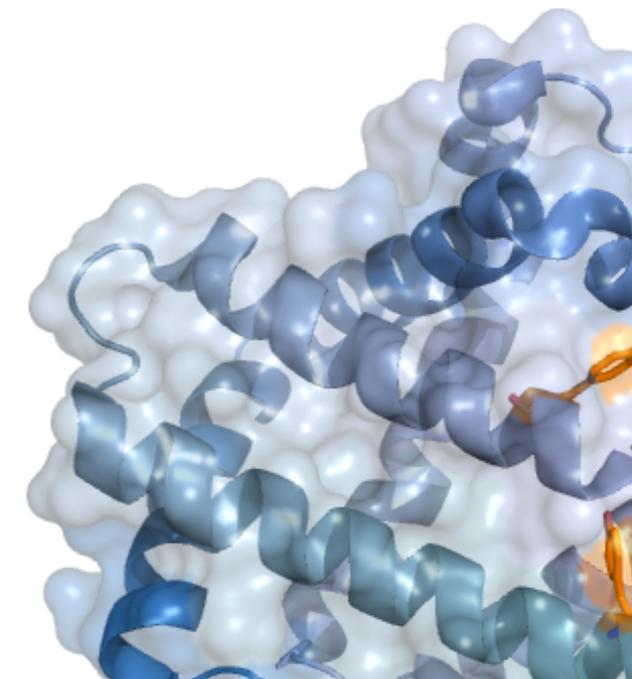
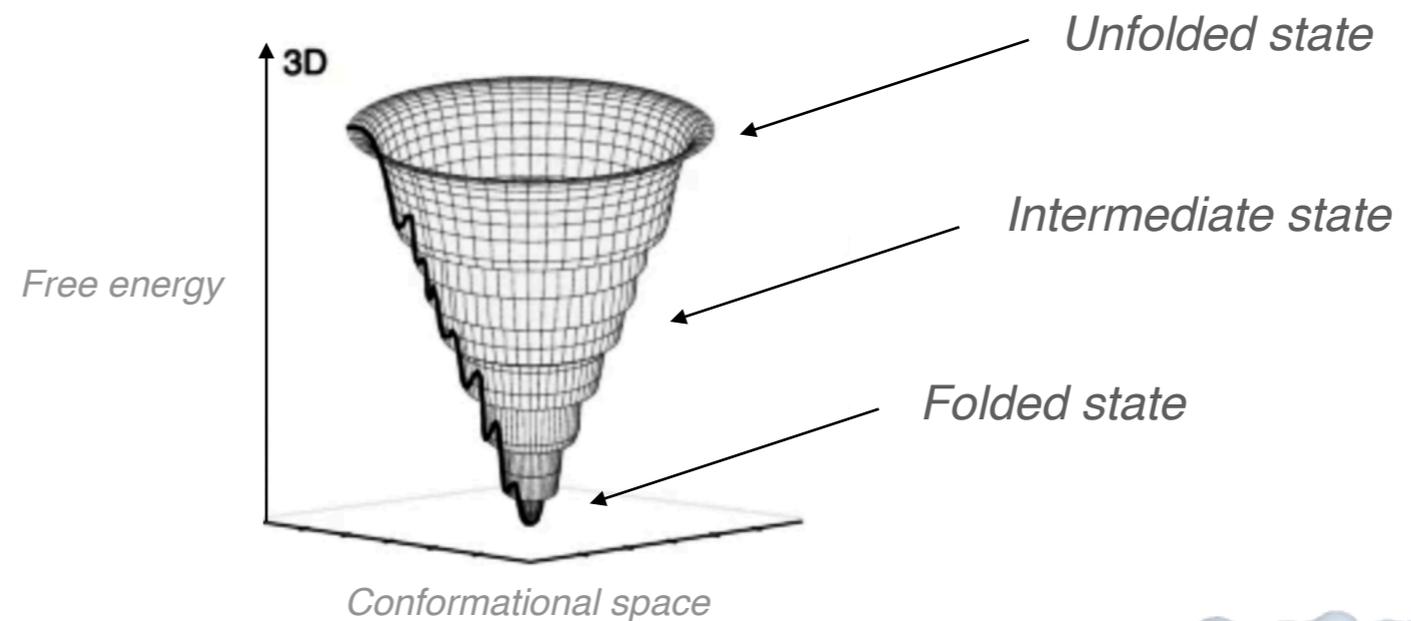
■ *Dynamic surfaces*

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Intrinsically disordered proteins (IDPs)

- *Lack well-defined structure*
- *Large entropic penalty of drug–target binding*

Folding funnel diagram



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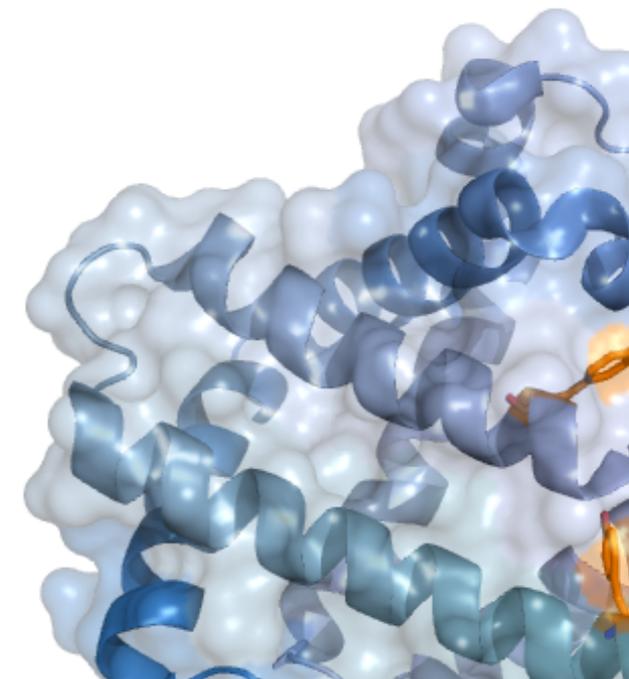
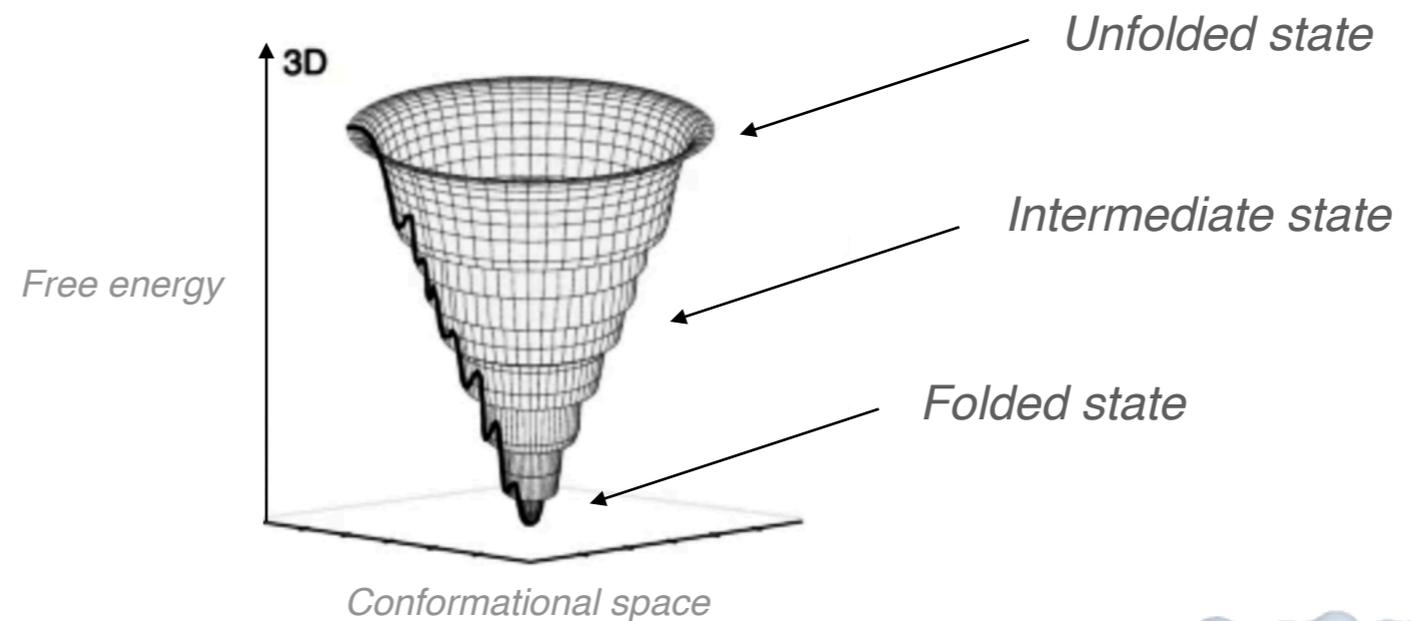
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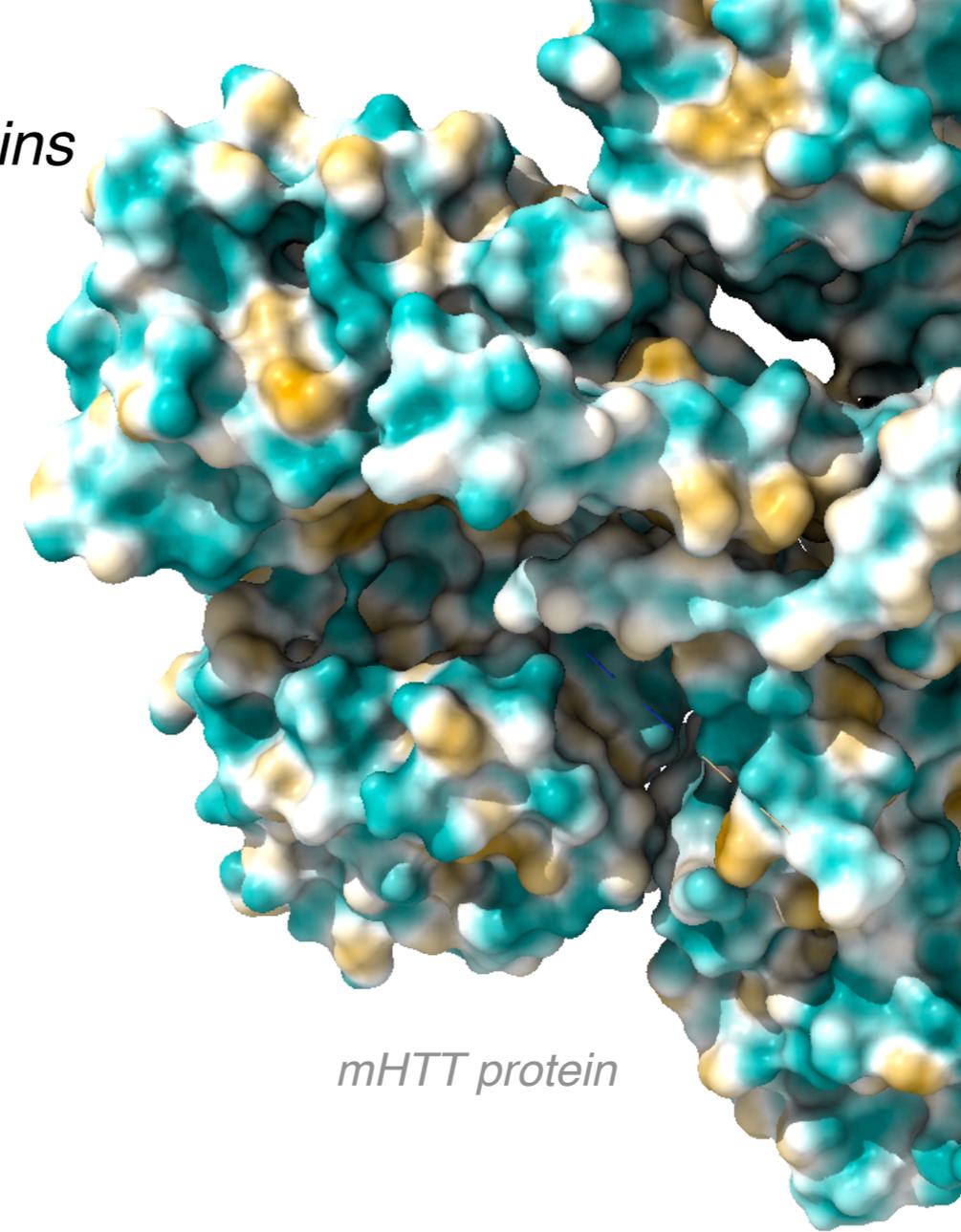
Hard to develop small molecule drugs

Folding funnel diagram



Intrinsically disordered proteins

Mutant Huntingtin protein (mHTT) = intrinsically disordered



mHTT protein

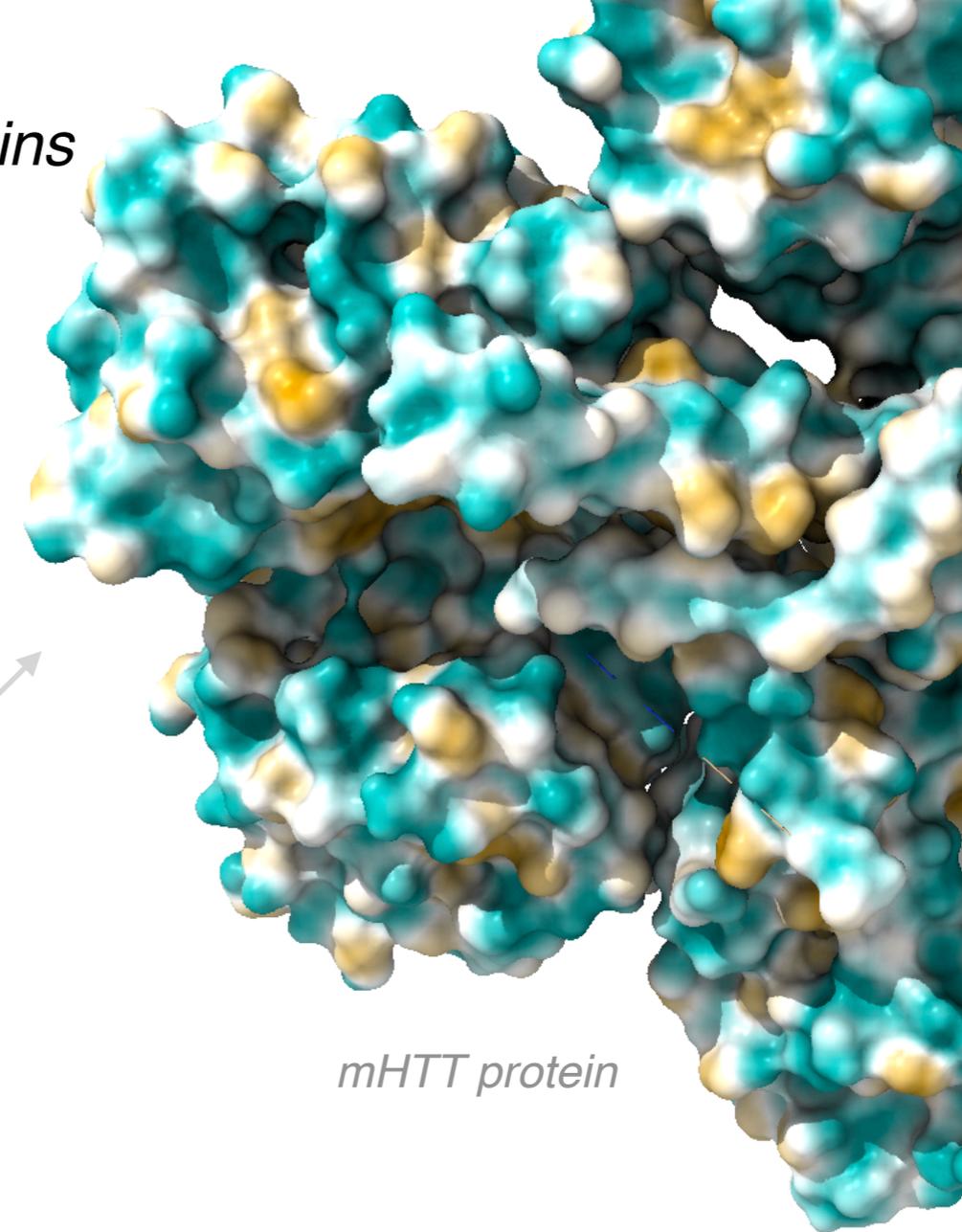
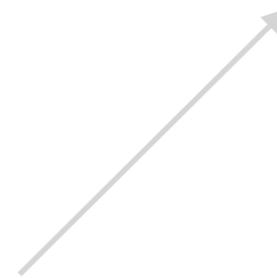
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Intrinsically disordered proteins

Mutant Huntingtin protein (mHTT) = intrinsically disordered

Multiple interconverting conformational states



mHTT protein

Intrinsically disordered proteins

Mutant Huntingtin protein (mHTT) = intrinsically disordered

CAG triplet repeat expansion disease

CAG

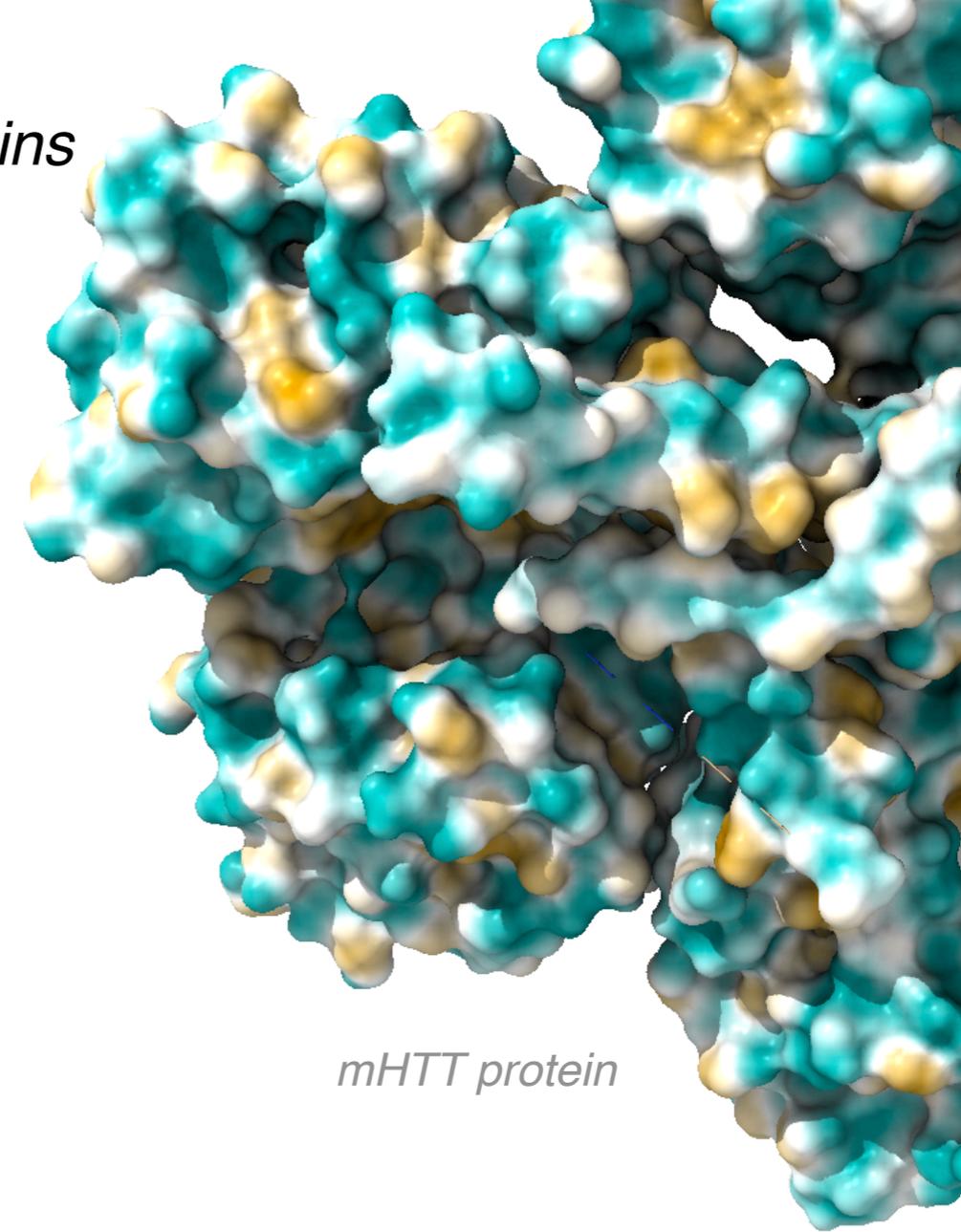
CAG

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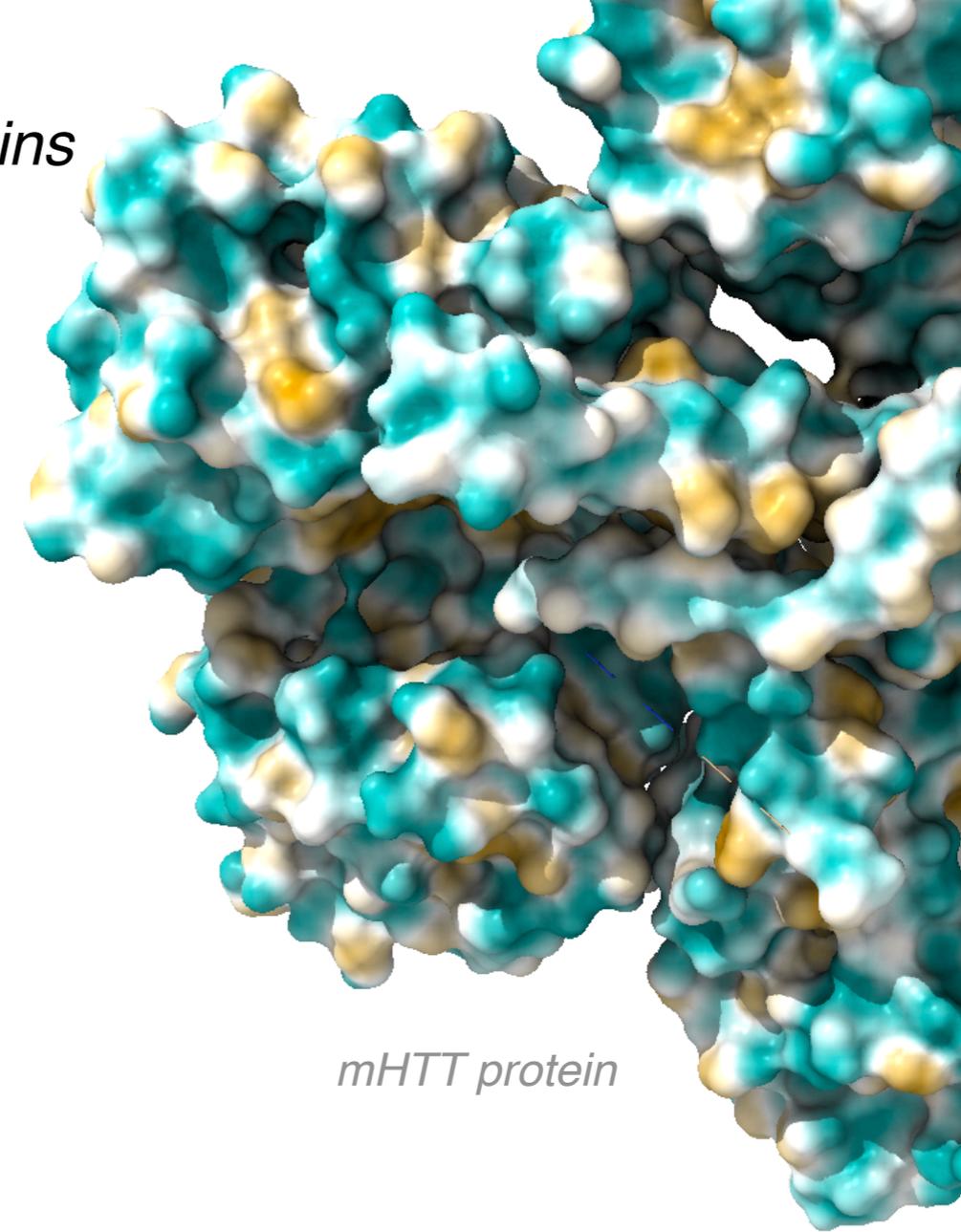
CAG

- *DNA-repeat expansion occurs throughout neuronal life*



mHTT protein

Intrinsically disordered proteins



mHTT protein

Mutant Huntingtin protein (mHTT) = intrinsically disordered

CAG triplet repeat expansion disease

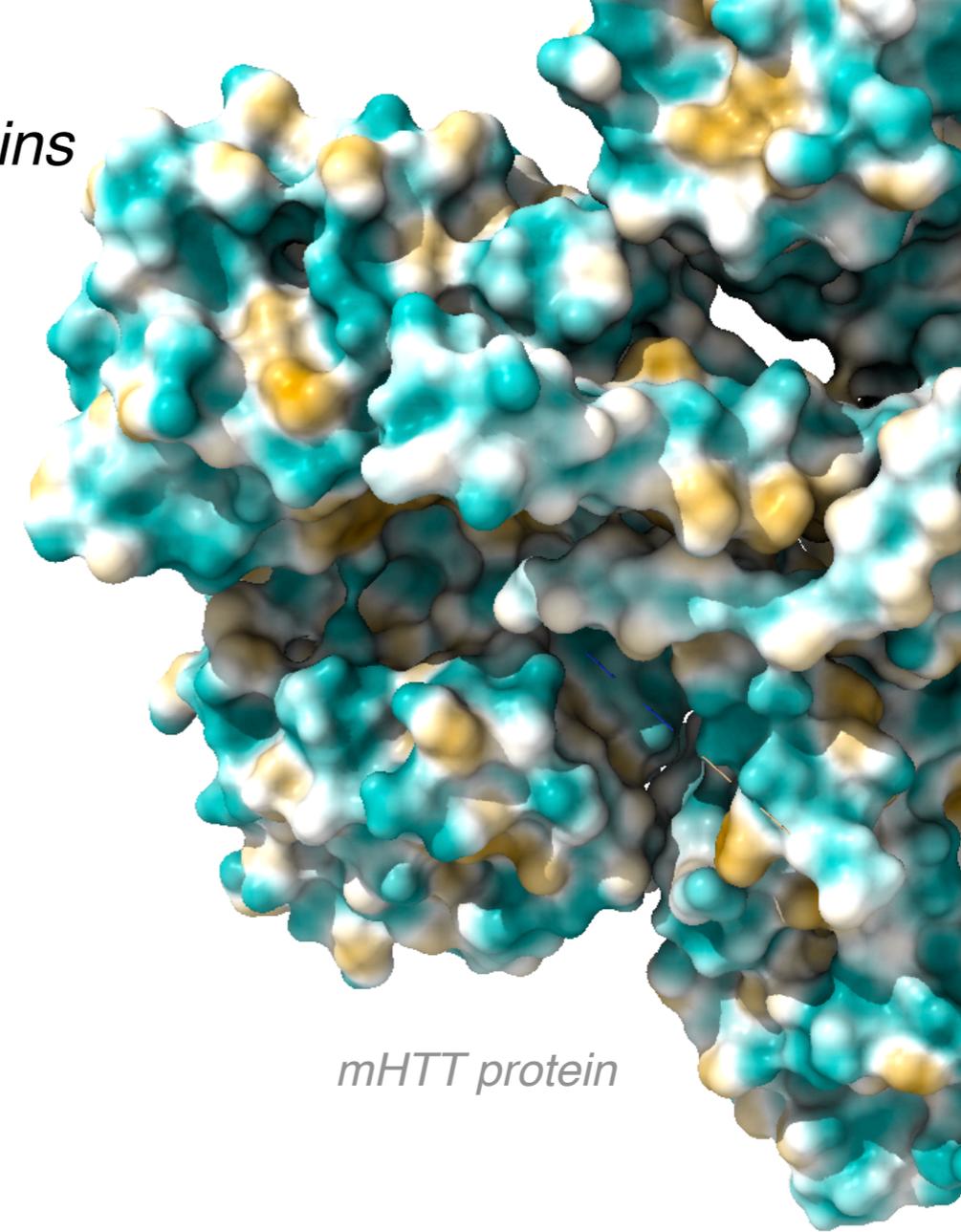


Abnormal polyglutamine tracts

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CAG triplet repeat expansion disease

CAG CAG CAG CAG CAG



Abnormal polyglutamine tracts



Irreversible aggregate formation

mHTT protein

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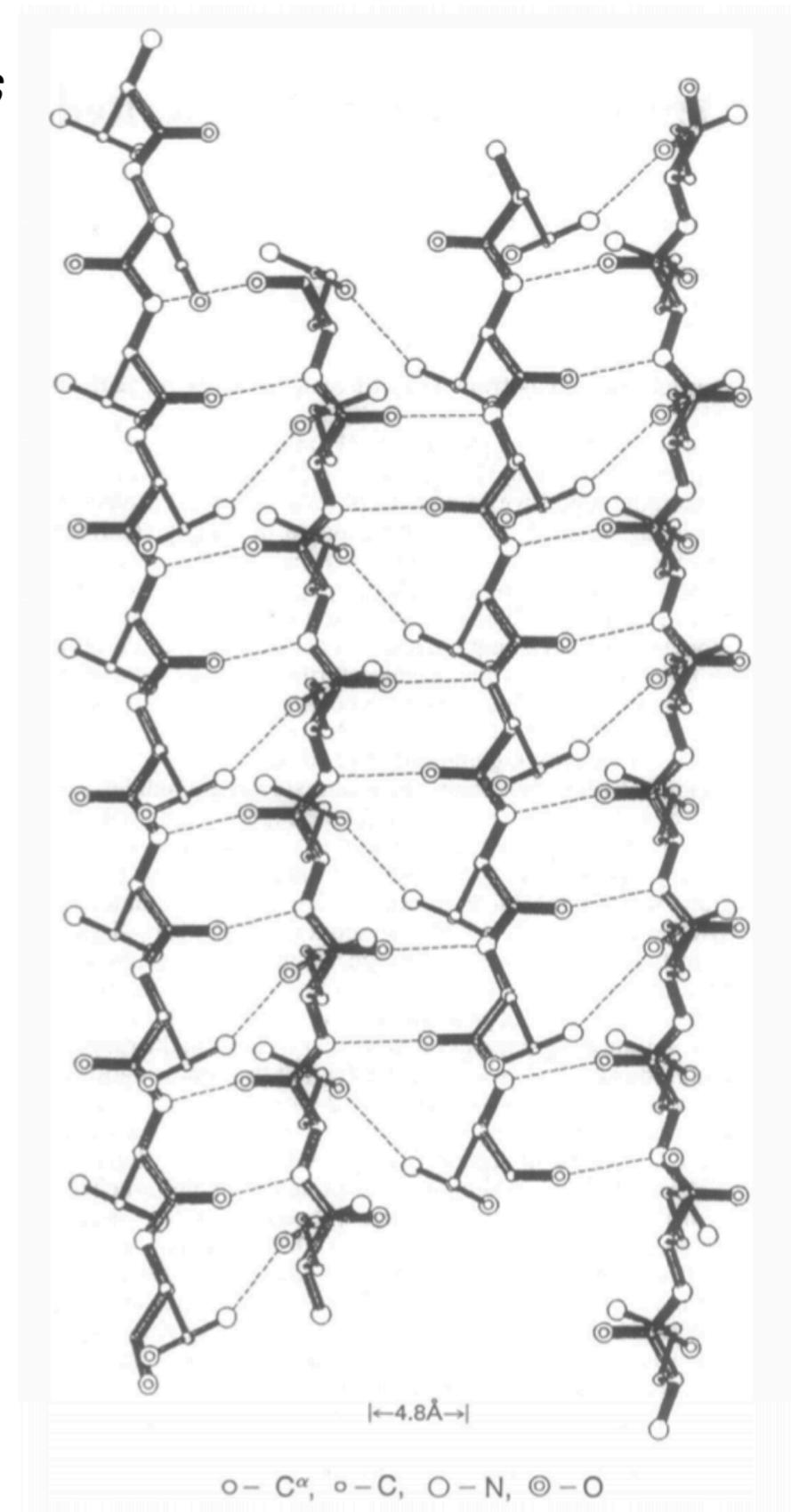
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Abnormal polyglutamine tracts



**Irreversible aggregate formation
Depends on length of polyglutamine stretch!**



Huntingtin polyglutamine repeat: β -sheets

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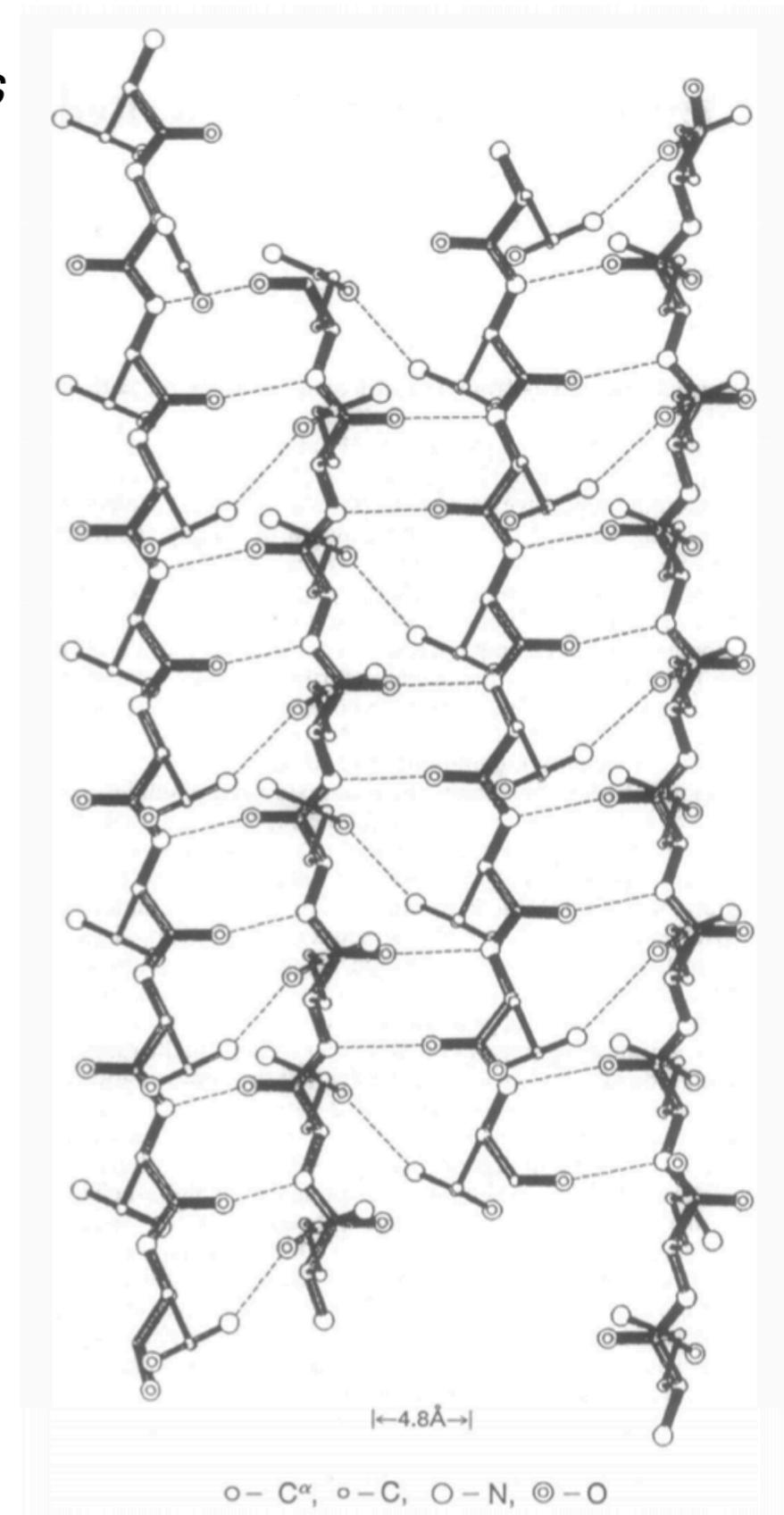
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Stabilized by hydrogen bonding networks

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Intrinsically disordered proteins

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Irreversible aggregates

Intrinsically disordered proteins

intrinsically disordered proteins



Irreversible aggregates

Not all intrinsically disordered proteins are pathological

Investigating Druggability

3 key factors to “Undruggability”:

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■ *Dynamic surfaces*

■ *Undefined binding pockets*

Investigating Druggability

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- *Protein–protein interactions (PPIs)*
- *Protein–nucleic acid interactions*

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*~130,000–650,000
types of PPIs in the
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***Disruption of PPIs can
promote disease states***

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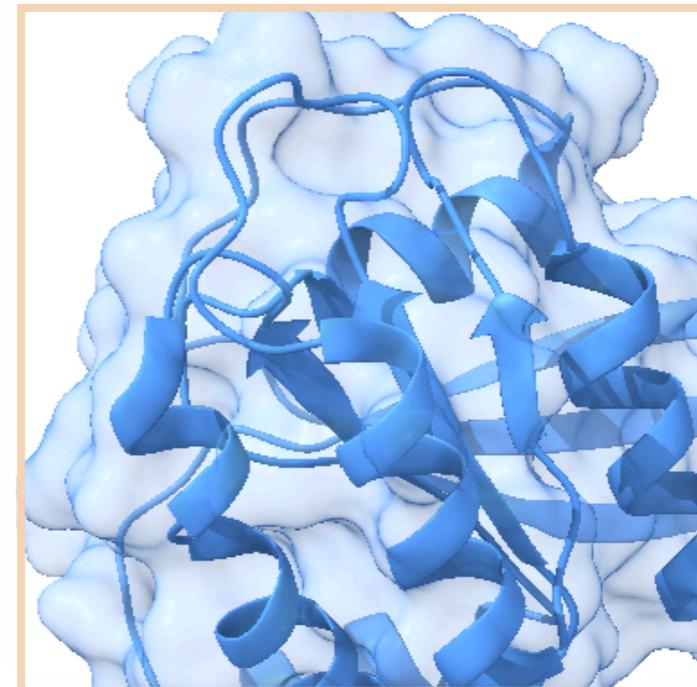
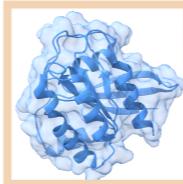
■ *Disordered Structures*

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Undefined binding pockets

- **Flat surfaces**
- **Lack grooves or binding sites**



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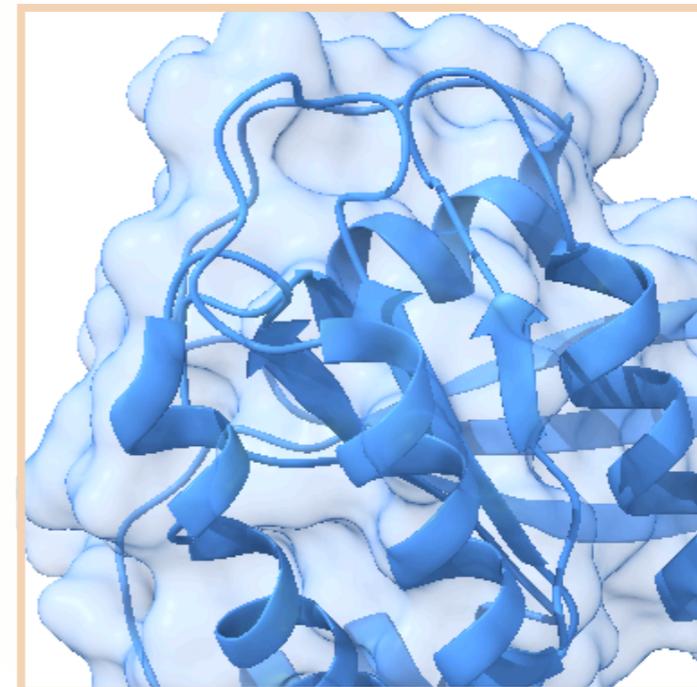
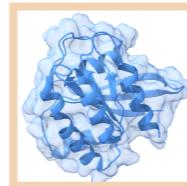
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KRAS proto-oncogene

- ***The most frequently mutated oncogene in cancer***



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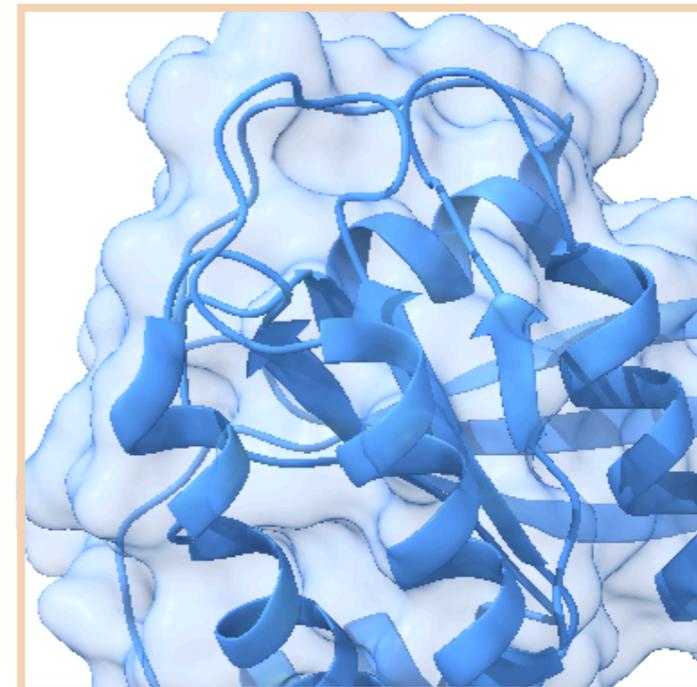
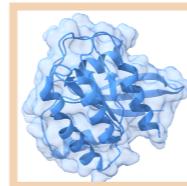
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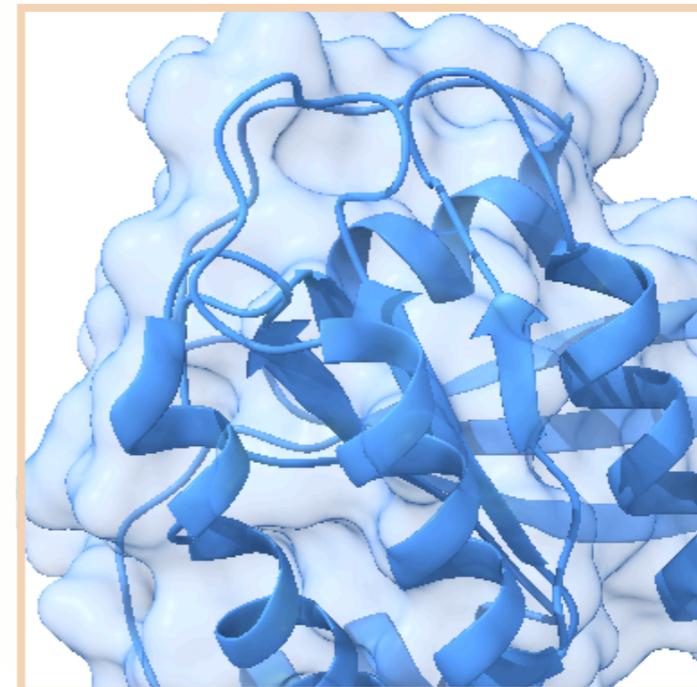
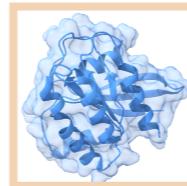
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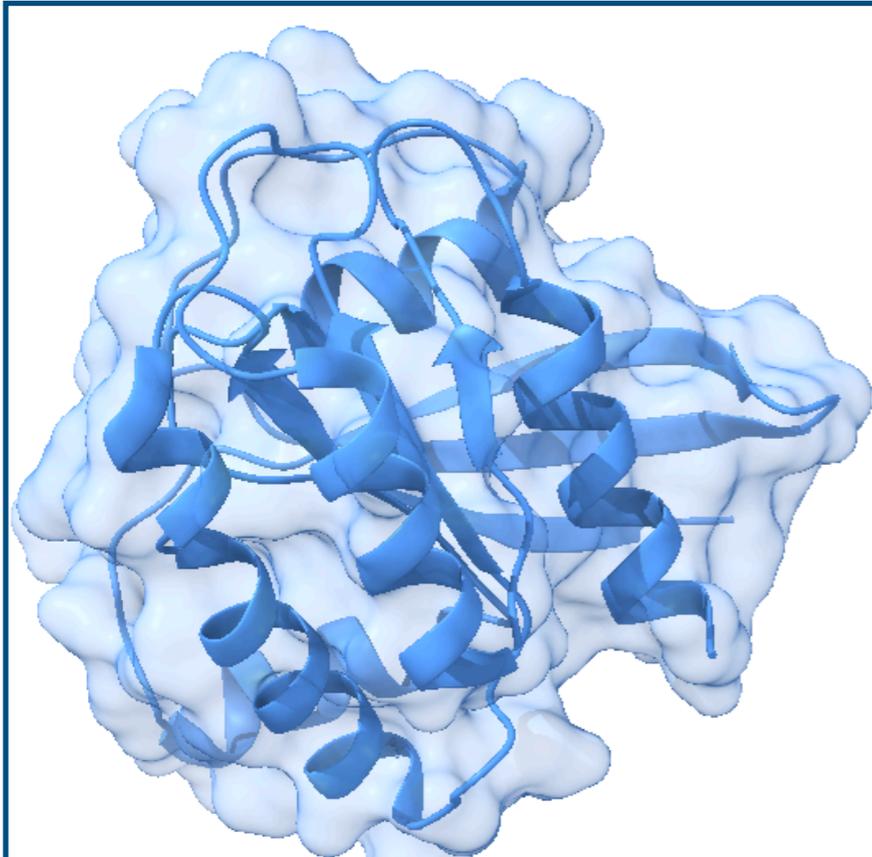
■ *Undefined binding pockets*

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The Ras Initiative



Killing Undruggable Targets

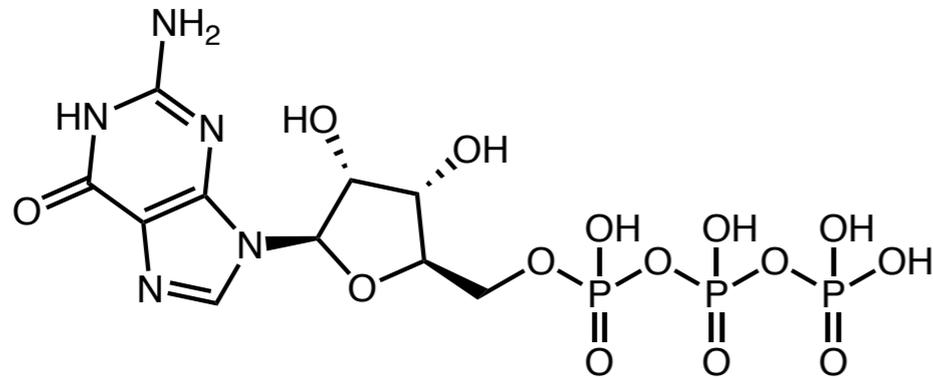
- ***Covalent inhibitors***

Part 1

Investigating Druggability

KRAS: to kill the undruggable

Ras proteins: Crucial in signal transduction (GTPase)



GTP-bound

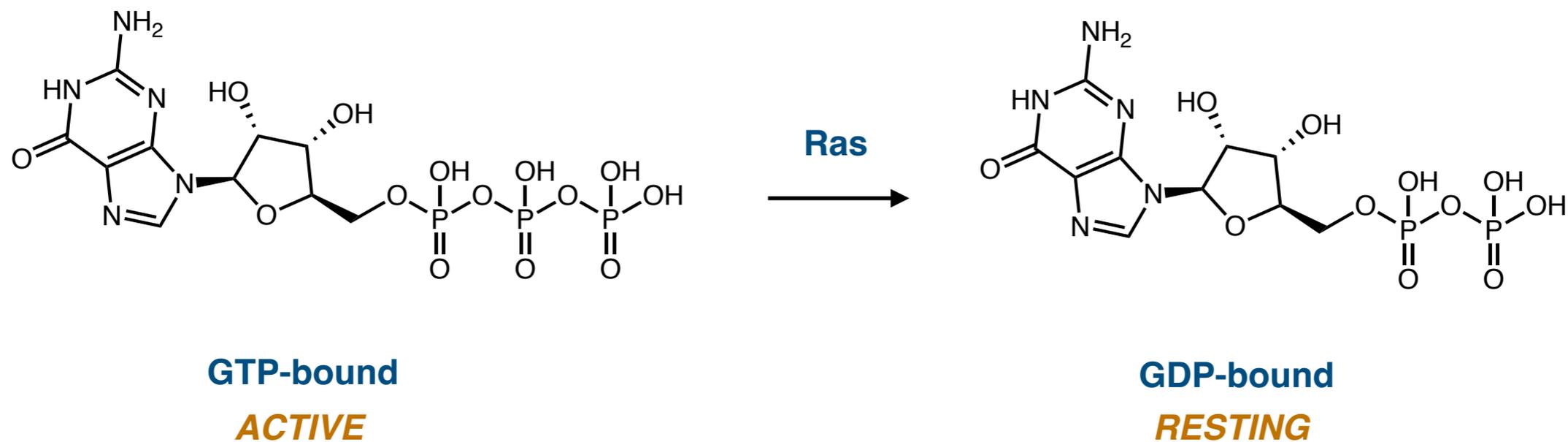
ACTIVE

Molecular switches to signaling networks

Investigating Druggability

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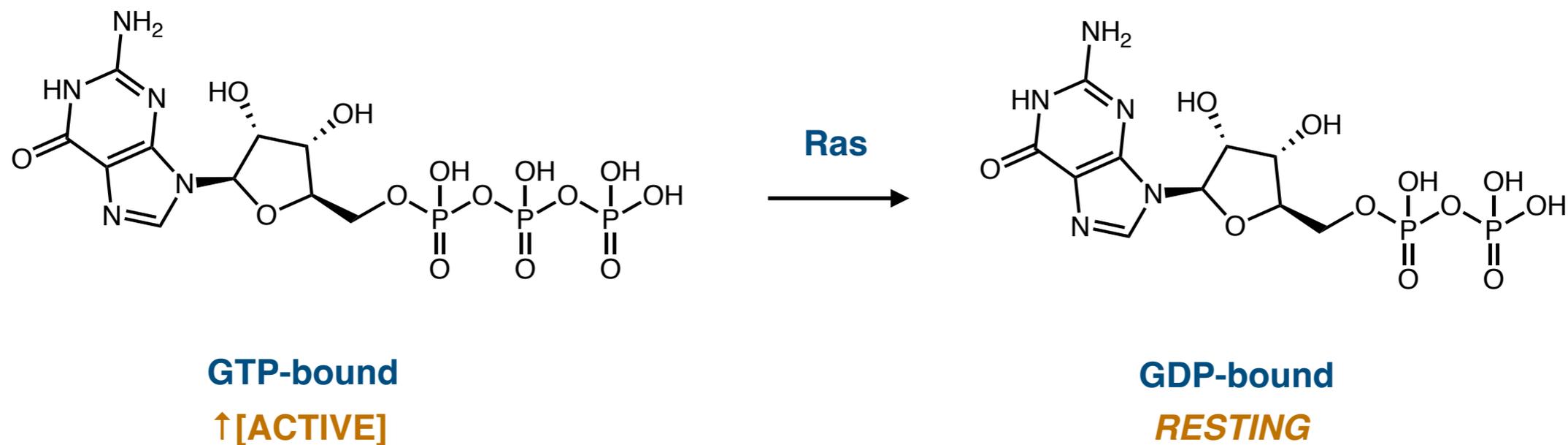


