

Outline of the talk

- Introduction
- Overview of main projects
- Protein binder design methodology



Team Sébastien GRANIER – Bernard MOUILLAC

Membrane Protein Structure and Function for Drug Discovery (MAGIC)

[Accueil](#) » [Teams](#) » [Team Granier-Mouillac](#) » [Project Protein and drug design](#)

PROJECT PROTEIN AND DRUG DESIGN

PRINCIPAL INVESTIGATORS



Cédric LEYRAT
CRCN, Inserm



Xiaojing CONG
CRCN, CNRS

IGF staff involved

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Post-doc CNRS

El Mehdi KARIM

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David ARANDA

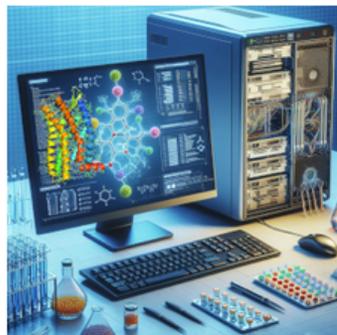
Post-doc INSERM

Paul MEDOUT-MARERE

IE INSERM

Tolith DERRICK GIDAGA

PhD UM



Our computational drug design pipeline spans from the virtual screening of large chemical libraries to the de novo design of small molecules, peptides and proteins. We integrate structural and functional data, molecular simulations and machine learning to boost efficiency and accuracy. The synergy between firsthand experimental data and computational approaches empowers us to address complex issues, such as drug side effects, and to explore novel drug targets. Our current focuses are GPCR targets and transmembrane proteins, as well as proteins involved in pneumovirus replication.

Main publications

- Healey R.D., et al. (2023) *Commun. Chem.*, 6(1), 160.
- Otun O., et al. (2024) *PNAS*, 121(30), e2404000121.
- Dumazer A., et al. (2025) *Biochemical Pharmacology*, 117065.

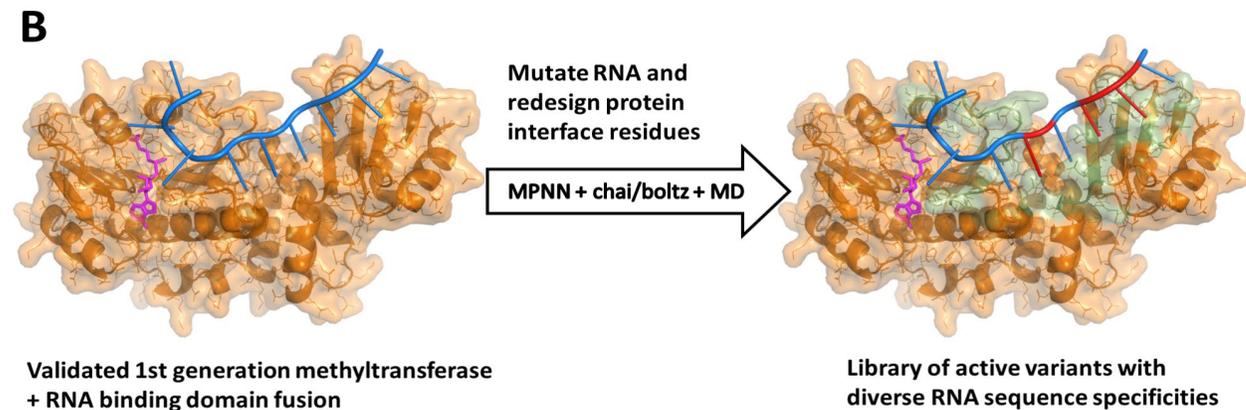
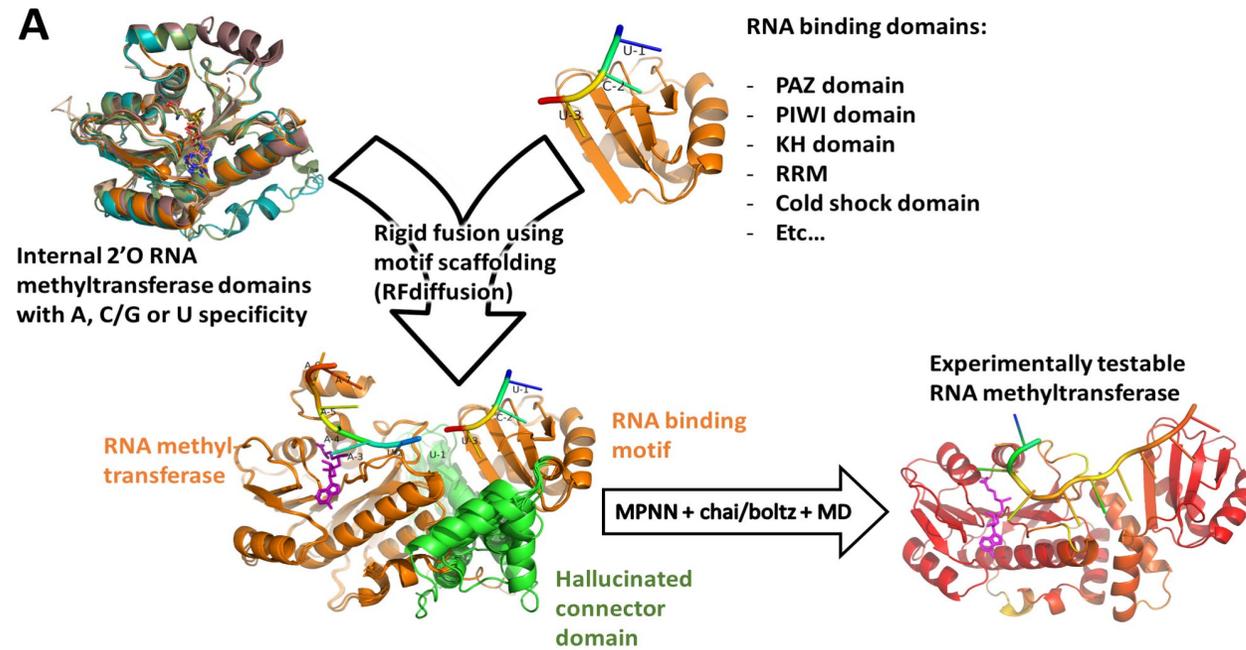
Funding

