



Agenzia nazionale per le nuove tecnologie,
l'energia e lo sviluppo economico sostenibile

AN *IN-SILICO* DRIVE-THROUGH FOR mAbs DISCOVERY

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CONFERENCE

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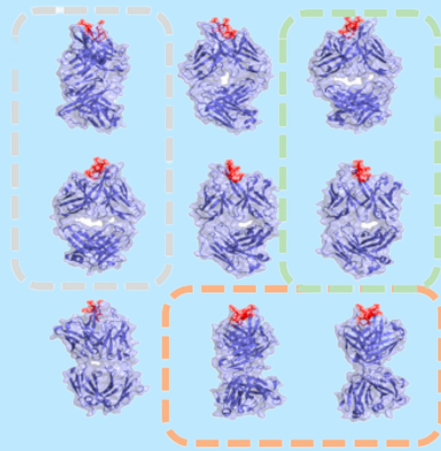
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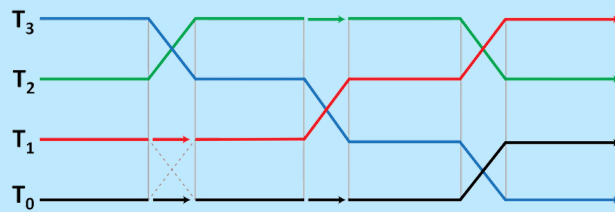
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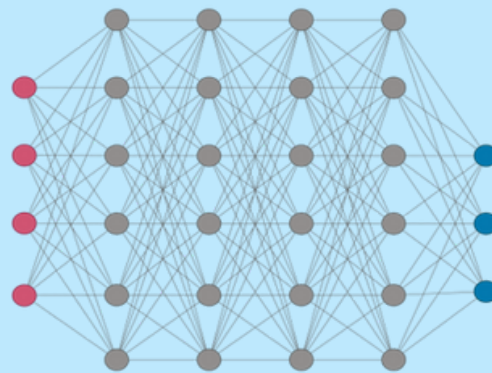
THE PIPELINE



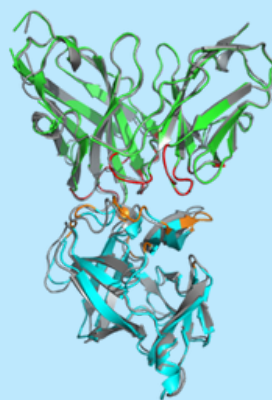
**De-novo design or
proprietary based Ab
optimization**



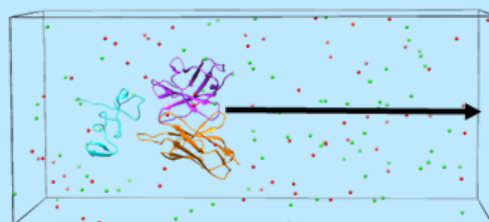
**Exhaustive Ab
conformational sampling
with Replica-Exchange-MD**



**Deep Learning selection of
binding conformer**



Ab-antigen docking



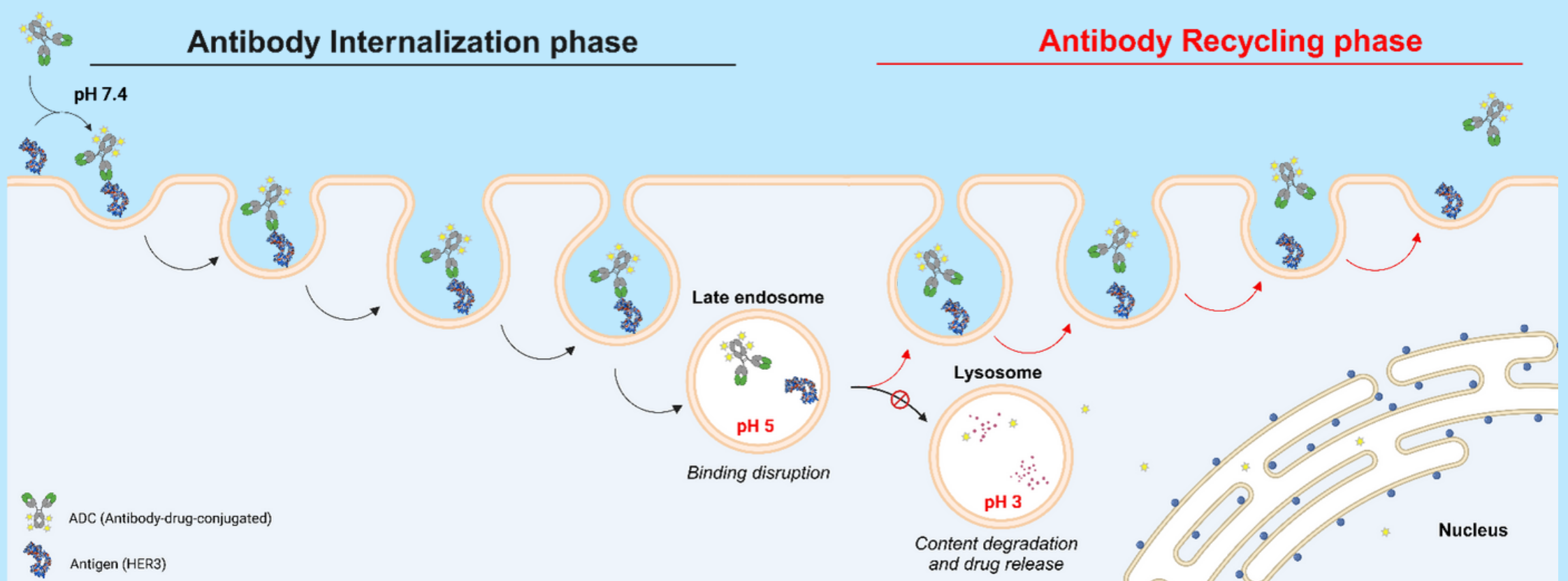
**Binding-force profiling
by steered MD**