Molecular switches to signaling networks

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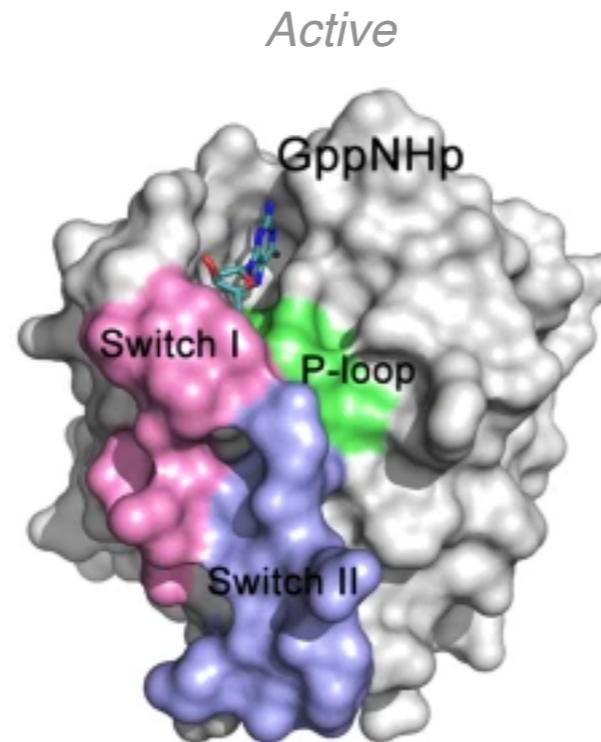
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Molecular switches to signaling networks

Stabilizing Surface Conformation

- **Surface representations of protein states:**



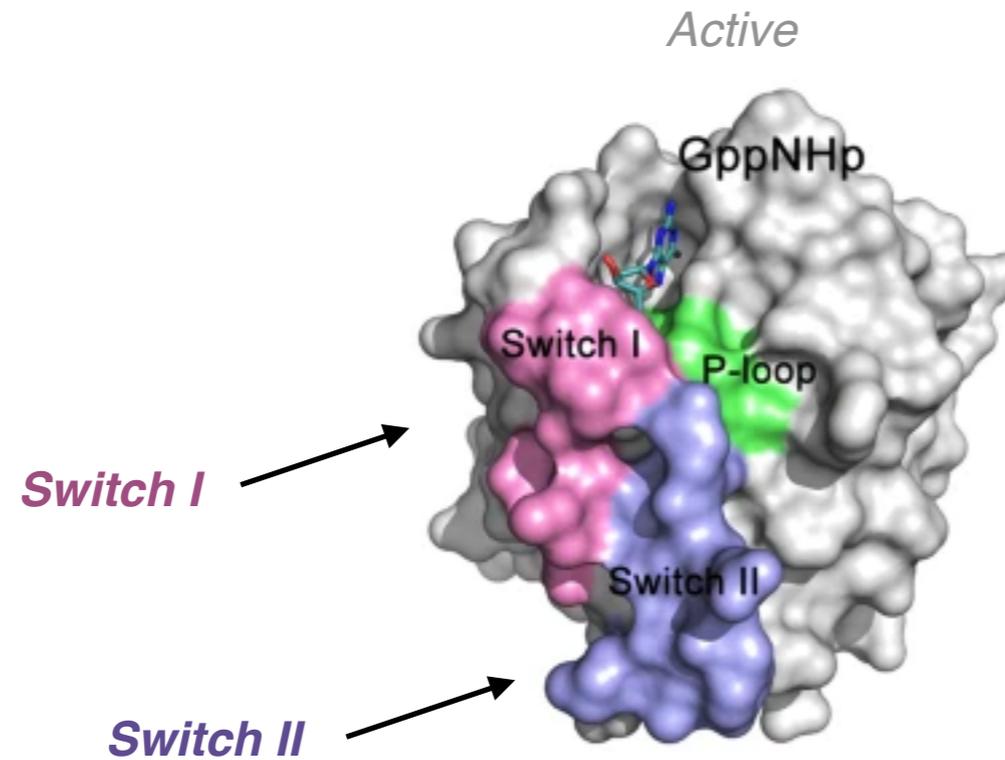
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- **2 regions change shape: Switch I, and Switch II**

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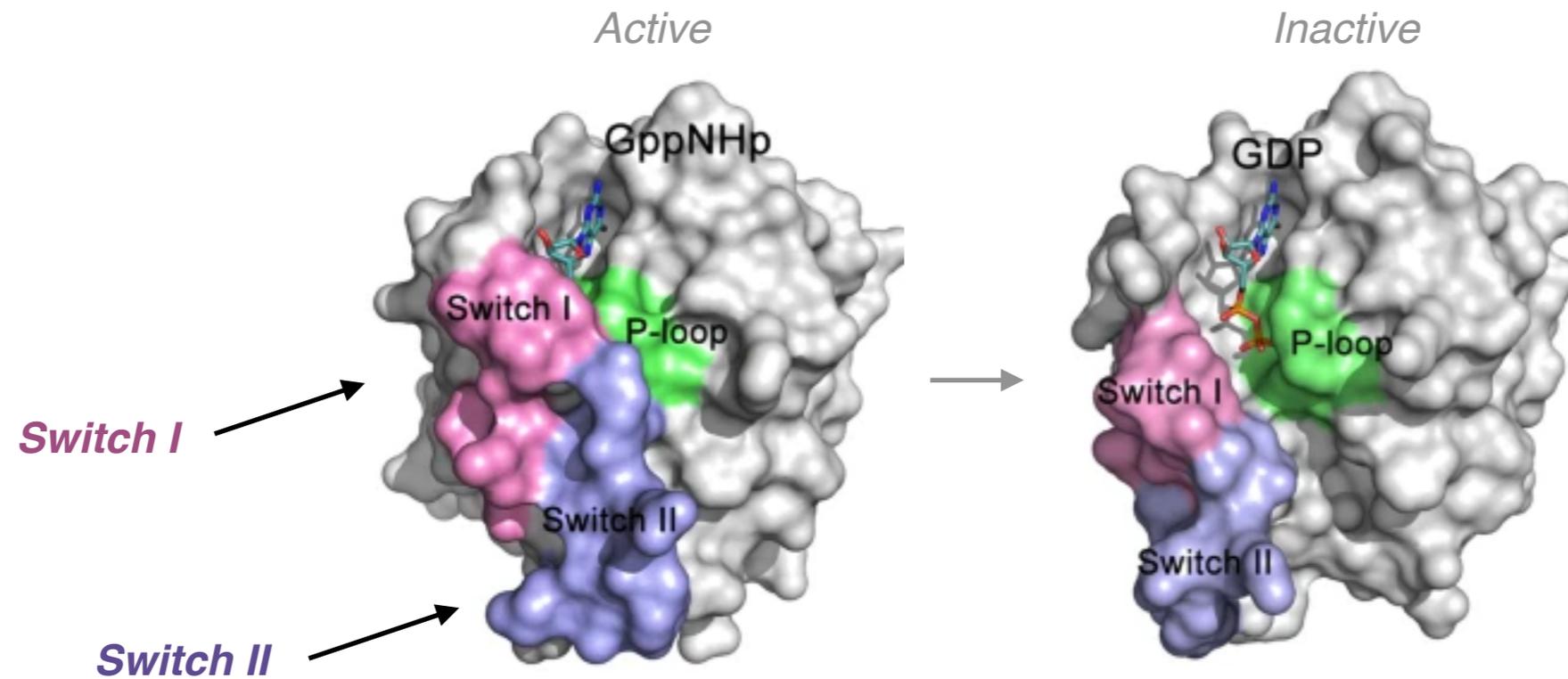
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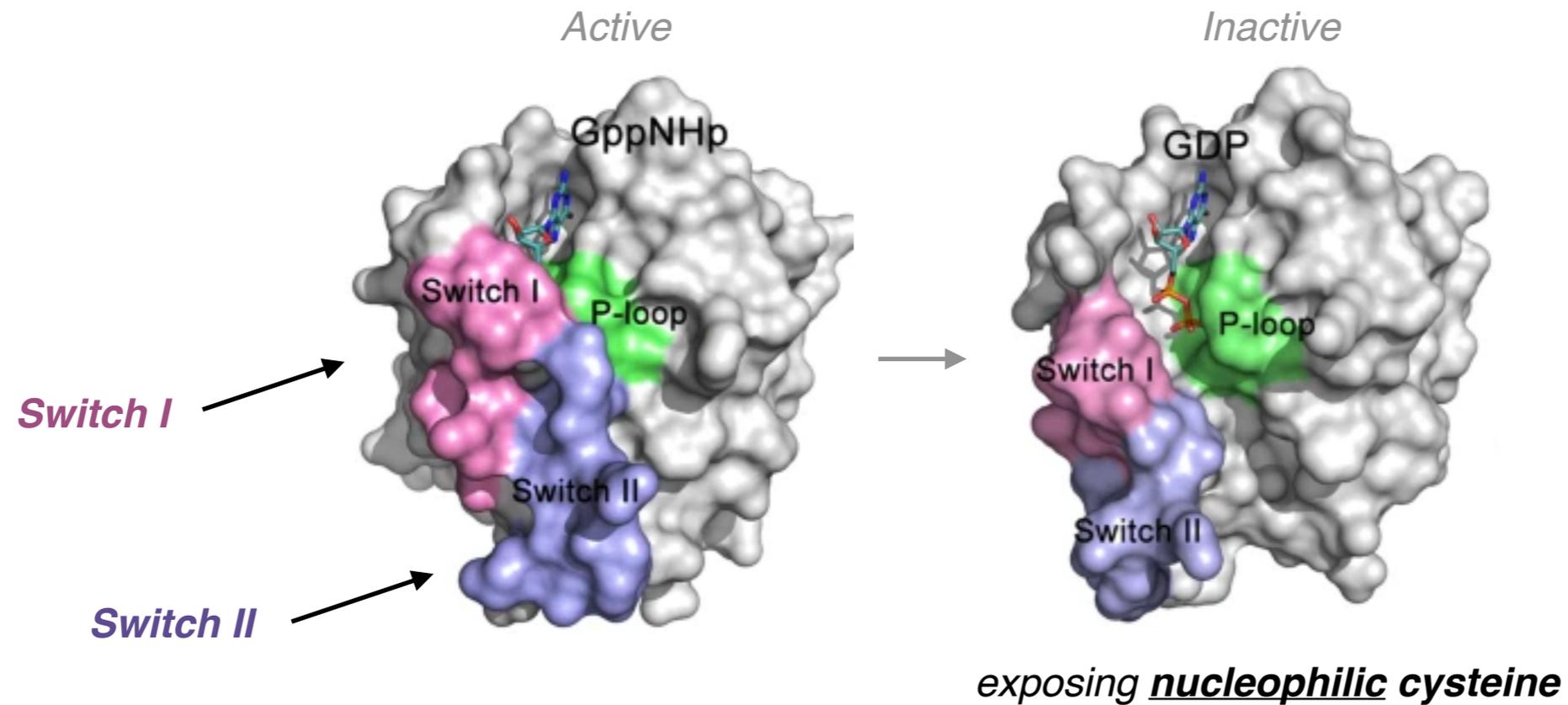
- **Signaling induces Ras conformational changes**
- **2 regions change shape: Switch I, and Switch II**

Milburn, M. V., Tong, L., Devos, A. M., Brünger, A., Yamaizumi, Z., Nishimura, S. *Science*. **1990**. 247, 939–945.

Pacold, M. E., Suire, S., Perisic, O., Lara-Gonzalez, S., Davis, C. T., Walker, E. H., Hawkins, P. T., Stephens, L., Eccleston, J. F., Williams, R. L. *Cell*. **2000**. 103, 931–944.

Stabilizing Surface Conformation

- **Surface representations of protein states:**



- **Switch II binding pocket changes in $G_{12}C$ mutant**

Milburn, M. V., Tong, L., Devos, A. M., Brünger, A., Yamaizumi, Z., Nishimura, S. *Science*. **1990**. 247, 939–945.

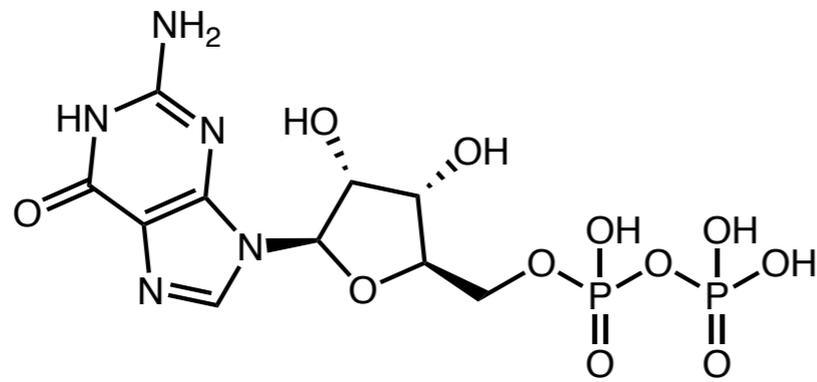
Pacold, M. E., Suire, S., Perisic, O., Lara-Gonzalez, S., Davis, C. T., Walker, E. H., Hawkins, P. T., Stephens, L., Eccleston, J. F., Williams, R. L. *Cell*. **2000**. 103, 931–944.

Investigating Druggability

KRAS: to kill the undruggable

KRAS targeting:

- *Covalent targeting to drug KRAS(G12C)*



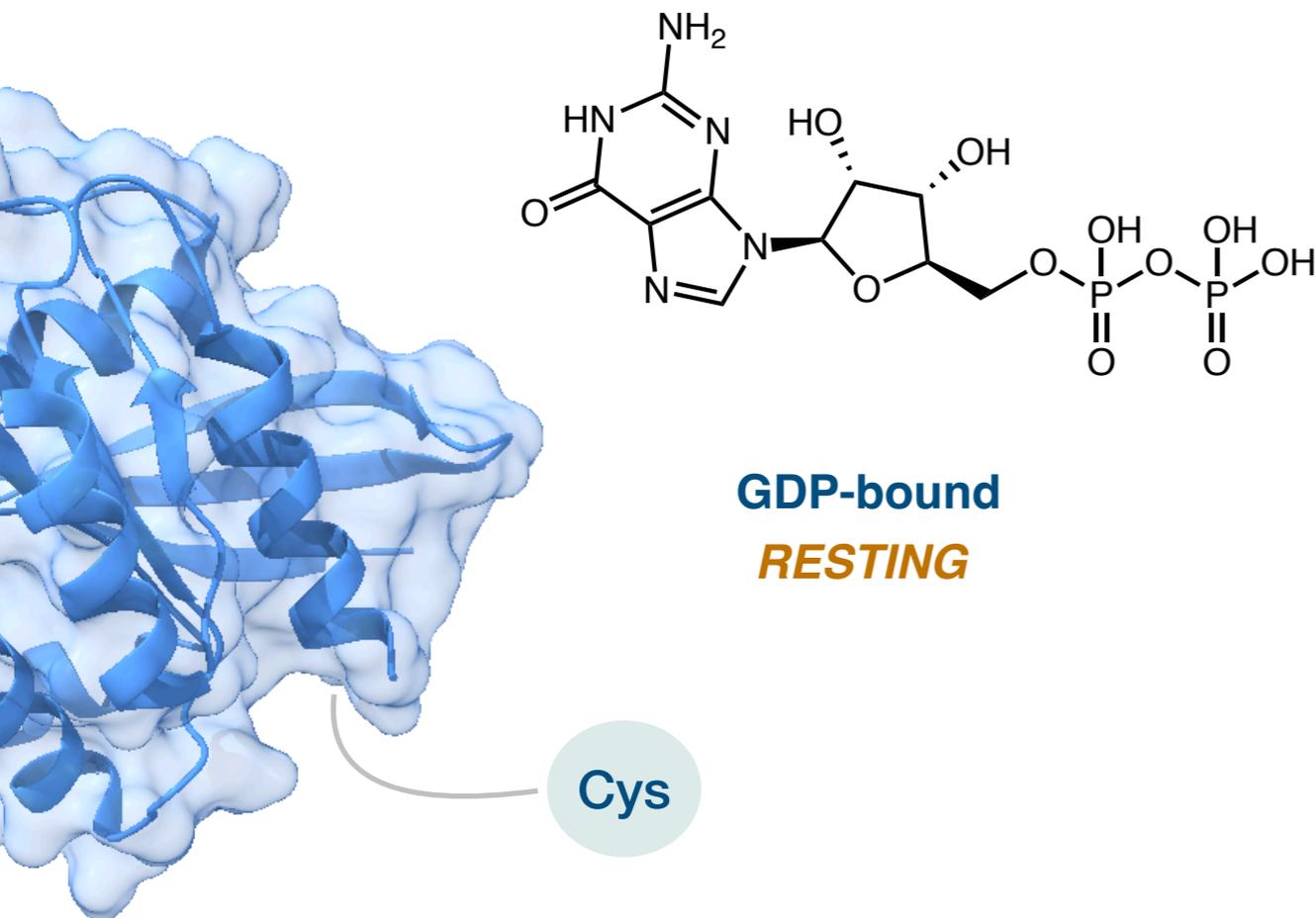
GDP-bound
RESTING

Investigating Druggability

KRAS: to kill the undruggable

KRAS targeting:

- *Covalent targeting to drug KRAS(G12C)*



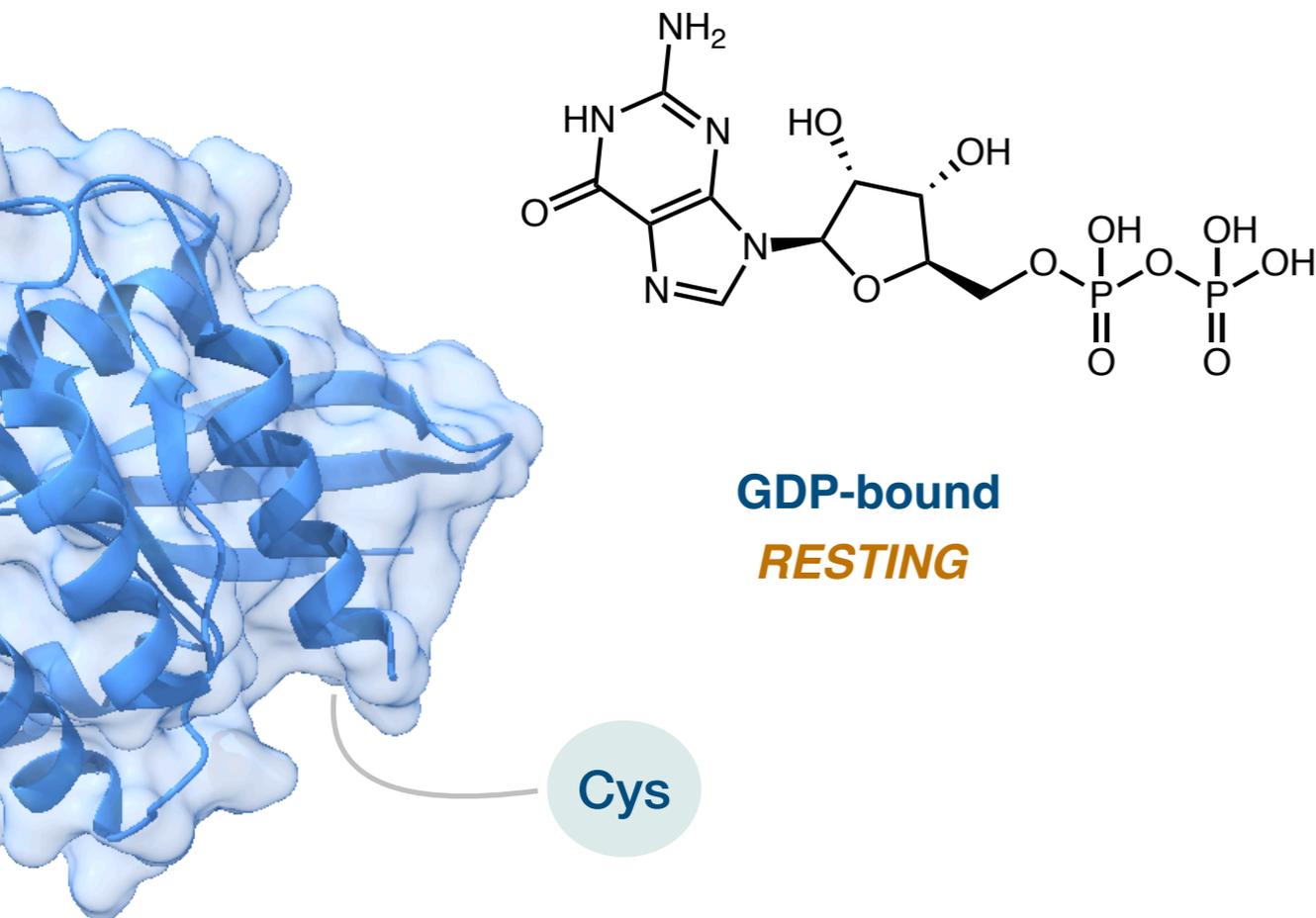
- *Drugs designed to target **nucleophilic cysteine 12** (Cys12) located in the hydrophobic switch-II pocket*

Investigating Druggability

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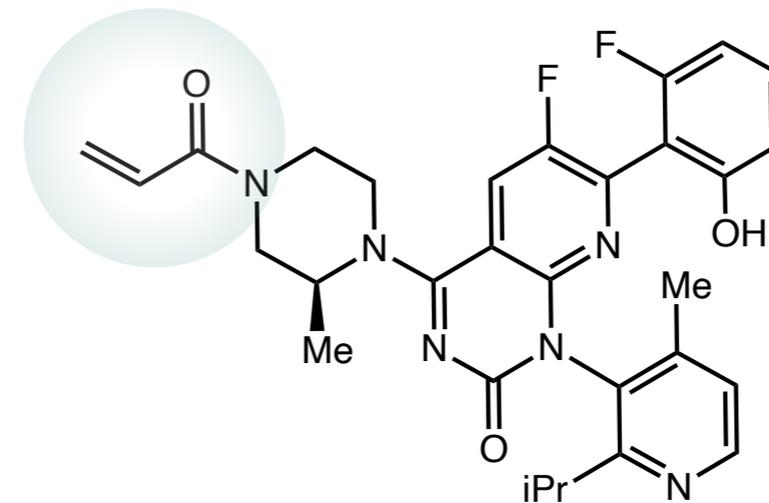
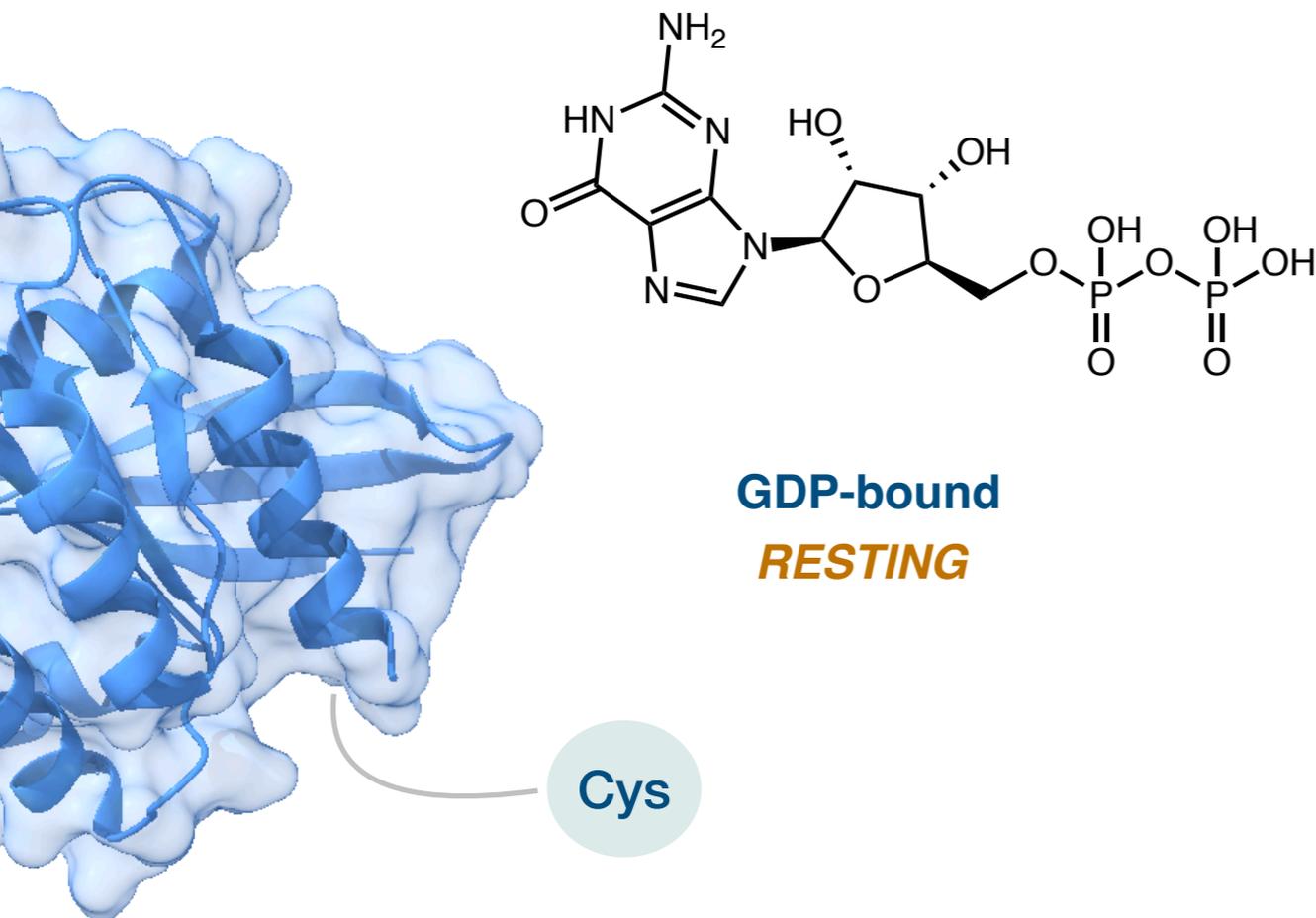
- *Drugs designed to target nucleophilic cysteine 12 (Cys12) located in the hydrophobic switch-II pocket*
 - *Optimization of an electrophilic warhead*

Investigating Druggability

KRAS: to kill the undruggable

KRAS targeting:

- Covalent targeting to drug KRAS(G12C)



Sotorasib
LUMAKRAS®

AMGEN

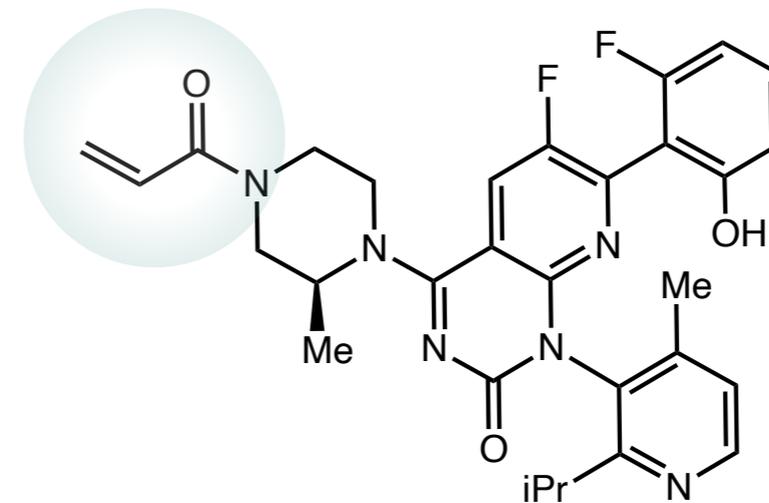
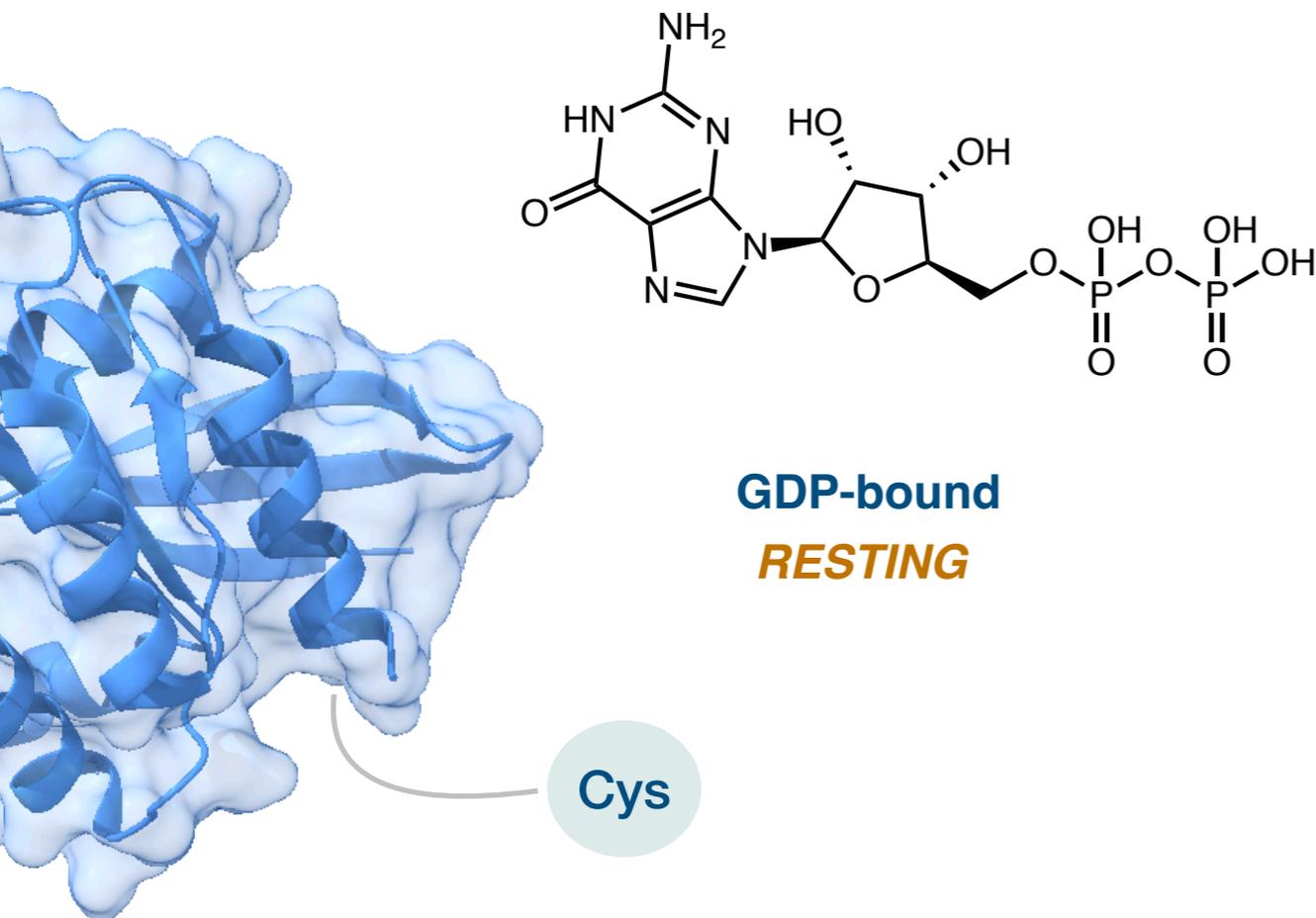
- Drugs designed to target **nucleophilic cysteine 12** (Cys12) located in the hydrophobic switch-II pocket
 - Optimization of an **electrophilic warhead**

Investigating Druggability

KRAS: to kill the undruggable

KRAS targeting:

- Covalent allosteric inhibitors to drug KRAS(G12C)



Sotorasib
LUMAKRAS®



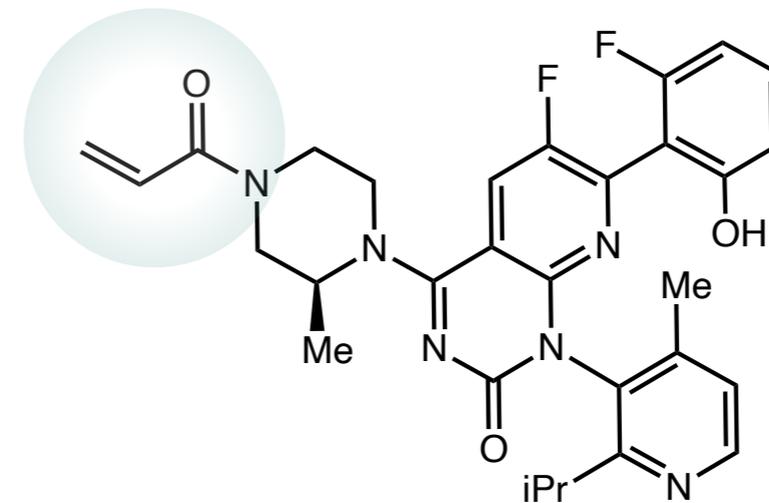
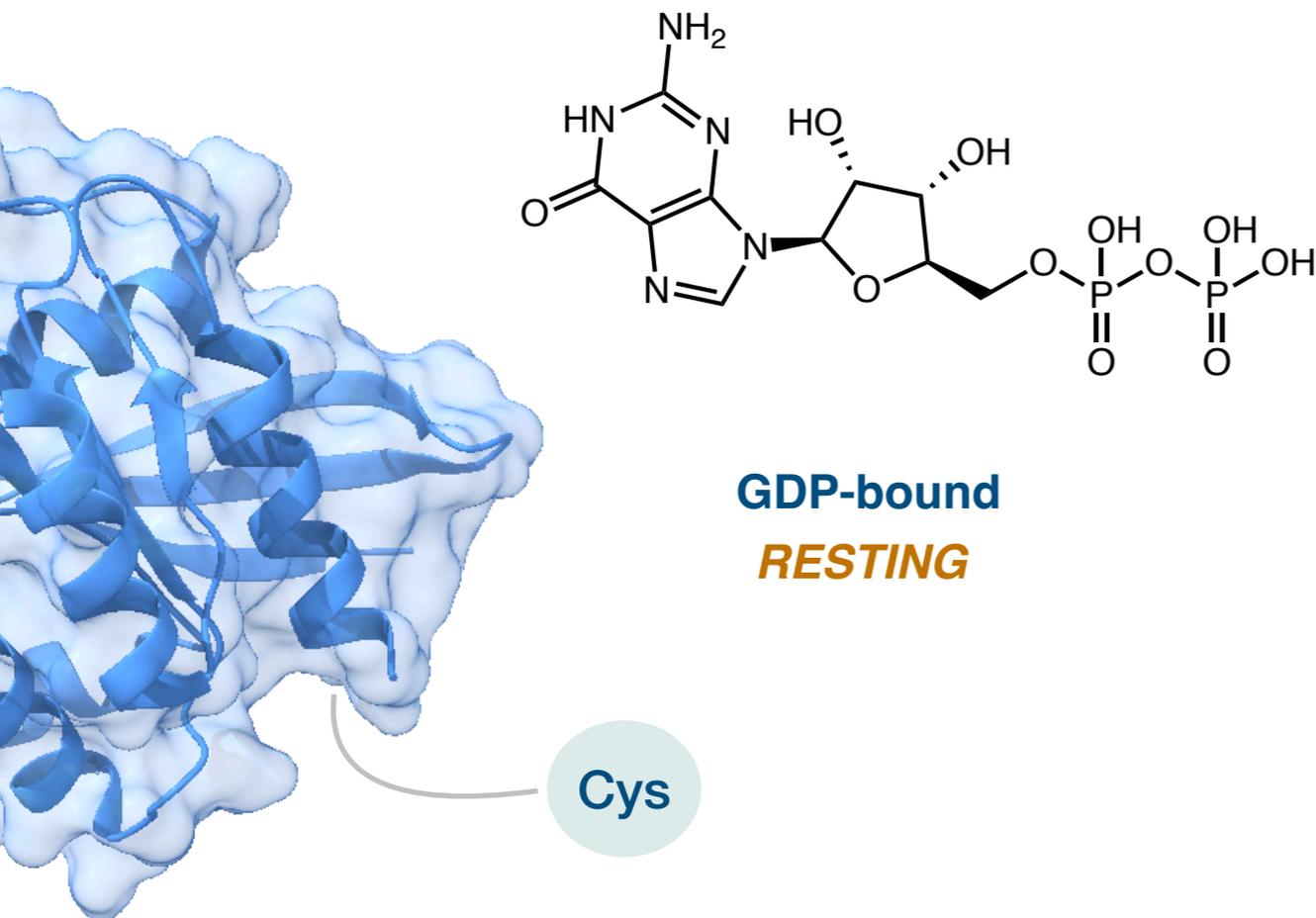
Sotorasib binds to the SII-P when KRAS(G12C) protein is **inactive GDP** bound state

Investigating Druggability

KRAS: to kill the undruggable

KRAS targeting:

- Covalent allosteric inhibitors to drug KRAS(G12C)



Sotorasib
LUMAKRAS®



Avoids pan RAS inhibition

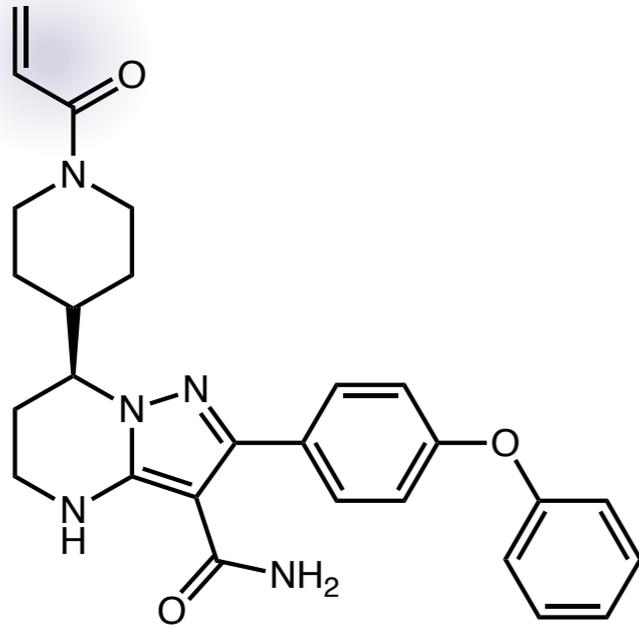
Covalent binding

Many immunomodulatory drugs covalently bind cysteine

- *Electrophilic probes are a key component of T cell research*

Covalent binding

Many immunomodulatory drugs covalently bind cysteine



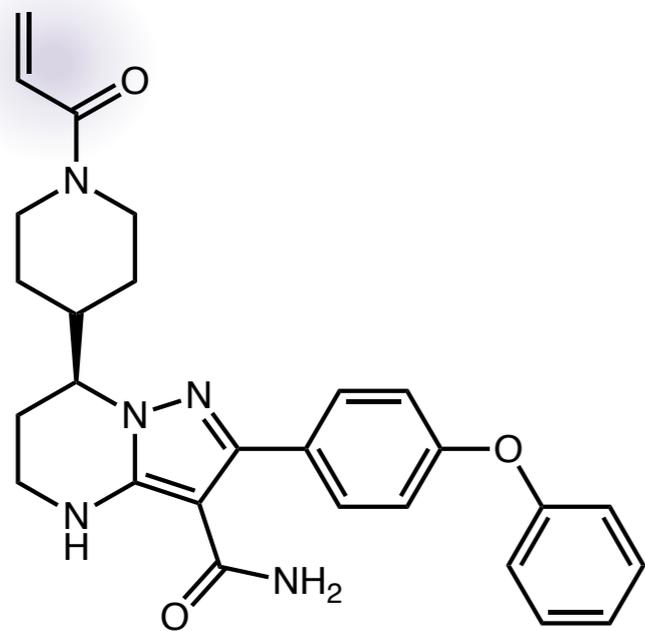
Brukina®

\$1.3 billion (USD)*

- ***Electrophilic probes are a key component of T cell research***

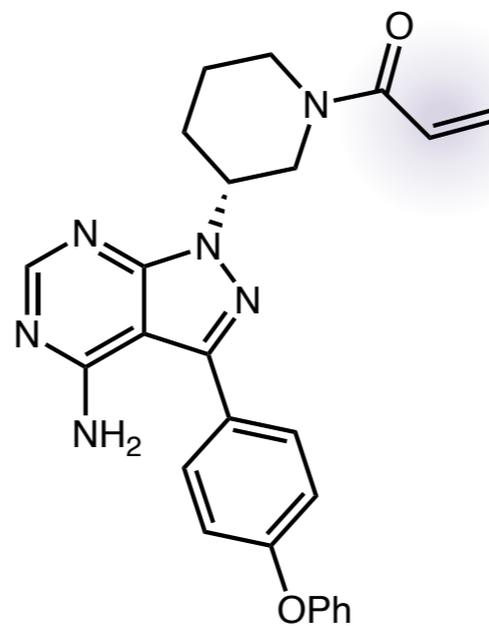
Covalent binding

Many immunomodulatory drugs covalently bind cysteine



Brukina®

\$1.3 billion (USD)*



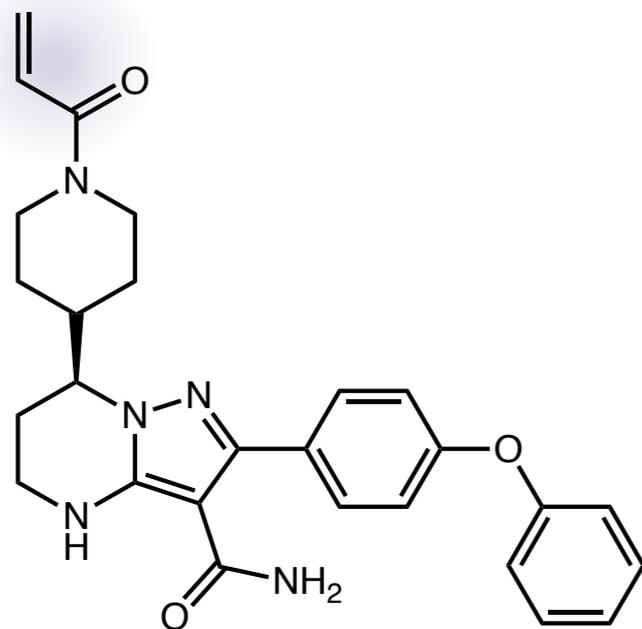
Ibruvica® (Ibrutinib)

\$4.9 billion (USD)*

- **Electrophilic probes are a key component of T cell research**

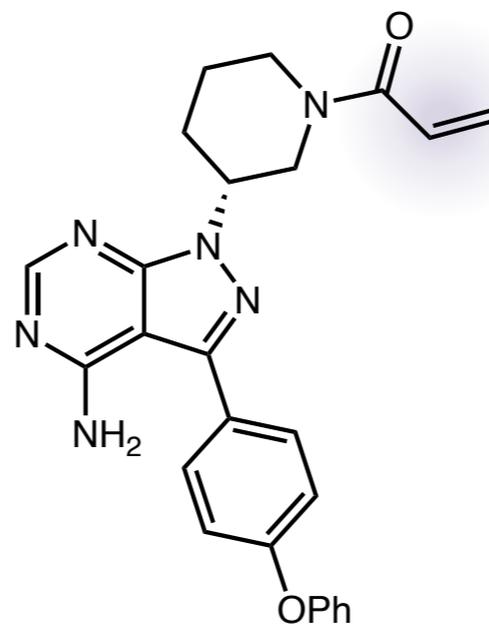
Covalent binding

Many immunomodulatory drugs covalently bind cysteine



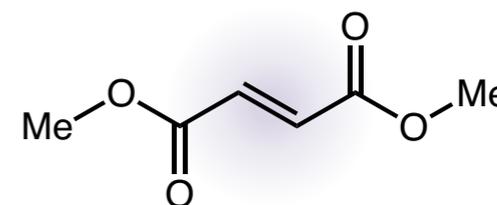
Brukinsa®

\$1.3 billion (USD)*



Ibruvica® (Ibrutinib)

\$4.9 billion (USD)*



Tecfidera®

\$4.2 billion (USD)*

- **Electrophilic probes are a key component of T cell research**

Covalent binding

- *How do you identify electrophilic probes?*

Activity Based Protein Profiling
Discovering drug–amino acid interactions

Activity Based Protein Profiling

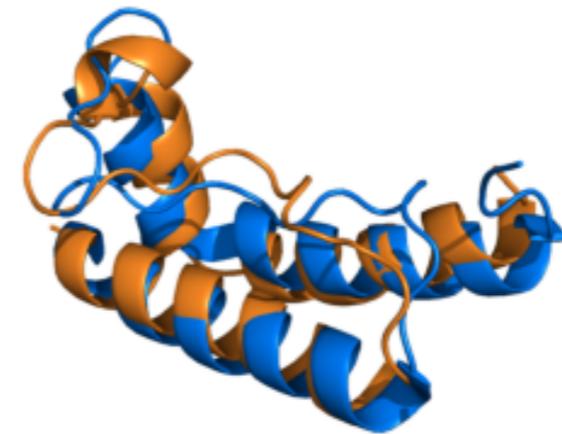
Activity Based Protein Profiling

Discovering drug–amino acid interactions

Genome sequencing



✓ *Predicted proteins*



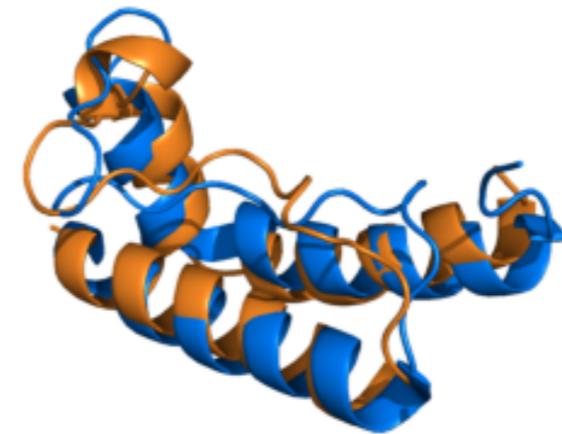
Activity Based Protein Profiling

Discovering drug–amino acid interactions

Genome sequencing



✓ *Predicted proteins*



- ***Assignment of protein function remains a challenge***

Activity Based Protein Profiling

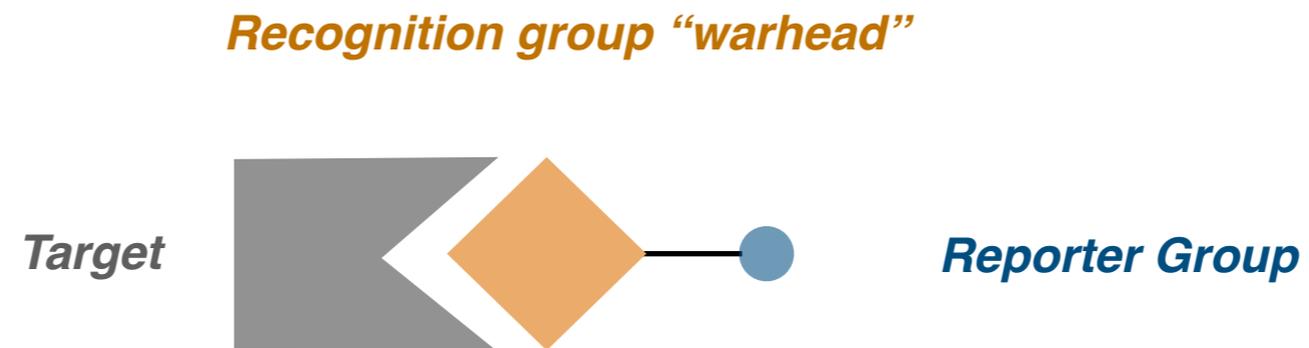
Discovering drug–amino acid interactions

- ***Activity-based protein profiling (ABPP)*** to probe small molecule–protein interactions
-

Activity Based Protein Profiling

Discovering drug–amino acid interactions

- **Activity-based protein profiling (ABPP)** to probe small molecule–protein interactions
-

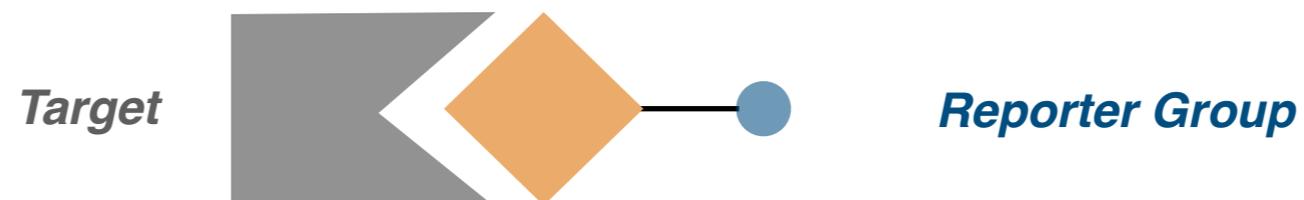


Activity Based Protein Profiling

Discovering drug–amino acid interactions

- **Activity-based protein profiling (ABPP)** to probe small molecule–protein interactions
-

Recognition group “warhead”



ABPP probes can be tuned towards:

- Cellular potency
- Stereochemical selectivity
- Site-specificity

Weerapana, E., Wang, C., Simon, G. M., Richter, F., Khare, S., Dillon, M. B. D., Bachovin, D. A., Mowen, K., Baker, D., Cravatt, B. F. *Nature*. **2010**. 468, 790–795

Porta, E. O. J., Steel, P. G. *Curr Res Pharmacol Drug Discov*. **2023**. 5. 100164–100171.