- 2024-2027 ANR-23-CE44-0043-03
- 2025-2029 ANR-24-RR11-0005
- 2026-2027 I-SITE RELAX-PRO
- 2026-2028 FRM-SPF202509050524
- 2026-2028 Inca_20069

Collaborations

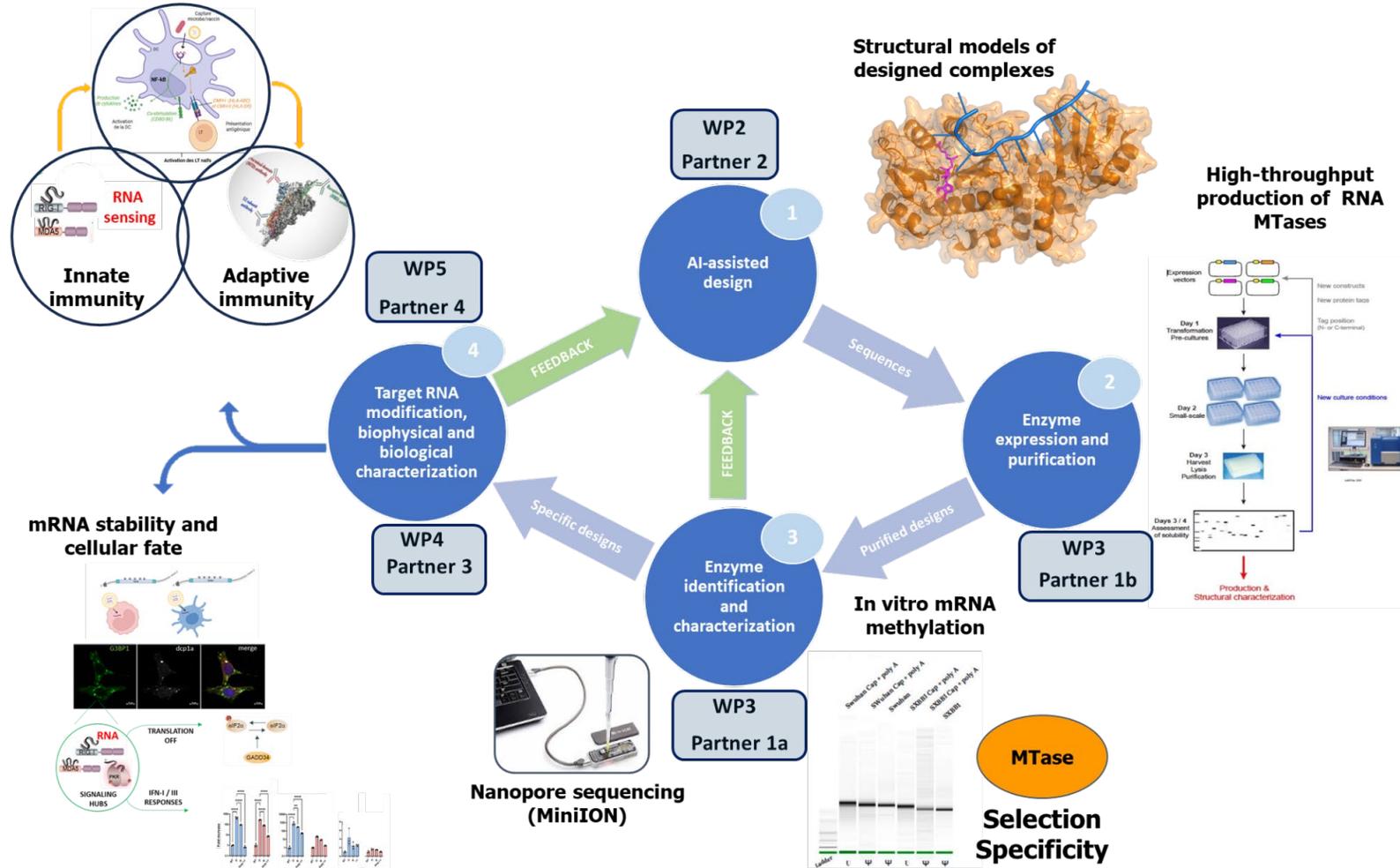
- Andrew C. Kruse (Boston)
- Christoph Arenz (Berlin)
- Dominique Bonnet (Illkirch-Graffenstaden)
- Cyril Rivat (Montpellier)
- Frederic Jean-Alphonse (Tours)
- Eric Reiter (Tours)
- Marie Galloux (Jouy-en-Josas)
- Jean-Marie Bourhis (Grenoble)
- Marc Jamin (Grenoble)
- Bruno Canard (Marseille)
- Jean-Marc Pascussi (Montpellier)
- Max Renner (Umea)

AIR-MT project: AI-based design of RNA Methyltransferases for RNA-based therapeutics

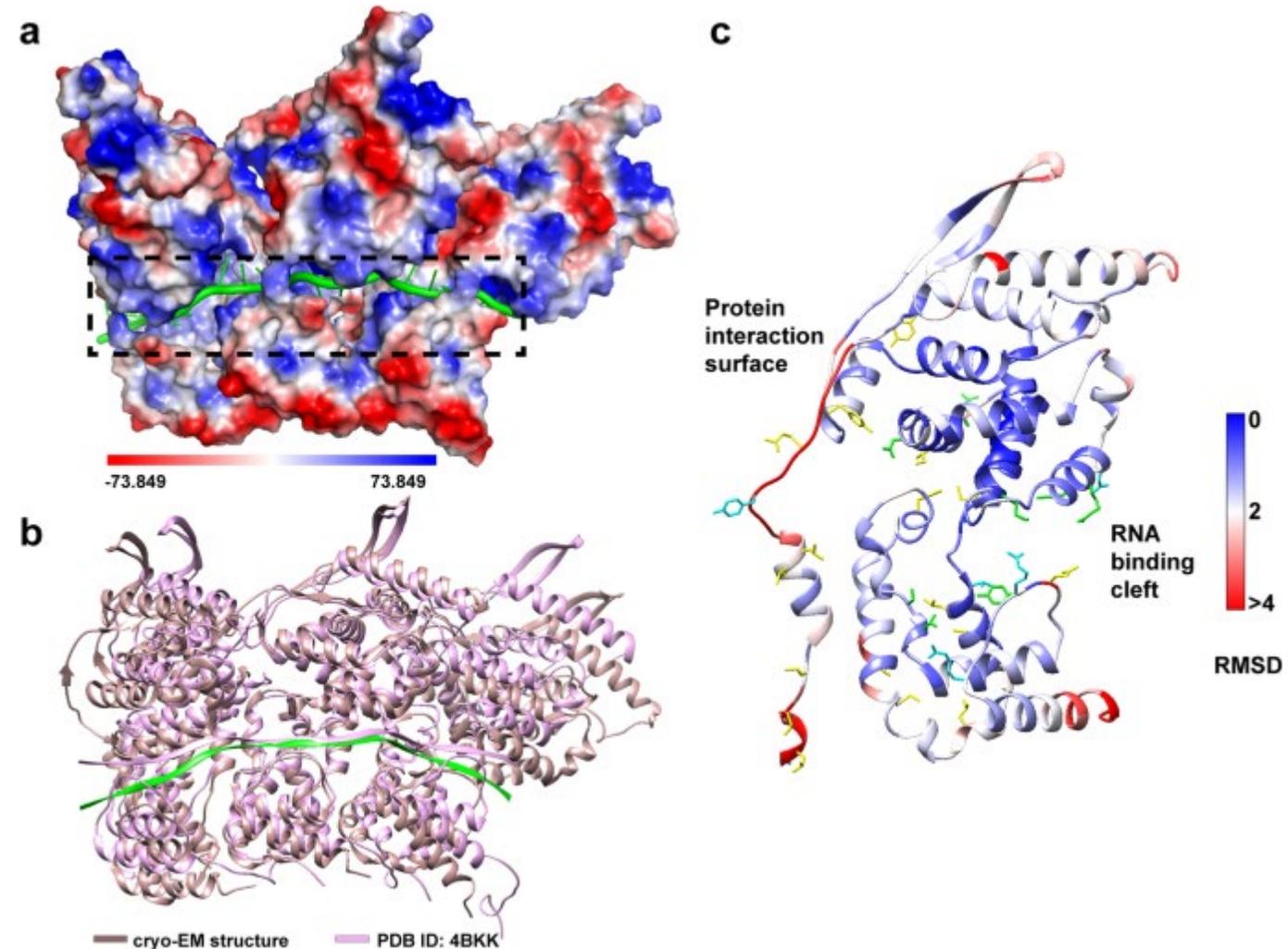
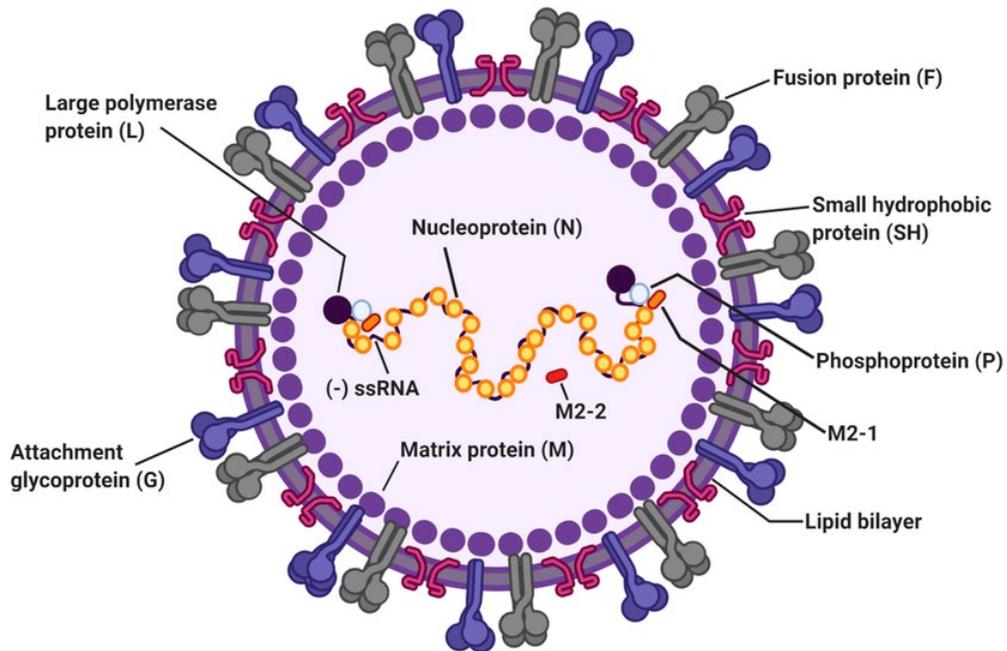


AIR-MT project: AI-based design of RNA Methyltransferases for RNA-based therapeutics

The project flow: Engineering of RNA MTases for internal site-specific methylation