Activity Based Protein Profiling
Discovering reactivity profiles of interactors

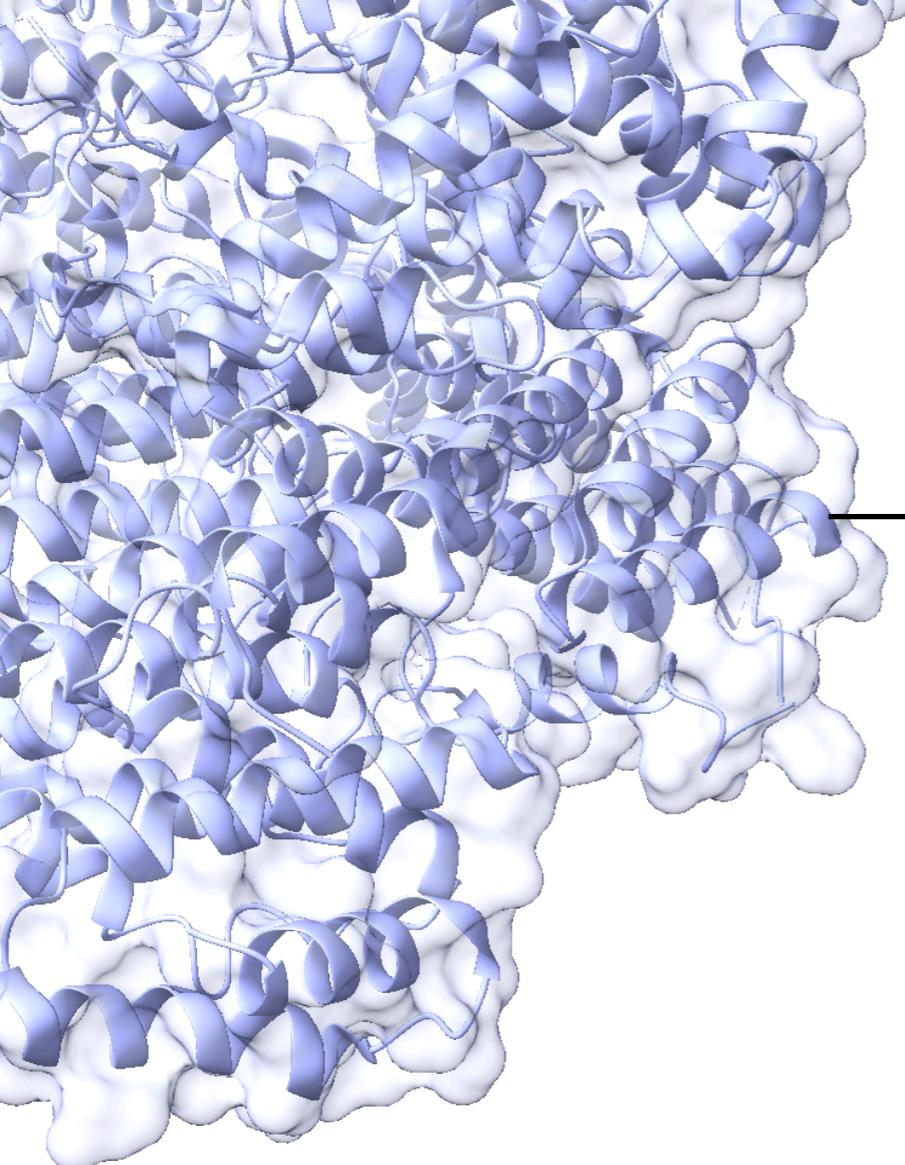
Article | Published: 17 November 2010

Quantitative reactivity profiling predicts functional cysteines in proteomes

[Eranthie Weerapana](#), [Chu Wang](#), [Gabriel M. Simon](#), [Florian Richter](#), [Sagar Khare](#), [Myles B. D. Dillon](#),
[Daniel A. Bachovchin](#), [Kerri Mowen](#), [David Baker](#) & [Benjamin F. Cravatt](#) 

[Nature](#) **468**, 790–795 (2010) | [Cite this article](#)

44k Accesses | **34** Altmetric | [Metrics](#)



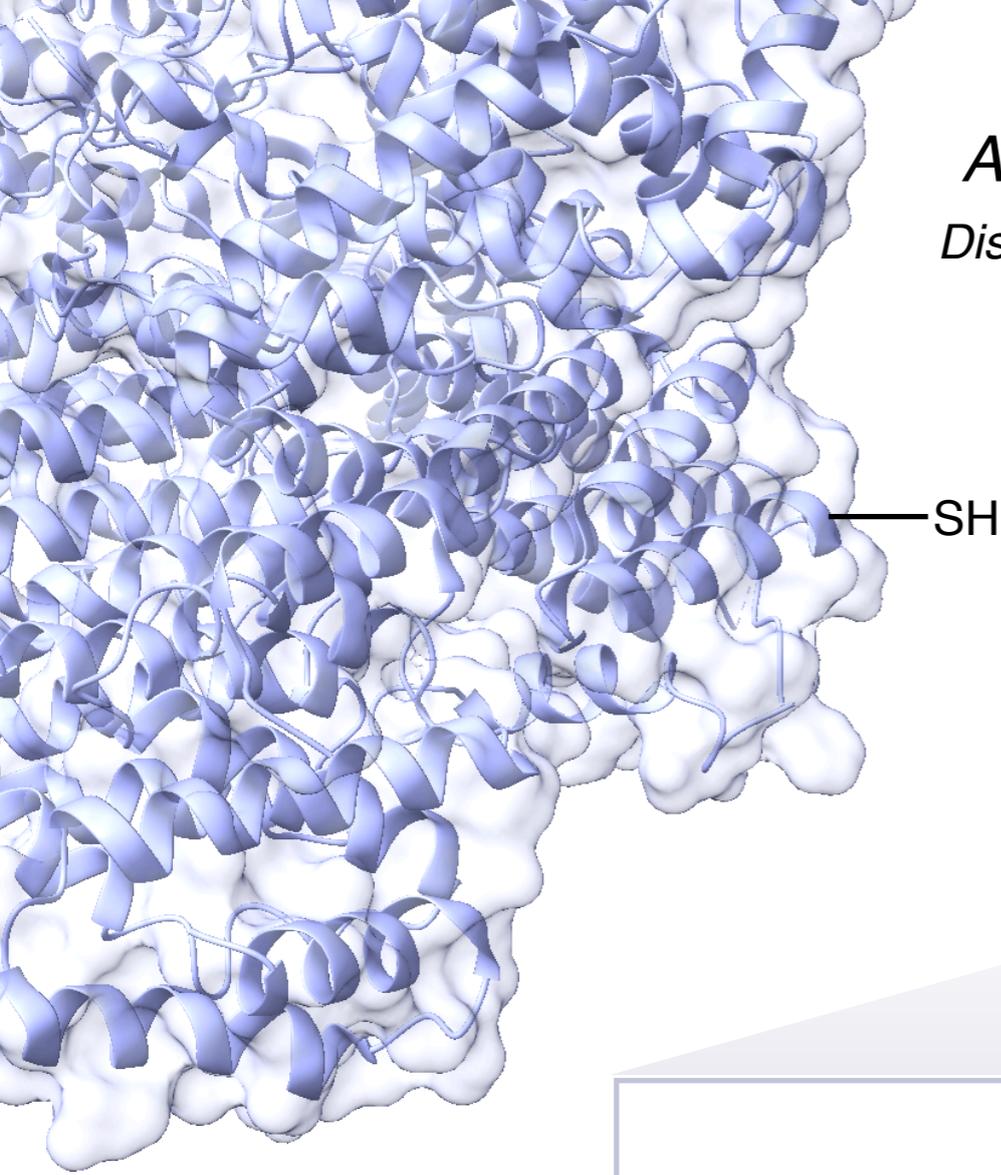
Activity Based Protein Profiling
Discovering reactivity profiles of interactors

—SH

- ***Cys is a nucleophilic amino acid***

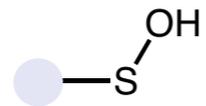
Activity Based Protein Profiling

Discovering reactivity profiles of interactors



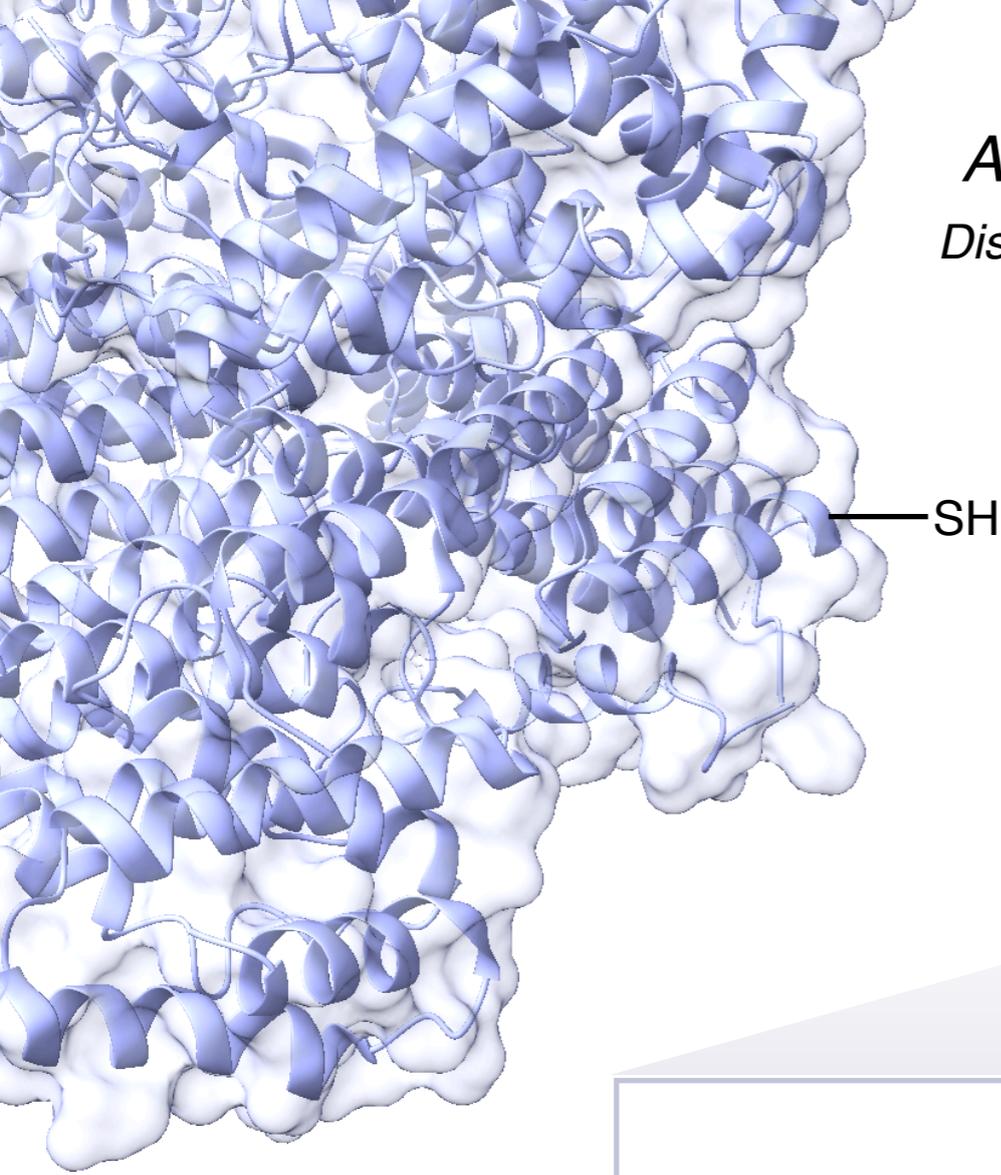
- ***Cys is a nucleophilic amino acid***

- ***Sulphenation***



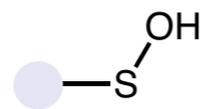
Activity Based Protein Profiling

Discovering reactivity profiles of interactors

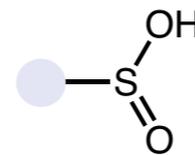


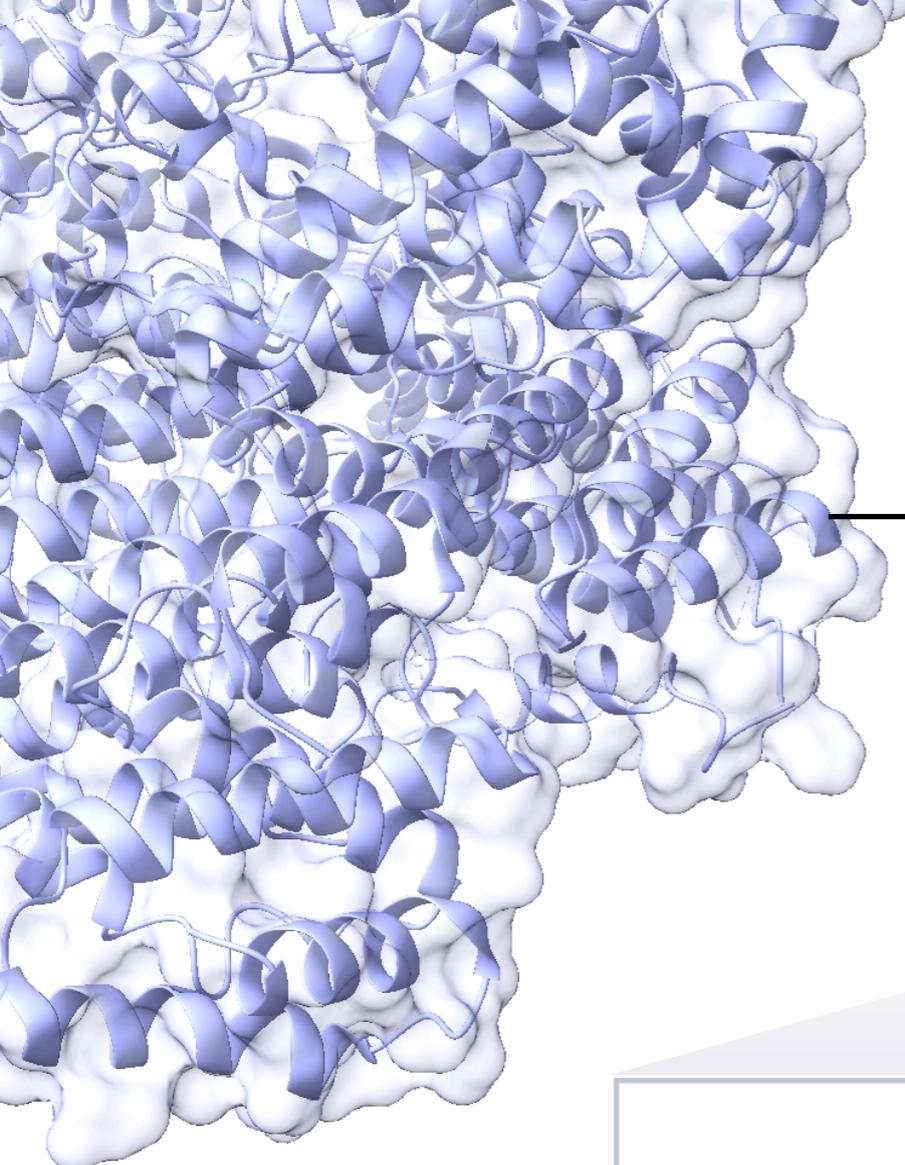
- **Cys is a nucleophilic amino acid**

- **Sulphenation**



- **Sulphination**





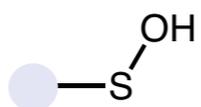
Activity Based Protein Profiling

Discovering reactivity profiles of interactors

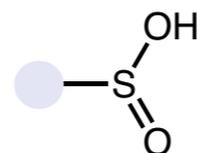
—SH

- ***Cys is a nucleophilic amino acid***

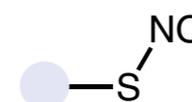
- ***Sulphenation***



- ***Sulphination***



- ***Nitrosylation***



- ***Oxidative PTMs enable regulatory behavior***

Activity Based Protein Profiling
Discovering reactivity profiles of interactors

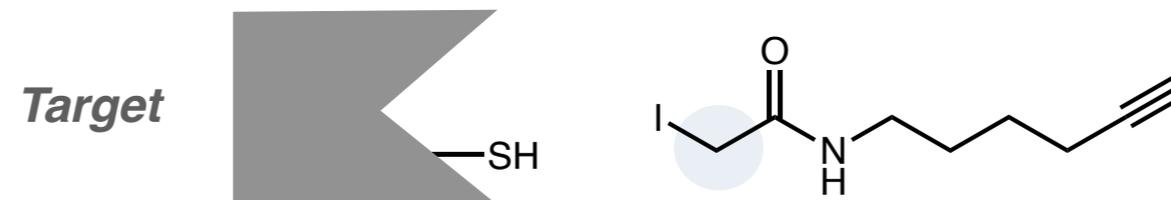
Isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling
(isoTOP-ABPP)

Activity Based Protein Profiling

Discovering reactivity profiles of interactors

Isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling (isoTOP-ABPP)

1. Labelling

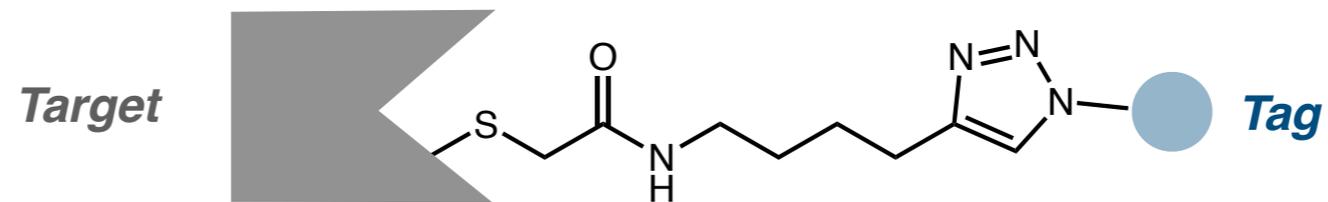


Activity Based Protein Profiling

Discovering reactivity profiles of interactors

Isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling (isoTOP-ABPP)

2. Conjugation

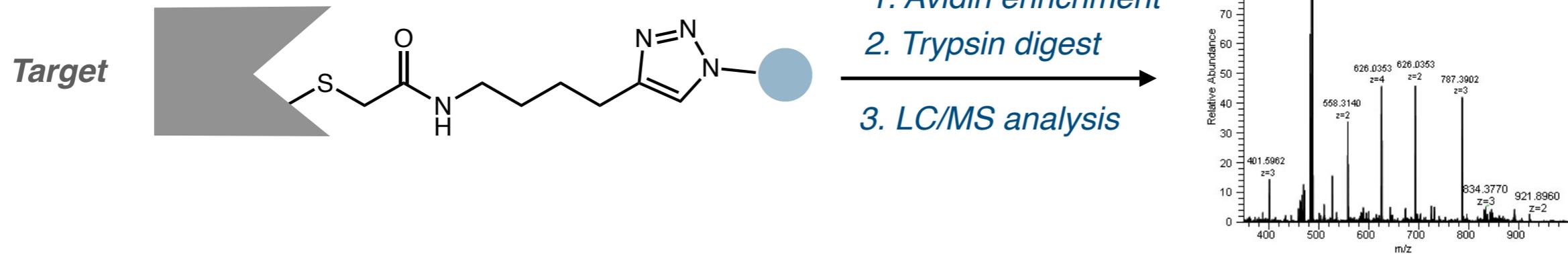


Activity Based Protein Profiling

Discovering reactivity profiles of interactors

Isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling (isoTOP-ABPP)

3. Enrichment and Digestion

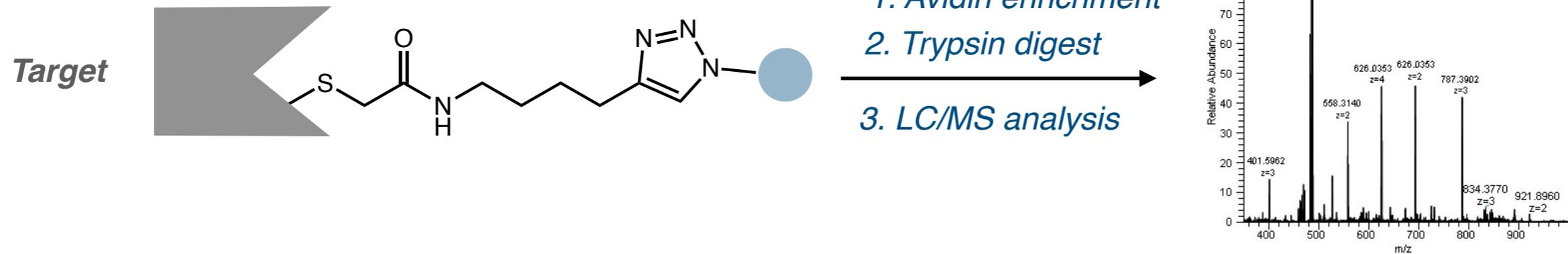


Activity Based Protein Profiling

Discovering reactivity profiles of interactors

Isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling (isoTOP-ABPP)

3. Enrichment and Digestion



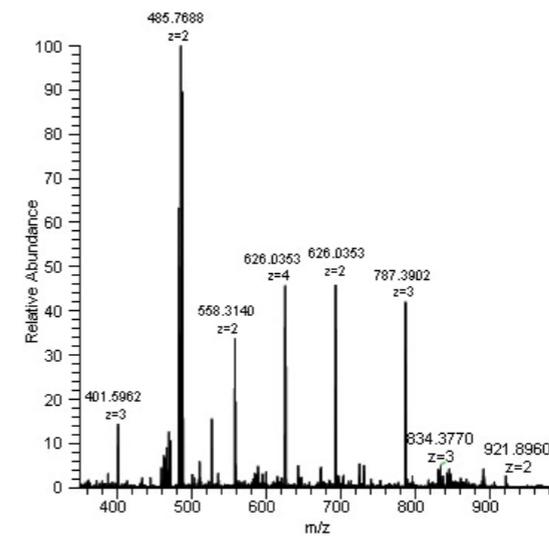
isotopic ratios of the peptides enable quantification in Cys reactivity

Activity Based Protein Profiling

Discovering reactivity profiles of interactors

- **Activity-Based Protein Profiling (ABPP)**

MS Quantifies extent of Cys labelling



LC/MS analysis

Activity Based Protein Profiling

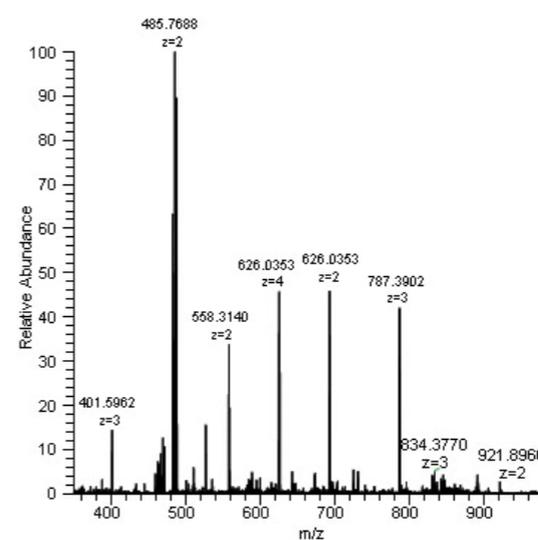
Discovering reactivity profiles of interactors

- **Activity-Based Protein Profiling (ABPP)**

MS Quantifies extent of Cys labelling



Enables Target ID and SAR



LC/MS analysis

Activity Based Protein Profiling

Discovering interactors

- *ABPP in drug discovery*



abbvie

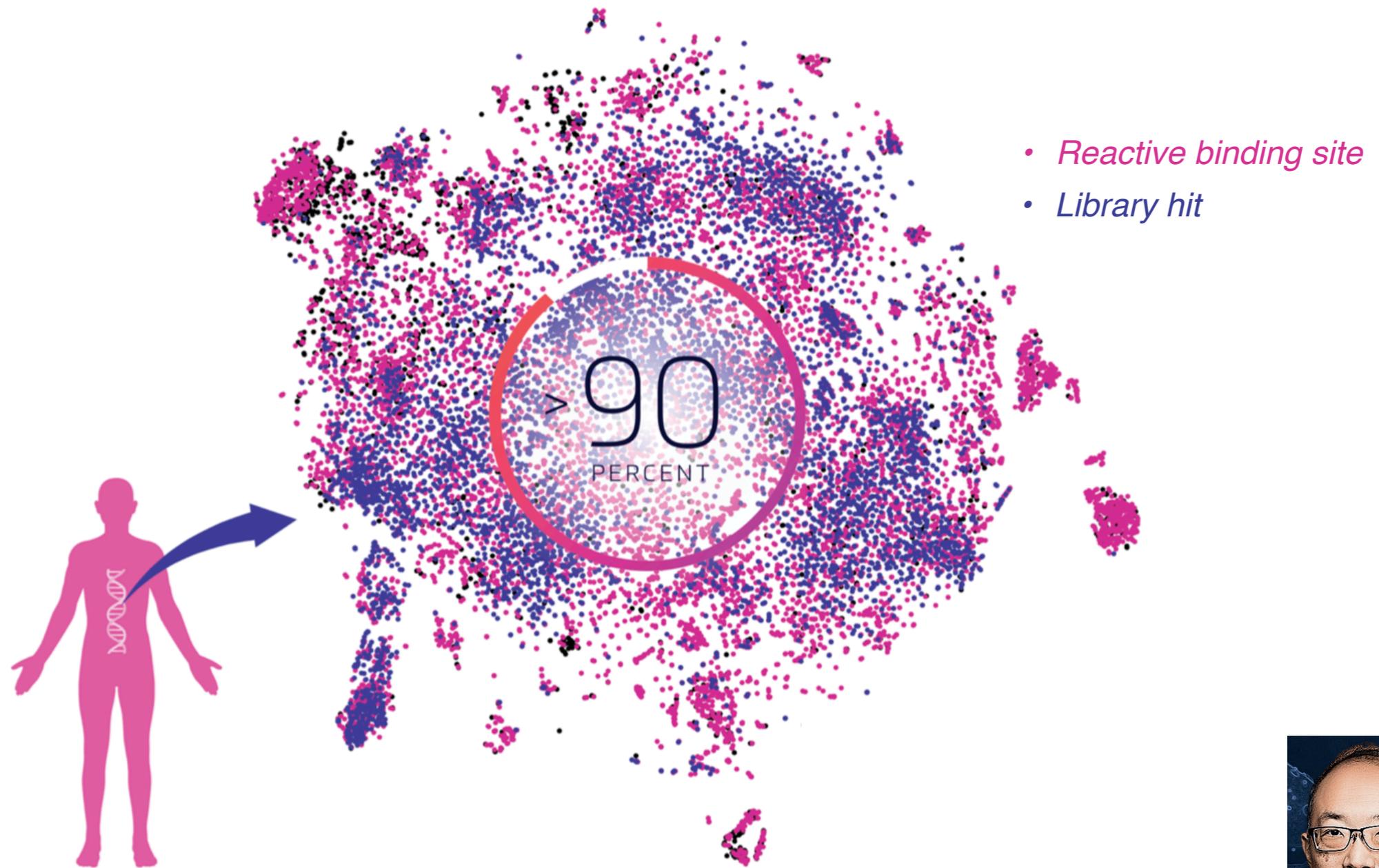
Founded in 2018



Prof. Dan Nomura

Activity Based Protein Profiling

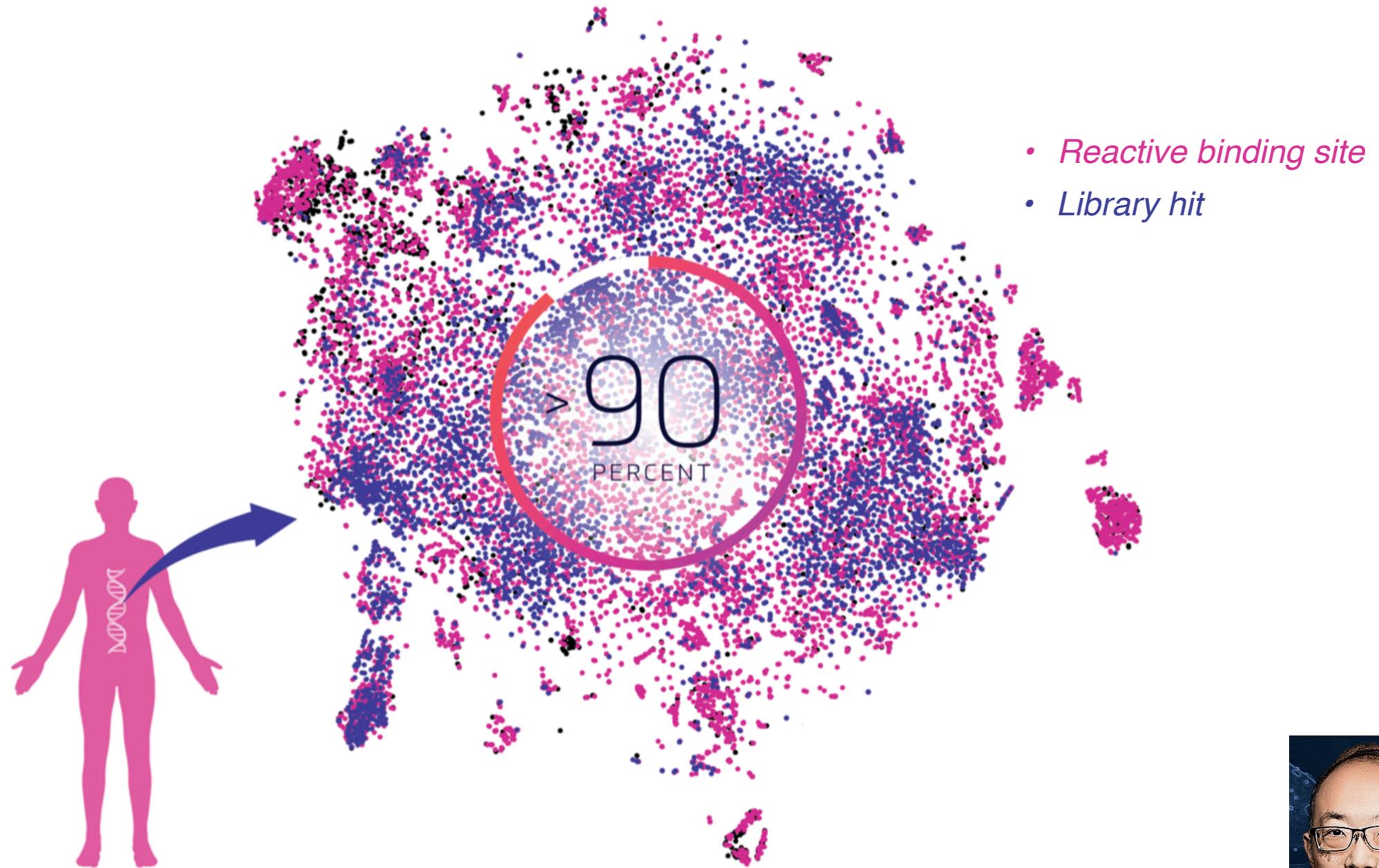
Discovering interactors



Prof. Dan Nomura

Activity Based Protein Profiling

Discovering interactors



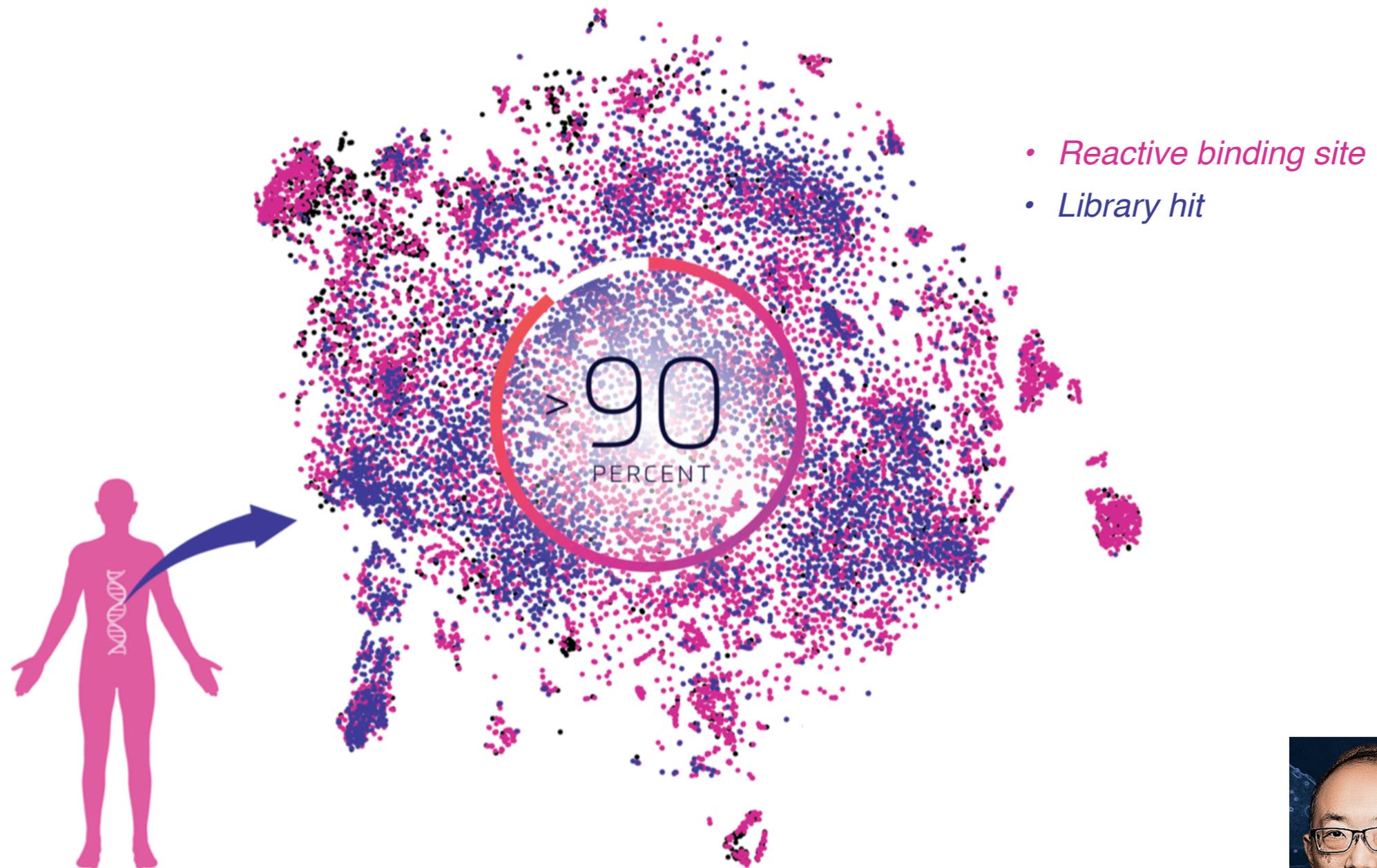
- **Activation score enables a rank-prioritization across the proteome**



Prof. Dan Nomura

Activity Based Protein Profiling

Discovering interactors



- **Activation score enables a rank-prioritization across the proteome**

- **Proposal: Informs drug discovery**

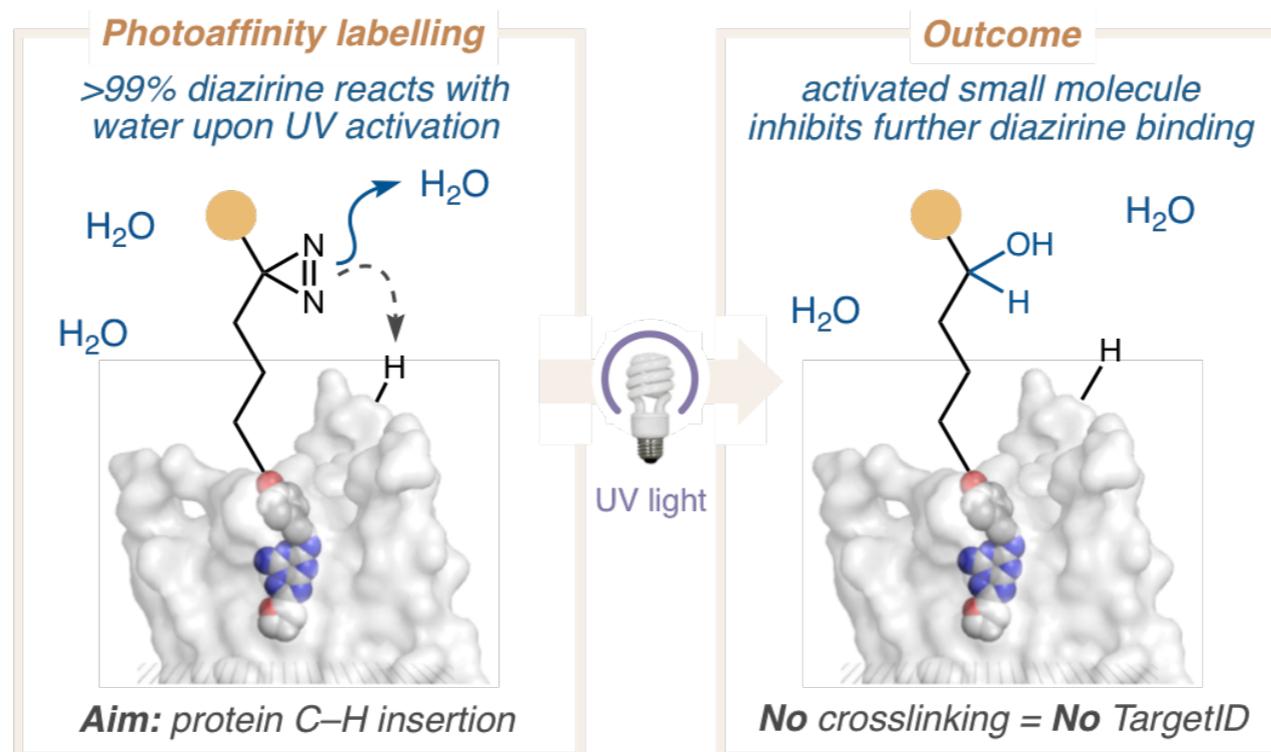


Prof. Dan Nomura

Small molecule photocatalysis enables drug target identification



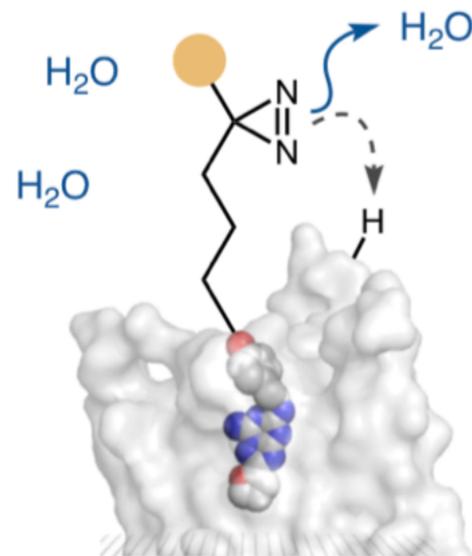
Small molecule photocatalysis enables drug target identification



Investigating Interactors

Modern Target ID methods:

1. PAL

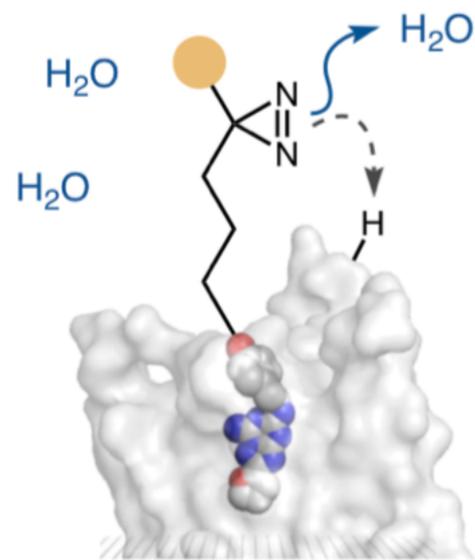


Directly tag the target

Investigating Interactors

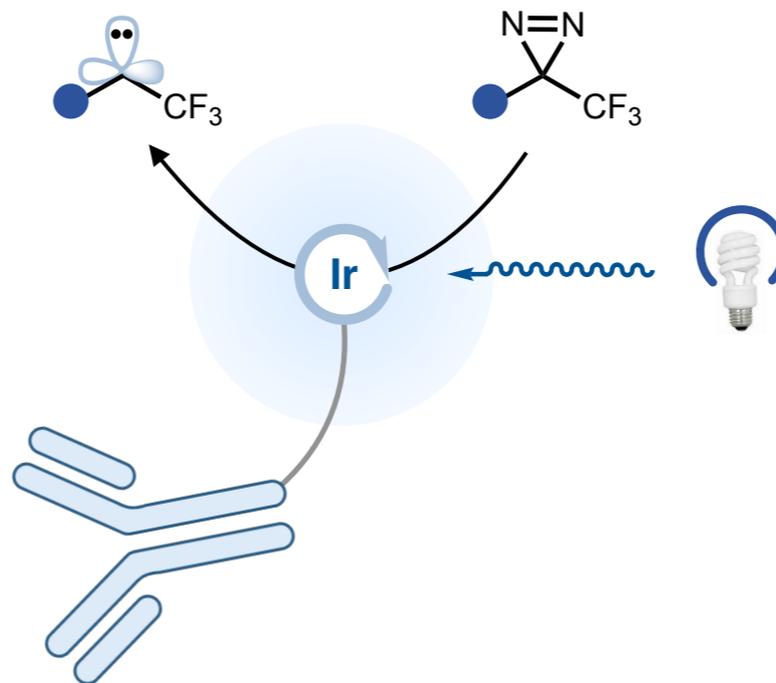
Modern Target ID methods:

1. PAL



Directly tag the target

2. Photoreactive probes

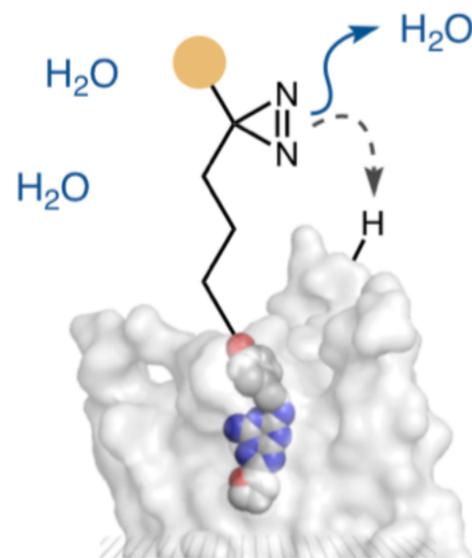


μmap

Investigating Interactors

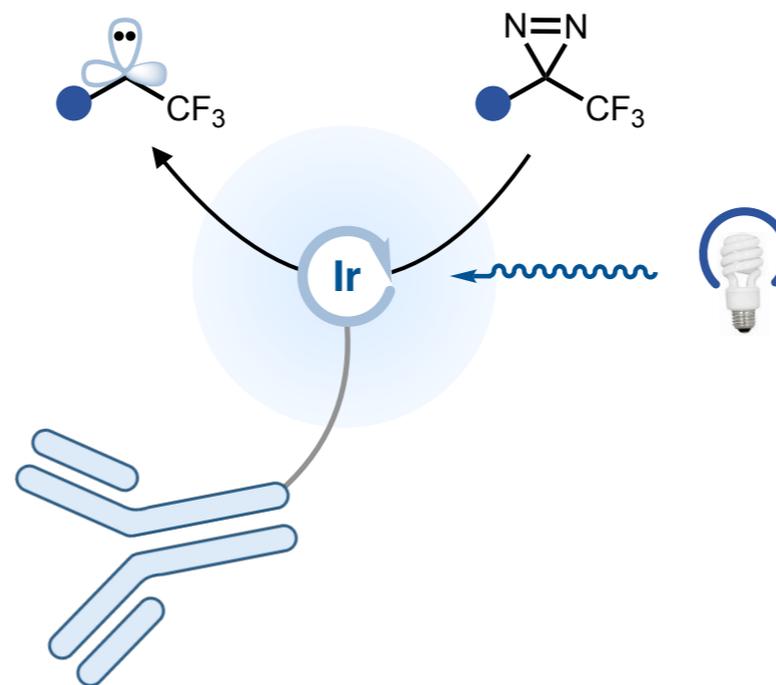
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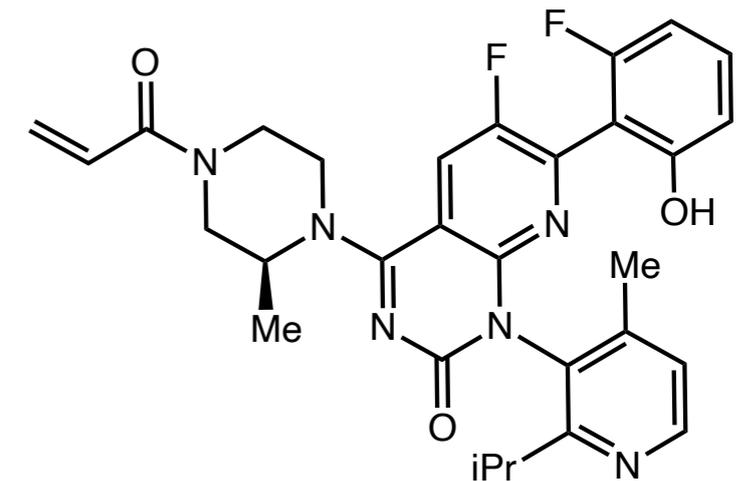
Directly tag the target

2. Photoreactive probes



μmap

3. Activity Based Protein Profiling

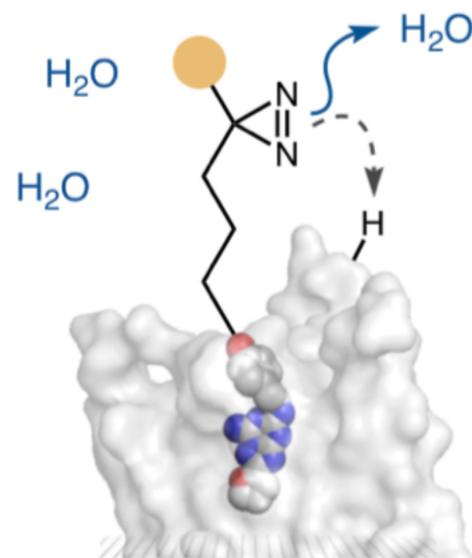


No target modification

Investigating Interactors

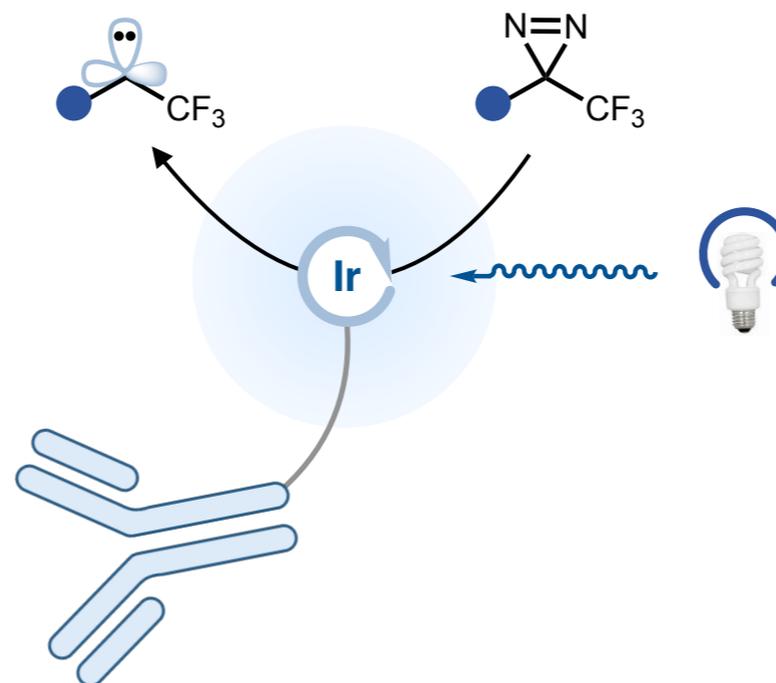
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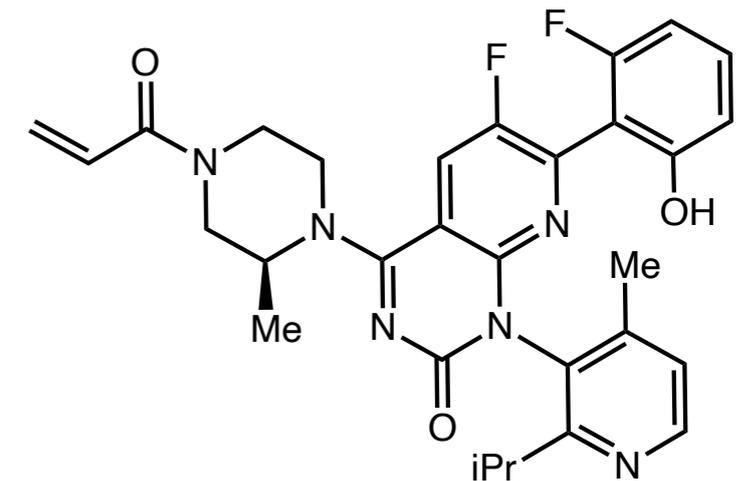
Directly tag the target

2. Photoreactive probes



μ map

3. Activity Based Protein Profiling

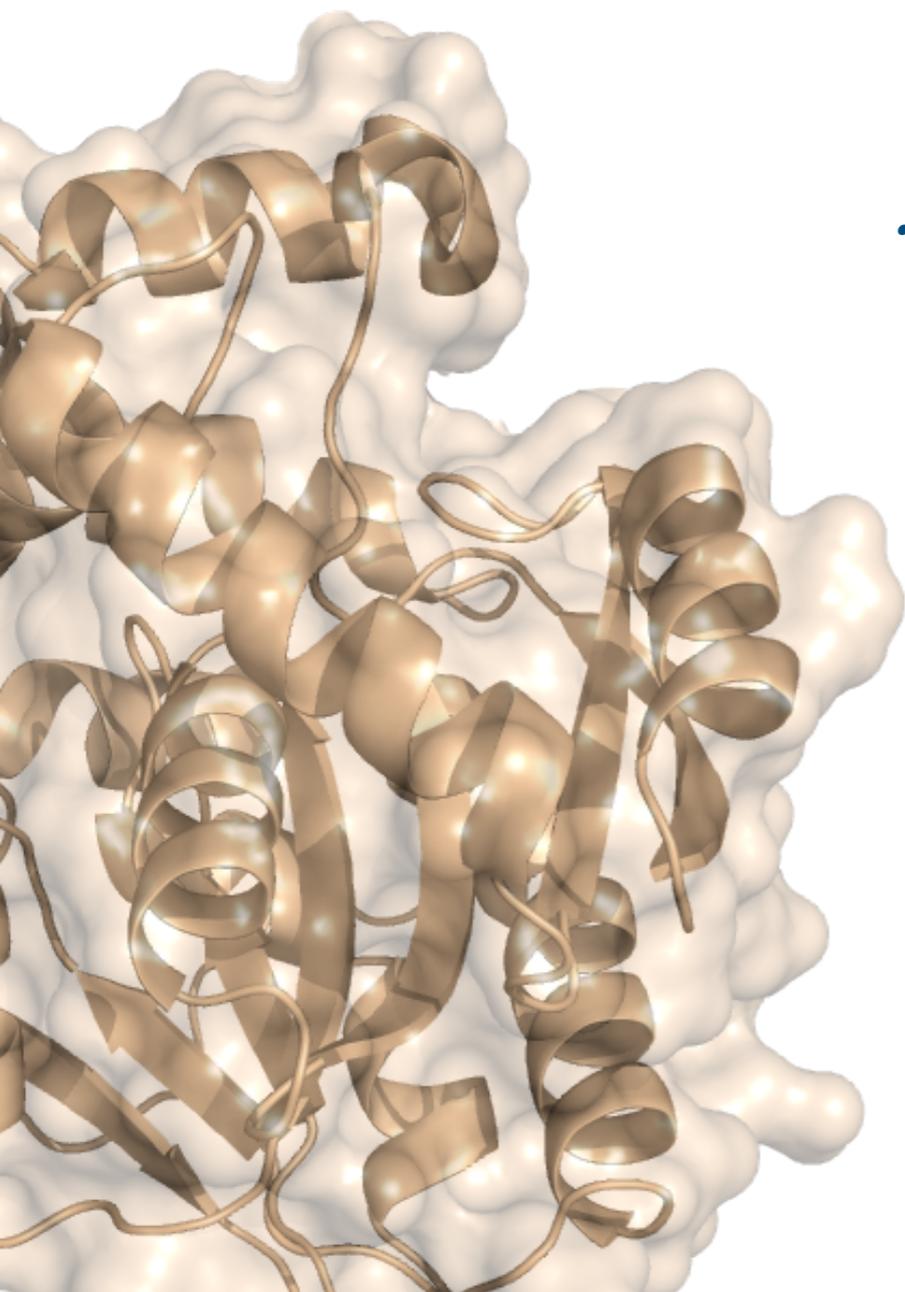


No target modification

Highly limited to Cys residues

Ligand Discovery

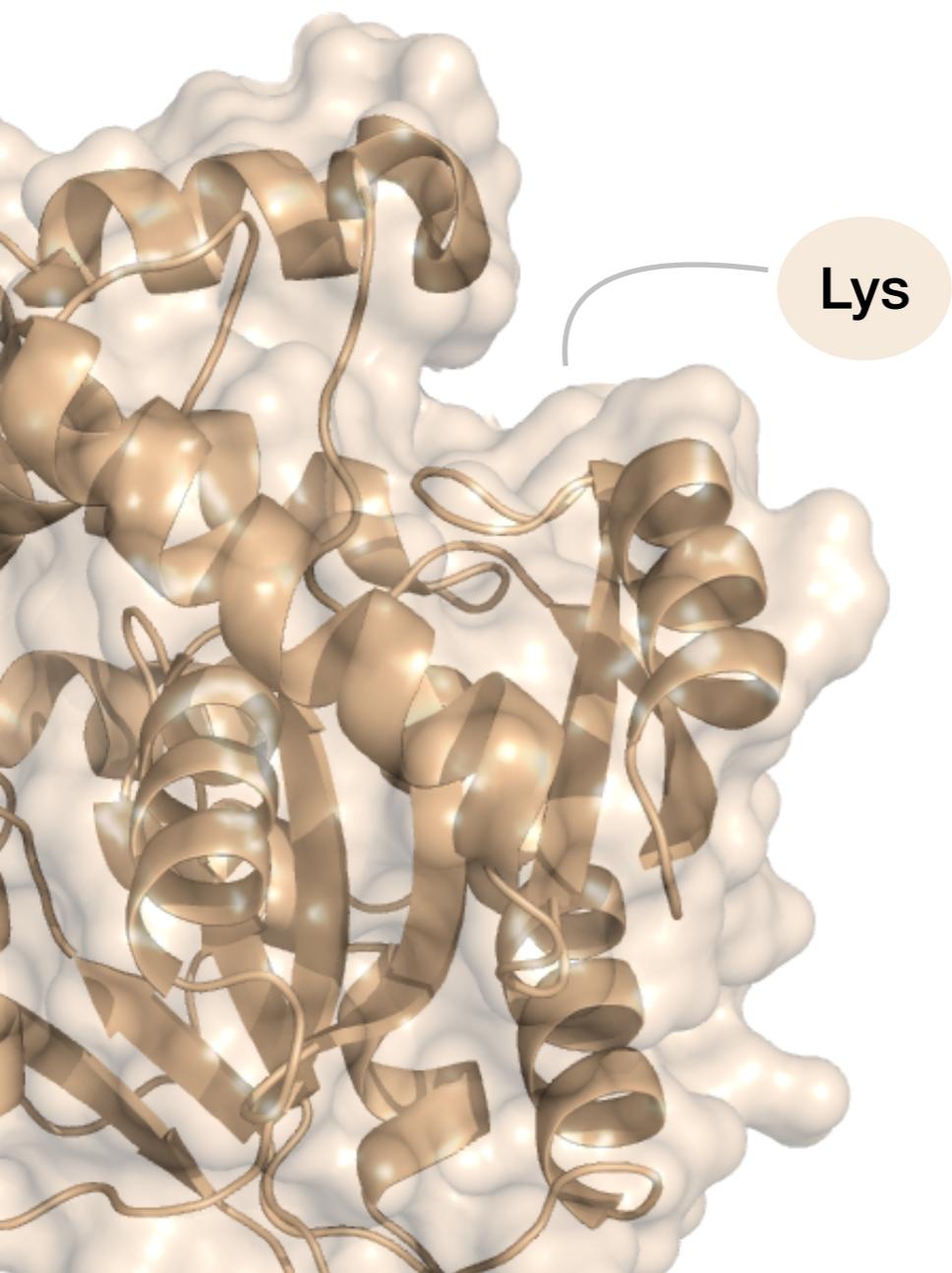
Expanding methods to drug nucleophilic residues