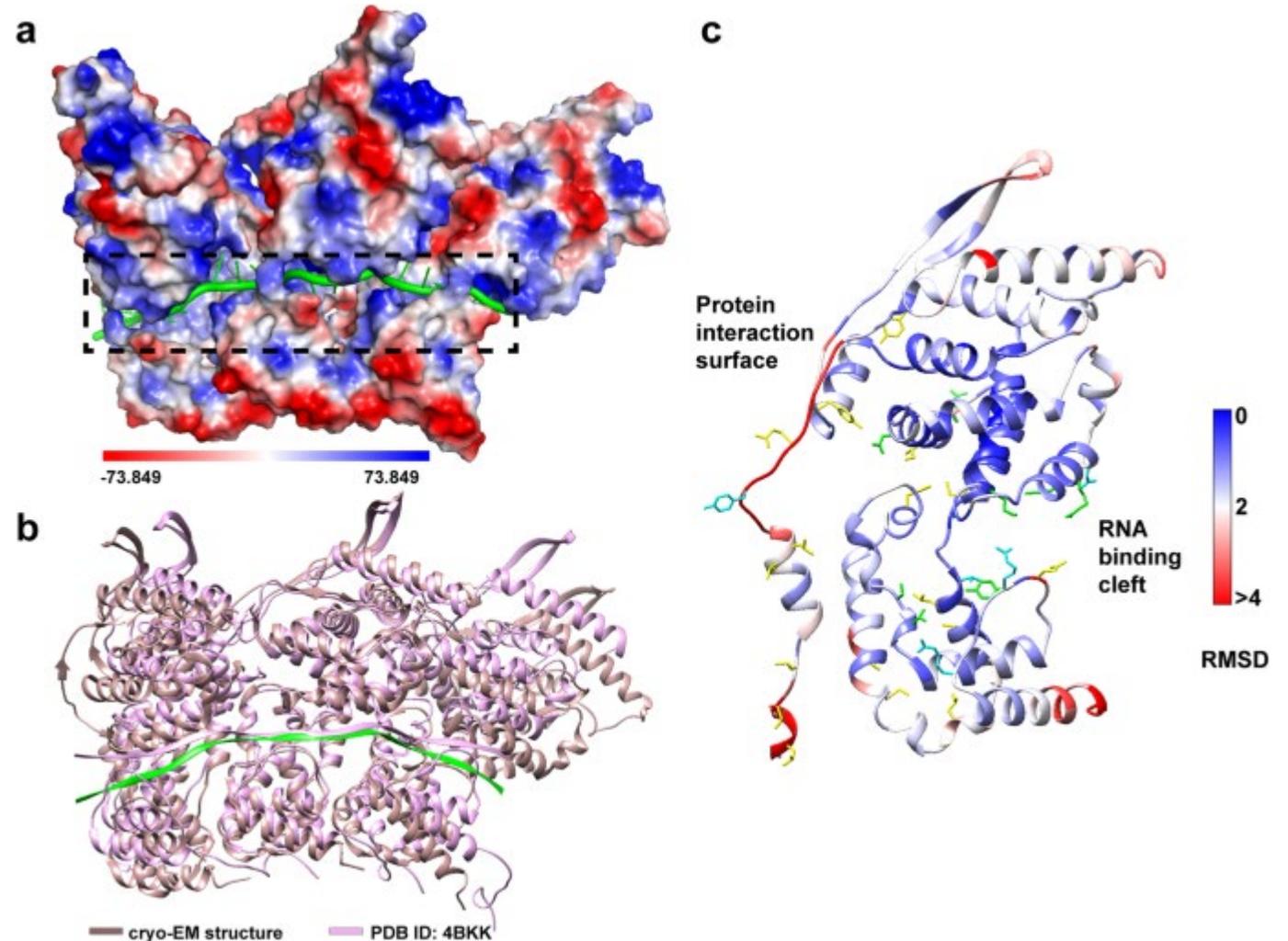
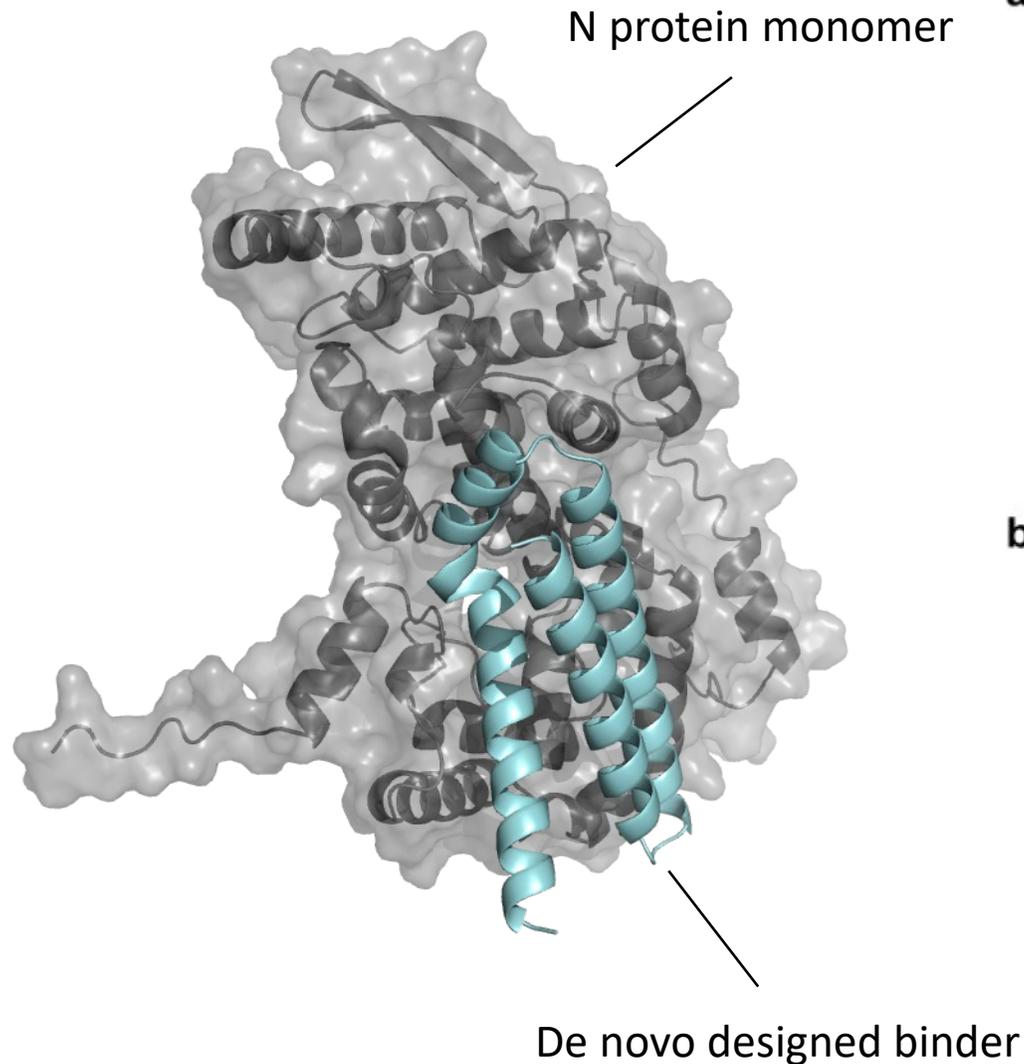
PNEUMOPEPS project: Targeting viral nucleocapsid assembly with designed protein binders



<https://doi.org/10.3390/v12010102>

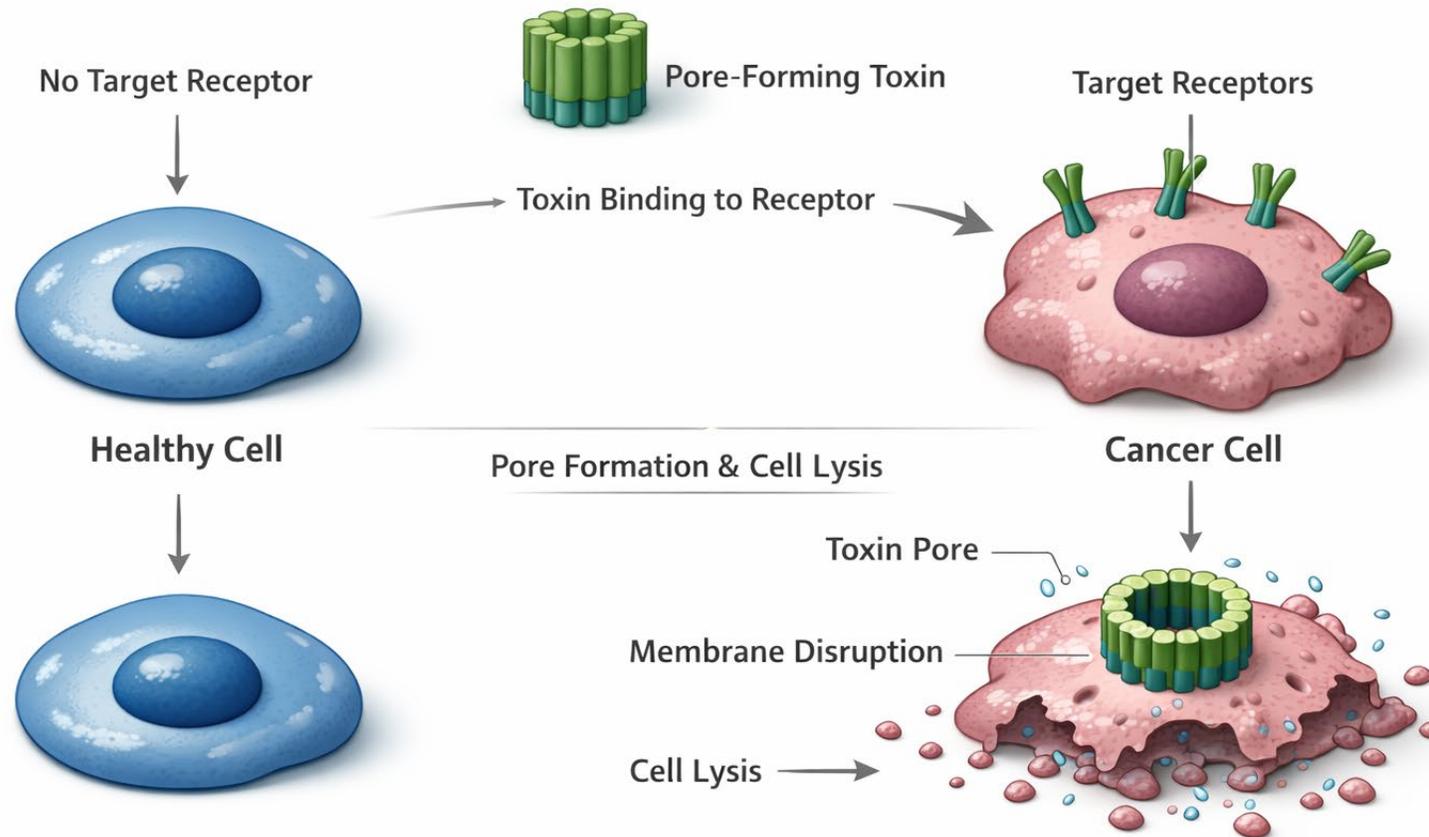
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PNEUMOPEPS project: Targeting viral nucleocapsid assembly with designed protein binders