- ***The human proteome contains druggable pockets with no proximal cysteines***

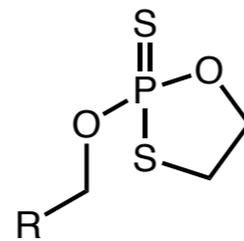
Ligand Discovery

Expanding methods to drug nucleophilic residues



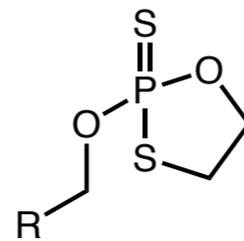
- *How do you drug other nucleophilic amino acids?*

Ligand Discovery



P(V)-Oxathiaphospholane (OTP)

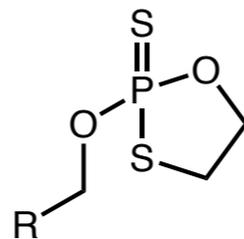
Ligand Discovery



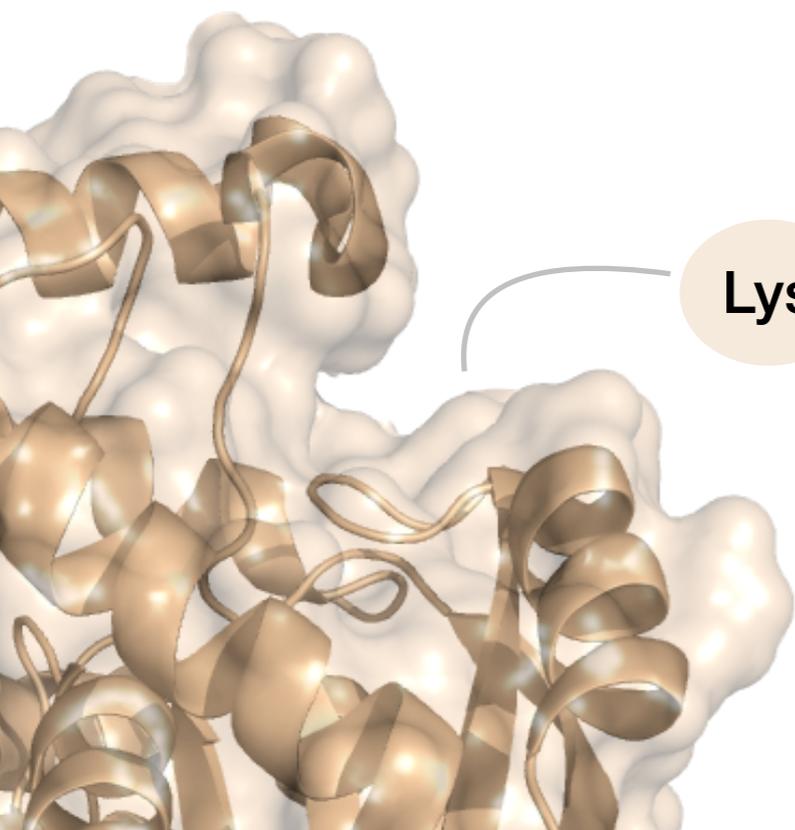
P(V)-Oxathiaphospholane (OTP)

selective bioconjugation

Ligand Discovery



P(V)-Oxathiaphospholane (OTP)



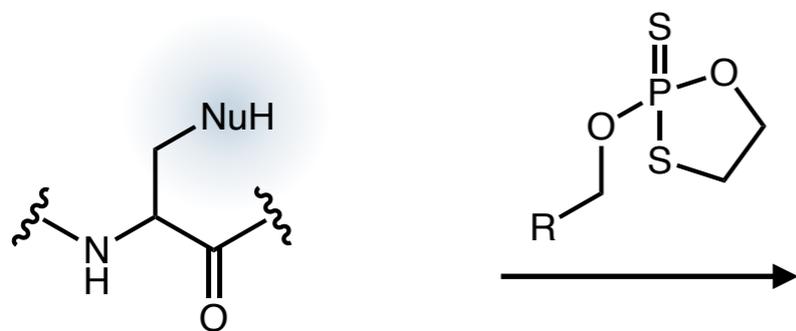
Lys

selective bioconjugation

Ligand Discovery

Expanding methods to drug nucleophilic residues

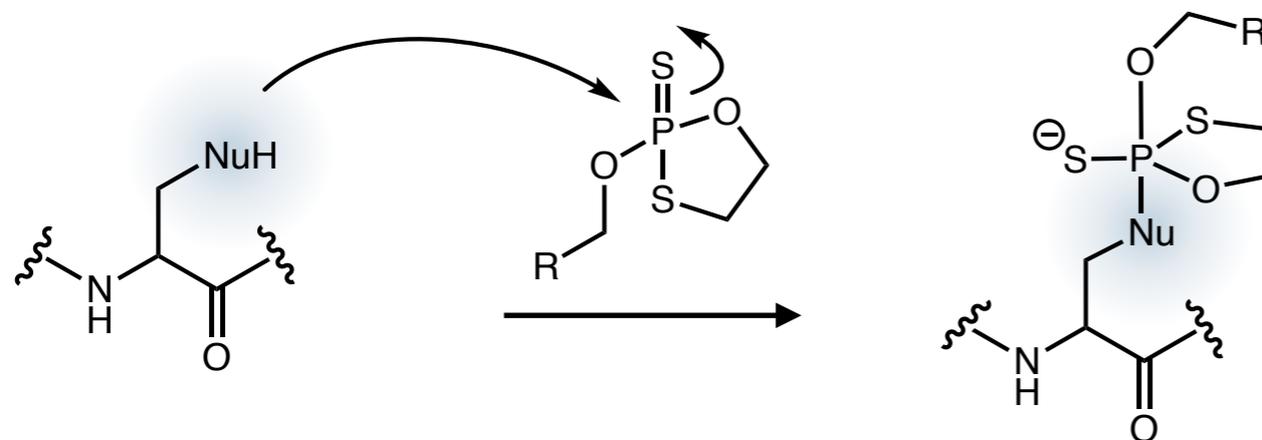
- **OTP probe for covalent targeting**



Ligand Discovery

Expanding methods to drug nucleophilic residues

- **OTP probe for covalent targeting**

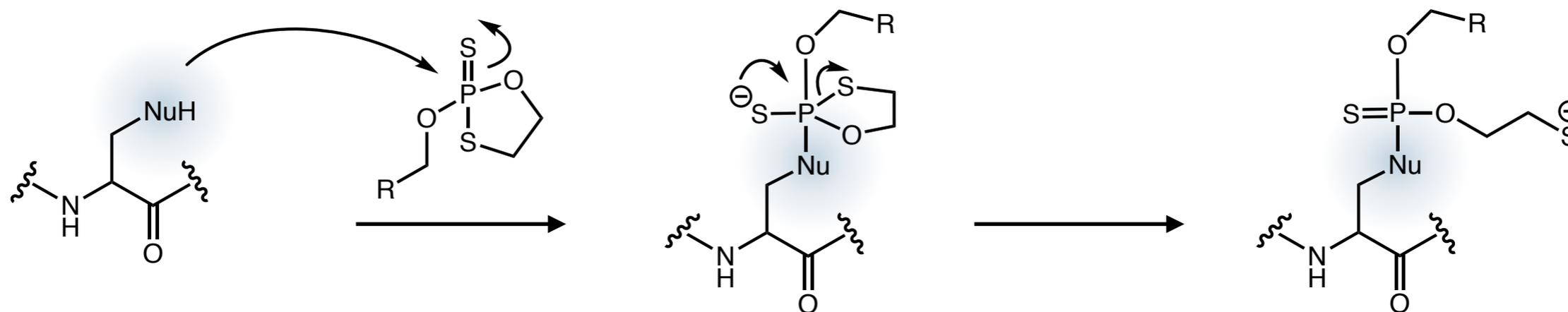


*Anionic, pentavalent
intermediate*

Ligand Discovery

Expanding methods to drug nucleophilic residues

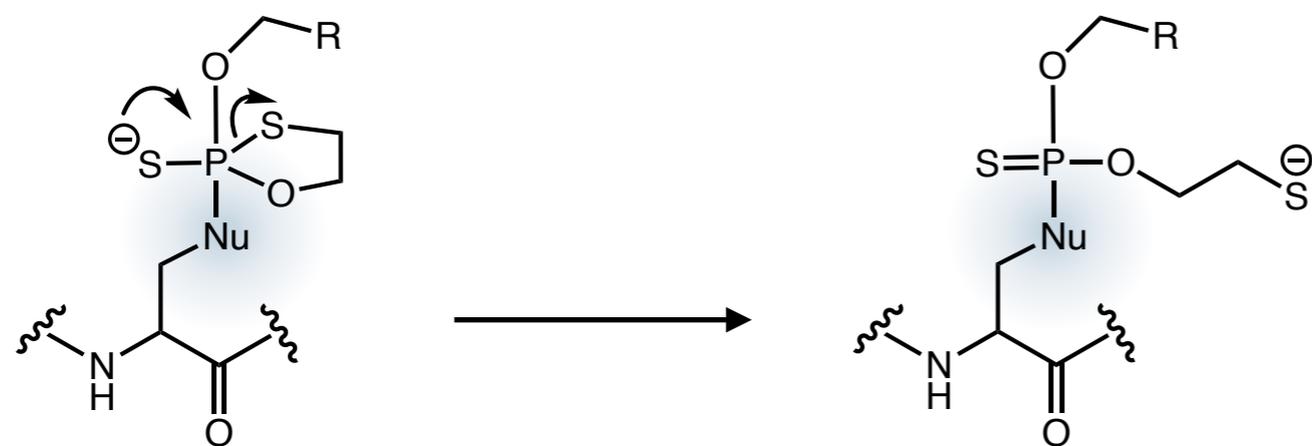
- **OTP probe for covalent targeting**



Ligand Discovery

Expanding methods to drug nucleophilic residues

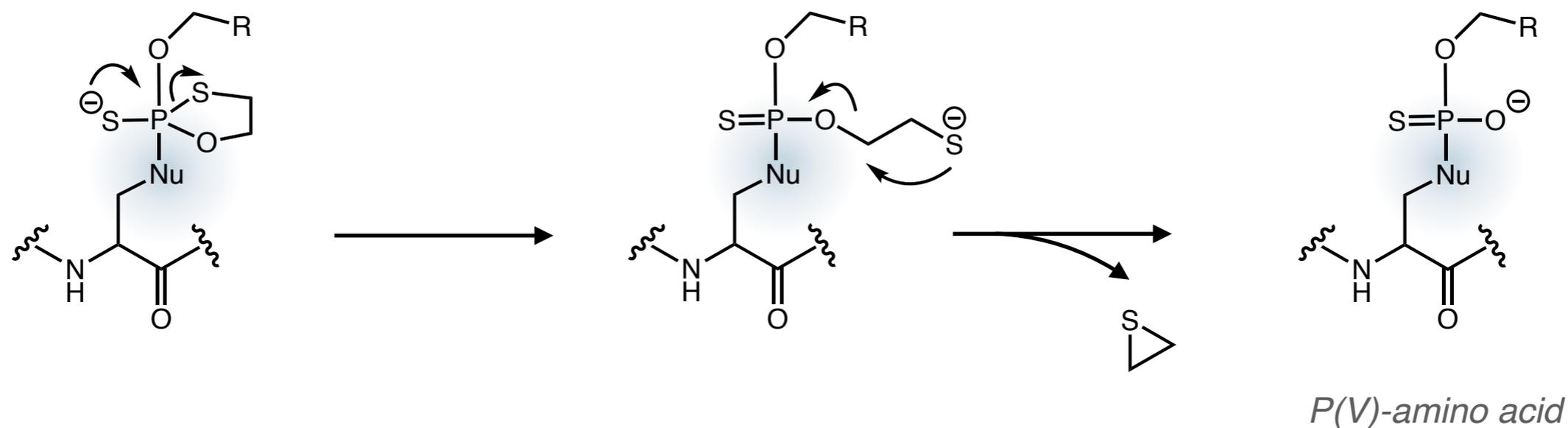
- **OTP probe for covalent targeting**



Ligand Discovery

Expanding methods to drug nucleophilic residues

- **OTP probe for covalent targeting**

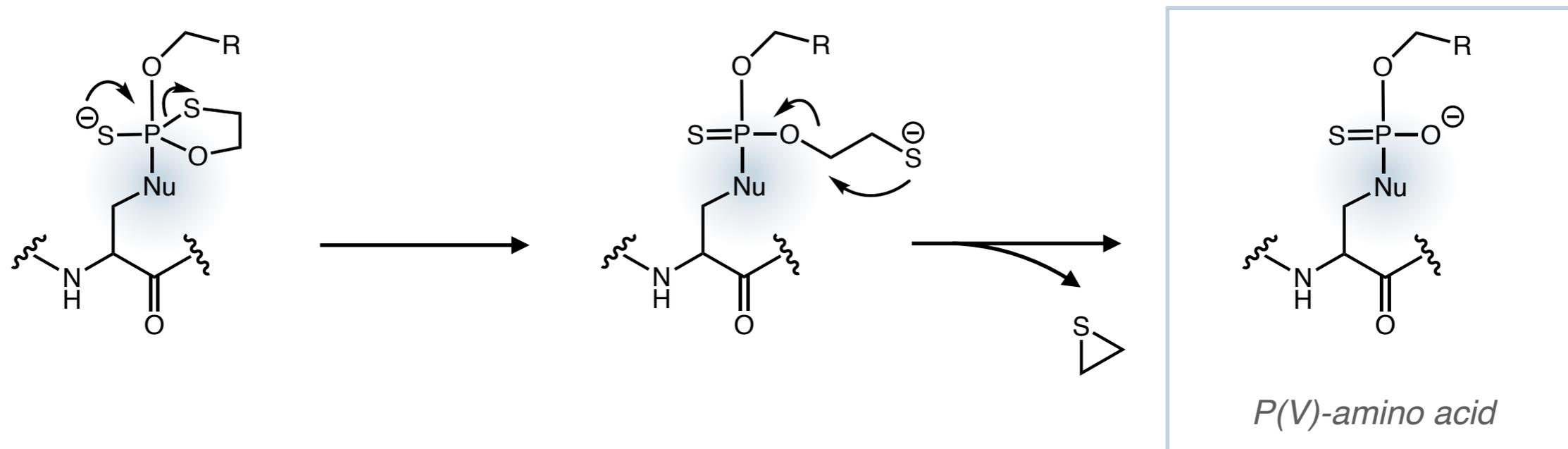


Modified P(V)-amino acid residue

Ligand Discovery

Expanding methods to drug nucleophilic residues

- **OTP probe for covalent targeting**

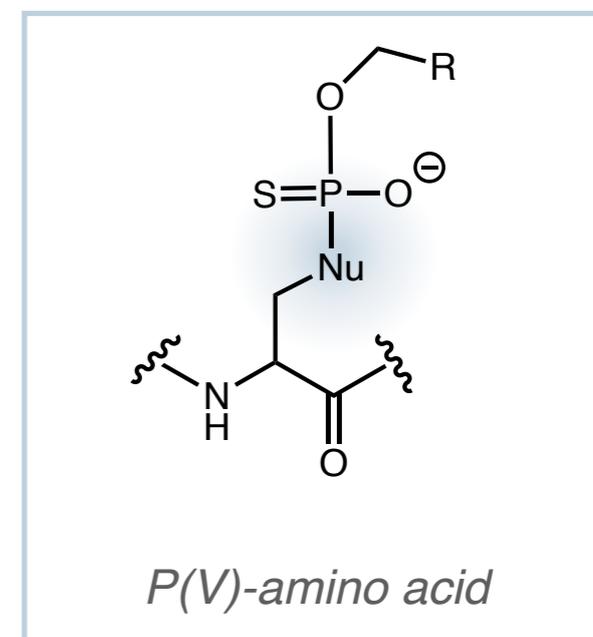
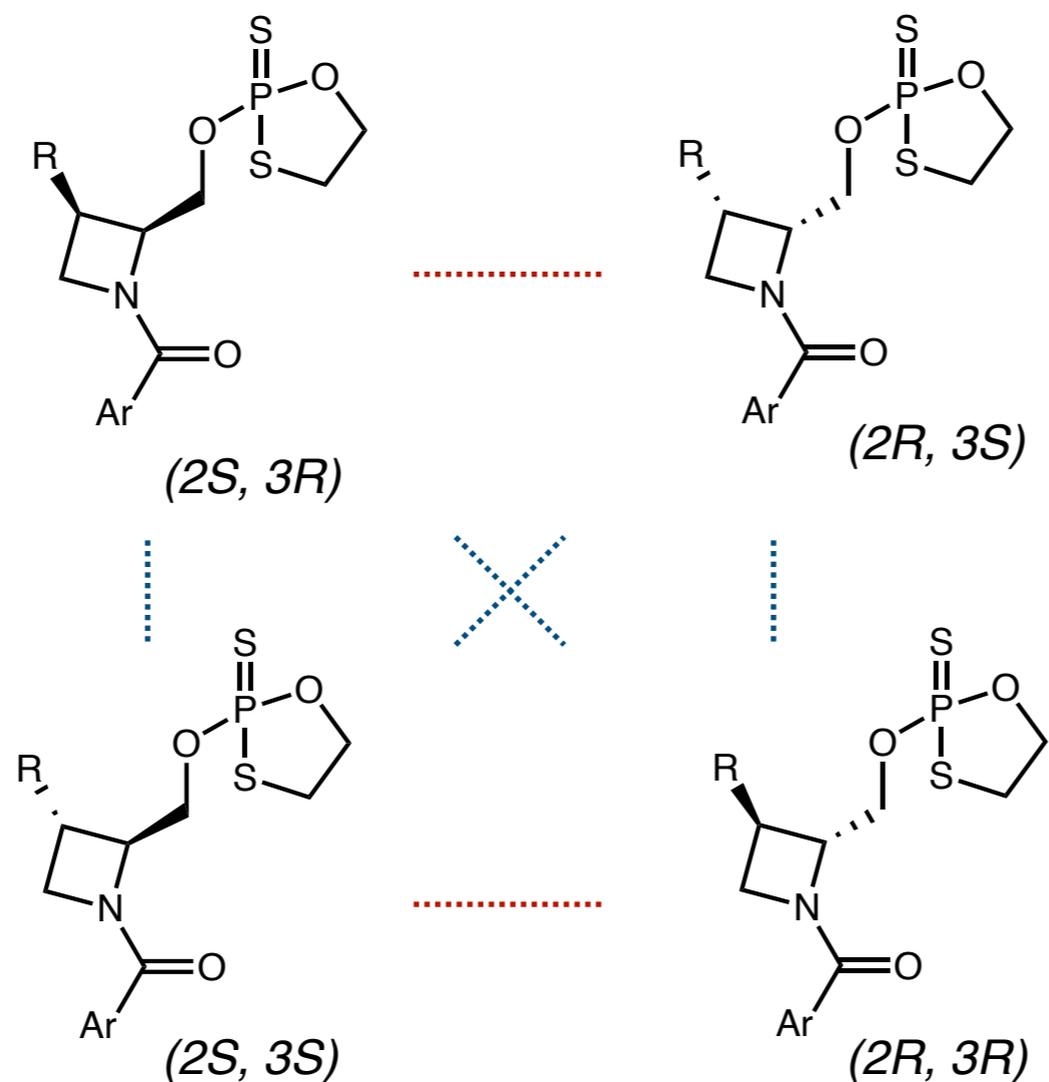


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Ligand Discovery

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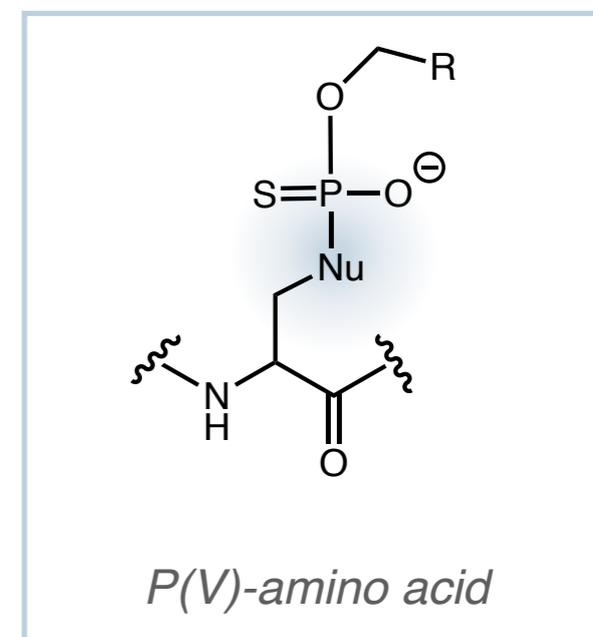
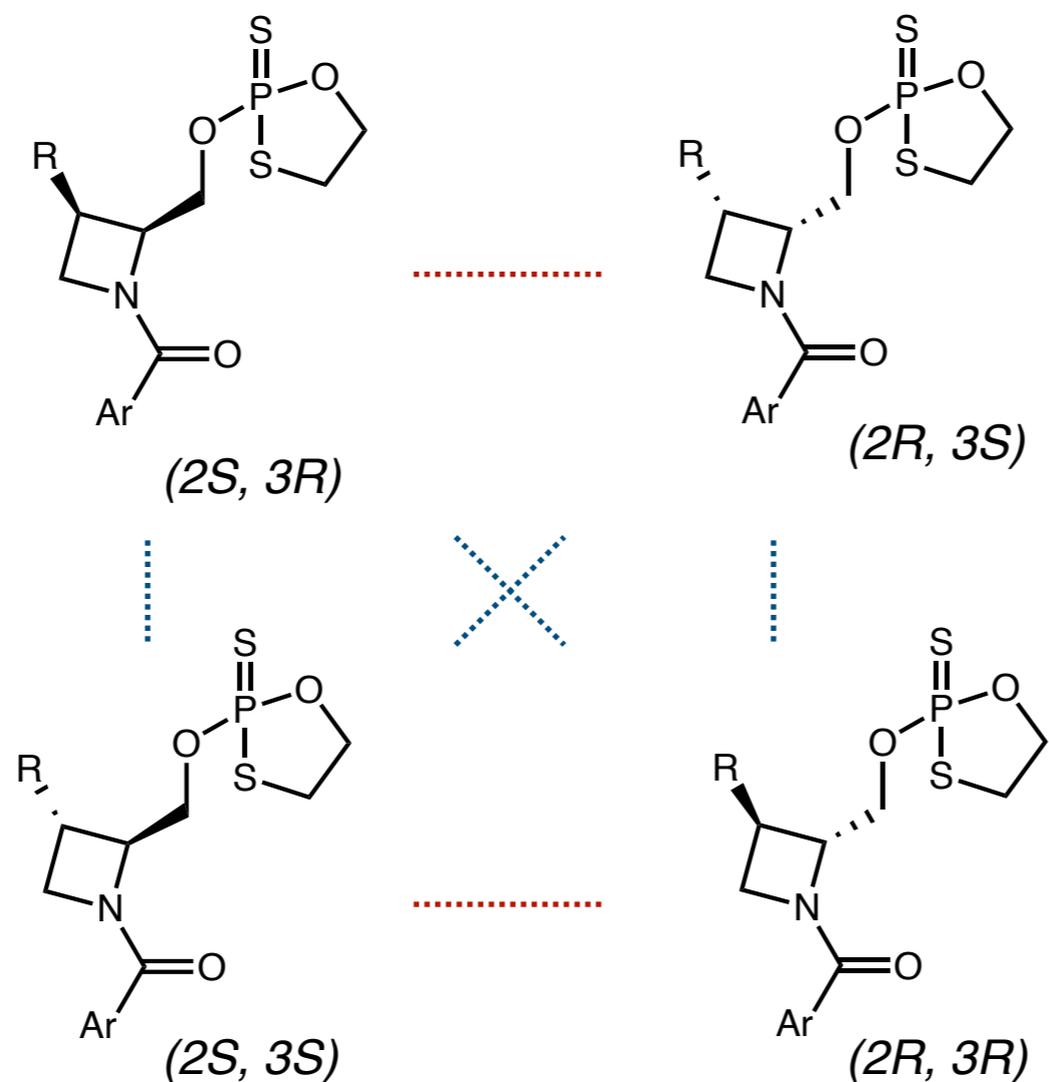


■ *P(V)* stereoprobes are stereosomerically defined

Ligand Discovery

Expanding methods to drug nucleophilic residues

- **OTP probe for covalent targeting**



- $P(V)$ stereoprobes are stereoisomerically defined

- Enables study of stereoselective protein-ligand interactions

Part 1

Covalent inhibitors

Part 2

Biologics

Non-covalent interactors

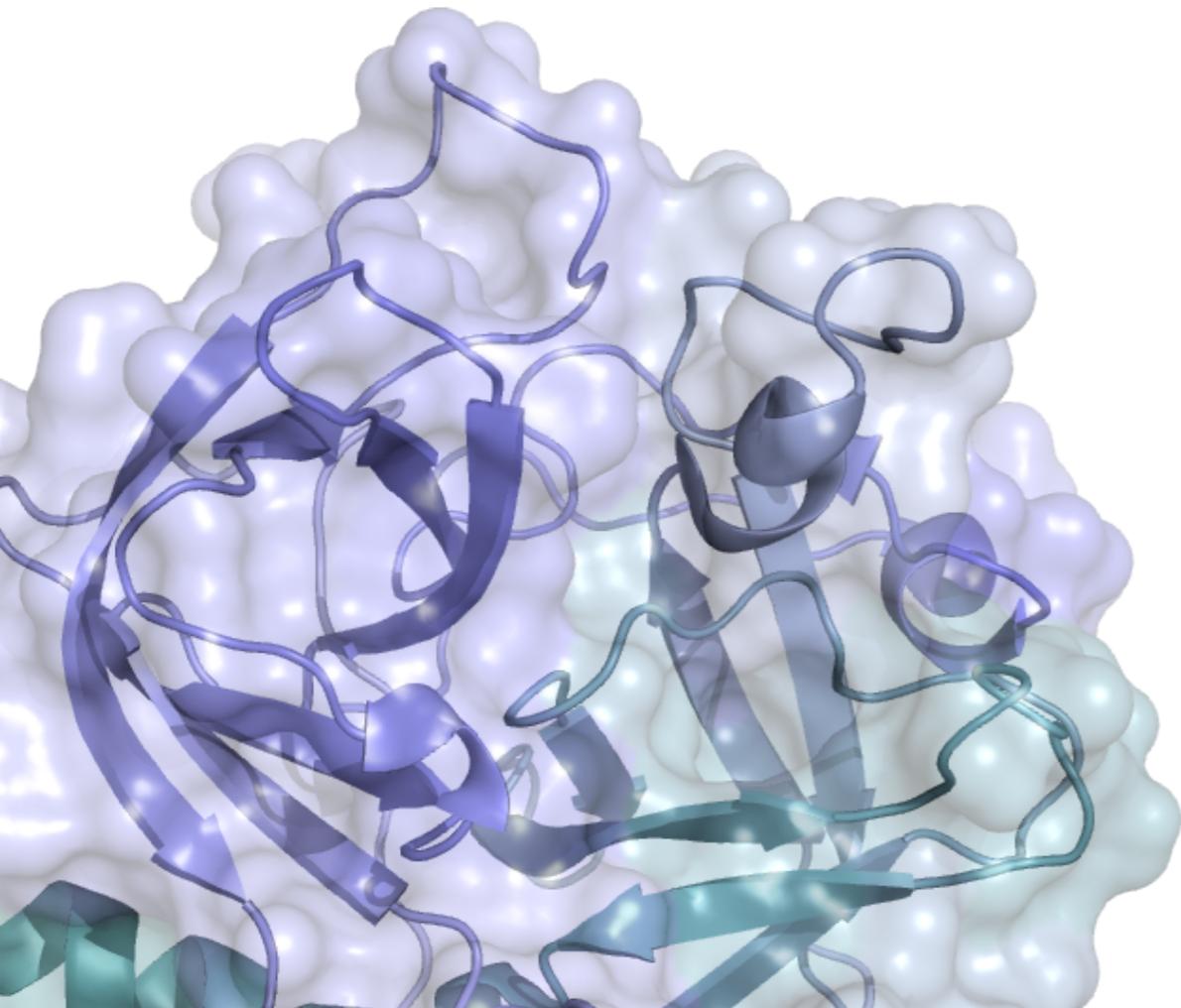
Part 3

*Prions and Multi drug
resistance: The Looming
Plagues*

Current Therapeutics

Targeted Protein Degradation (TPD) technology

***A major limitation to targeted protein degradation is
reliance on **small molecule drugs*****

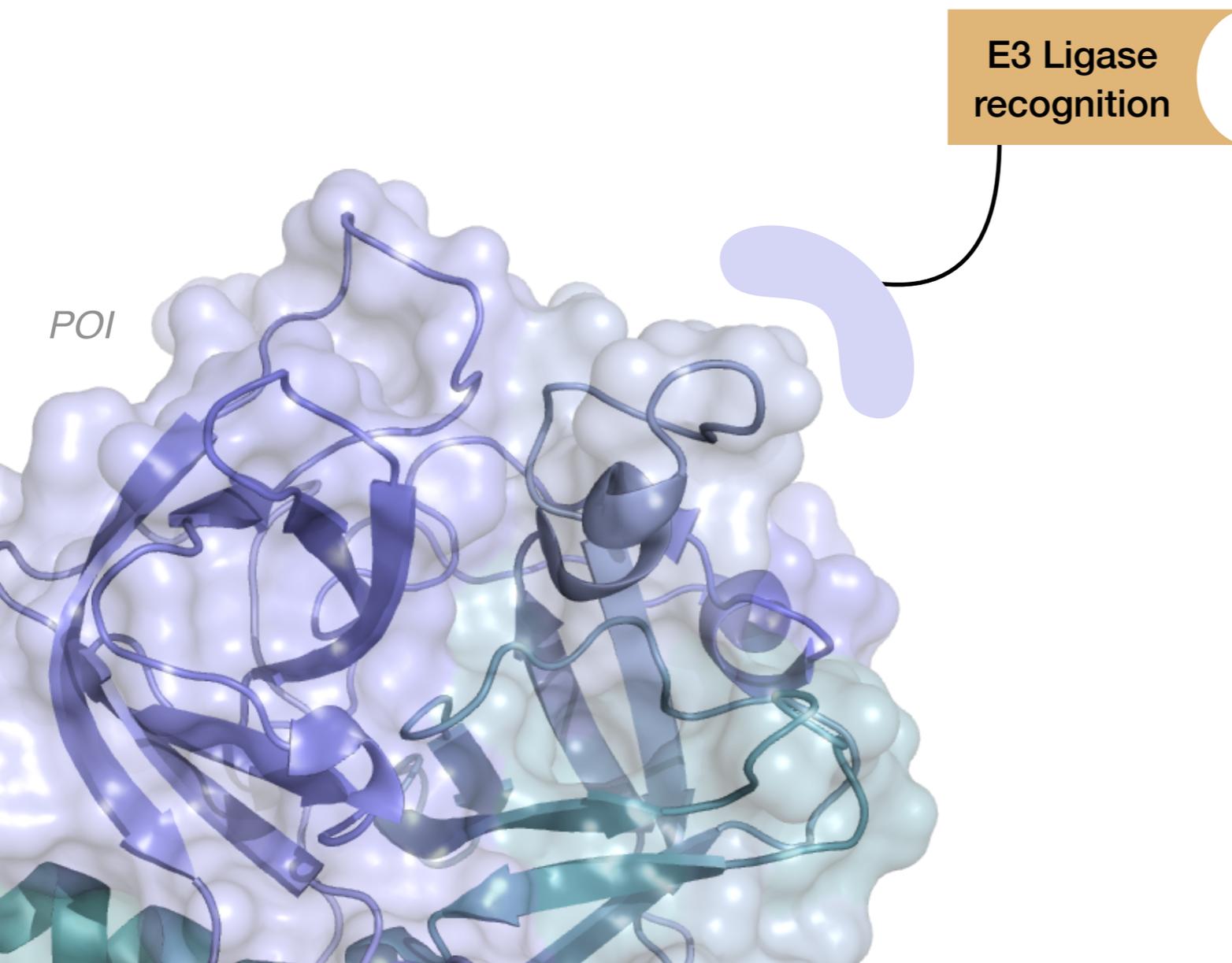


Current Therapeutics

Targeted Protein Degradation (TPD) technology

- **2 major classes of small molecules for TPD:**

1. PROTACs

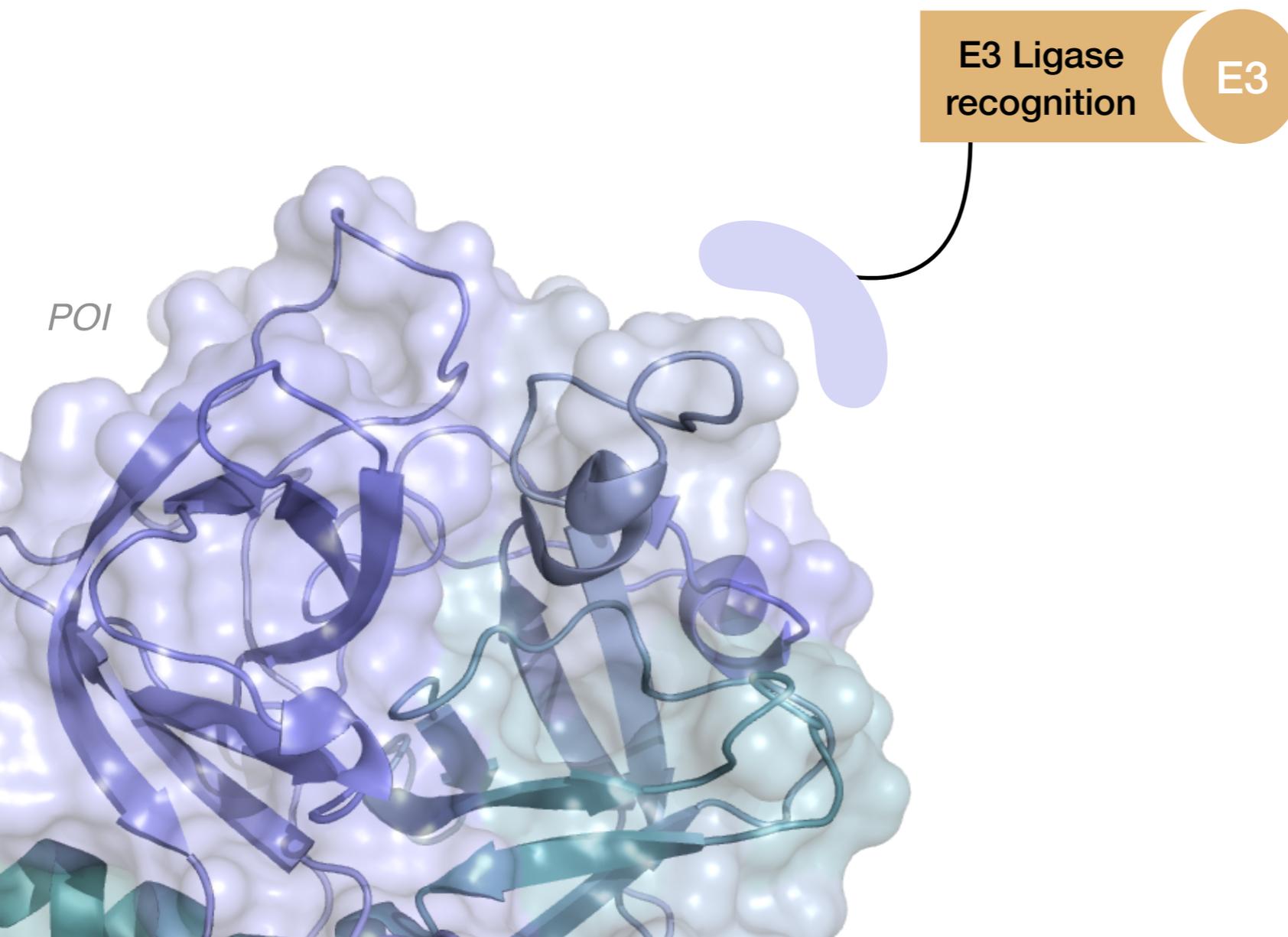


Current Therapeutics

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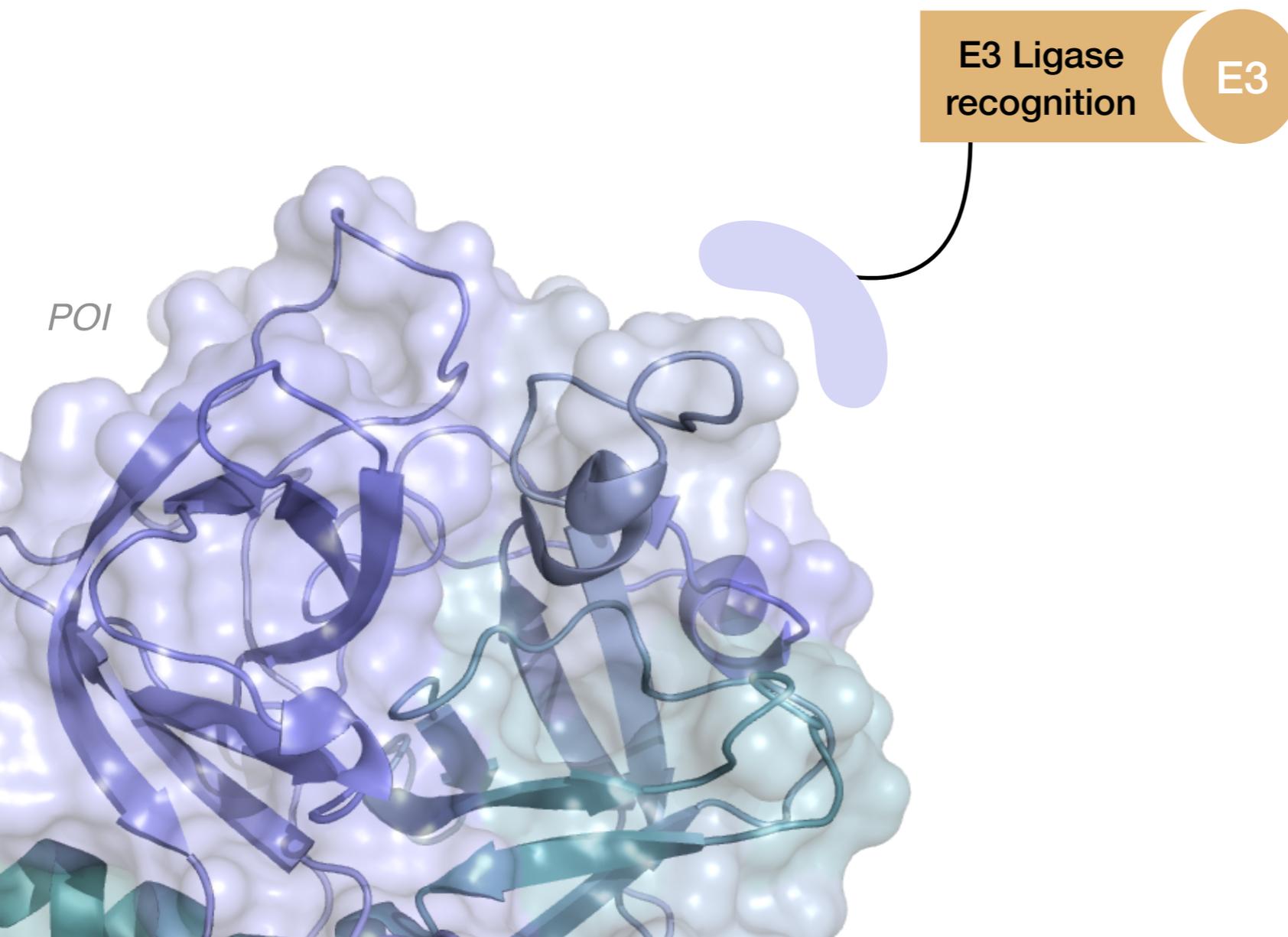
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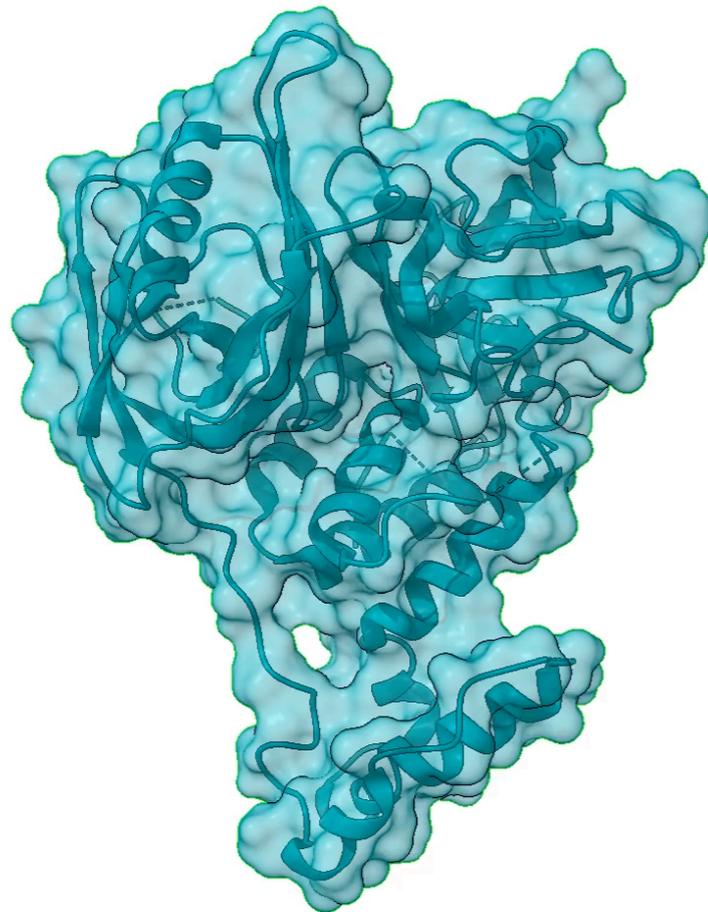
2. Molecular glues



Protein Targeting

Heterobifunctionals

Cereblon

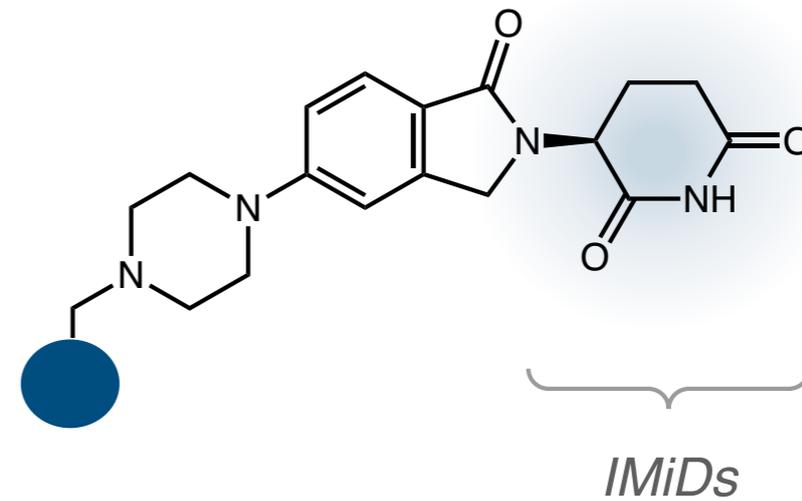
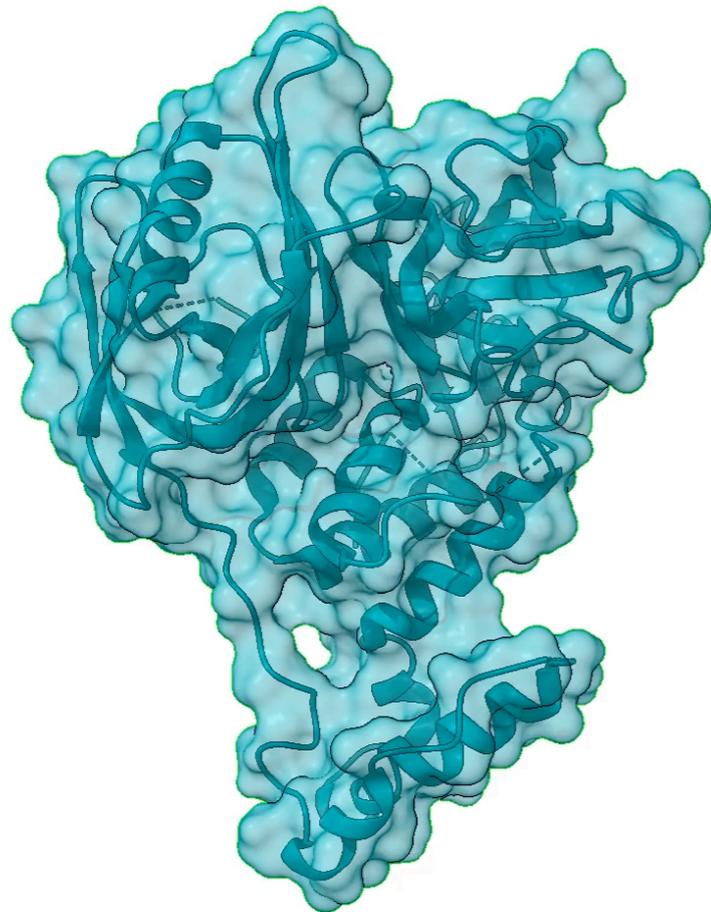


IMiDs bind the E3 ligase protein, Cereblon

Protein Targeting

Heterobifunctionals

Cereblon

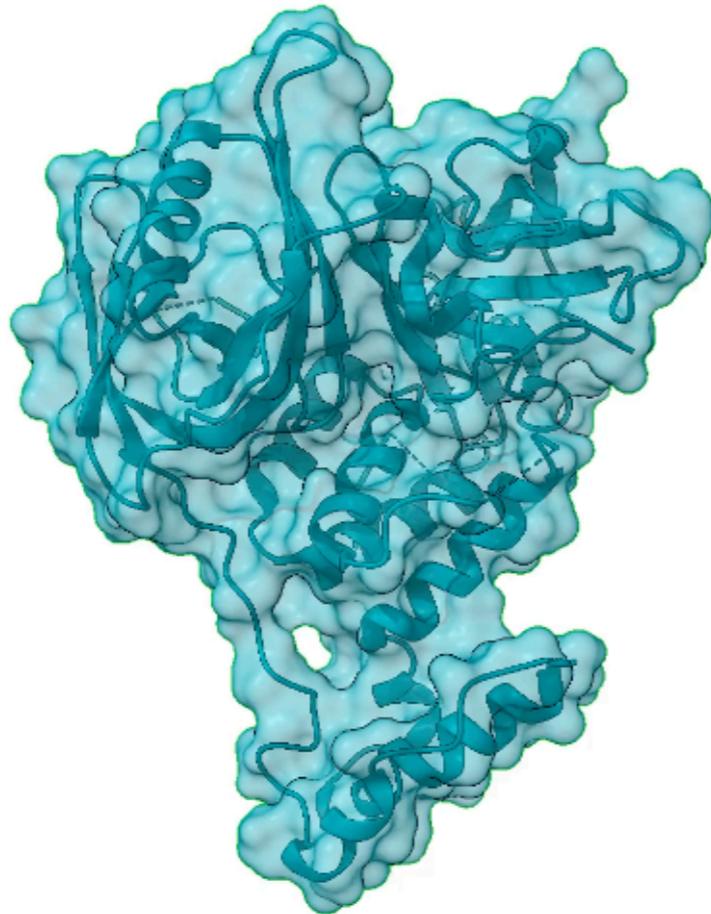


IMiDs bind the E3 ligase protein, Cereblon

Protein Targeting

Induced proximity

Cereblon



Benefits to Heterobifunctionals:

- 1. Target non-enzymatic pockets**
- 2. Catalytic degraders**
- 3. Degradation removes entire protein**
- 4. PROTAC warheads don't require high binding affinity**

Current Strategies

PROTACs in the clinic

- **PROTACs**

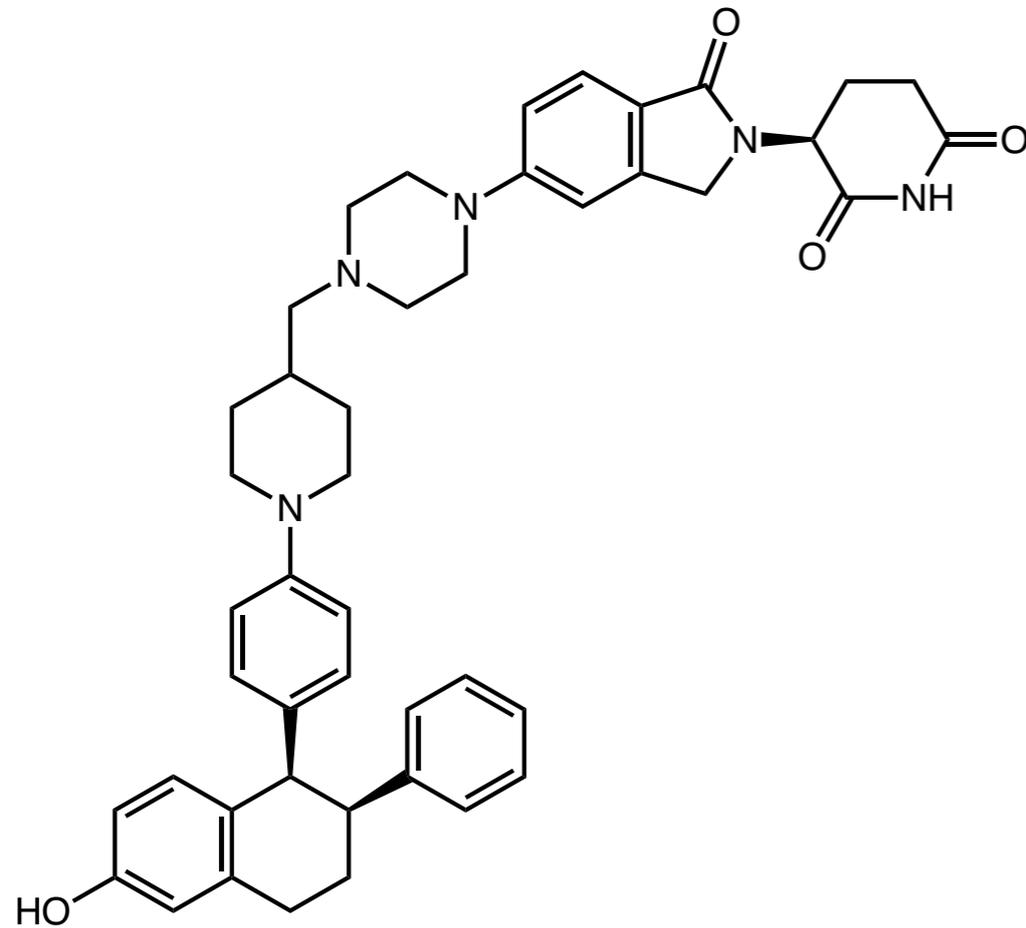


Prof. Craig Crews

Current Strategies

PROTACs in the clinic

- **PROTACs**



Vepdegestrant

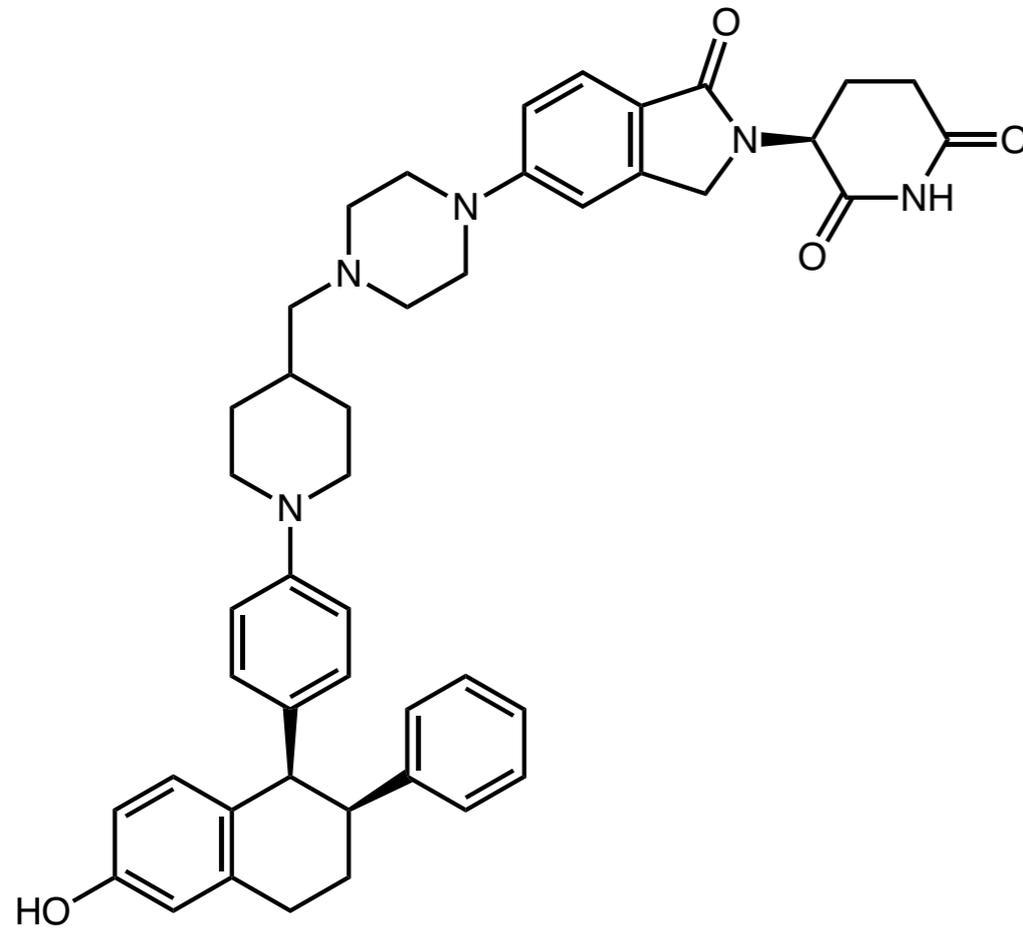


Prof. Craig Crews

Current Strategies

PROTACs in the clinic

PROTACs



Vepdegestrant

- **PROTAC protein degrader**
- **ER+, HER2- breast cancer**
- **Targets estrogen receptor (ER)**



Prof. Craig Crews

Current Strategies

PROTACs in the clinic

Press Release Details

Arvinas and Pfizer Announce Positive Topline Results from Phase 3 VERITAC-2 Clinical Trial

March 11, 2025

- *VERITAC-2 achieved its primary endpoint in the estrogen receptor 1-mutant population, demonstrating statistically significant and clinically meaningful improvement in progression-free survival –*
- *Vepdegestrant is the first PROTAC degrader to demonstrate clinical benefit in a Phase 3 trial –*

NEW HAVEN, Conn. and NEW YORK, March 11, 2025 (GLOBE NEWSWIRE) -- Arvinas, Inc. (Nasdaq: ARVN) and Pfizer Inc. (NYSE: PFE) today announced positive topline results from the Phase 3 VERITAC-2 clinical trial (NCT05654623) evaluating vepdegestrant monotherapy versus fulvestrant in adults with estrogen receptor-positive, human epidermal growth factor receptor 2-negative (ER+/HER2-) advanced or metastatic breast cancer whose disease progressed following prior treatment with cyclin-dependent kinase (CDK) 4/6 inhibitors and endocrine therapy. These are the first pivotal data for vepdegestrant, a potential first-in-class investigational oral PROteolysis TArgeting Chimera (PROTAC) ER degrader.