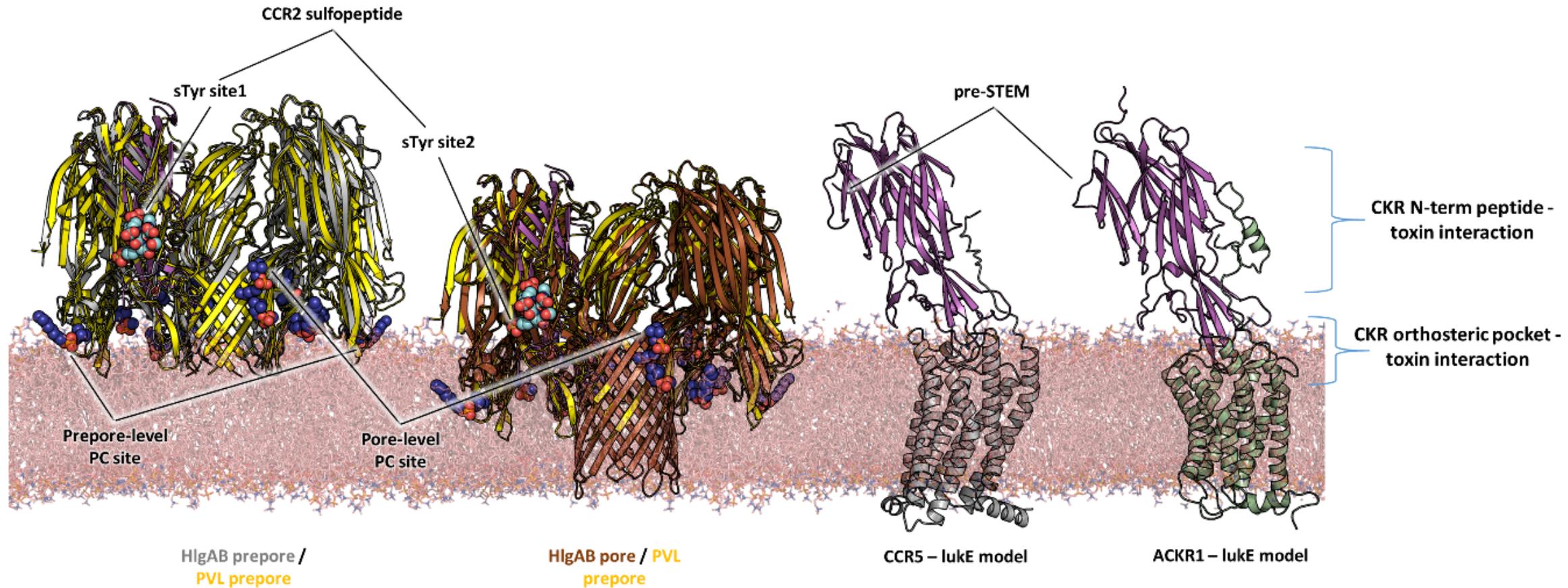


Toxin engineering project: Optimizing bicomponent pore forming toxins for CXCR4-targeted cancer cell killing

Targeting Cells via Specific Receptor Using Pore-Forming Toxins

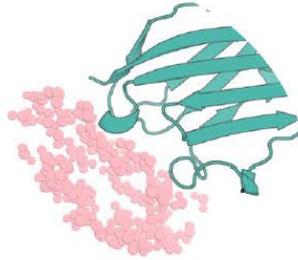
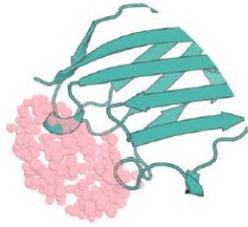
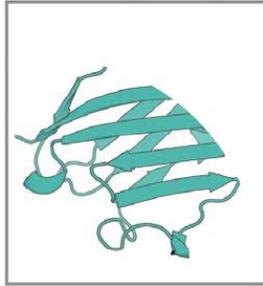


Toxin engineering project: Optimizing bicomponent pore forming toxins for CXCR4-targeted cancer cell killing

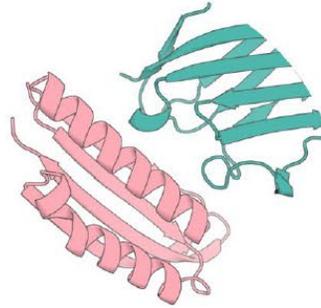


Binder design pipeline

Binding target



Binder design



1

Backbone
generation
(Rfdiffusion,
RFdiffusion3)

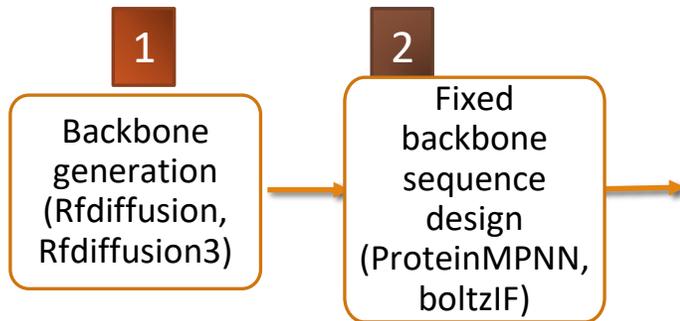
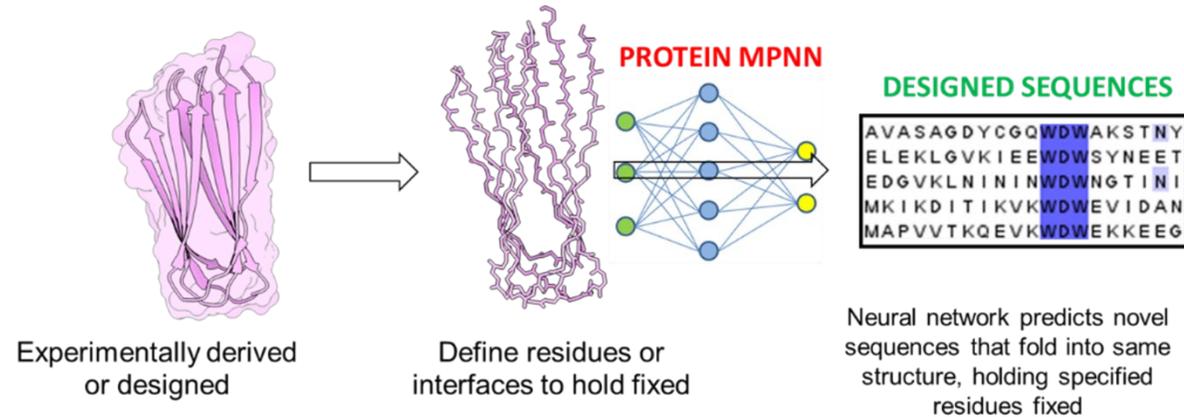


<https://doi.org/10.1038/s41586-023-06415-8>

<https://doi.org/10.1101/2025.09.18.676967>

- Example of a *de novo* design pipeline for generating proteins binding a specified target

Binder design pipeline

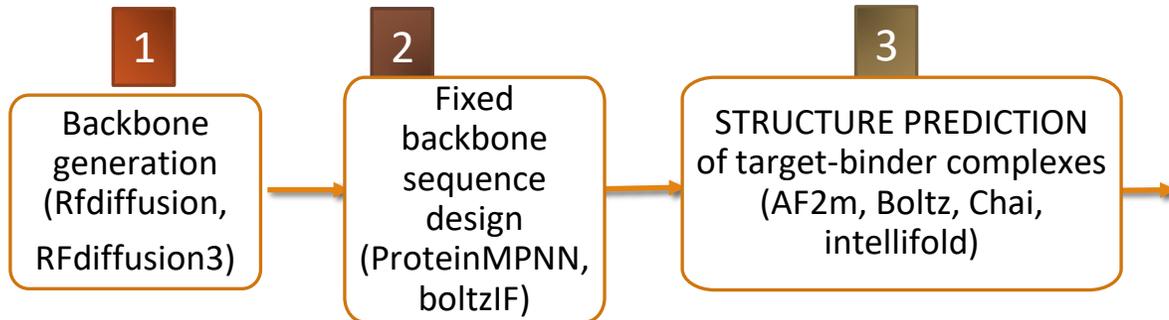
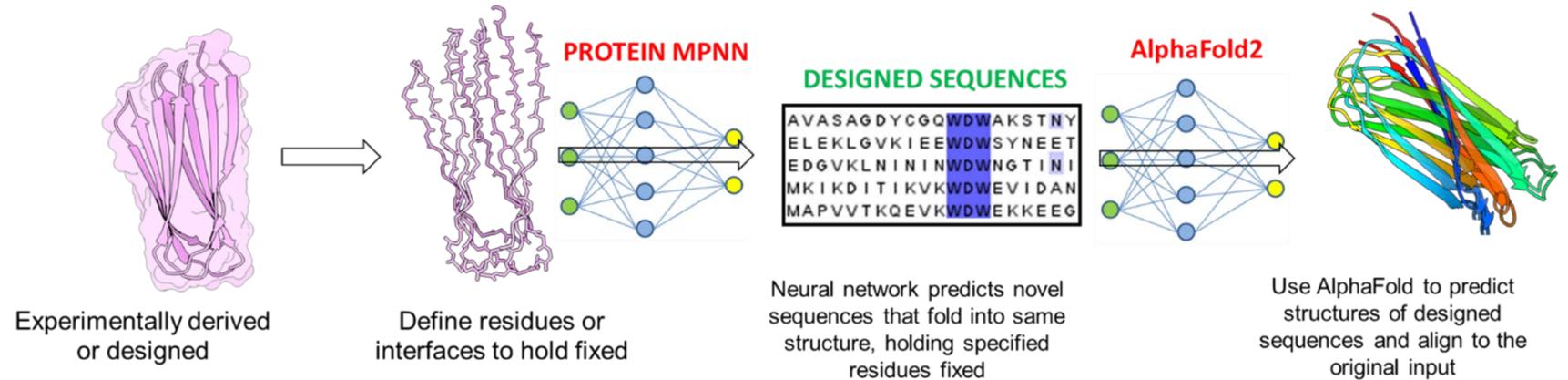


[DOI: 10.1126/science.add2187](https://doi.org/10.1126/science.add2187)

<https://doi.org/10.1038/s41592-025-02626-1>

- Example of a *de novo* design pipeline for generating proteins binding a specified target

Binder design pipeline



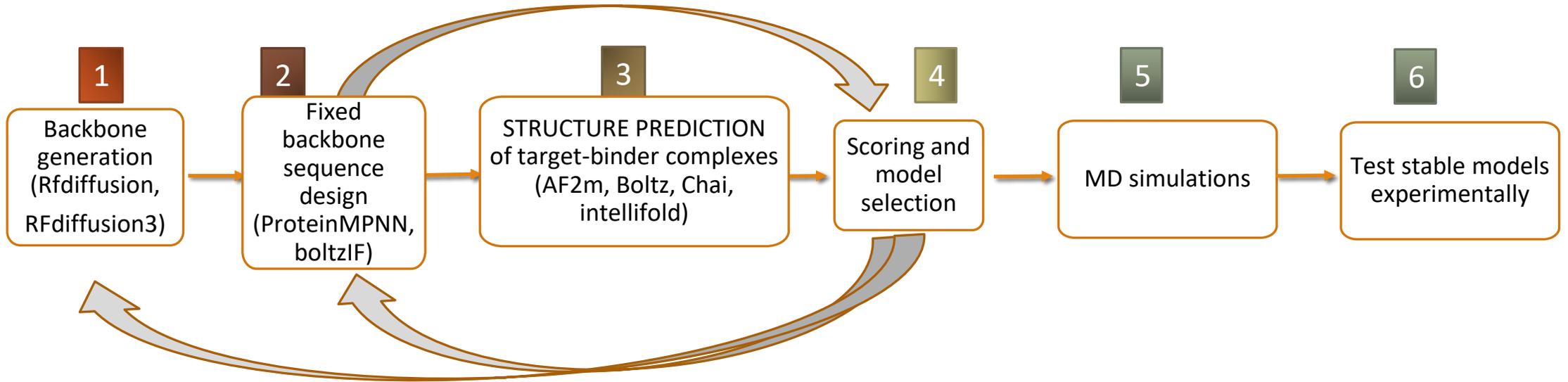
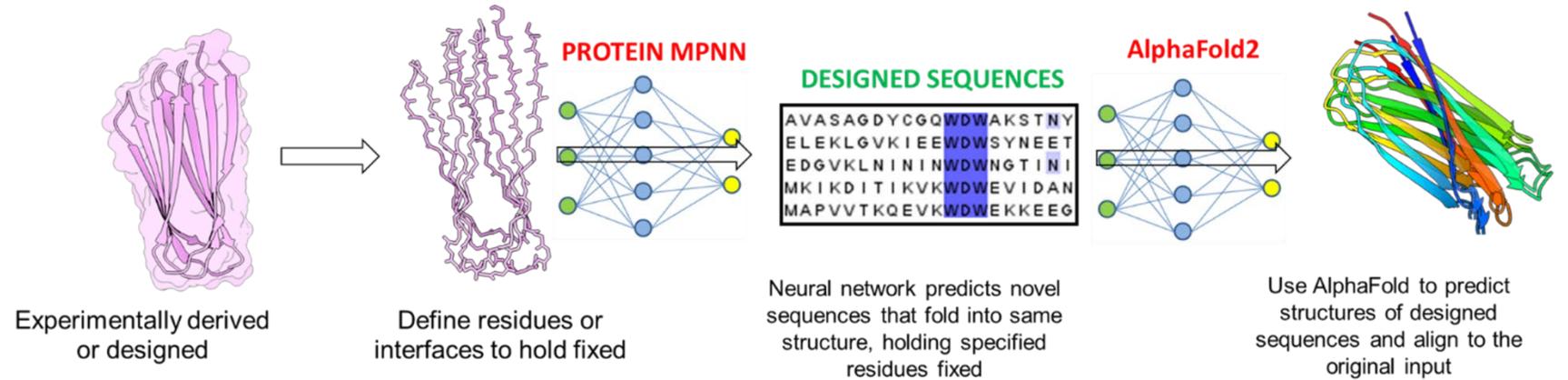
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<https://doi.org/10.1101/2024.11.19.624167>