Current Strategies

PROTACs in the clinic

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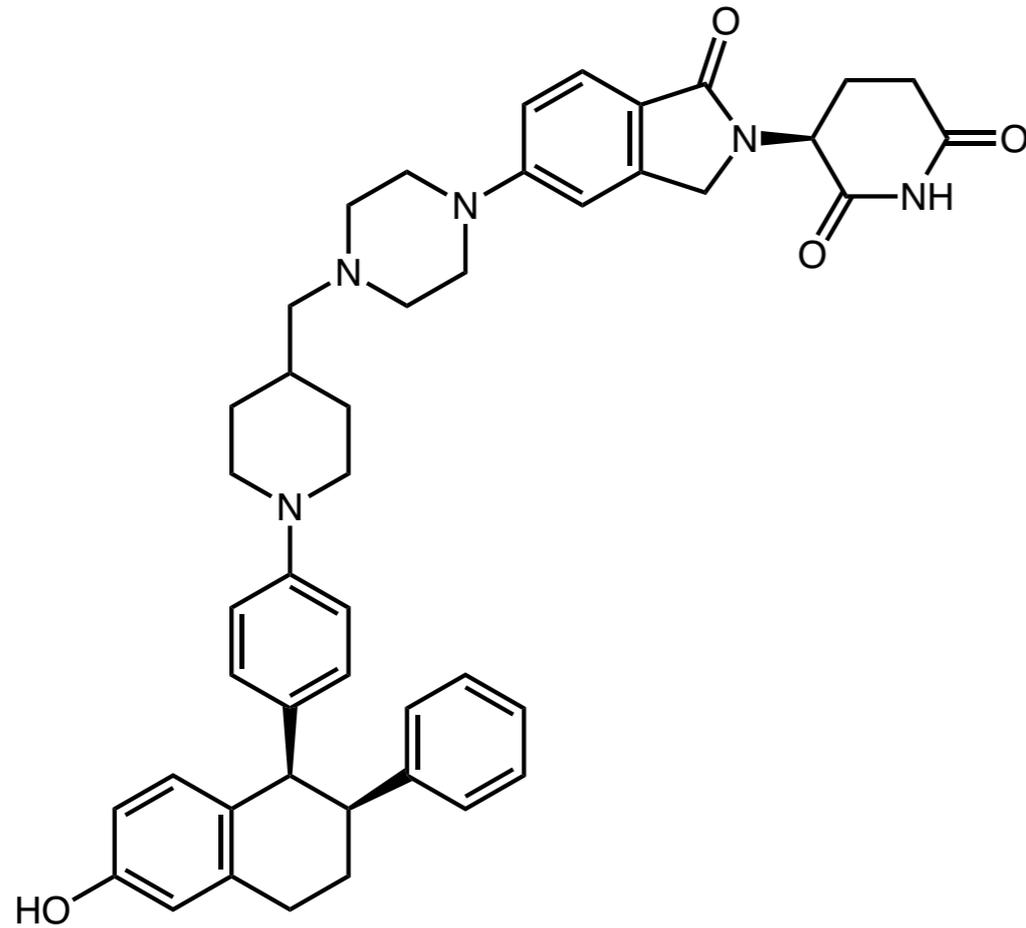
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- ***1st PROTAC degrader to show clinical benefit in Phase III trial***

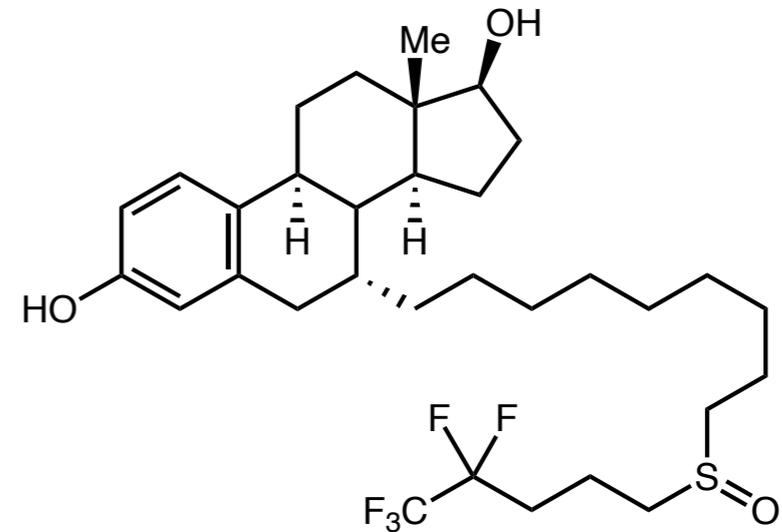
Current Strategies

Vepdegestrant PROTAC in the clinic



Vepdegestrant

versus

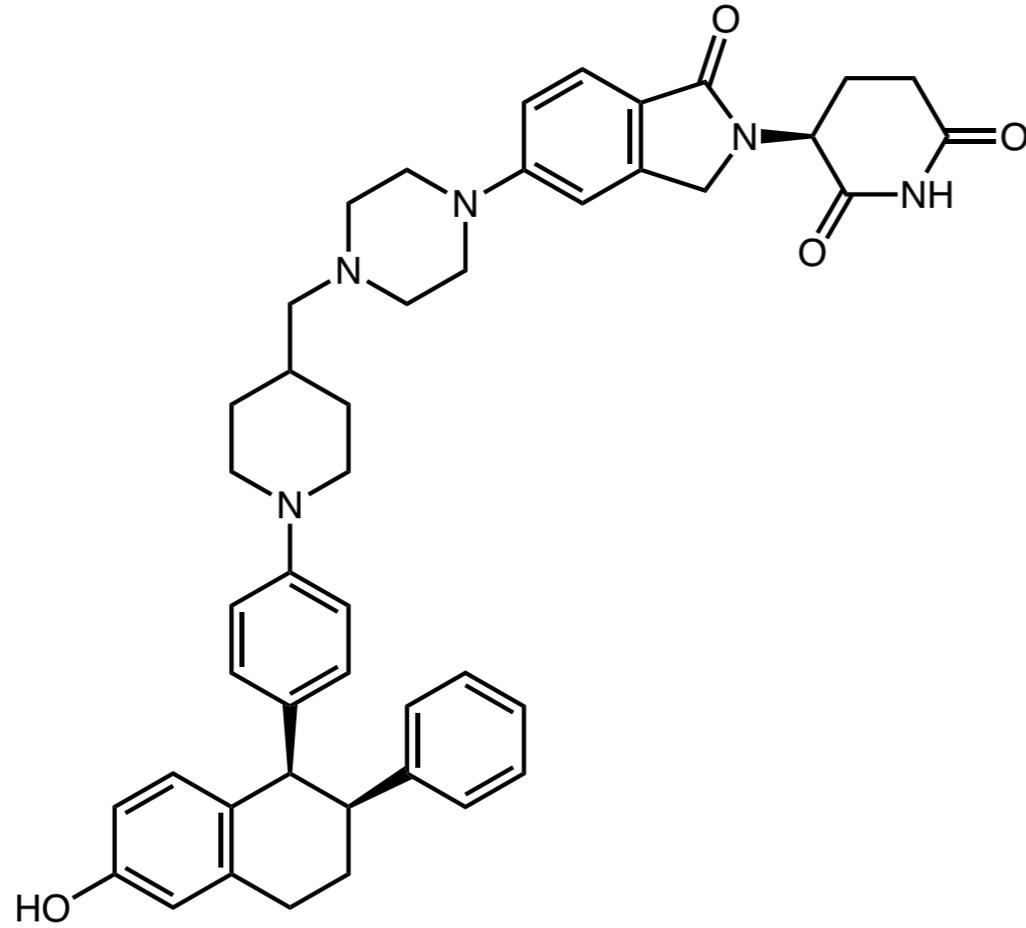


Fulvestrant



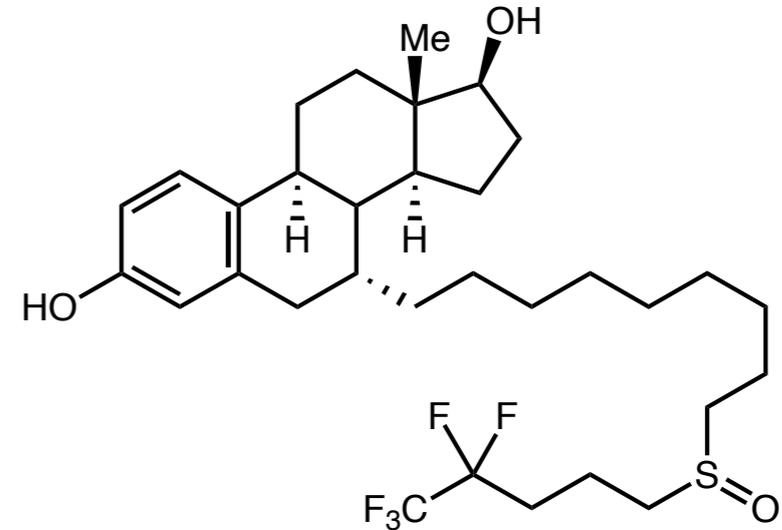
Current Strategies

Vepdegestrant PROTAC in the clinic



Vepdegestrant

versus



Fulvestrant



- *Vepdegestrant failed to meet key clinical study endpoints*

Strategies to Access Undruggable Targets

What other strategies can be used to target the undruggable proteome?

Current Strategies

peptidomimetics

Pharmacophores designed to mimic a natural peptide

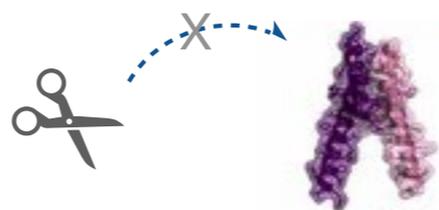
Current Strategies

peptidomimetics

Pharmacophores designed to mimic a natural peptide



1. Stabilization against proteolysis



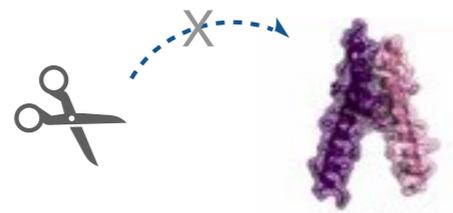
Current Strategies

peptidomimetics

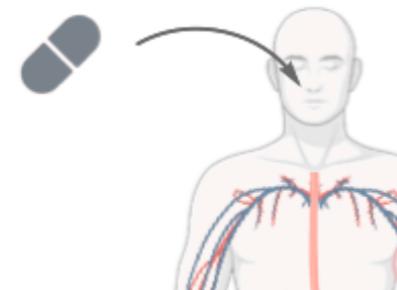
Pharmacophores designed to mimic a natural peptide



1. Stabilization against proteolysis



2. Increased oral bioavailability



Investigating Druggability

3 key factors to “Undruggability”:

■ *Disordered Structures*

■ *Dynamic surfaces*

■ *Undefined binding pockets*

- *Protein–protein interactions (PPIs)*
- *Protein–nucleic acid interactions*

*~130,000–650,000
types of PPIs in the
human interactome*

***Disruption of PPIs can
promote disease states***

Investigating Druggability

3 key factors to “Undruggability”:

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■ *Undefined binding pockets*

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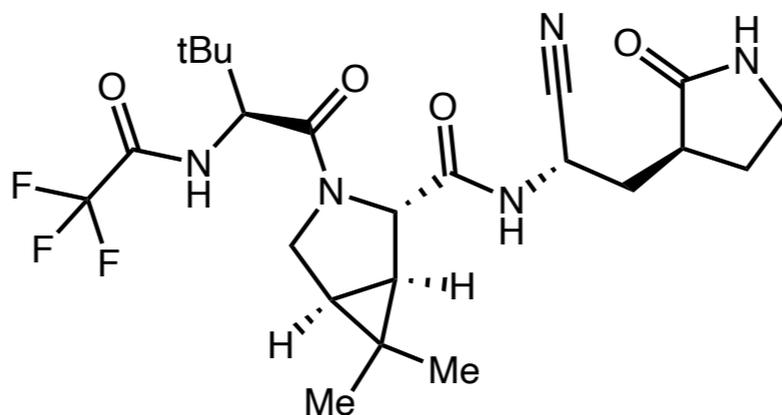
peptidomimetics

- *exhibit specific interactions with PPI and protein–nucleic acids*

Peptidomimetic inhibitors

- *Peptidomimetic inhibitors are ubiquitous*

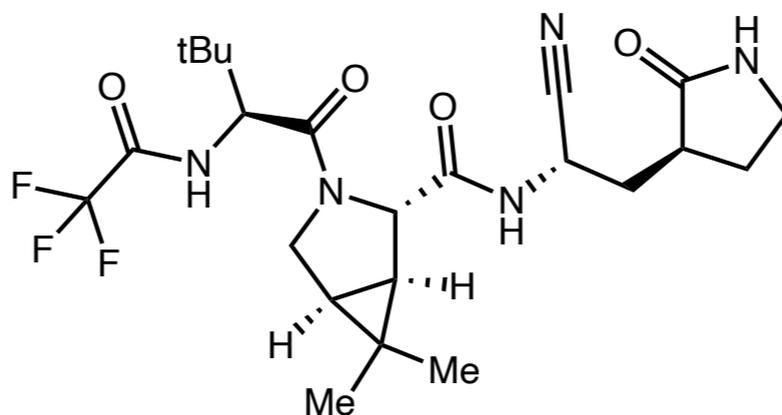
Peptidomimetic inhibitors



Nirmatrelvir

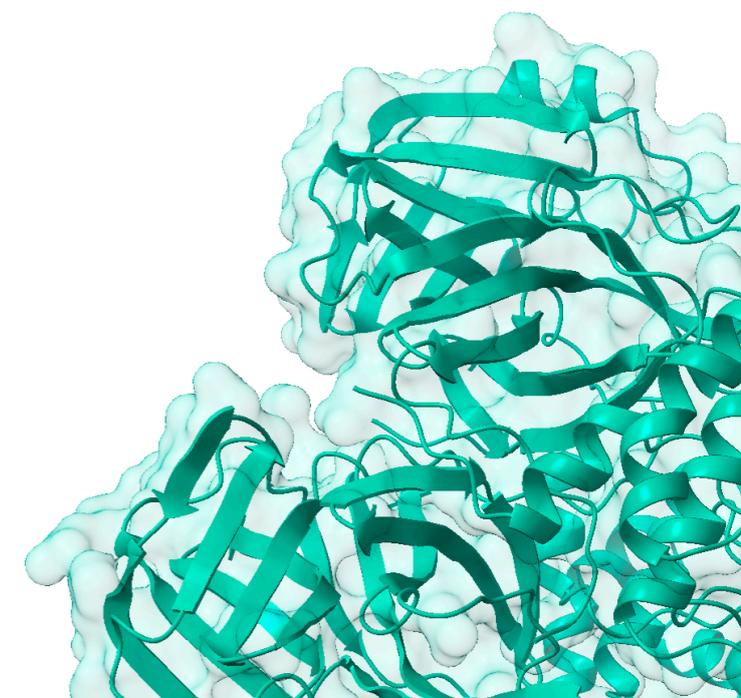
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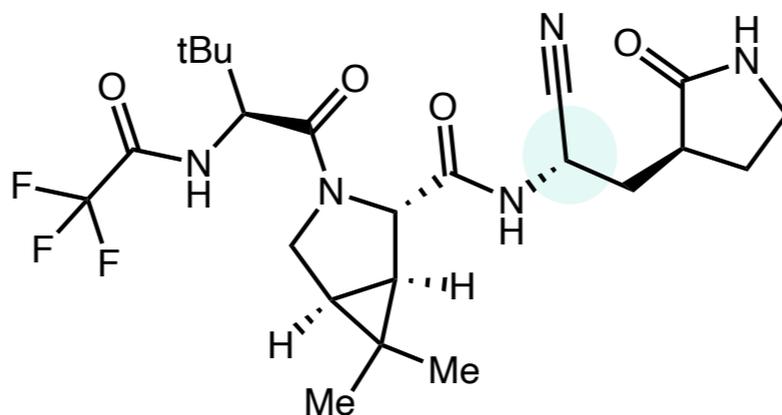


Nirmatrelvir

- *Peptidomimetic inhibitors are ubiquitous*
- *MPro SARS-CoV-2 main protease*

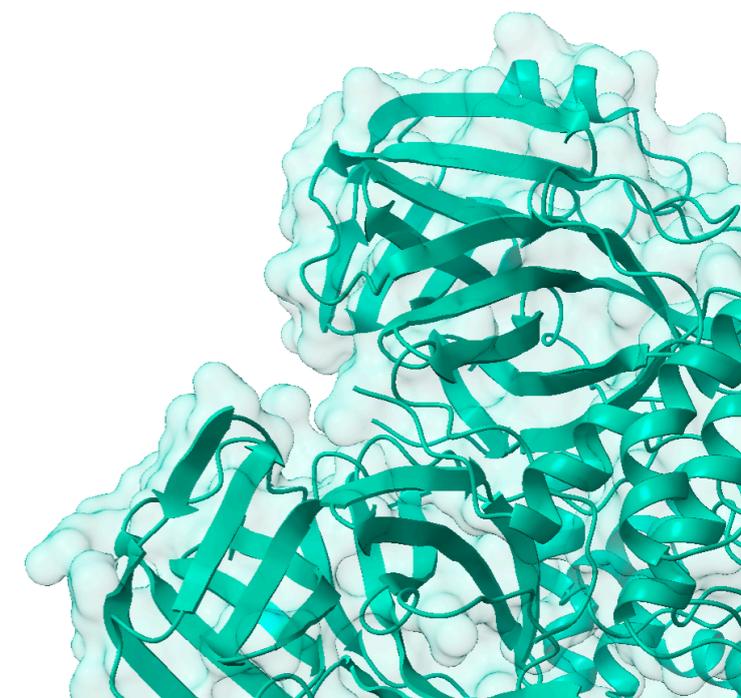


Peptidomimetic inhibitors

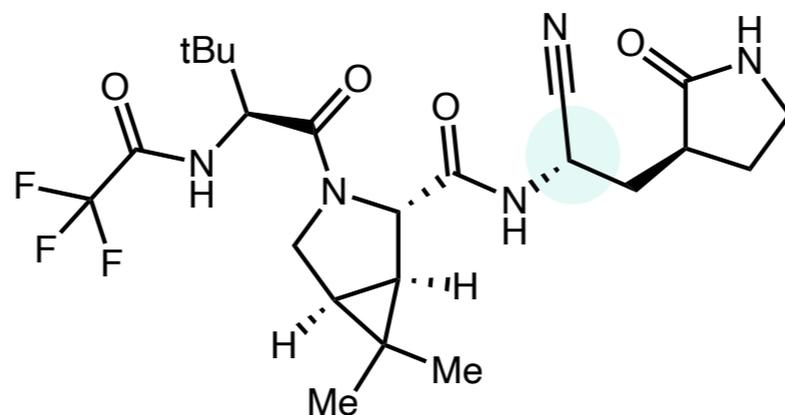


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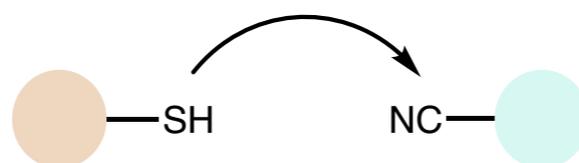


Peptidomimetic inhibitors

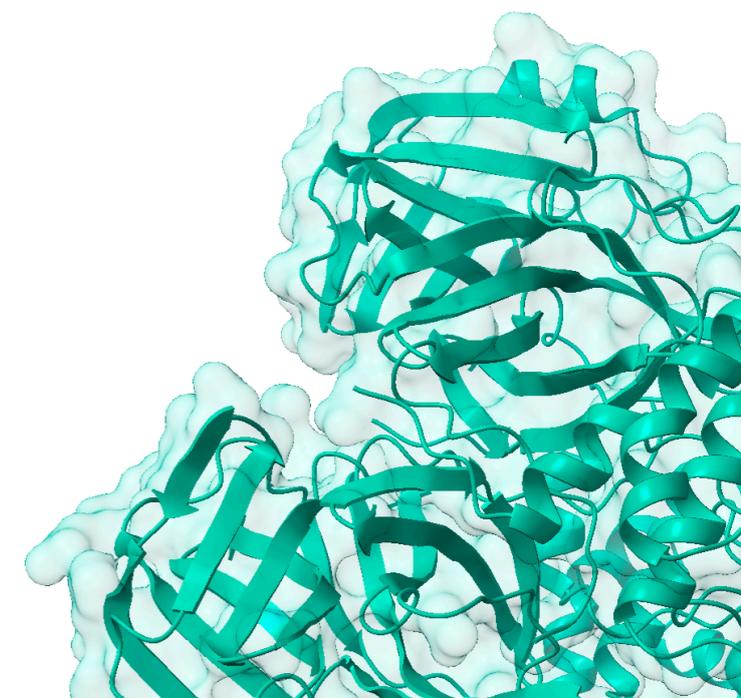


Nirmatrelvir

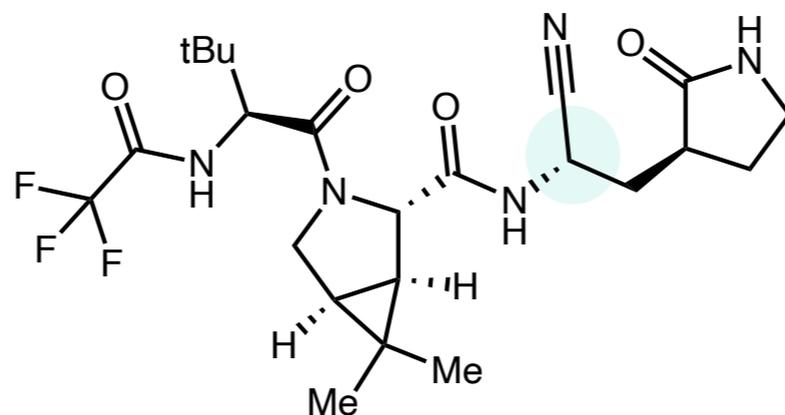
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Cys145 M^{pro}

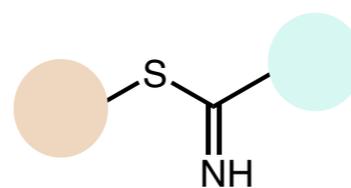


Peptidomimetic inhibitors

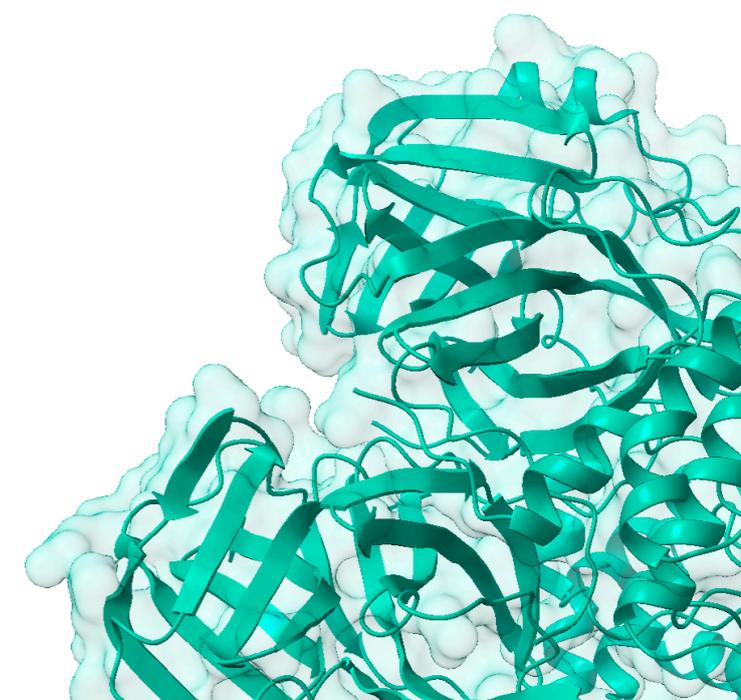


Nirmatrelvir

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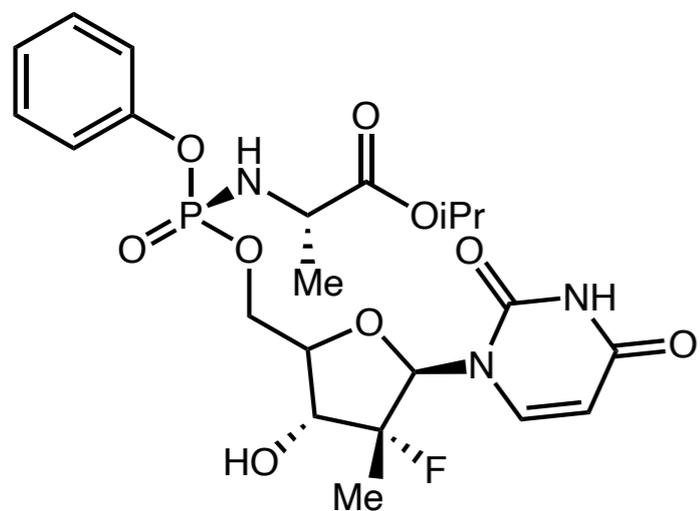


Thioimide

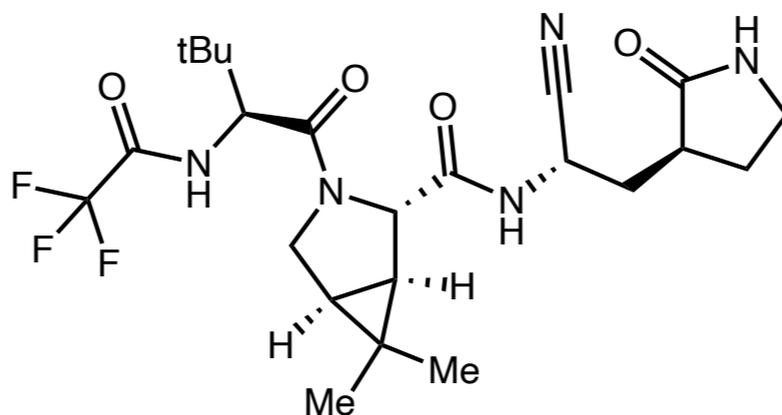


Peptidomimetic inhibitors

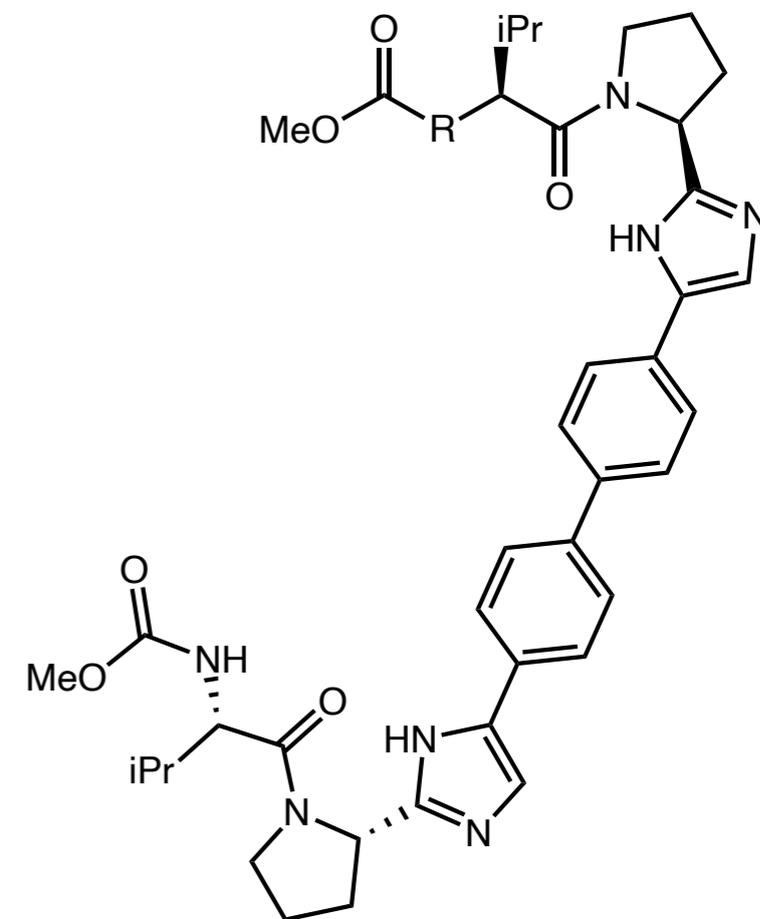
To name just a few...



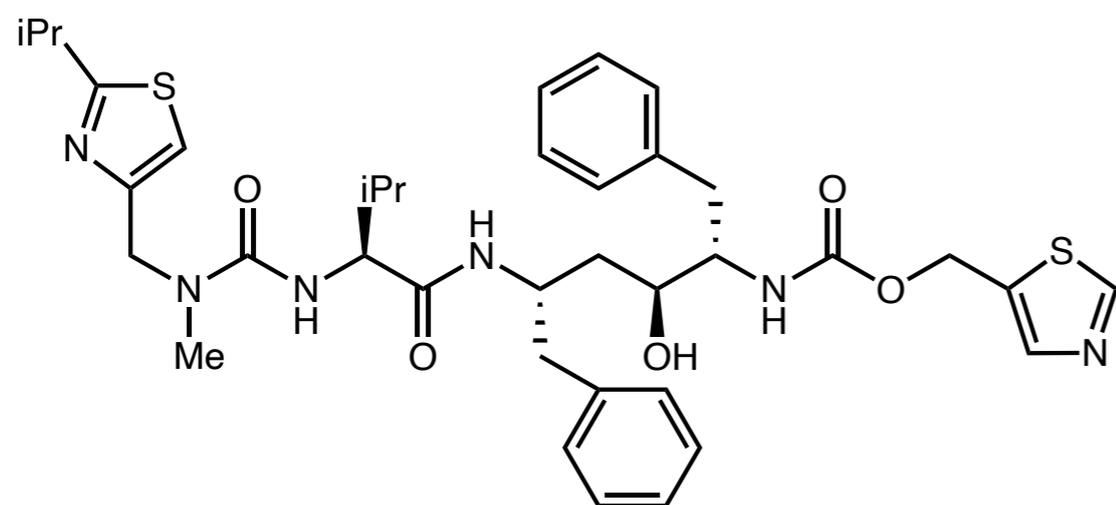
Sofosbuvir
Hep C



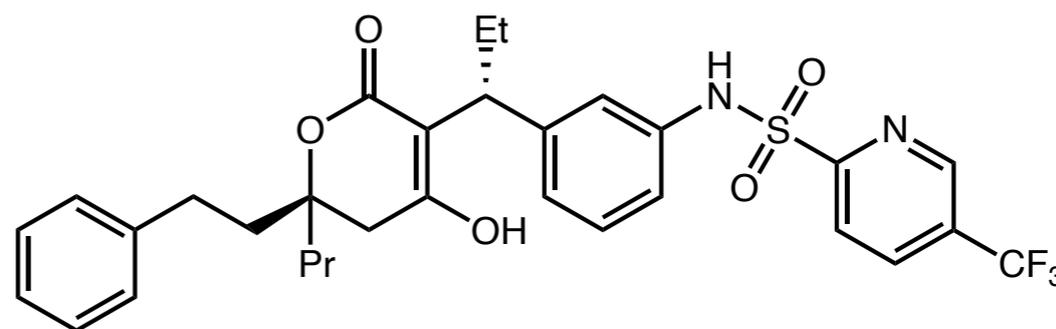
Nirmatrelvir
SARS CoV-2



Daclatasvir
Hep C

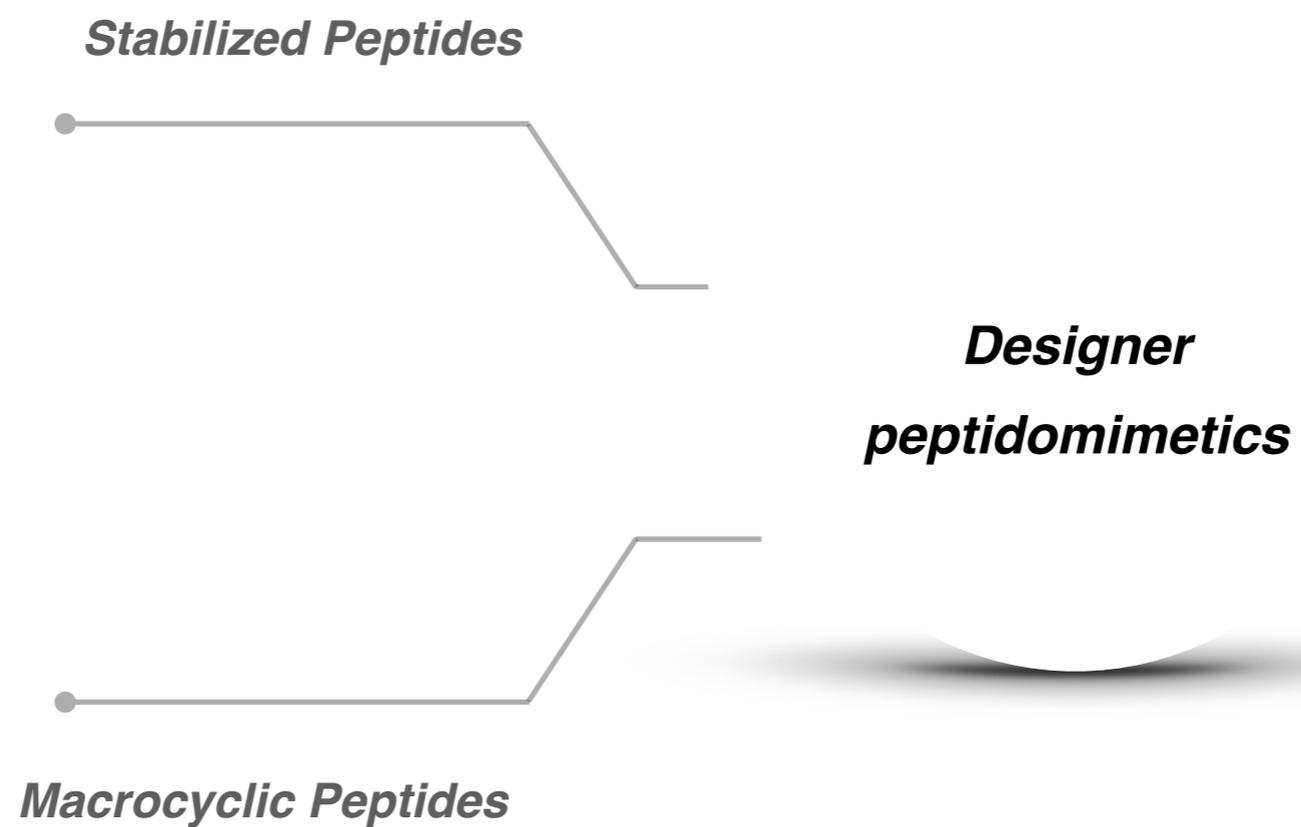


Ritonavir
HIV

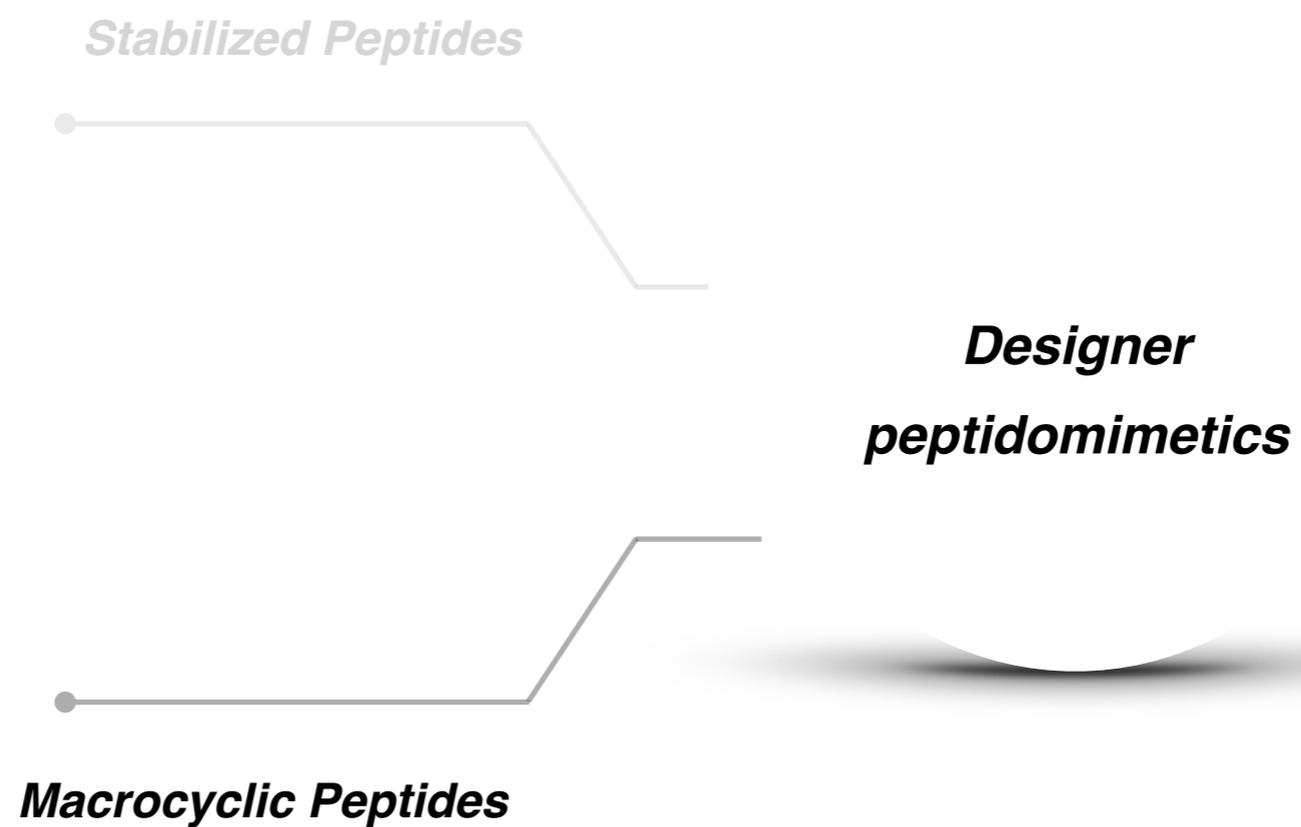


Tipranavir
HIV

Strategies to Access Undruggable Targets

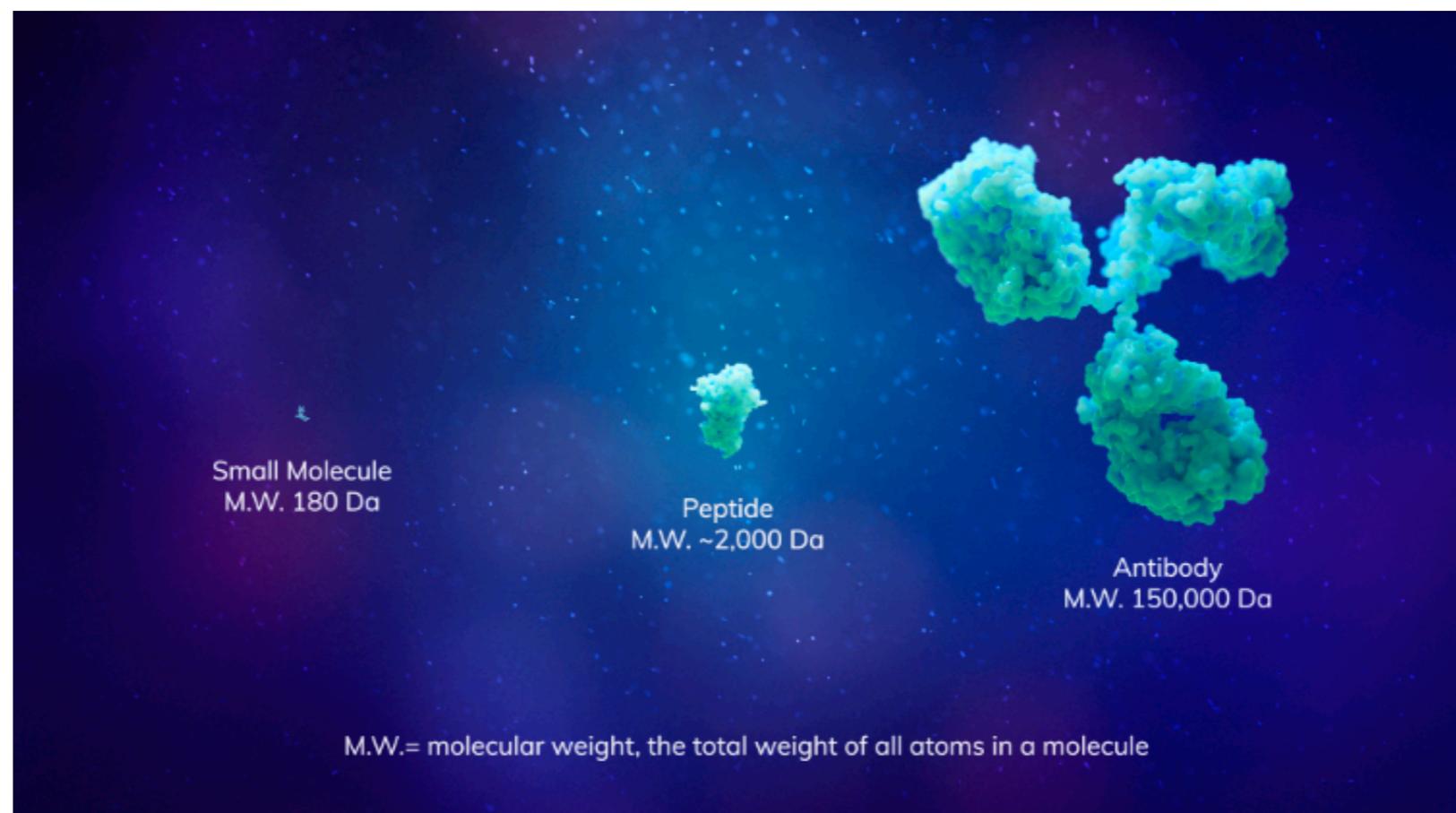


Strategies to Access Undruggable Targets



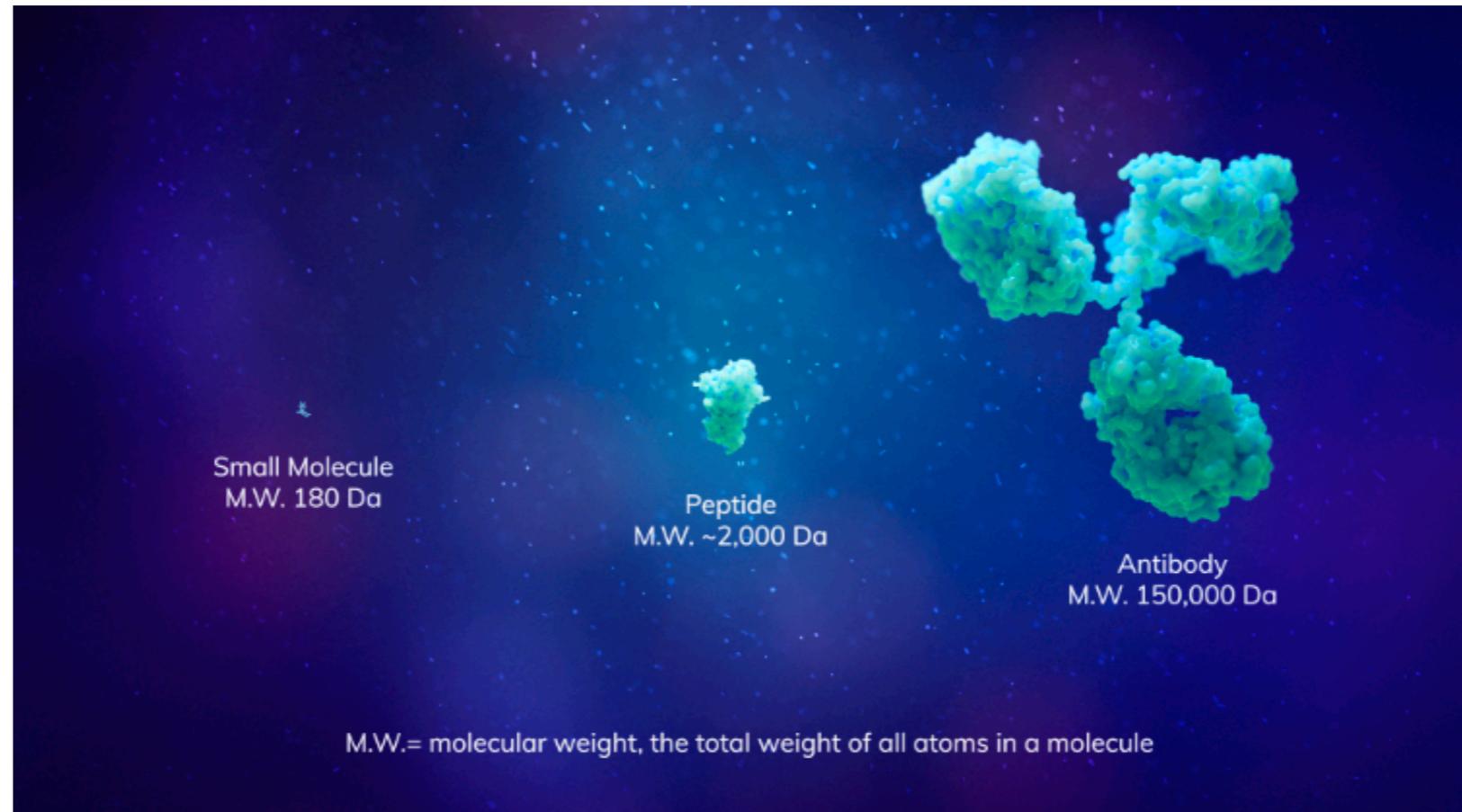
Macrocyclic Peptides

MCPs = The “goldilocks” chemical modality



Macrocyclic Peptides

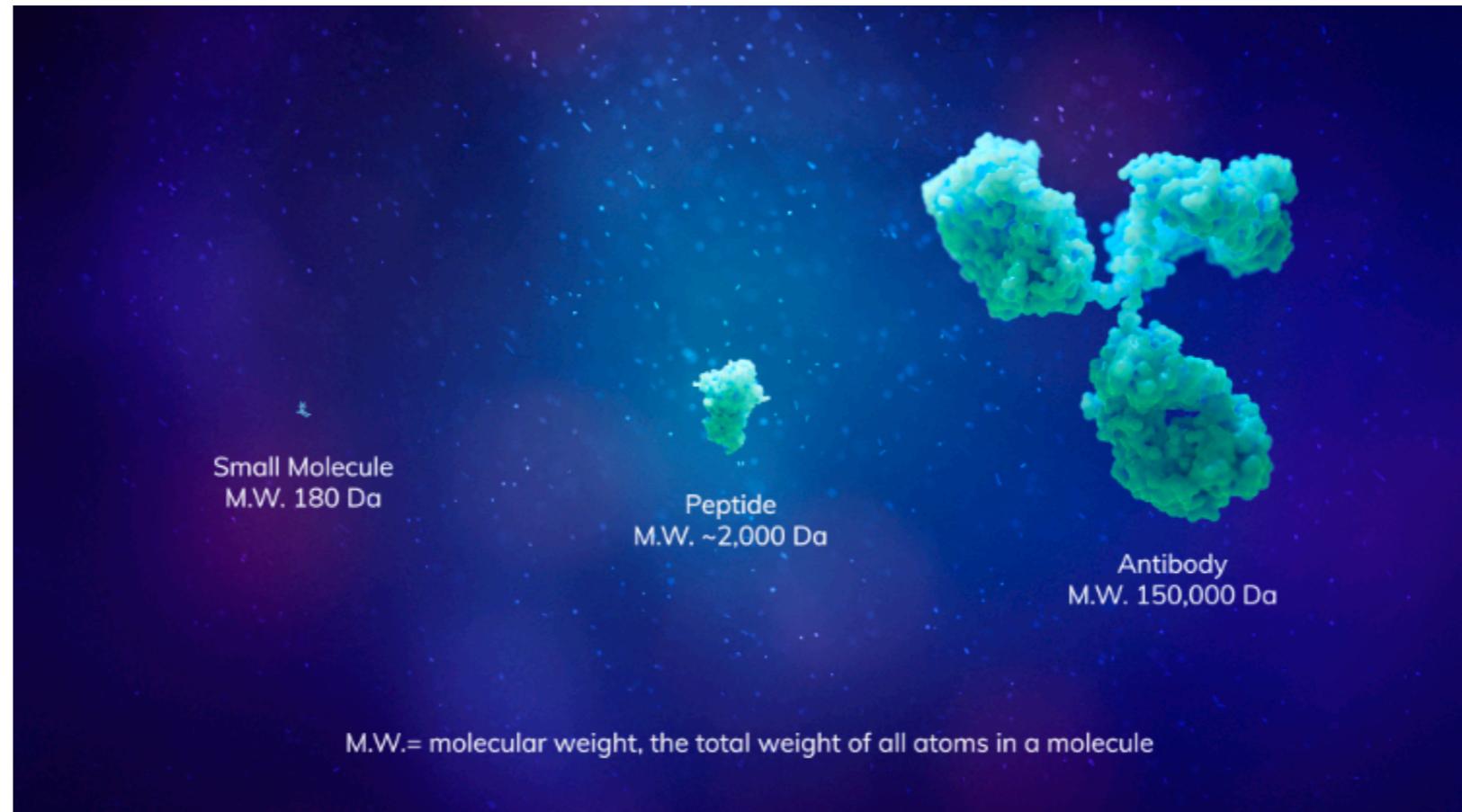
MCPs = The “goldilocks” chemical modality



greater surface area: useful to disrupting protein–protein interactions

Macrocyclic Peptides

MCPs = The “goldilocks” chemical modality



MCPs for Undruggable targets:

- ***Large compound library screening a powerful approach for the de novo discovery of MCPs***

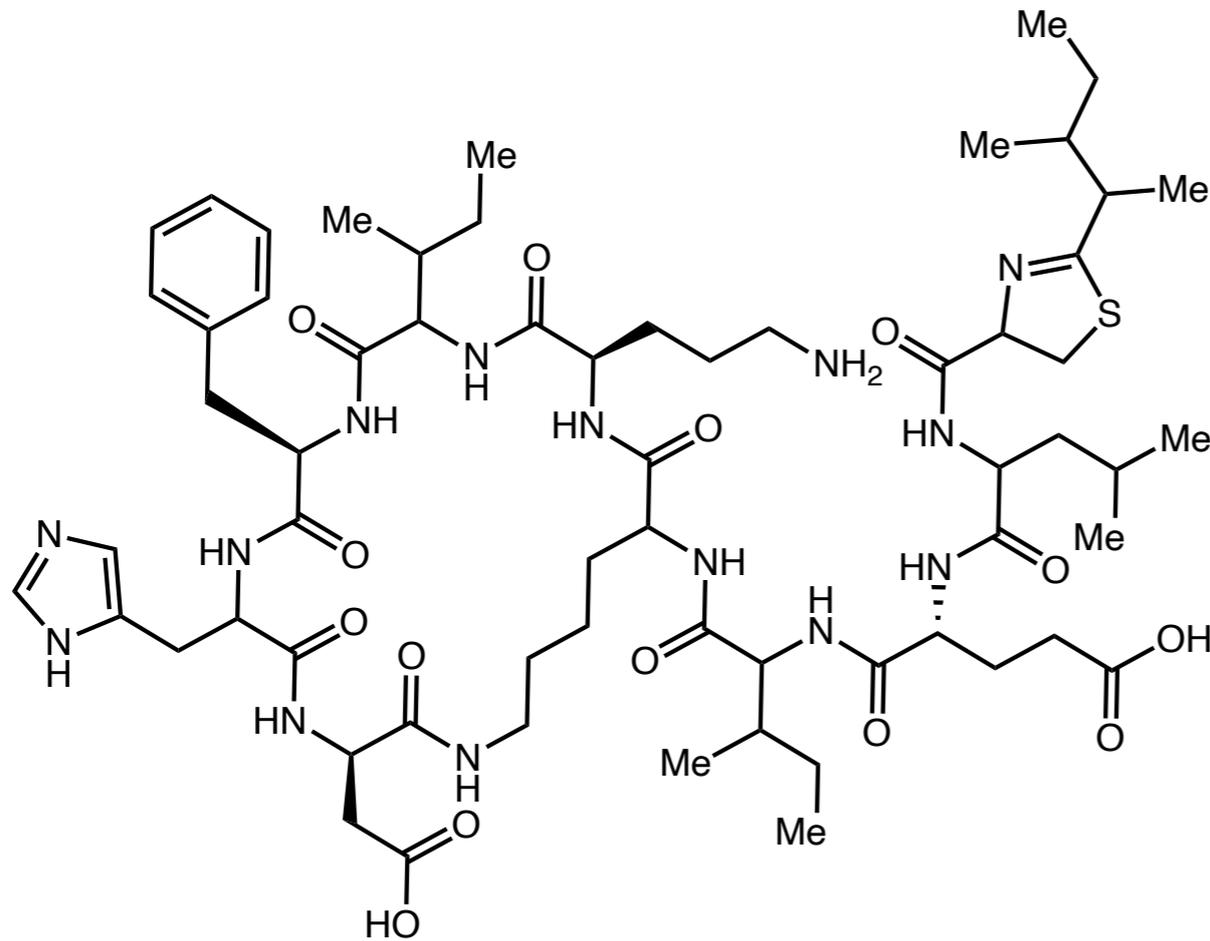
Macrocyclic Peptides (MCPs)

- *MCPs in drug discovery:*

- ***MCPs exhibit constrained conformations and chemical stability***

Macrocyclic Peptides (MCPs)

■ MCPs in drug discovery:



Bacitracin A



- ***MCPs are important sources for antibiotic discovery due to their constrained conformations and chemical stability***

Macrocyclic Peptides (MCPs)

Targeting drug–resistance

- *MCPs in drug discovery:*

drug–resistant bacterial infections:
Undruggable targets that were previously treatable

Macrocyclic Peptides (MCPs)

Targeting drug-resistance

■ MCPs in drug discovery:



Carbapenem-resistant Acinetobacter baumannii (CRAB)

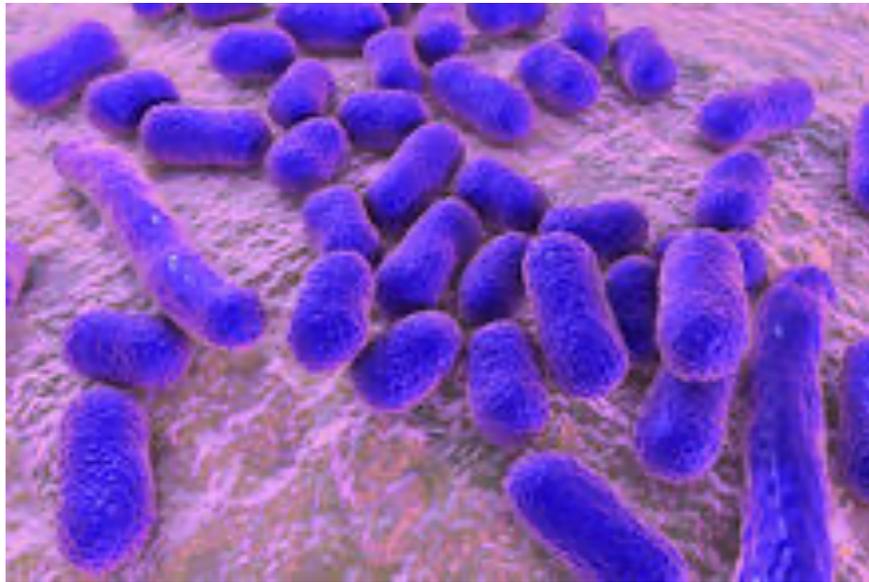
- **Gained multi-drug resistance 50 years ago**
- **Resistant to β -lactam and carbapenem antibiotics**



Macrocyclic Peptides (MCPs)

Targeting drug-resistance

■ *MCPs in drug discovery:*



Priority 1 Critical WHO Pathogen



Carbapenem-resistant Acinetobacter baumannii (CRAB)

- ***Gained multi-drug resistance 50 years ago***
- ***Resistant to β -lactam and carbapenem antibiotics***

Macrocyclic Peptides (MCPs)

Targeting drug-resistance

- MCPs in drug discovery:



Macrocyclic peptide
drug

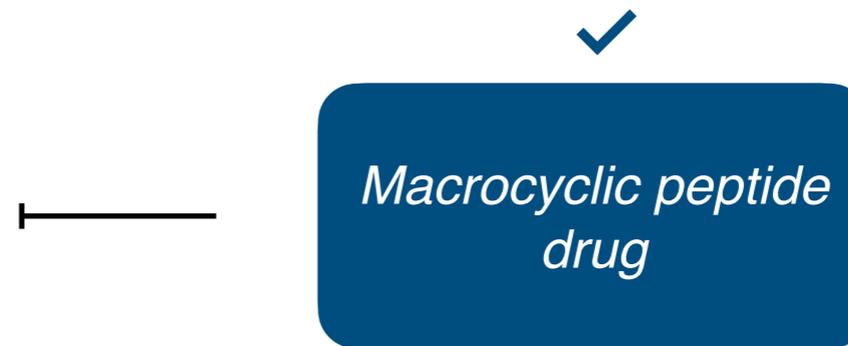
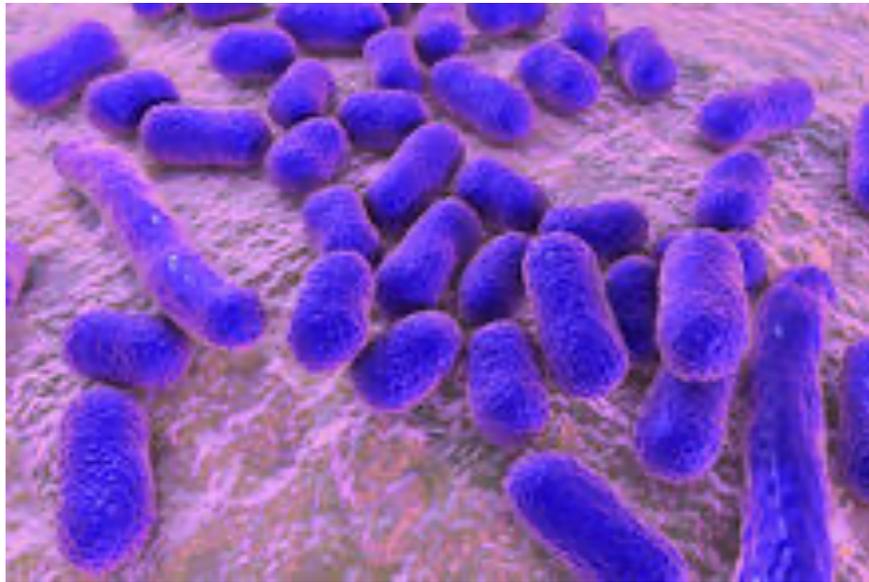
Carbapenem-resistant Acinetobacter baumannii (CRAB)



Macrocyclic Peptides (MCPs)

Targeting drug-resistance

■ MCPs in drug discovery:



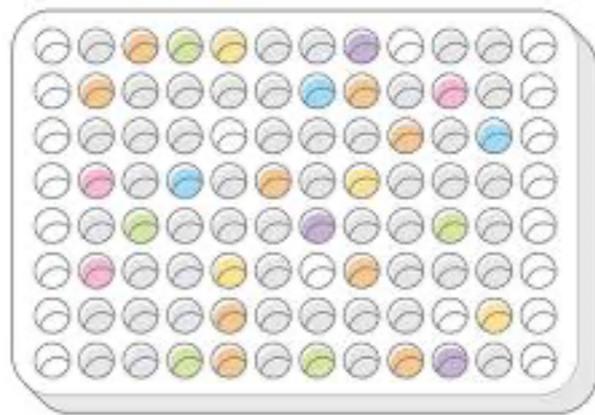
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Macrocyclic Peptides (MCPs)

Targeting drug-resistance



Screened > 45,000 MCPs

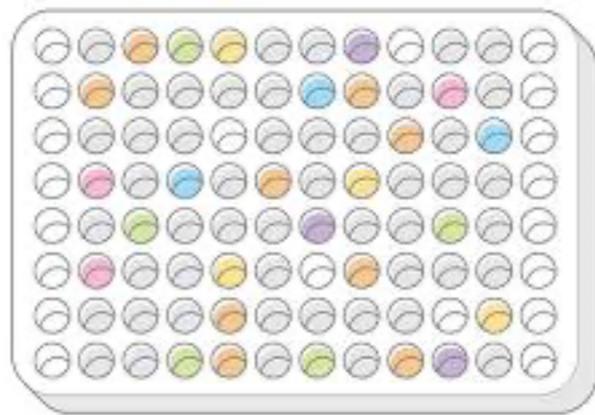


1 MCP selectively kills *A. baumannii*



Macrocyclic Peptides (MCPs)

Targeting drug-resistance



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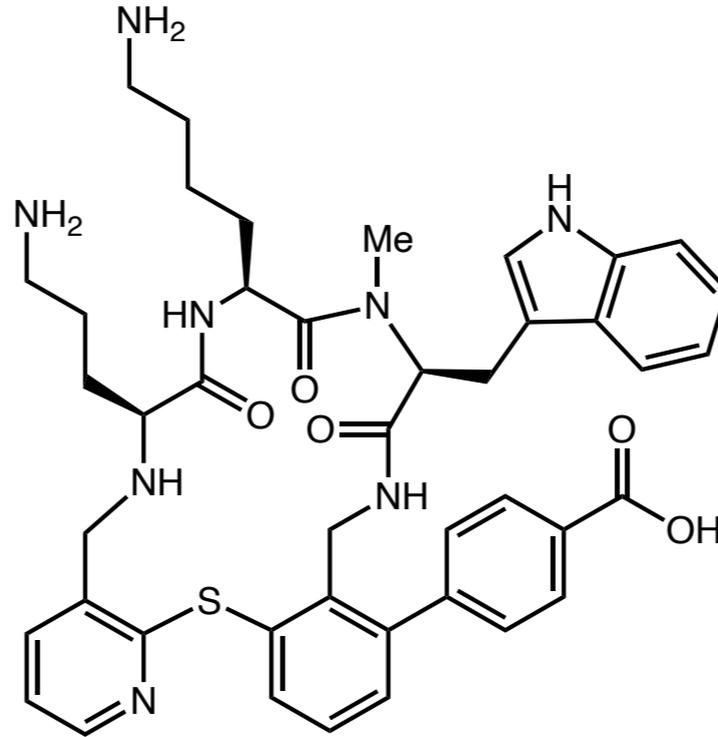
1 MCP selectively kills *A. baumannii*

- **Further optimization performed for efficacy and blood-plasma compatibility**



Macrocyclic Peptides (MCPs)

Targeting drug-resistance



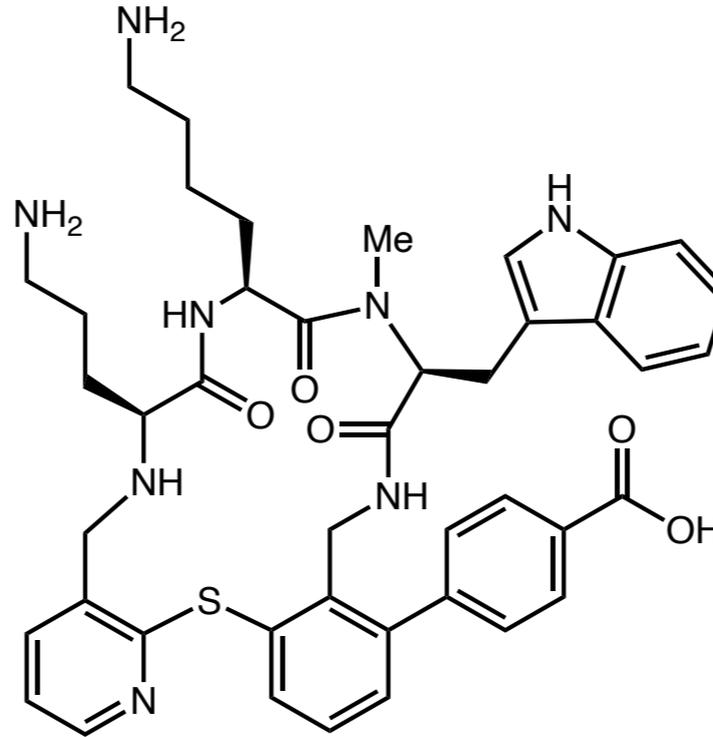
Zosurabalpin®

1 MCP selectively kills *A. baumannii*



Macrocyclic Peptides (MCPs)

Targeting drug-resistance



Zosurabalpin®

1 MCP selectively kills *A. baumannii*

Operative via novel mode of action



Macrocyclic Peptides (MCPs)

Targeting drug–resistance

- *MCPs in drug discovery:*

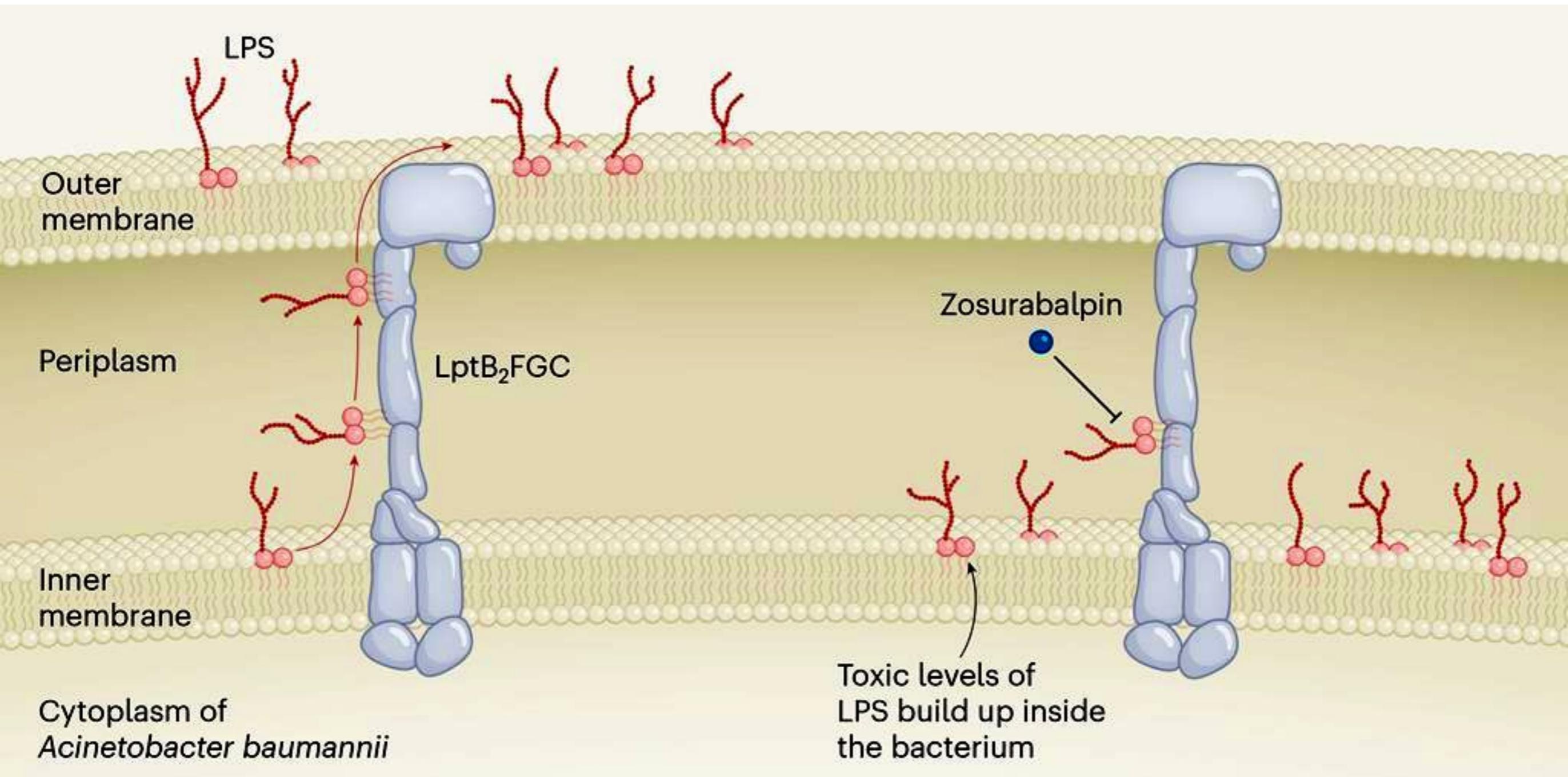
- ***Zosurabalpin inhibits transport of the molecule lipopolysaccharide (LPS)***



Macrocyclic Peptides (MCPs)

Targeting drug-resistance

■ MCPs in drug discovery:



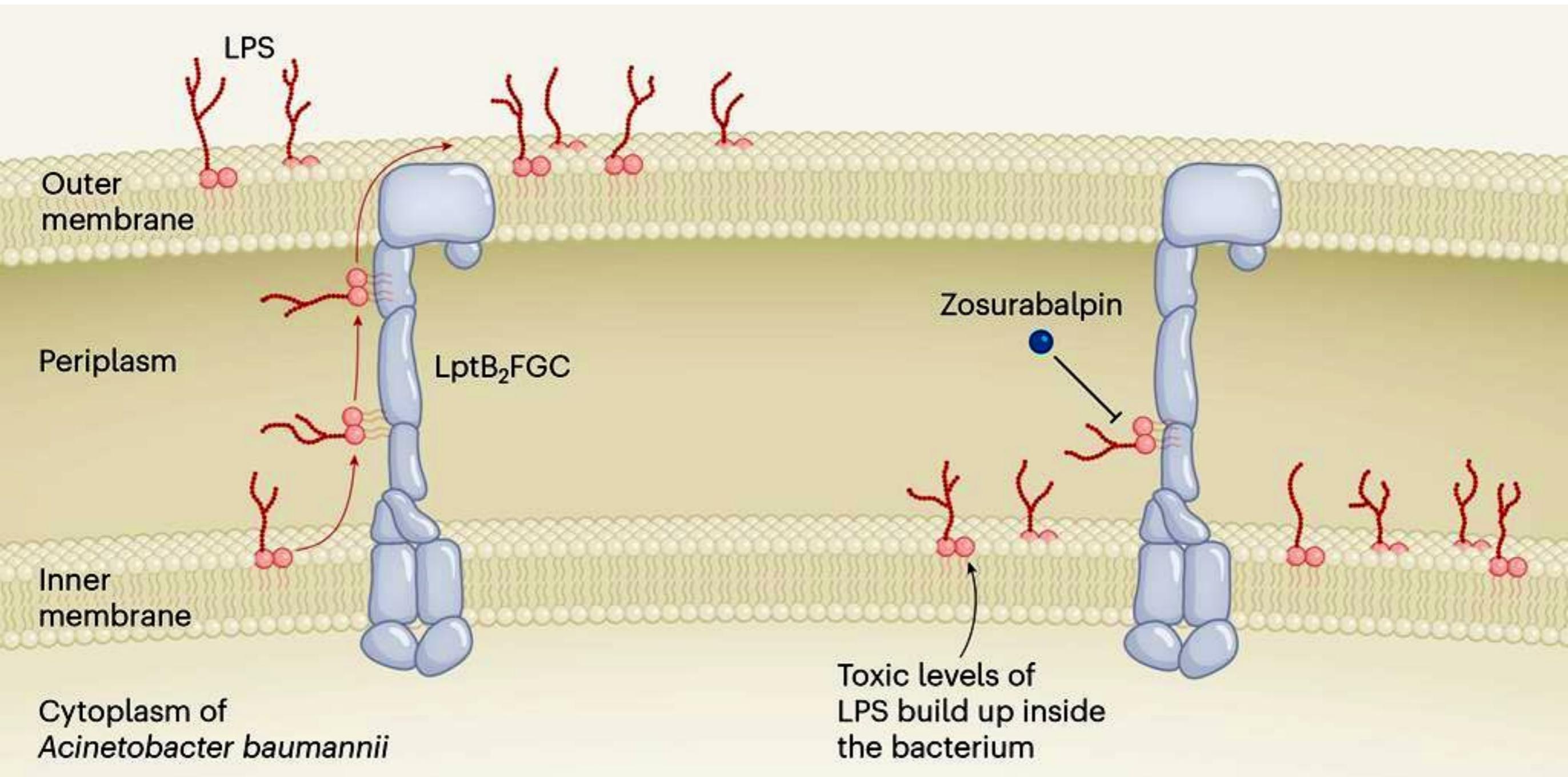
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Macrocyclic Peptides (MCPs)

Targeting drug-resistance

- MCPs in drug discovery: inhibits LptB₂FGC complex



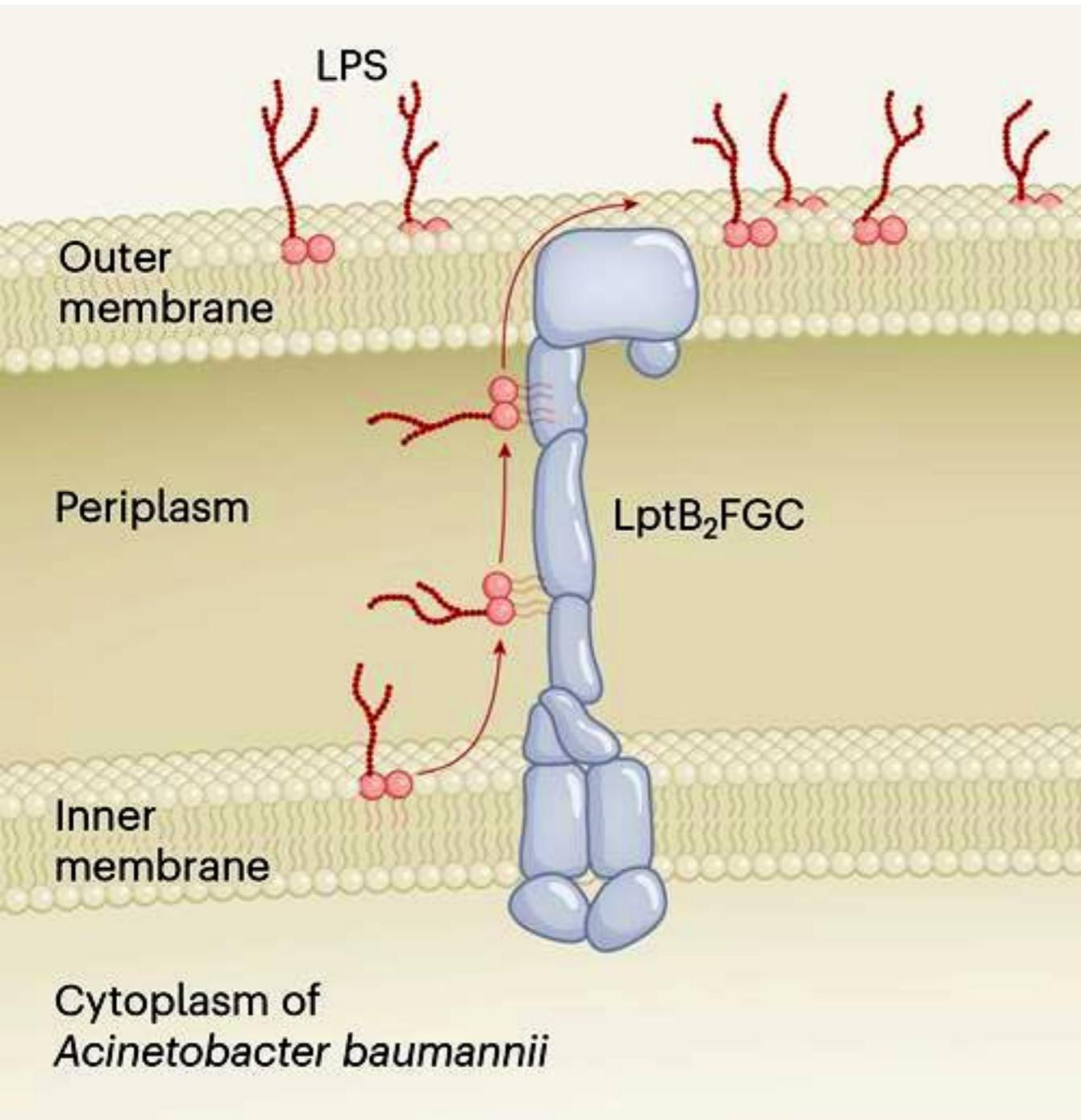
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Macrocyclic Peptides (MCPs)

Targeting drug-resistance

- MCPs in drug discovery: reaching novel targets



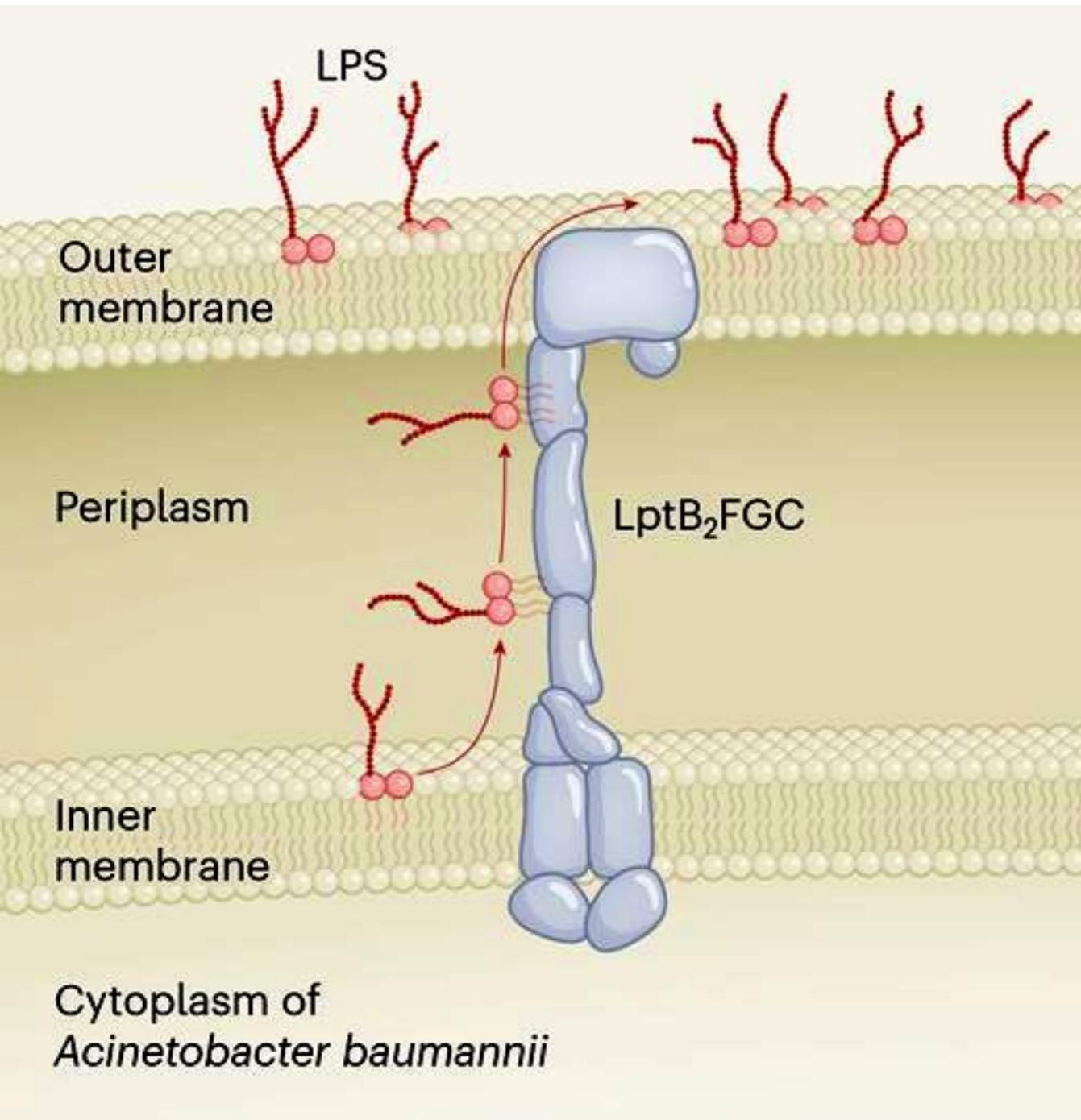
- **Antibiotics have focused on reaching cytoplasmic targets**



Macrocyclic Peptides (MCPs)

Targeting drug-resistance

- MCPs in drug discovery: reaching novel targets



- **Antibiotics have focused on reaching cytoplasmic targets**



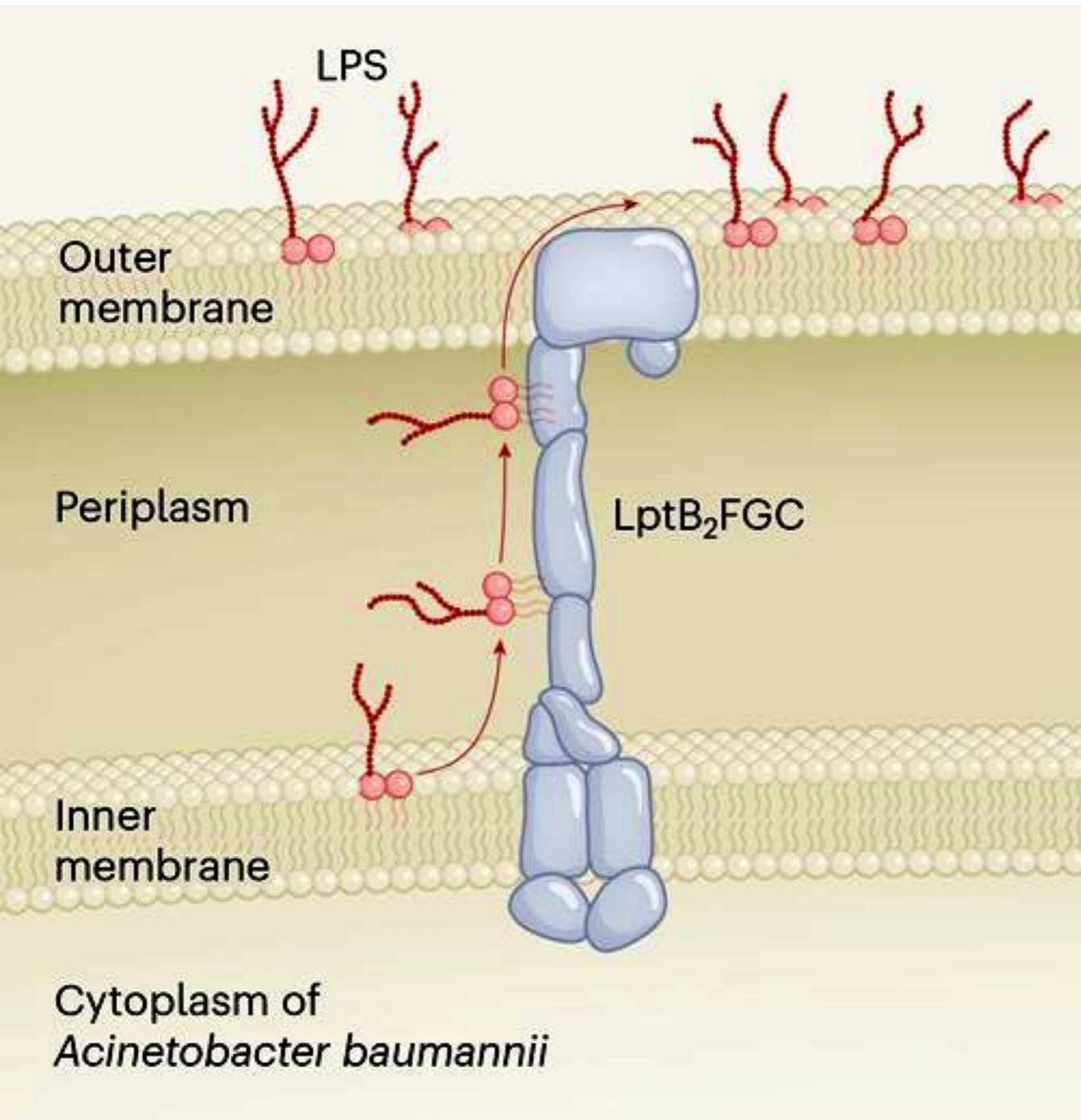
- **This limits prospective targets to cell surface**



Macrocyclic Peptides (MCPs)

Targeting drug-resistance

- MCPs in drug discovery: reaching novel targets



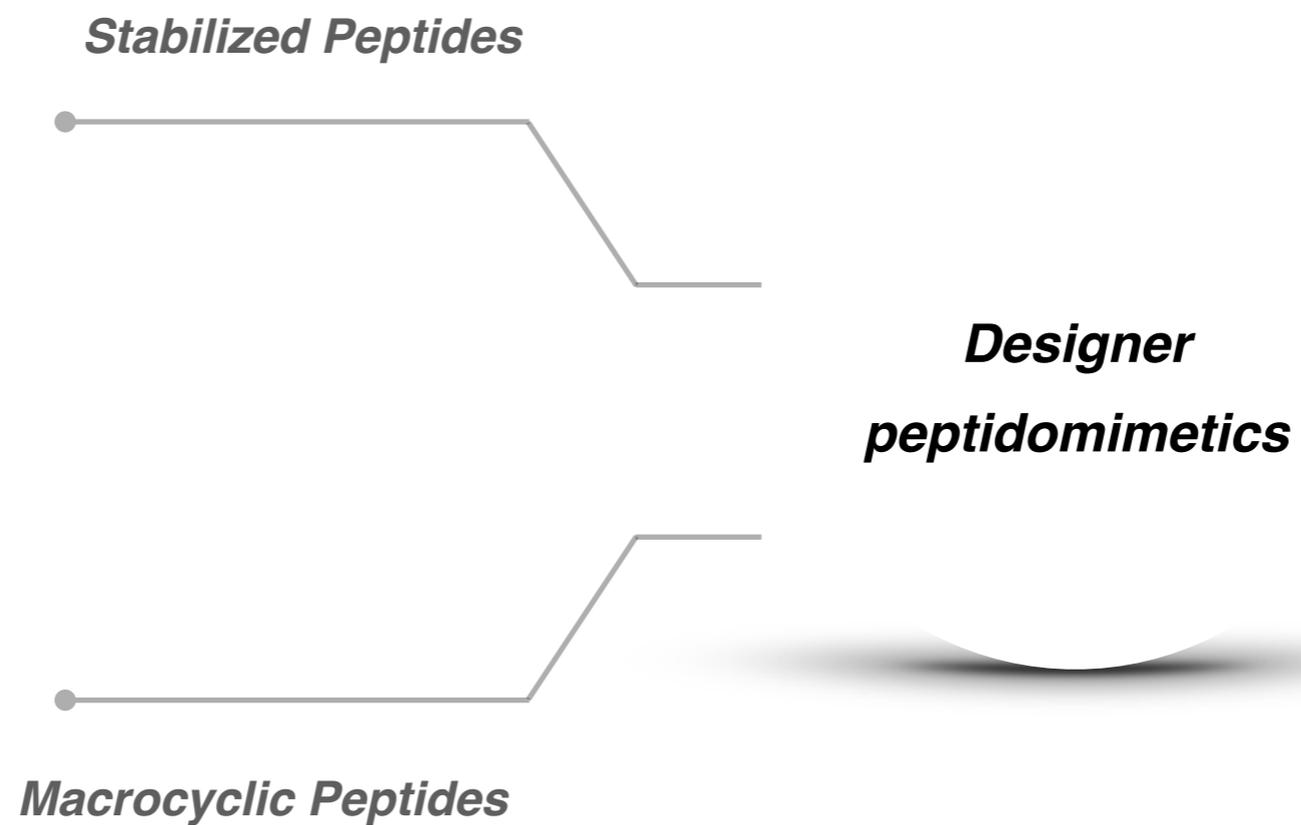
- **Antibiotics have focused on reaching cytoplasmic targets**



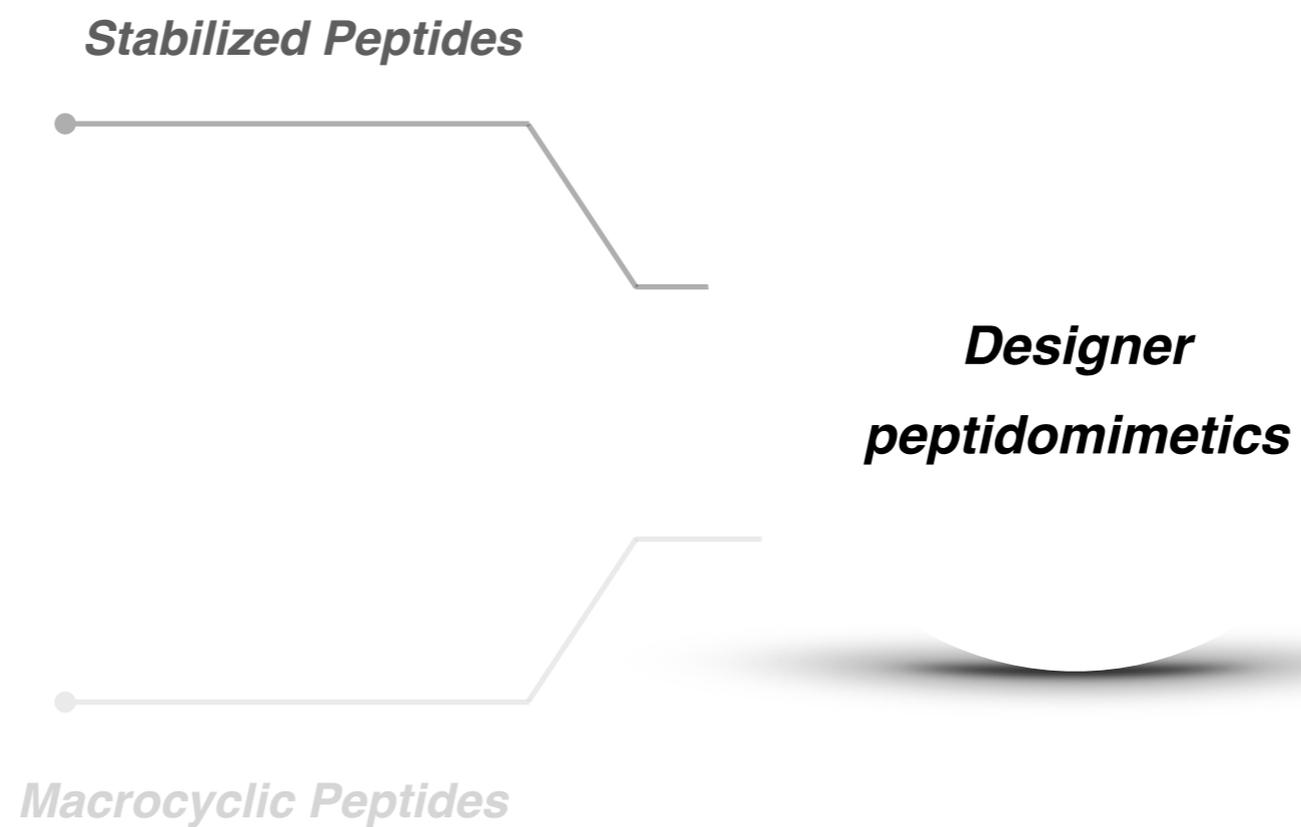
- ***LptB₂FGC* resides in the periplasm, enabling Zosurabalpin delivery**



Strategies to Access Undruggable Targets



Strategies to Access Undruggable Targets



Strategies to Access Undruggable Targets

Stabilized Peptides



Strategies to Access Undruggable Targets

Stabilized Peptides



- *synthetic modifications to **stabilize local and global structural motifs***

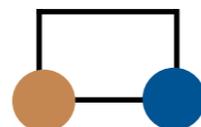


Strategies to Access Undruggable Targets

Stabilized Peptides



- *synthetic modifications to **stabilize local and global structural motifs***



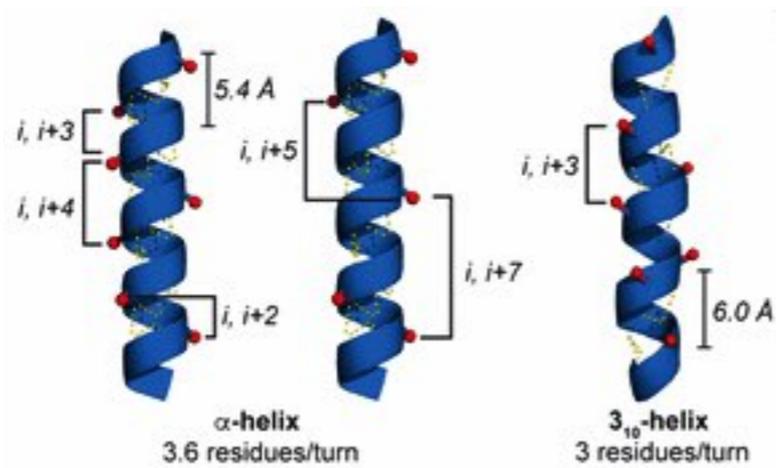
Confers enhanced affinity and specificity

Stabilized Peptides

- *Imposing structure*

Naturally occurring motifs:

Helix motifs

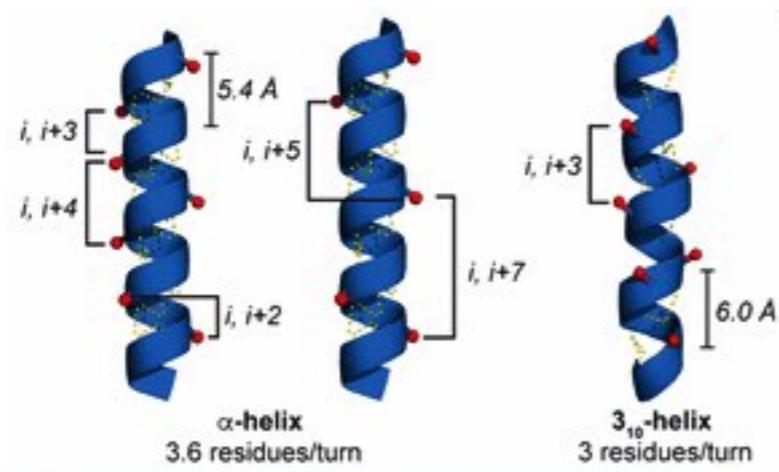


Stabilized Peptides

■ Imposing structure

Naturally occurring motifs:

Helix motifs



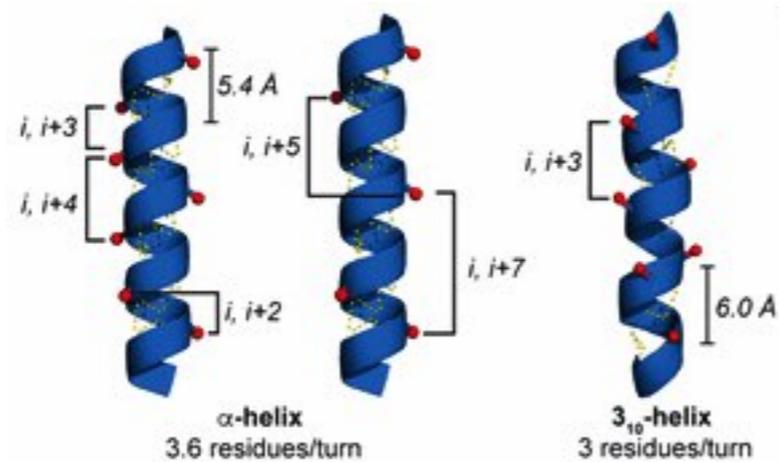
- **The majority of interactions reported in PDB involve α -helices**

Stabilized Peptides

■ Imposing structure

Naturally occurring motifs:

Helix motifs



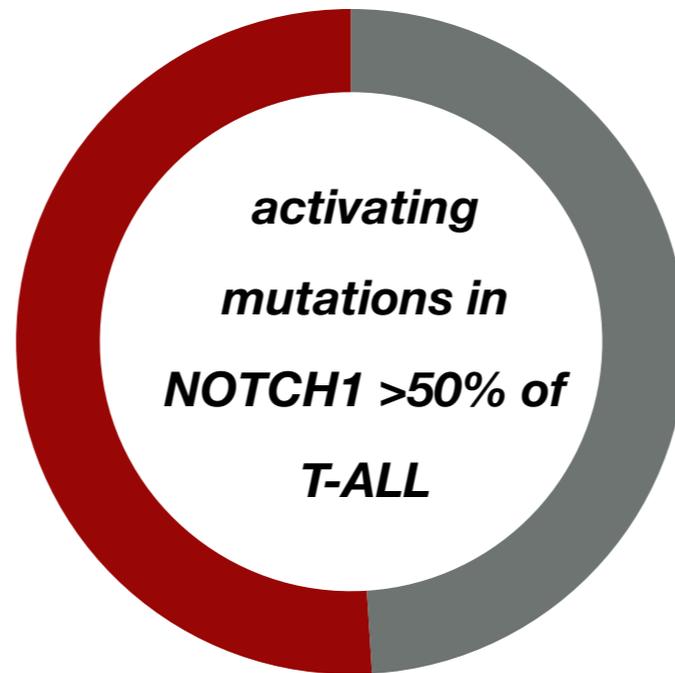
Hairpin motifs



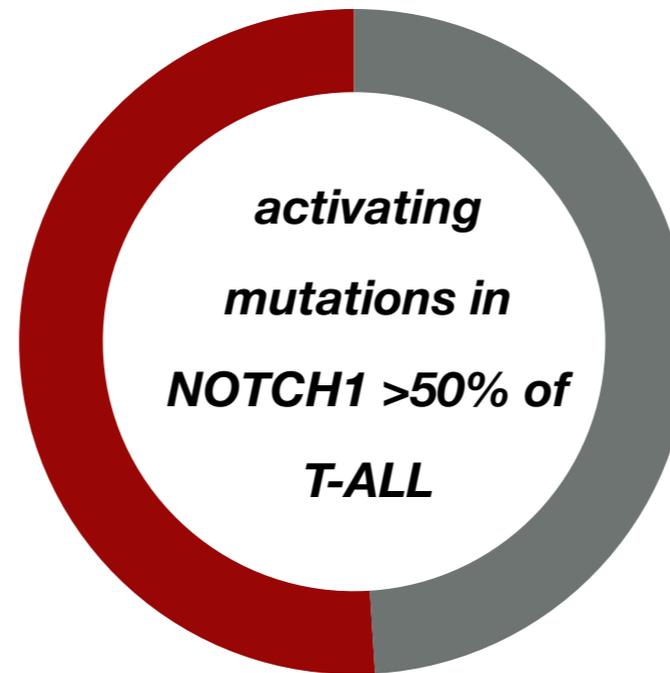
• **Both exhibit internal hydrogen bonding**

• **stabilizing mutations locks the peptide into desired conformation**

Stabilized Peptides
Inhibition of NOTCH



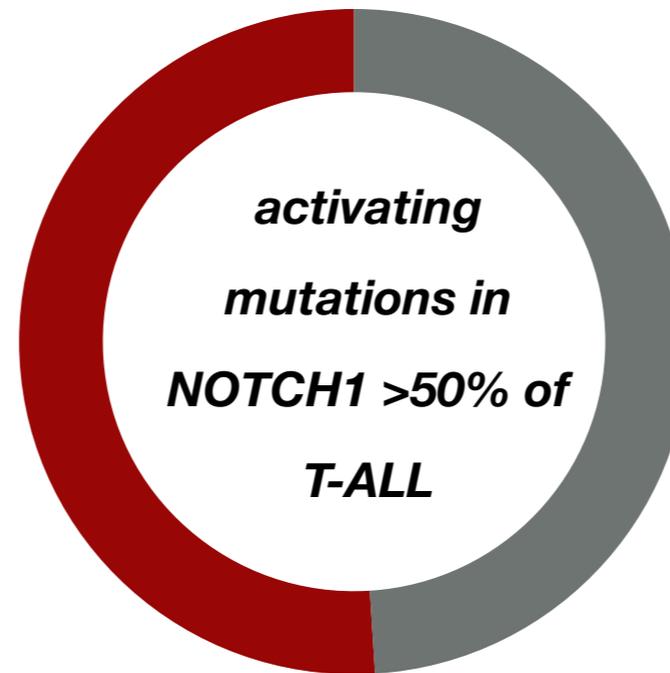
Stabilized Peptides
Inhibition of NOTCH



***Inappropriate NOTCH activation is directly implicated in T-cell Acute
Lymphoblastic Leukaemia (T-ALL)***

Stabilized Peptides

Inhibition of NOTCH



NOTCH1 = transcription factor

- ***transcription factors are challenging to target***

Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex

Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*

*Binding by
extracellular ligands
induces signaling*

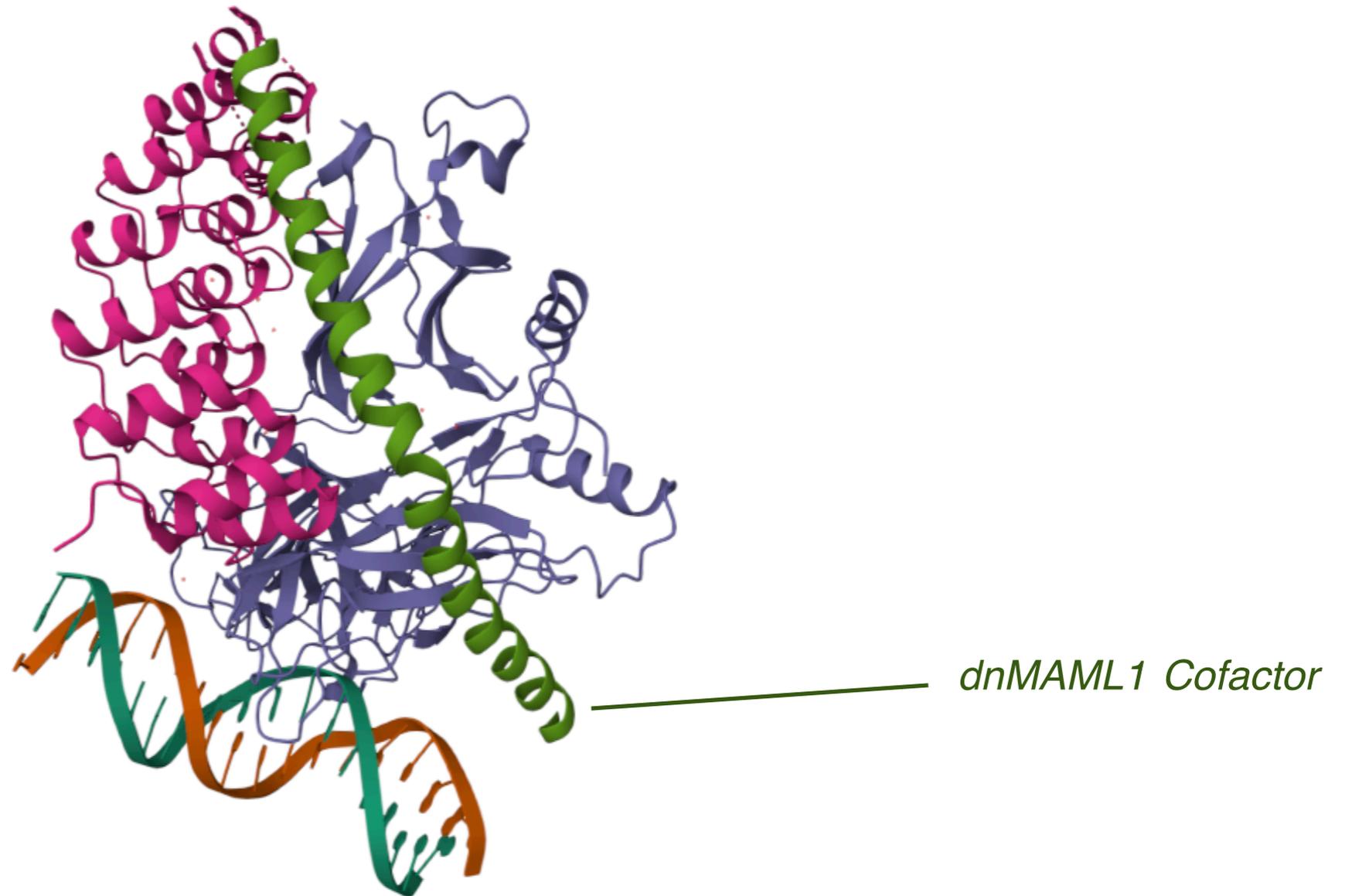


NOTCH1 ternary complex

Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*

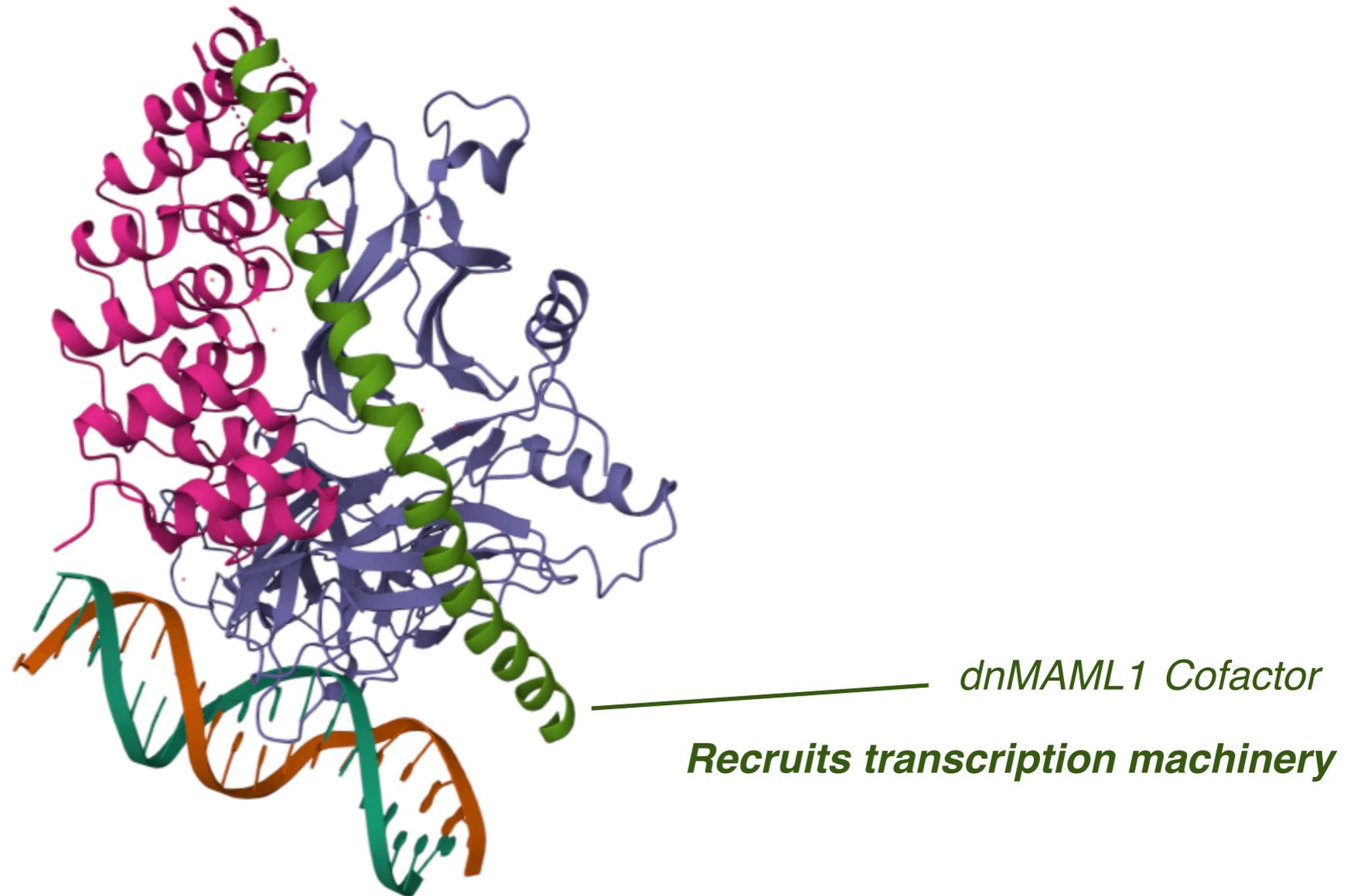


NOTCH1 ternary complex

Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex

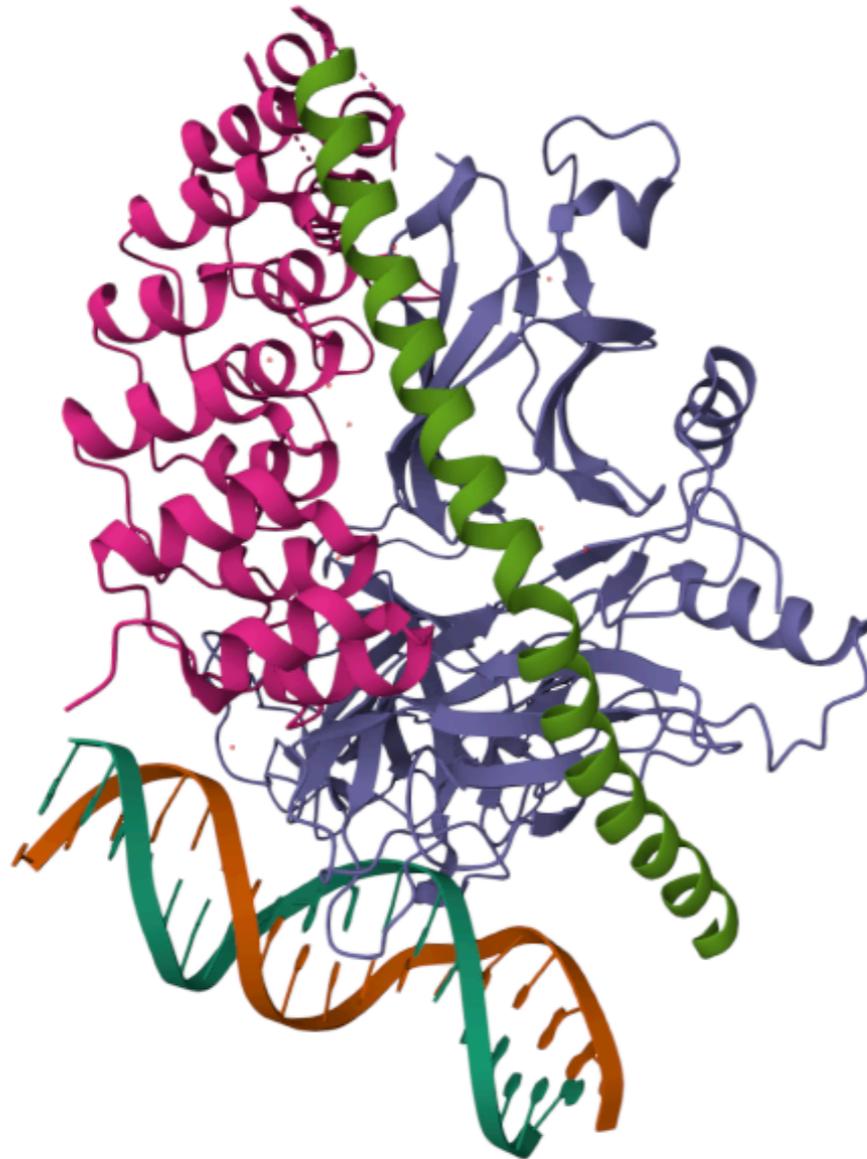
Assembly promotes signalling



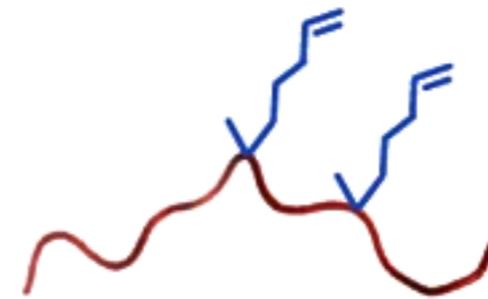
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex



ICN1 normally binds MAML1



Derived from MAML1 binding domain!

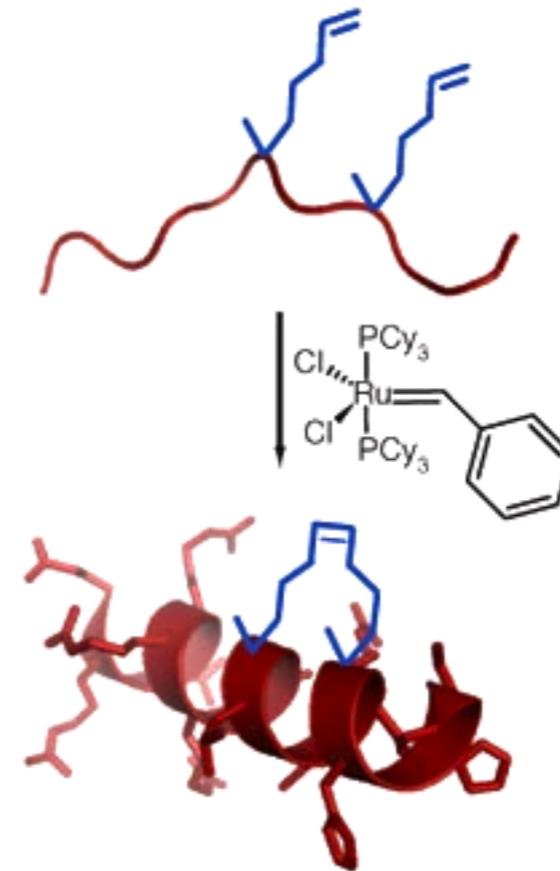
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex



stapled α -helical peptides

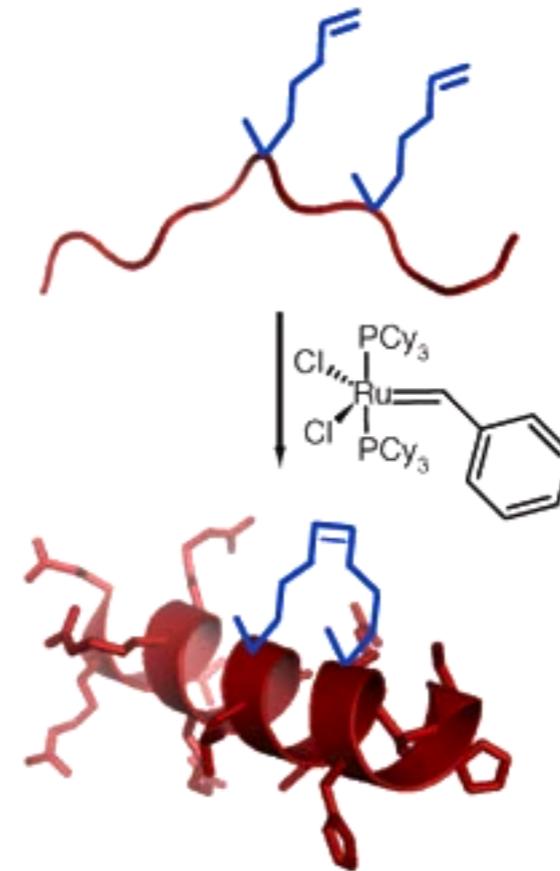
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex



stapled α -helical peptides

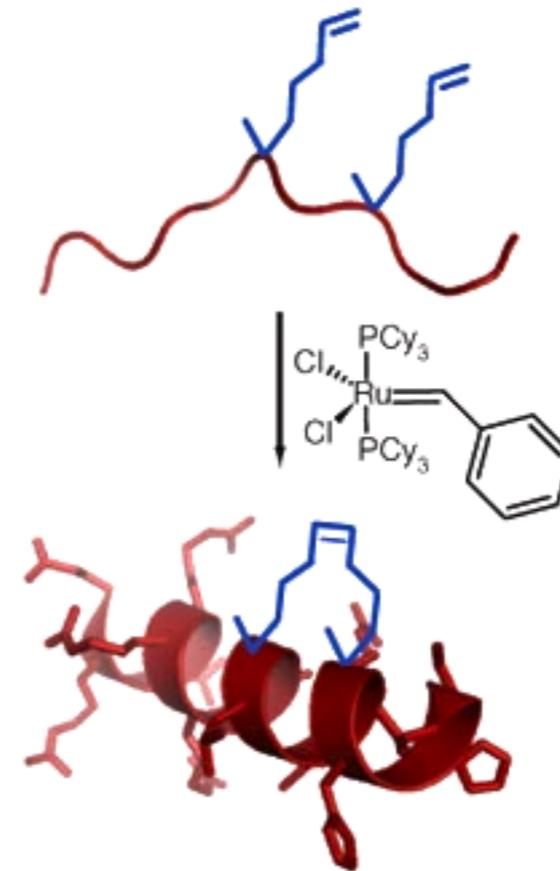
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex



Forced as a helix (despite being short) due to stapling

stapled α -helical peptides

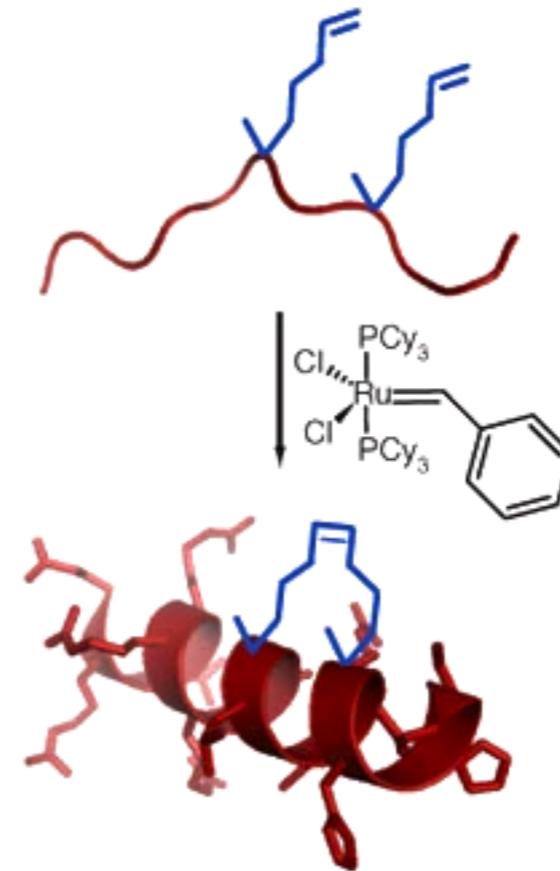
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure:*



NOTCH1 ternary complex



Forced as a helix (despite being short) due to stapling

stapled α -helical peptides

(No binding)

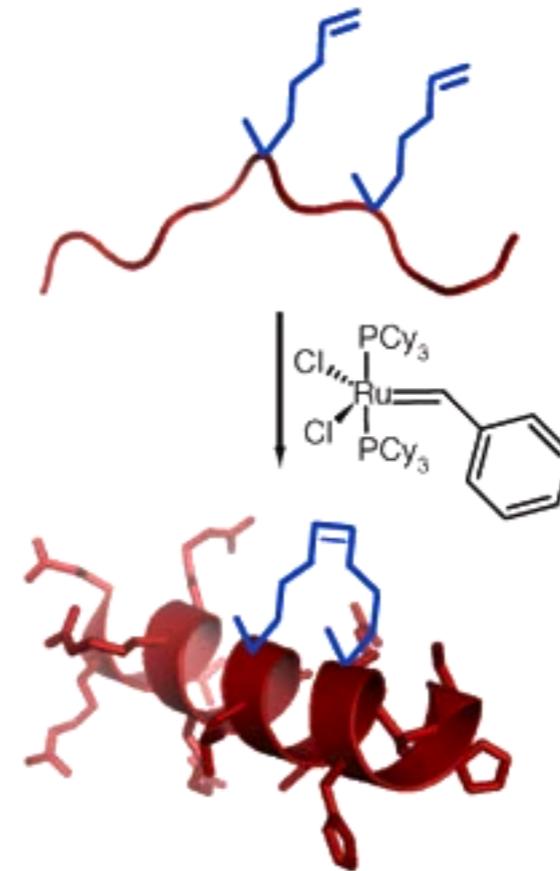
Stabilized Peptides

Inhibition of NOTCH

- *Imposing structure: Previous peptide stapling had never targeted a complex*



NOTCH1 ternary complex



Forced as a helix (despite being short) due to stapling

stapled α -helical peptides

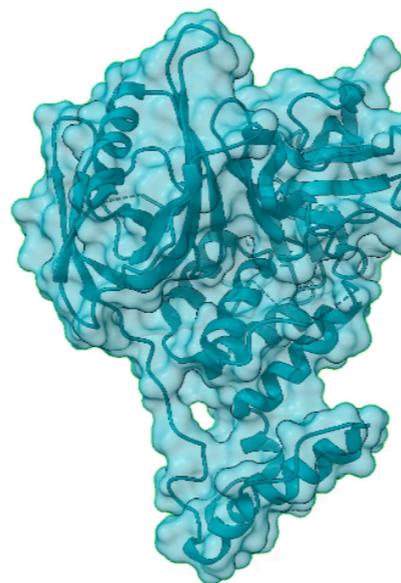
Modification Strategies for Undruggable Targets: Target ID and druggability



Part 2

Non-covalent interactors, peptidomimetics, etc.

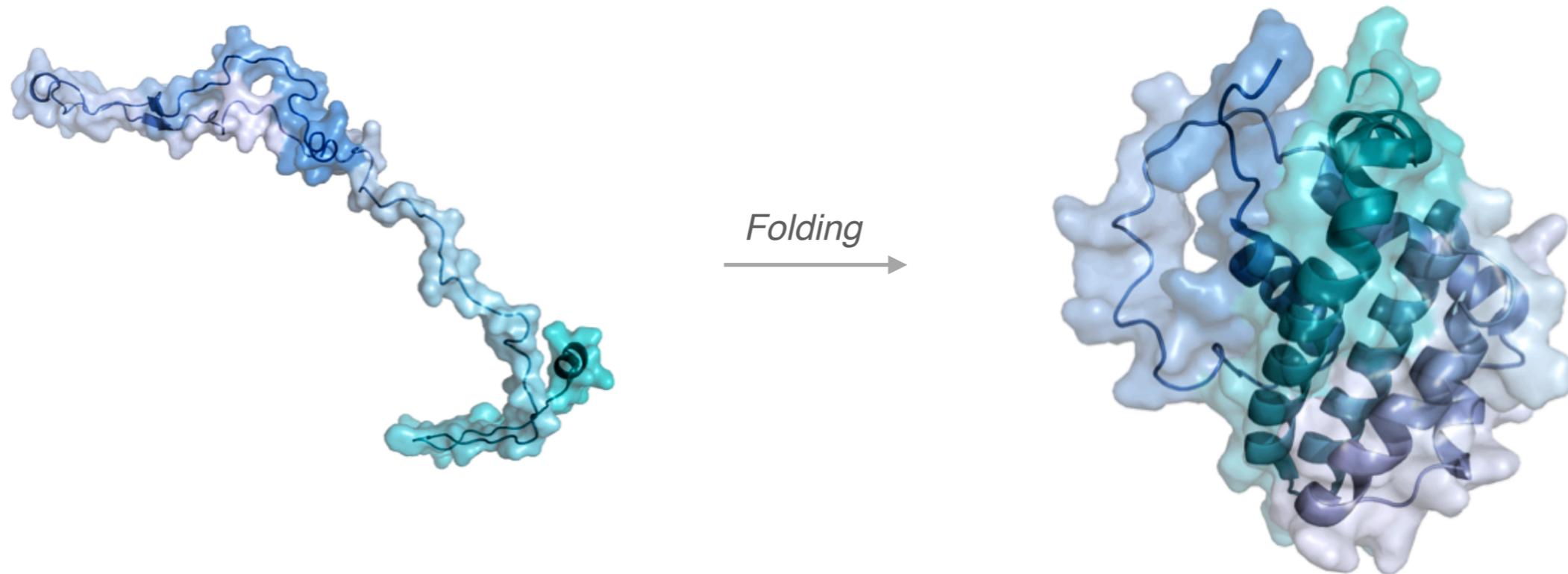
- *Exploiting structure–function to investigate therapeutics*



Part 3

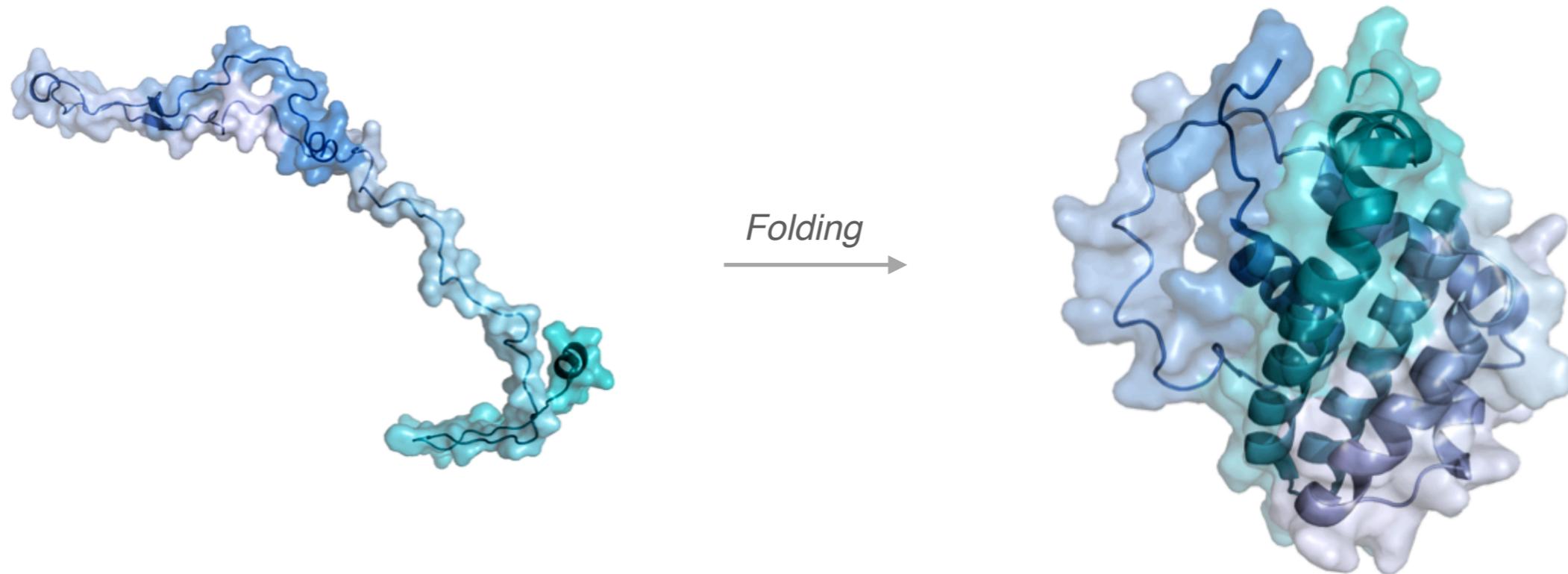
Prions: Protein Misfolding

Intrinsically disordered proteins



Intrinsically disordered proteins

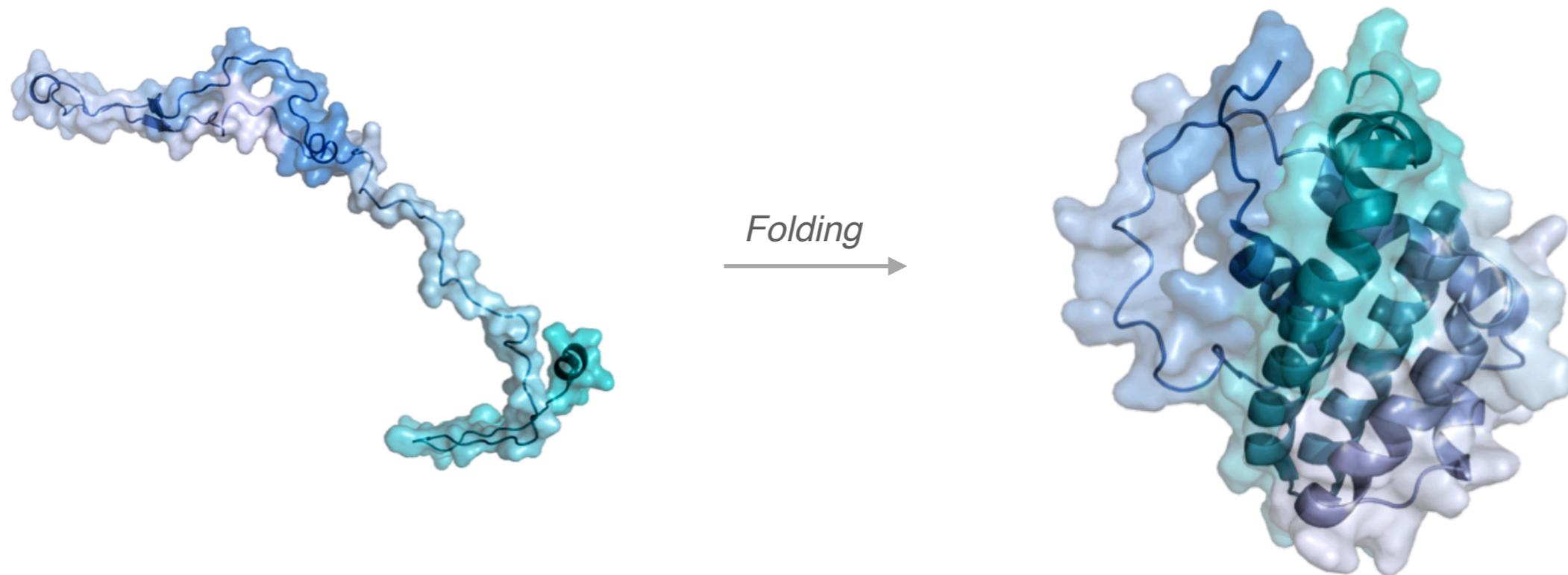
Prion disease = proteopathic disease



Levinthal's paradox

Intrinsically disordered proteins

Prion disease = proteopathic disease

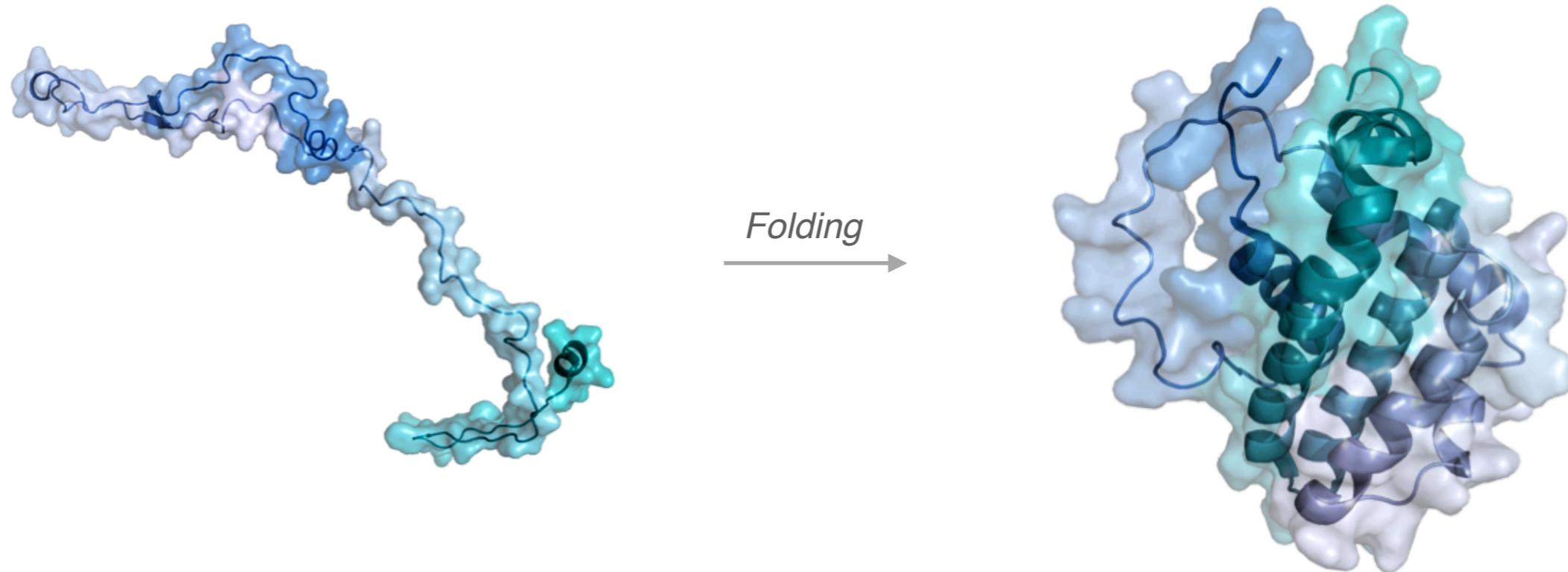


Levinthal's paradox

*“A protein with N amino acids should have 10^{2N} degrees of freedom. Thus a small protein (e.g. 150 amino acids) would have 10^{300} degrees of freedom. There is not enough time in the universe to try each of these combinations, and yet the protein is **folded within a second.**”*

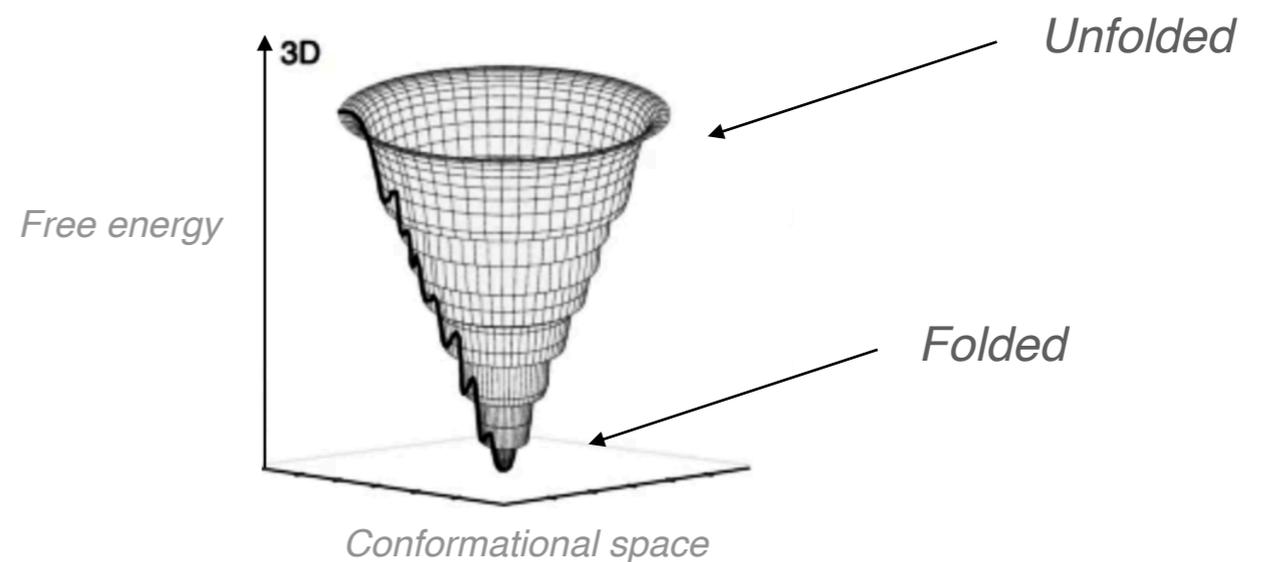
Intrinsically disordered proteins

Prion disease = proteopathic disease

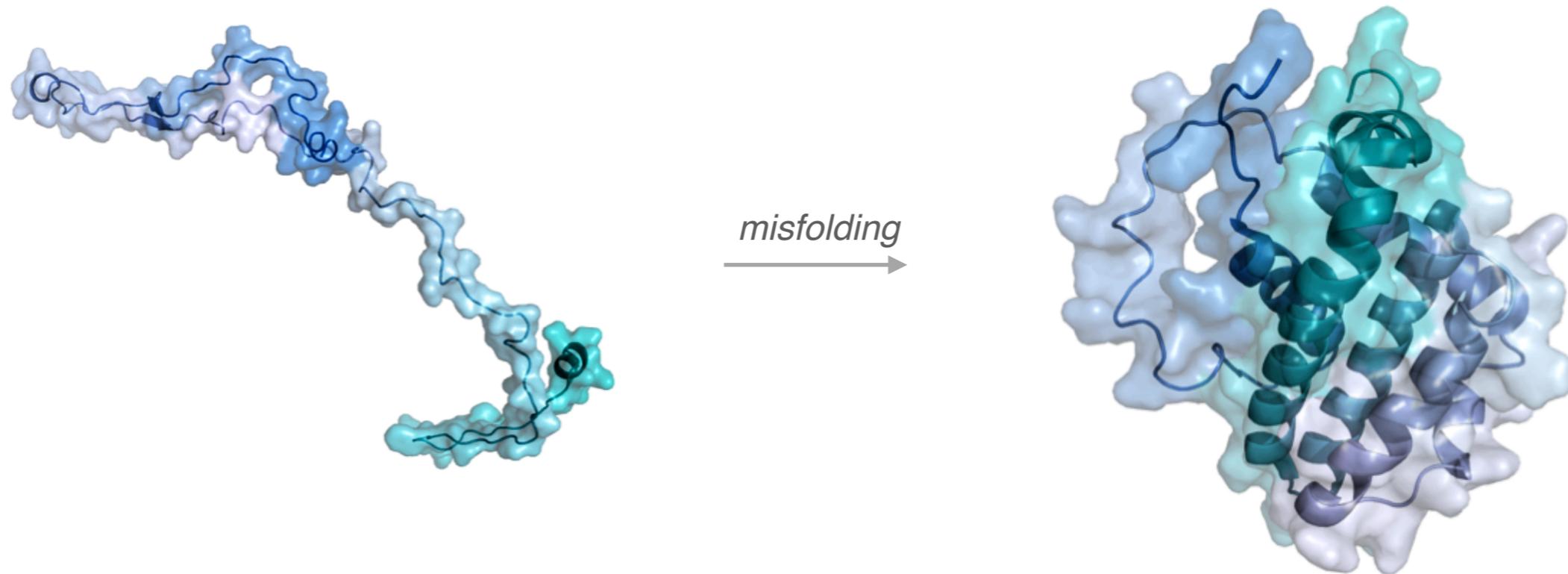


Levinthal's paradox

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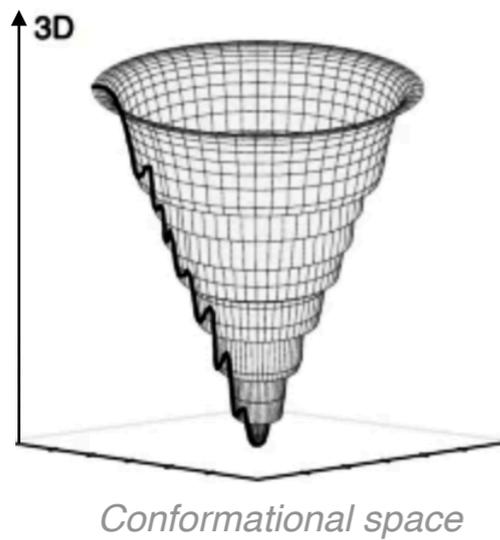
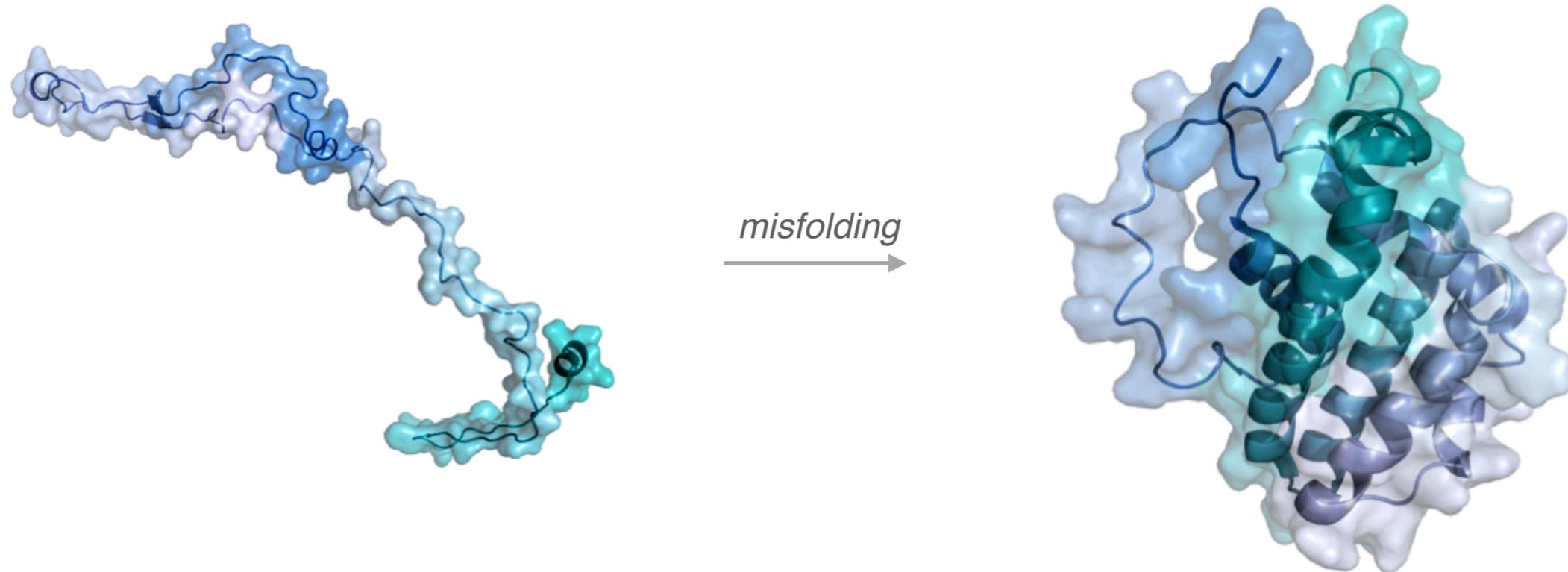


Intrinsically disordered proteins



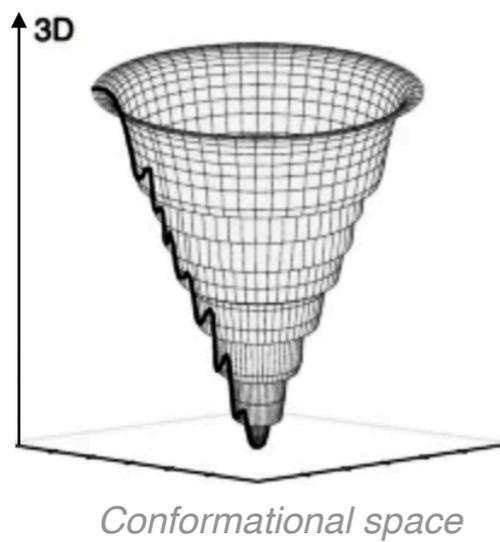
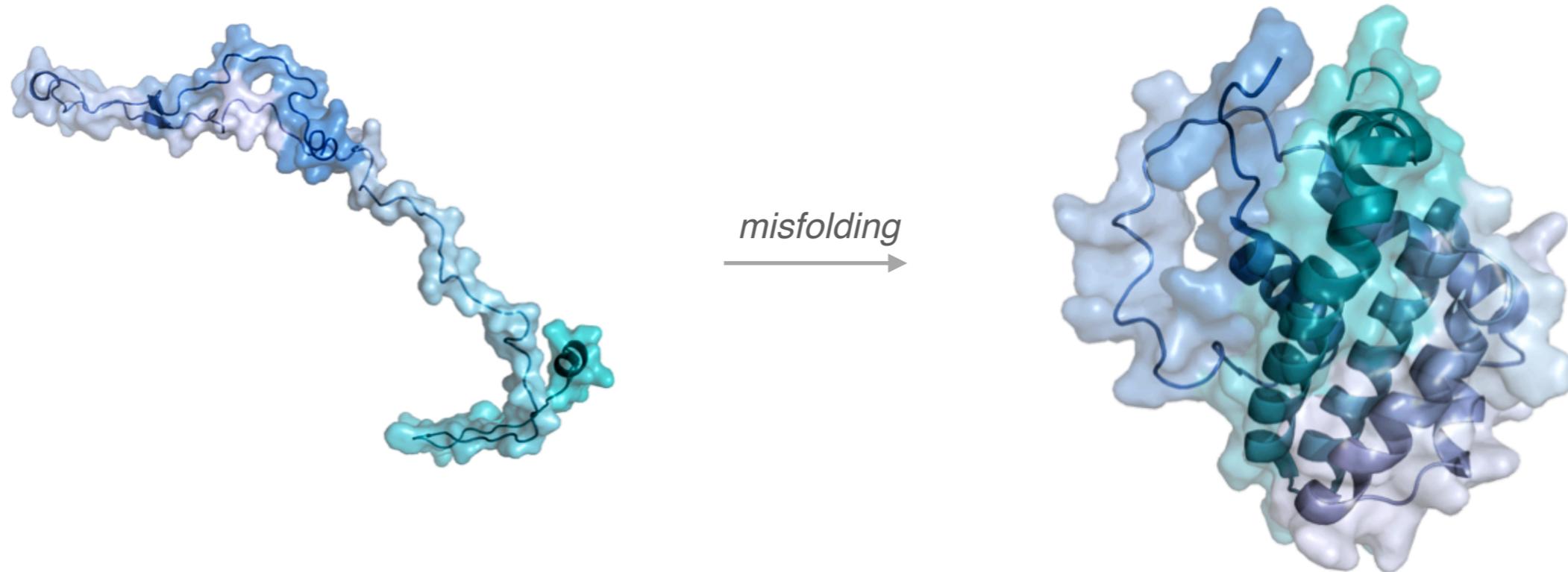
“Proteinaceous infection” = Prion

Intrinsically disordered proteins



“Proteinaceous infection” = Prion

Intrinsically disordered proteins

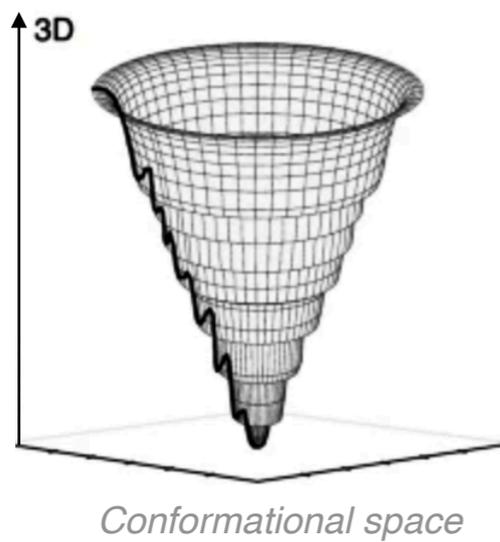
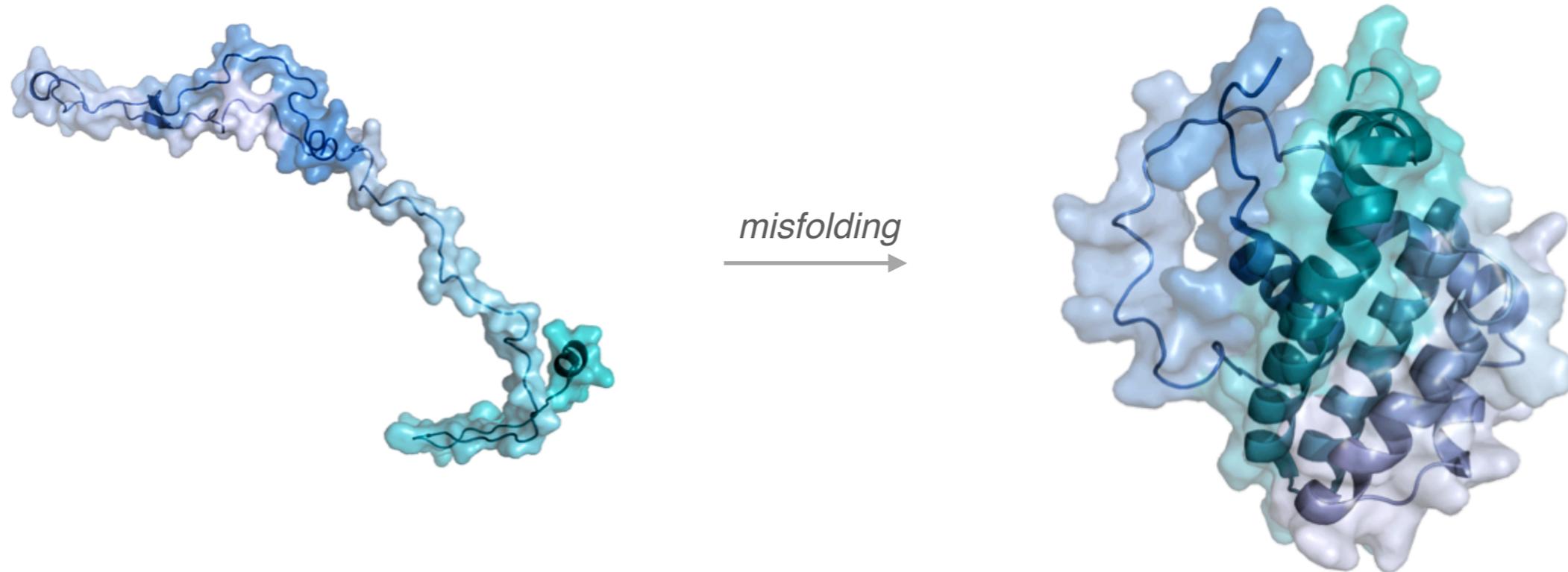