<https://doi.org/10.1101/2024.10.10.615955>

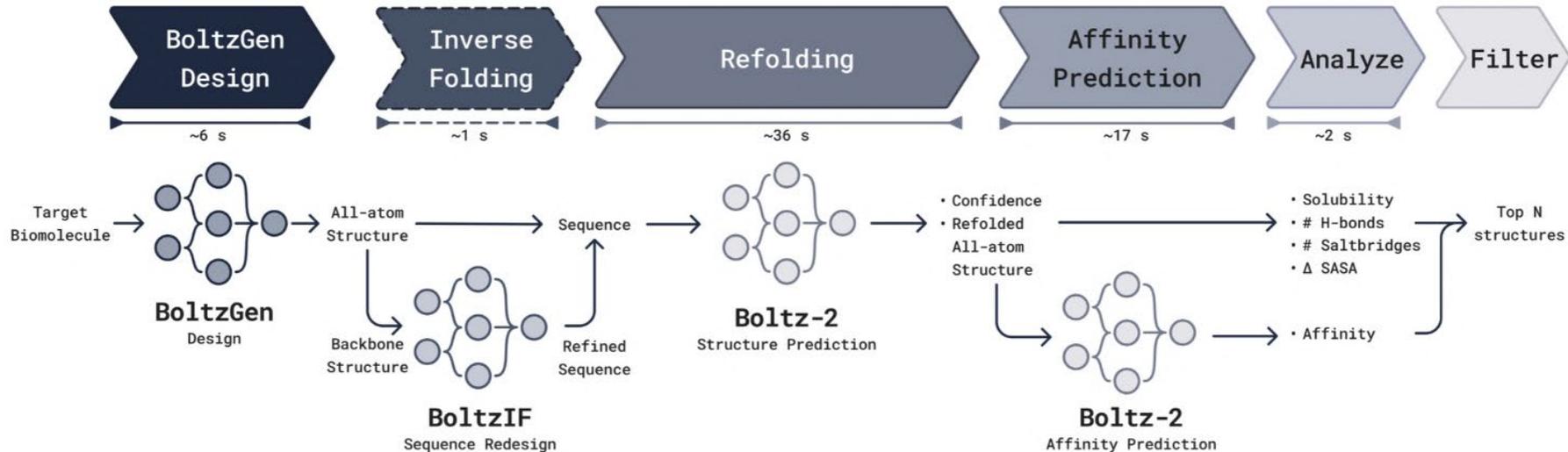
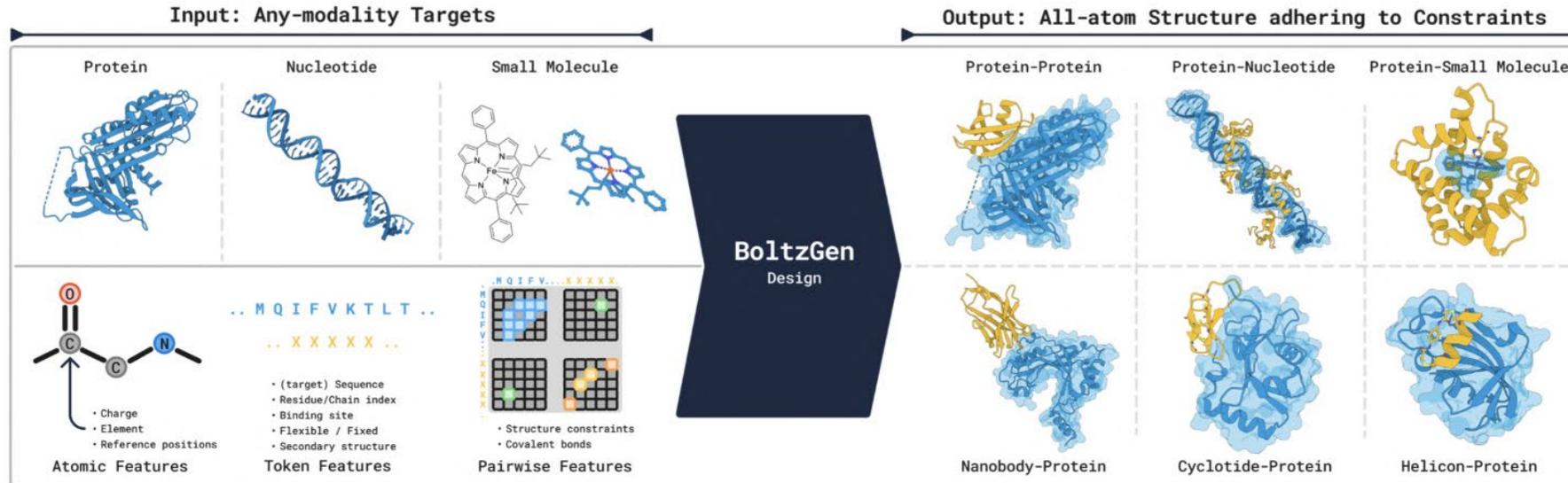
<https://doi.org/10.48550/arXiv.2507.02025>

Binder design pipeline



- Example of a *de novo* design pipeline for generating proteins binding a specified target

Example of an automated, modular design pipeline



Acknowledgements