“Proteinaceous infection” = Prion



Dr. Stanley Prusiner

Intrinsically disordered proteins

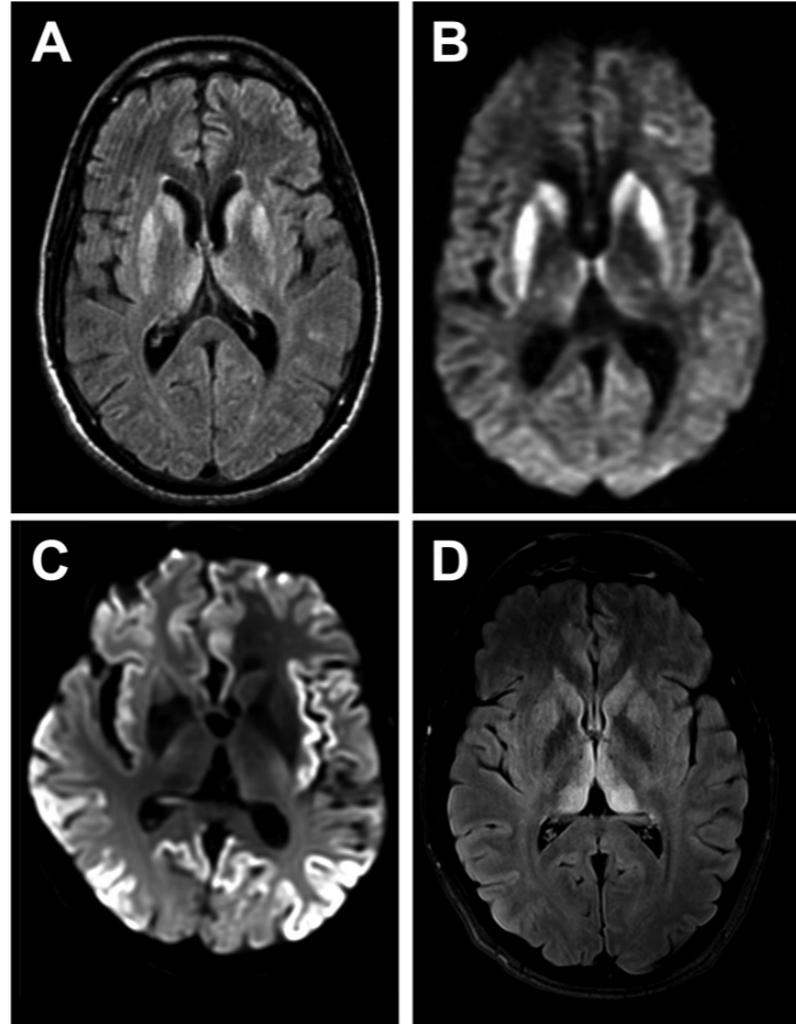


“Proteinaceous infection” = Prion
Prions are exceedingly hard to sterilize/inactivate



Dr. Stanley Prusiner

Intrinsically disordered proteins



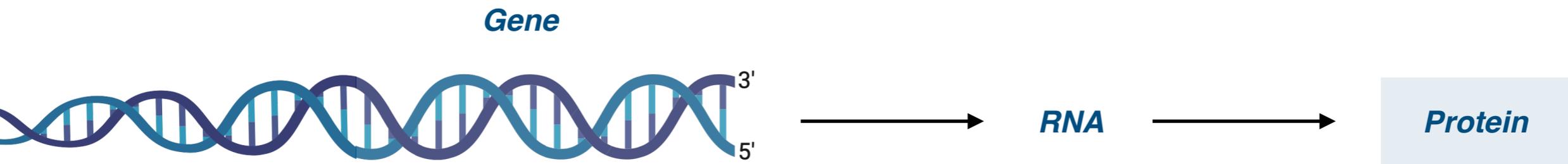
“Proteinaceous infection” = Prion

Jakob-Creutzfeldt disease, or Kuru

- *No known cure*

Intrinsically disordered proteins

Strategies to target the undruggable



Intrinsically disordered proteins

Strategies to target the undruggable

In vivo base editing extends lifespan of a humanized mouse model of prion disease

[Meirui An](#), [Jessie R. Davis](#), [Jonathan M. Levy](#), [Fiona E. Serack](#), [John W. Harvey](#), [Pamela P. Brauer](#),
[Catherine P. Pirtle](#), [Kiara N. Berríos](#), [Gregory A. Newby](#), [Wei-Hsi Yeh](#), [Nikita Kamath](#), [Meredith Mortberg](#),
[Yuan Lian](#), [Michael Howard](#), [Kendrick DeSouza-Lenz](#), [Kenia Guzman](#), [Aaron Thai](#), [Samantha Graffam](#),
[Vanessa Laversenne](#), [Alissa A. Coffey](#), [Jeannine Frej](#), [Sarah E. Pierce](#), [Jiri G. Safar](#), [Benjamin E.](#)
[Deverman](#), ... [David R. Liu](#)  [+ Show authors](#)

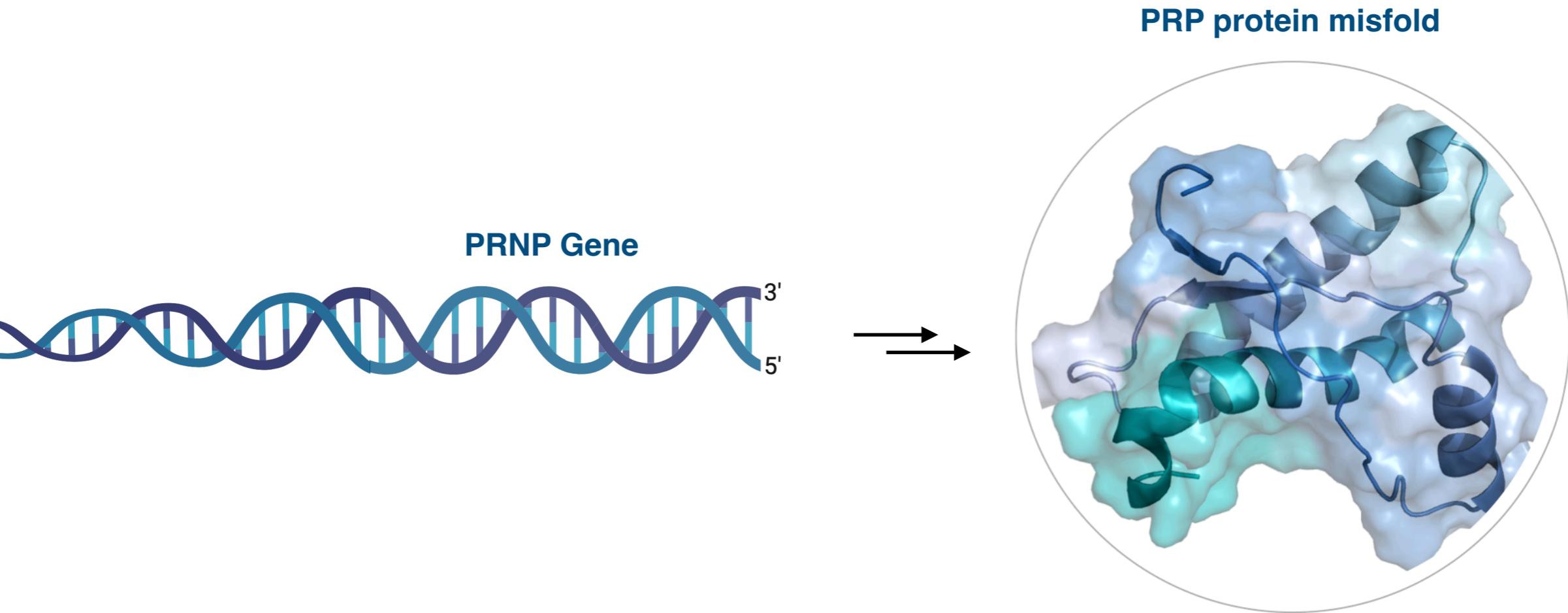
[Nature Medicine](#) **31**, 1319–1328 (2025) | [Cite this article](#)

19k Accesses | **156** Altmetric | [Metrics](#)



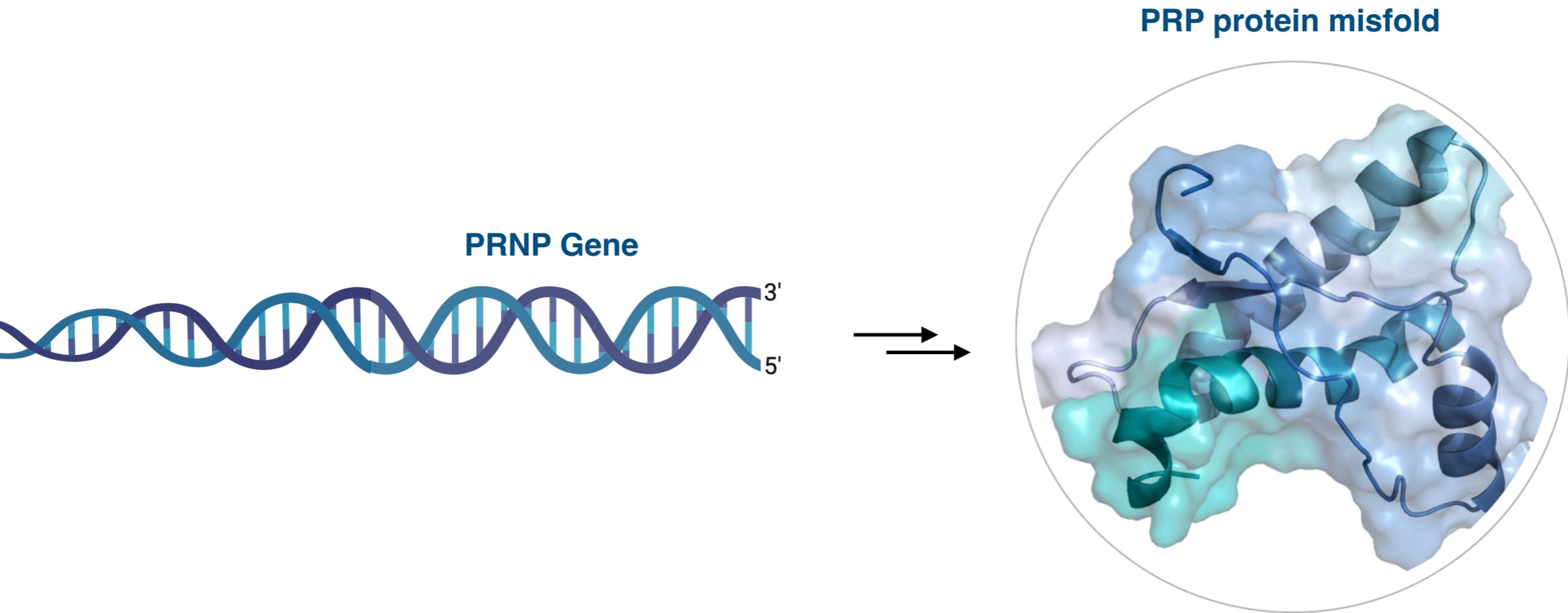
Intrinsically disordered proteins

Strategies to target the undruggable



Intrinsically disordered proteins

Strategies to target the undruggable



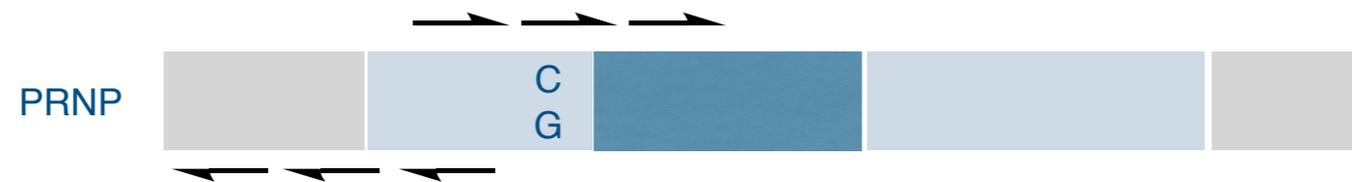
- ***strategy: gene therapy***

Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**

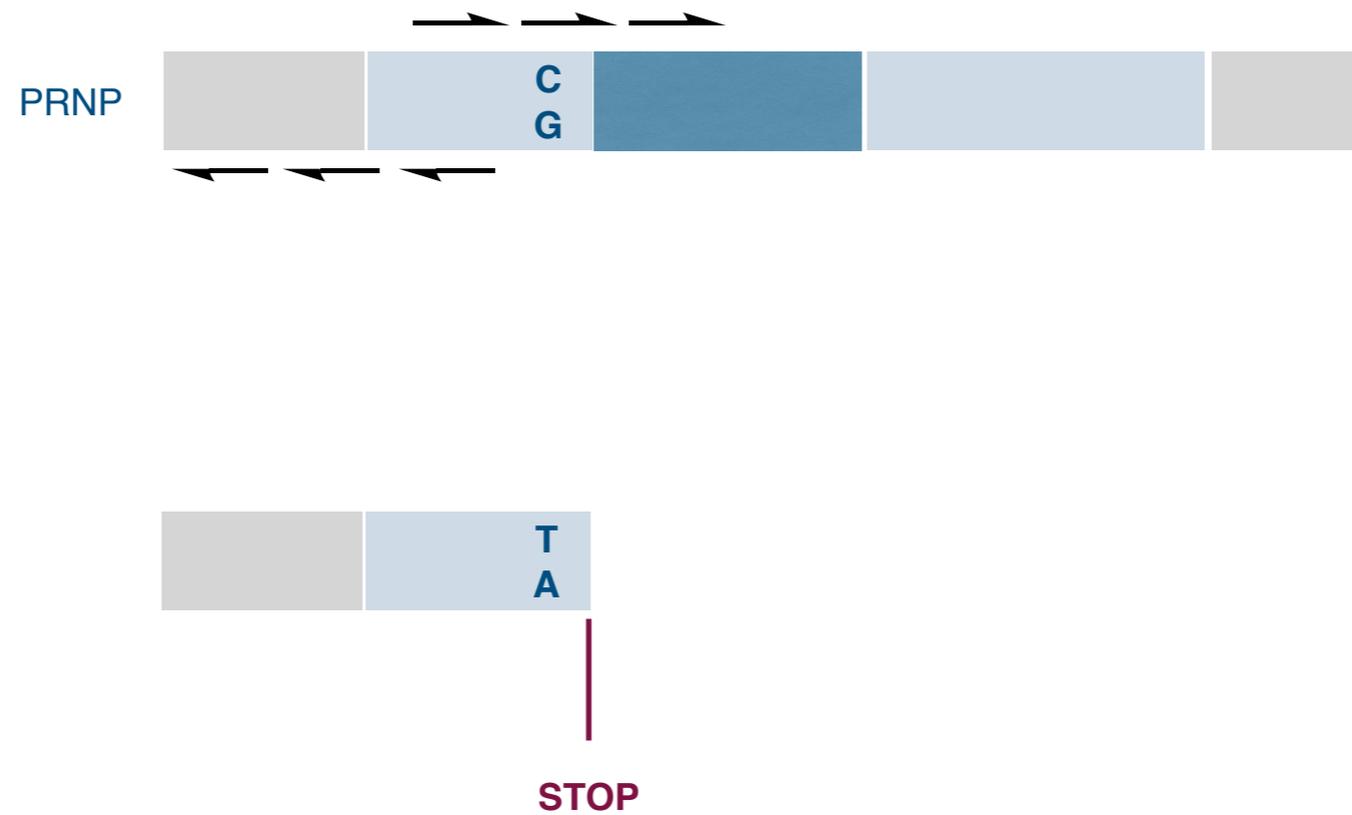


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Cytosine base editor (CBE)**

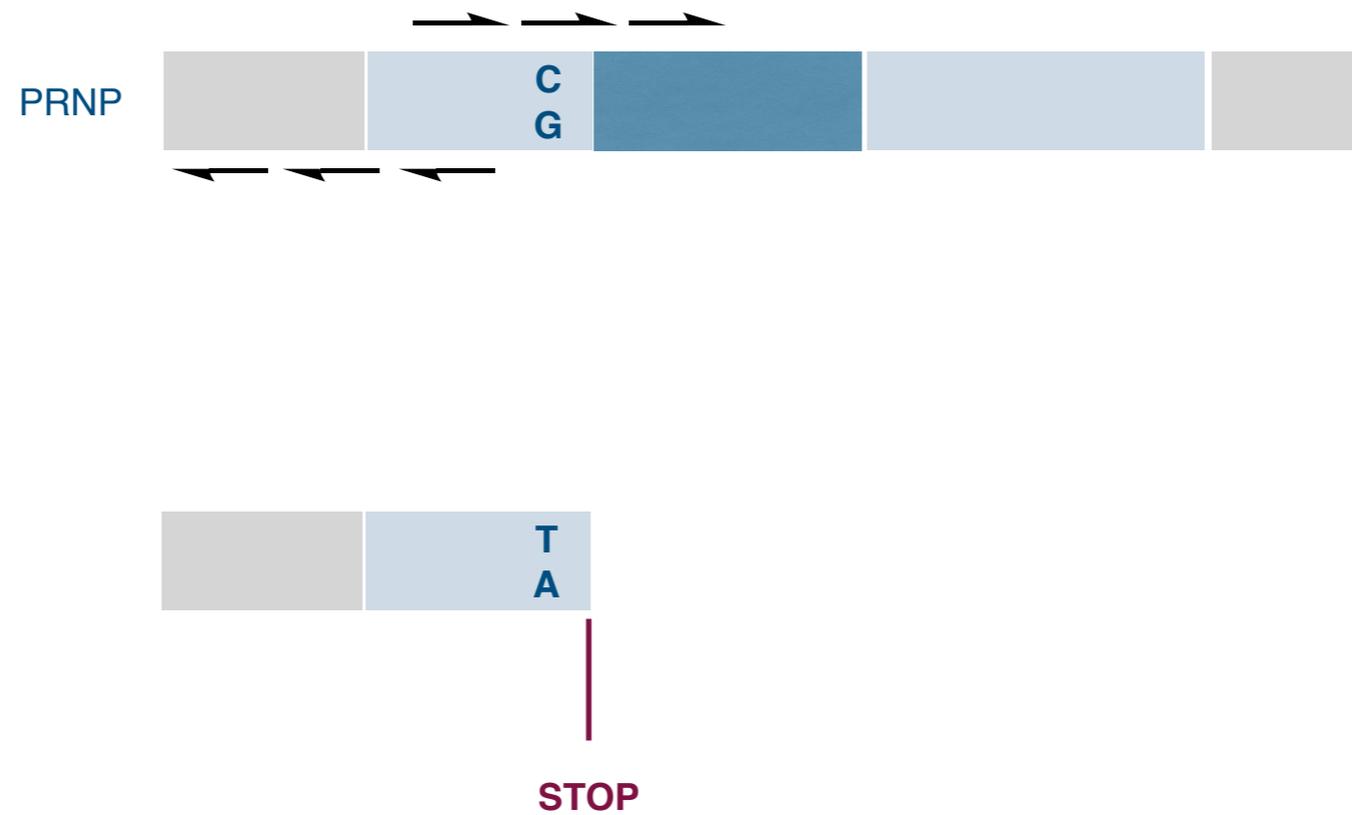


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Cytosine base editor (CBE)**



Key point: Arg, Gln, Trp codons



stop codons

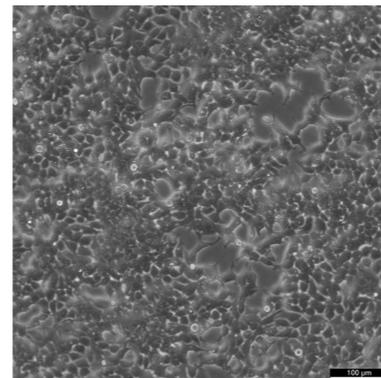


LIU GROUP

Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**



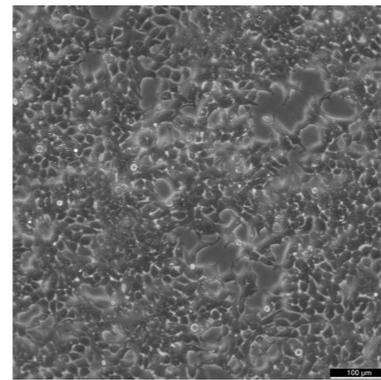
HEK293T cells



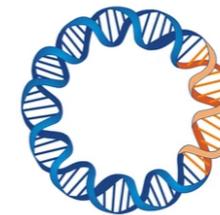
Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**



HEK293T cells



***Transfected with plasmid encoding
base editing tools***

***Base editing targeting Arg37 exhibited high
editing efficiency (54%!)***

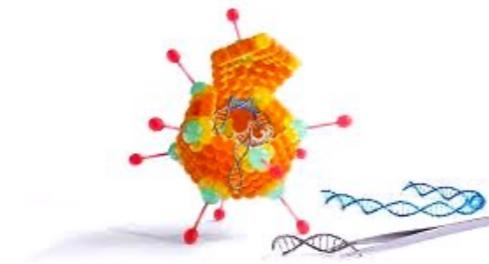


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**

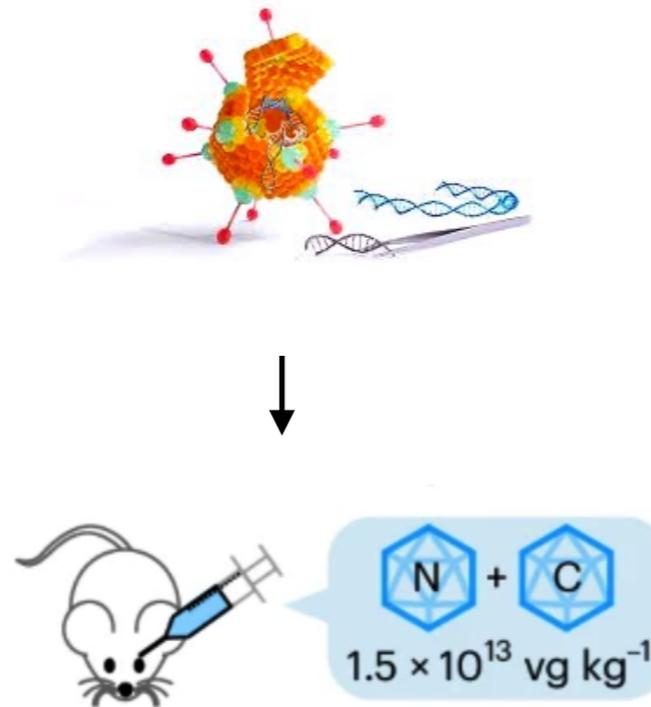


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**



Tg25109 mice
(Humanized prion mice)

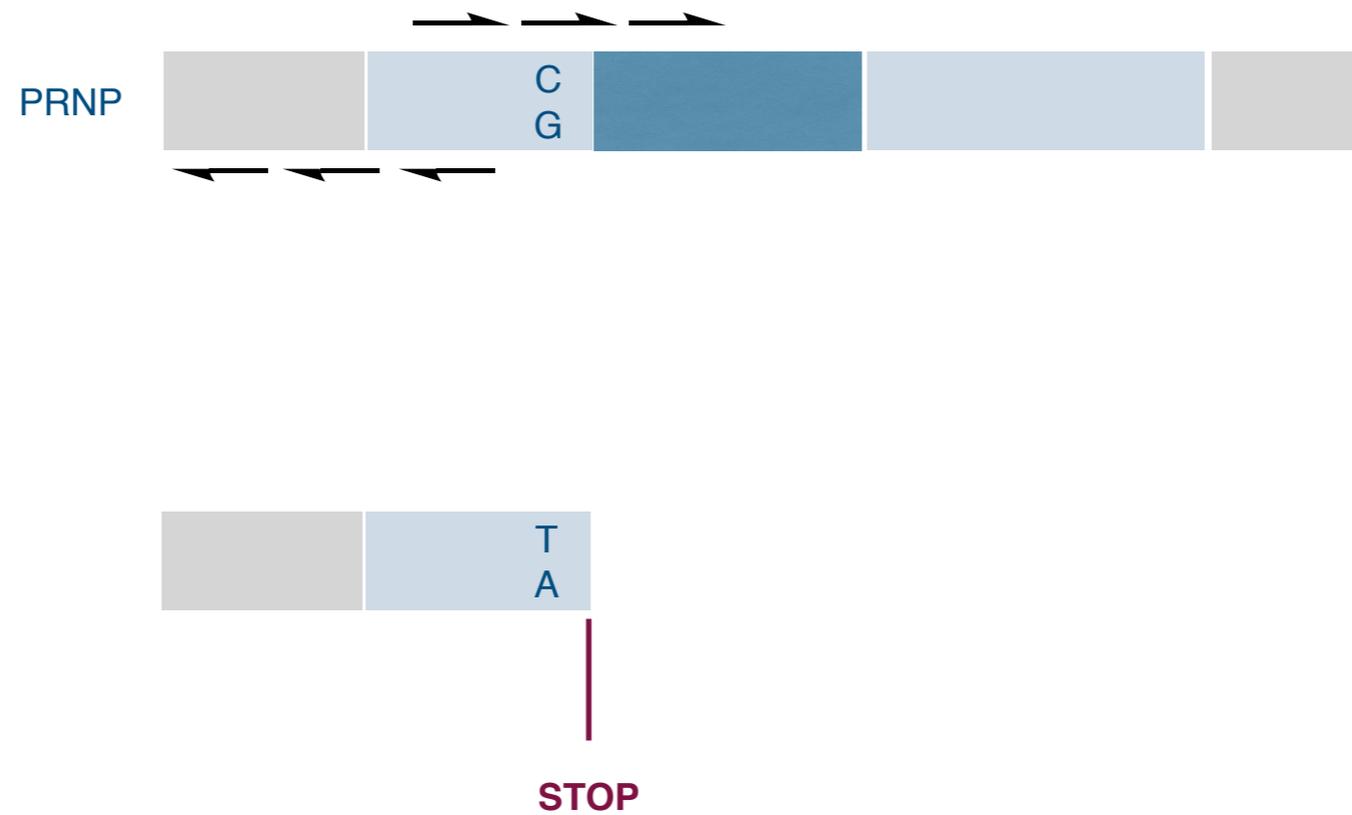


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

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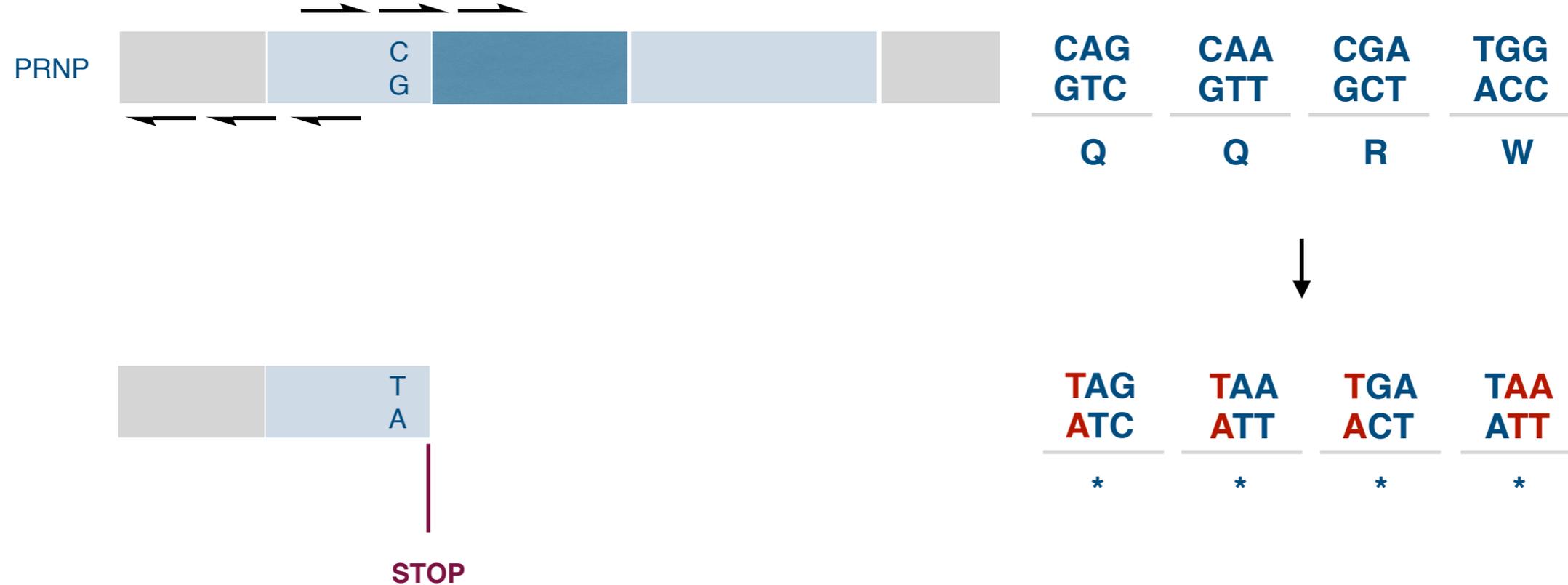


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**

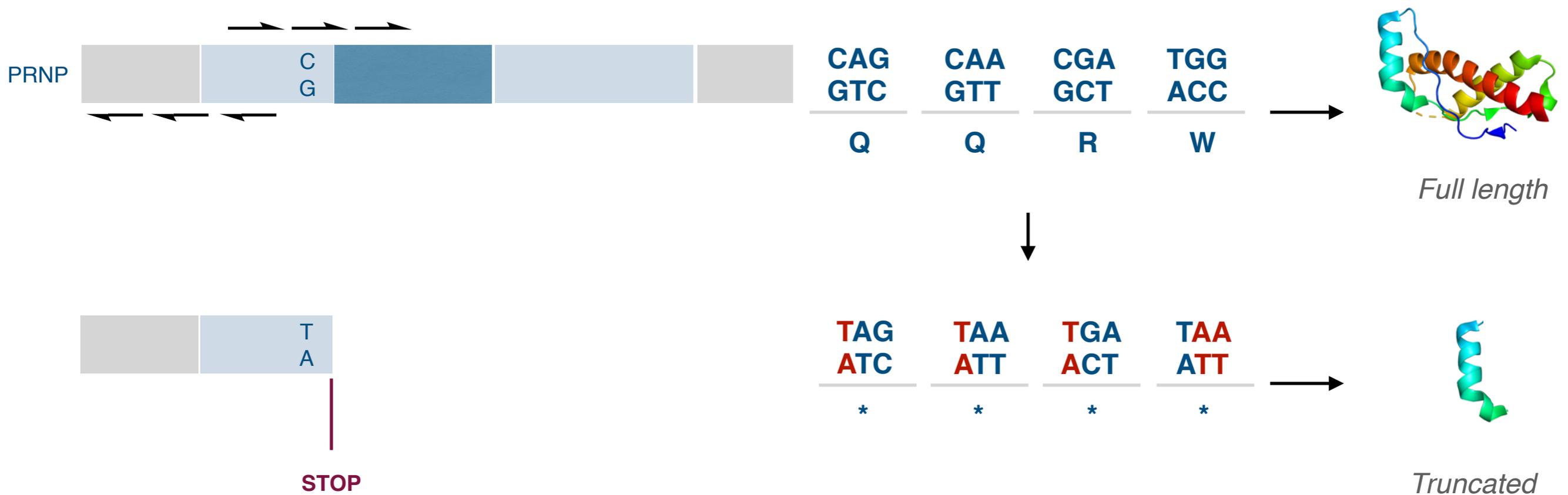


Intrinsically disordered proteins

Strategies to target the undruggable

- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**

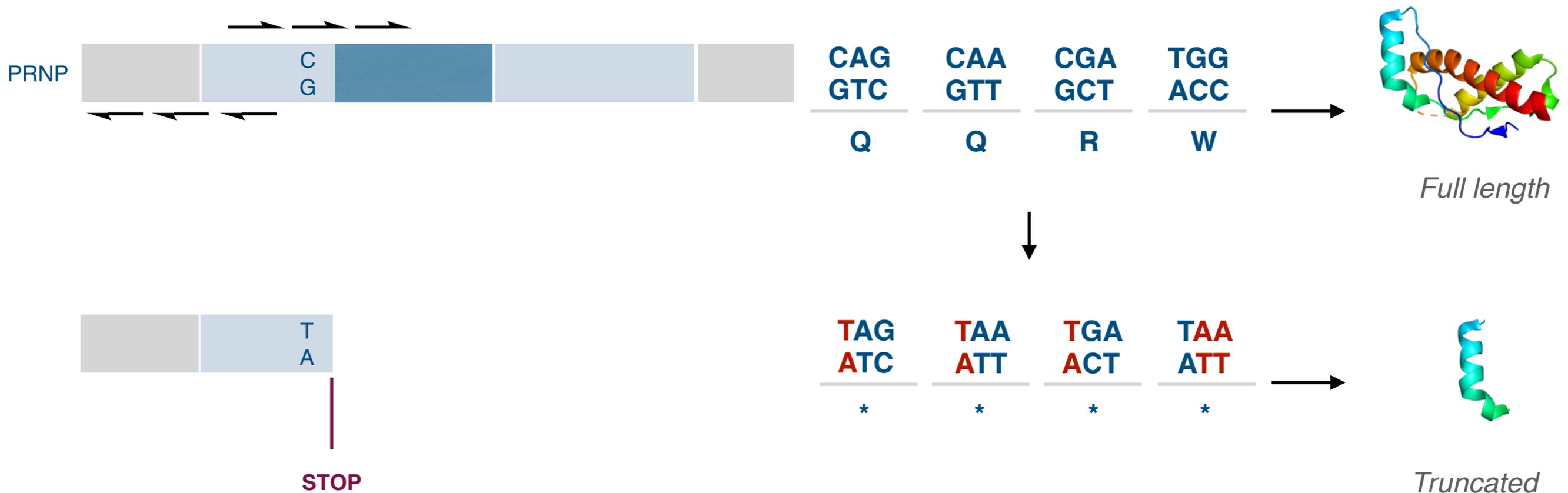


Intrinsically disordered proteins

Strategies to target the undruggable

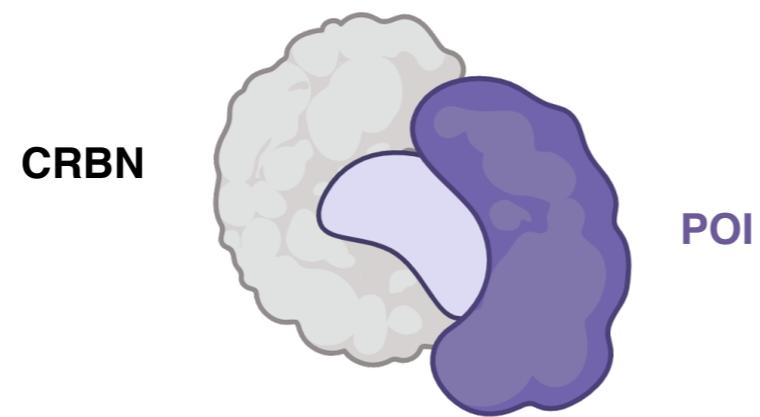
- **Base editing a single gene: treating prion disease**

- **Adenovirus to modify PRNP locus:**



- **50% increase in lifespan in a humanized mouse model of prion disease!**

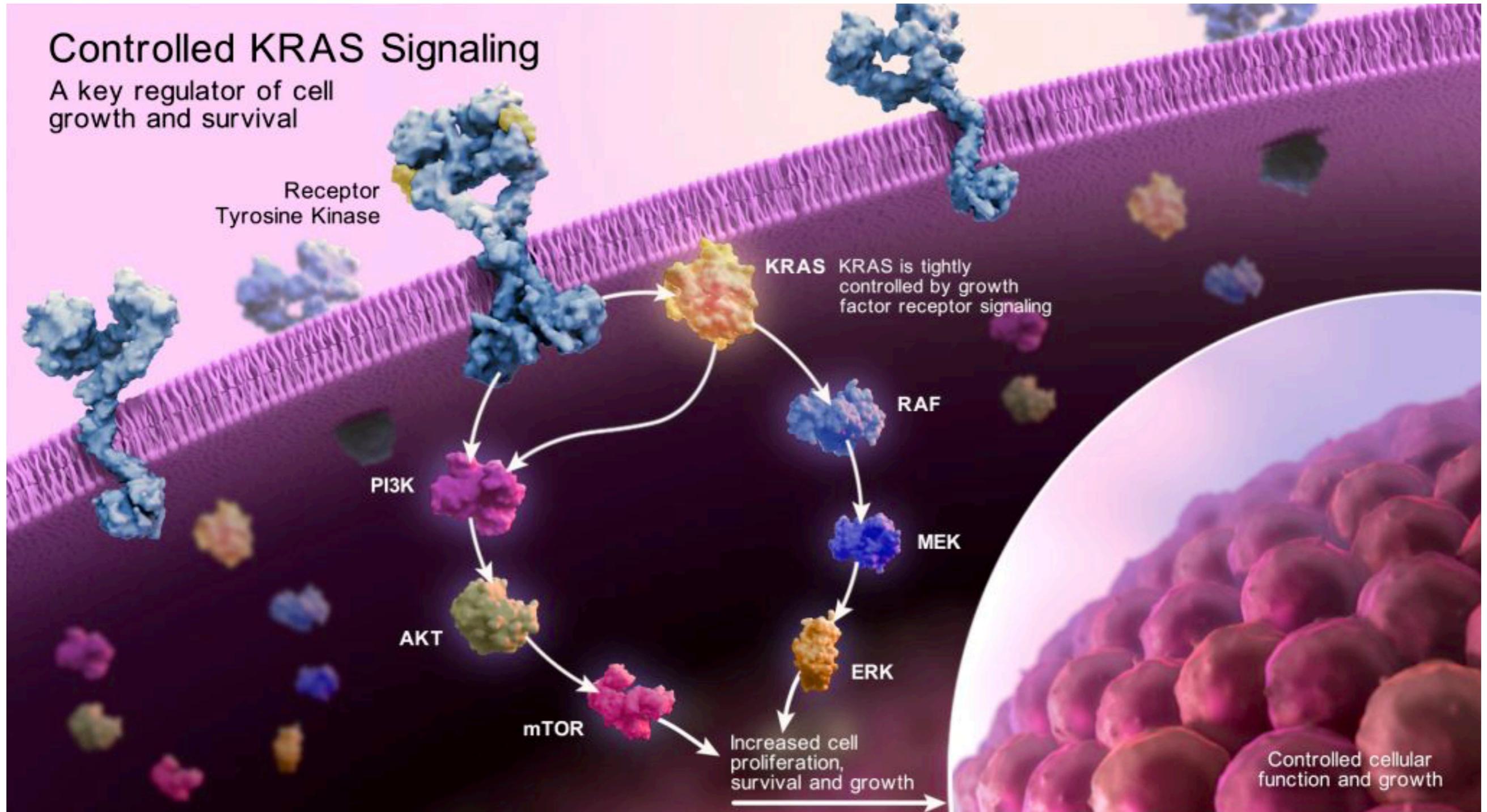
Questions?



Questions?

KRAS signalling

Controls cell proliferation and growth



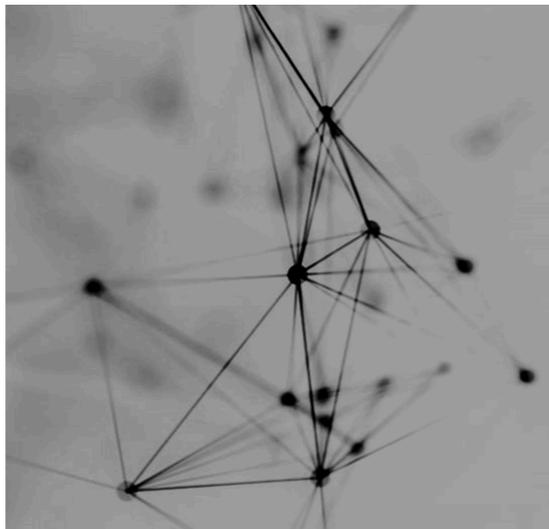
Druggable Targets

Identification of disease-causal targets has been driven by:

1. Data-driven “-omics”

2. protein and nucleic acid ID

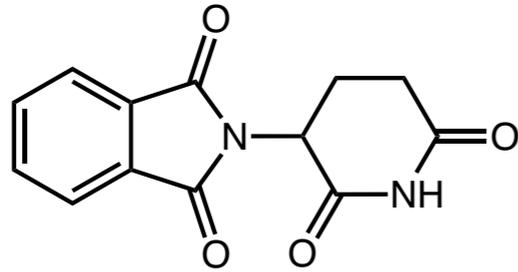
- **gives expression level data**



Molecular Glues

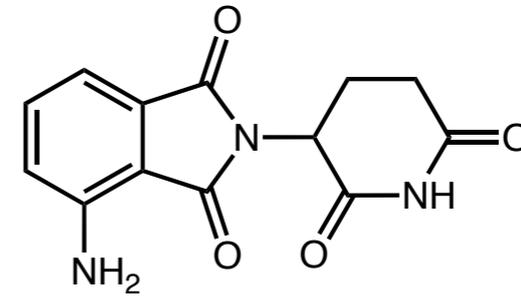
Immunomodulatory drugs

- Molecular glue mechanism of IMiDs influenced PROTAC design

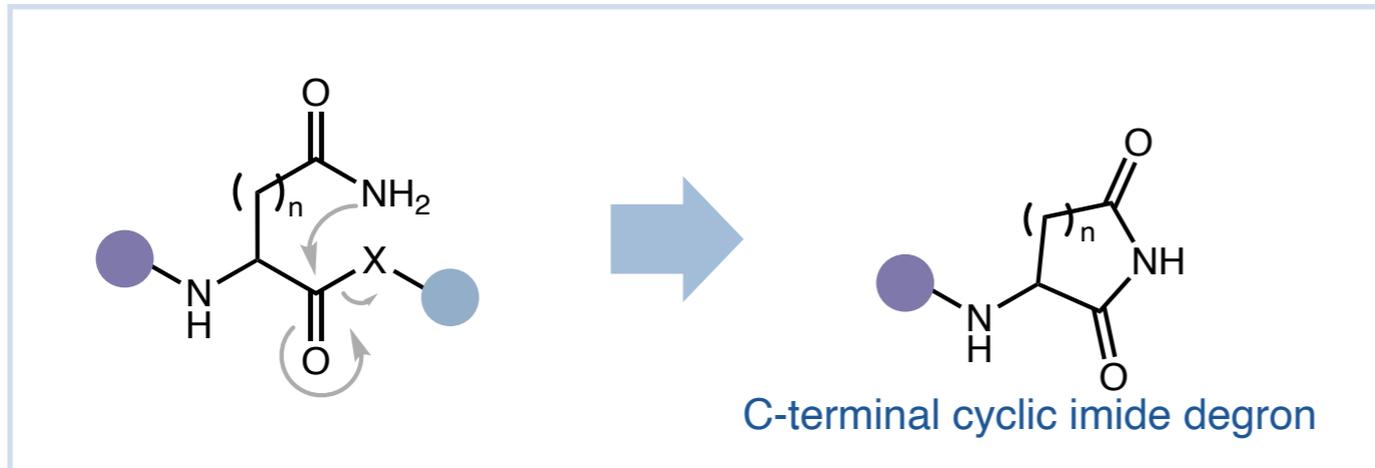


Thalidomide

induces protein degradation

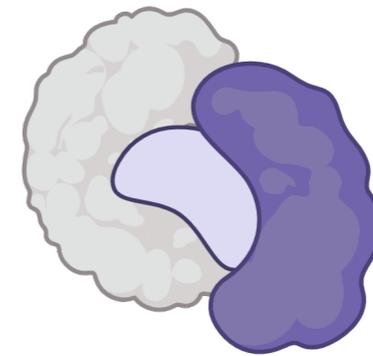


Lenalidomide



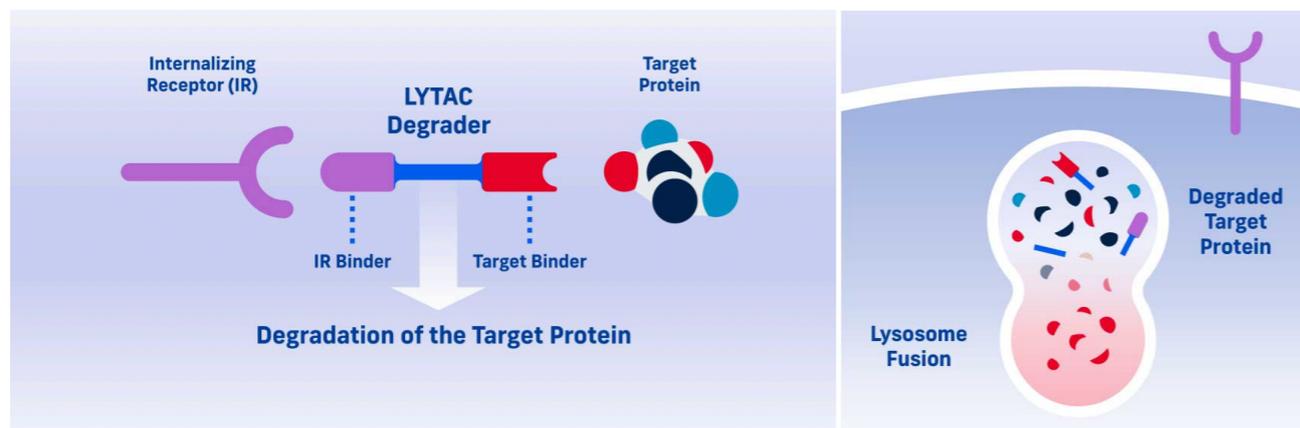
IMiDs mimic a PTM that recruits degradation machinery

CRBN



POI

LYTAC: Lysosome Targeting Chimeras

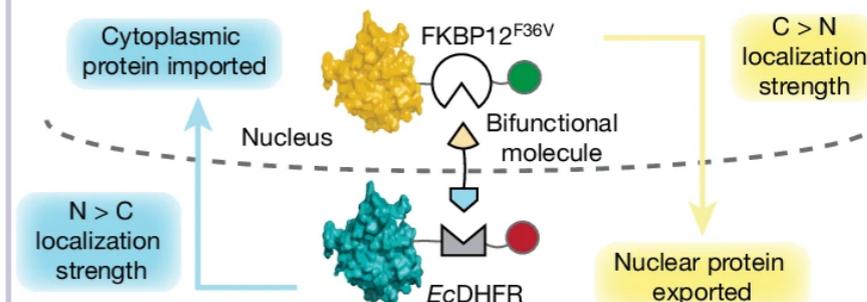


nature

LYCIA
THERAPEUTICS



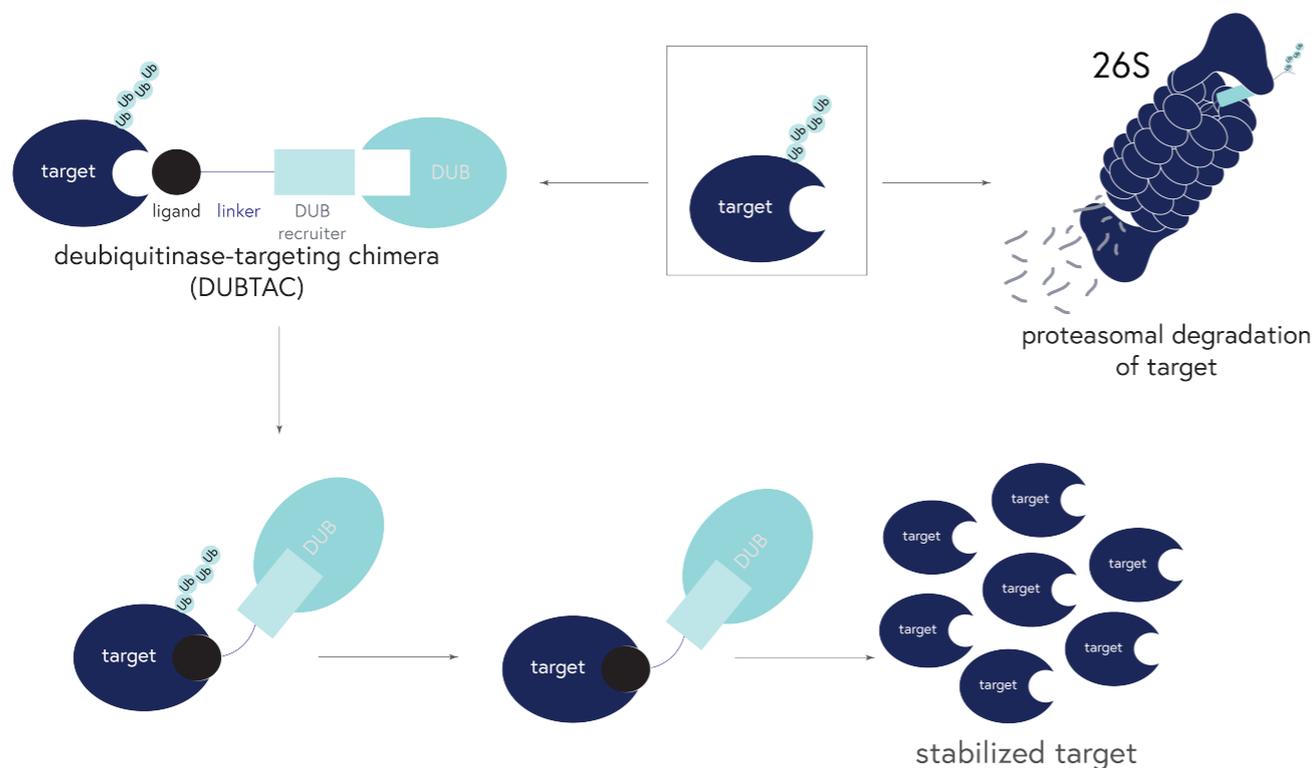
TRAM: Targeted Relocalization Activating Molecules



nature

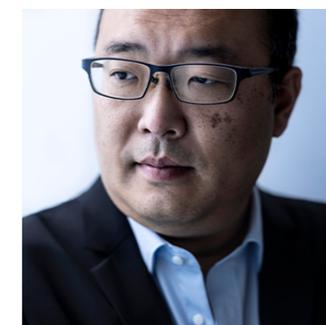
Steven Banik, Stanford

DUBTAC: Deubiquitinase Targeting Chimeras



VICINITAS
THERAPEUTICS

nature
chem bio



Novel Chemical Reactivity Through AI-Augmented Experimentation