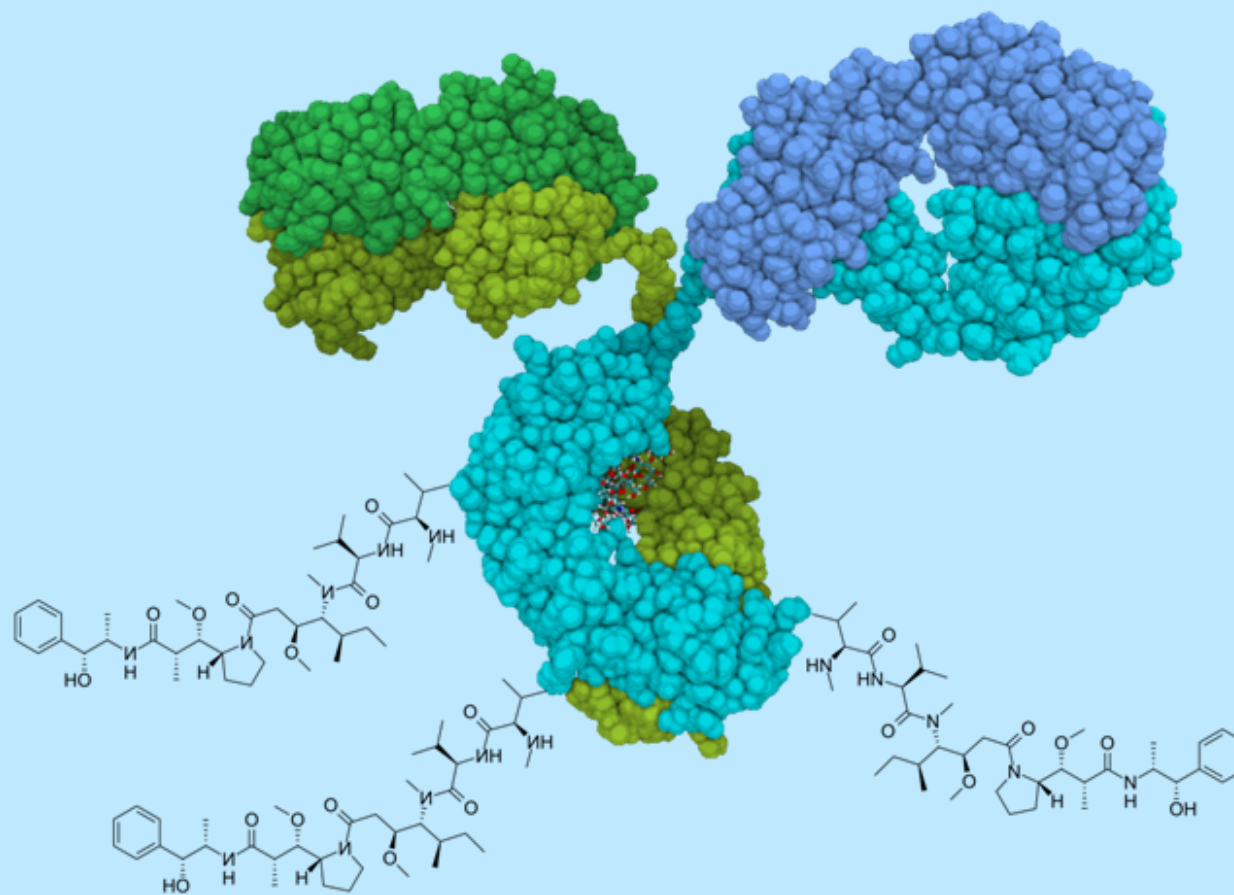
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THE CHALLENGE

- Monoclonal antibodies (mAbs) have **irreversibly revolutionized** current **medicine**.
- Although extremely efficient, **identification of mAbs** candidates to enter clinical trials **remains challenging**.
- With a landscape of **>10¹³ possible variants** **experimental studies** are both time and cost prohibitive.
- Modellization of **molecular interactions on High Performance Computing (HPC)** clusters offers the chance to address both problems and narrow down the plethora of ideal candidates to be experimentally validated.



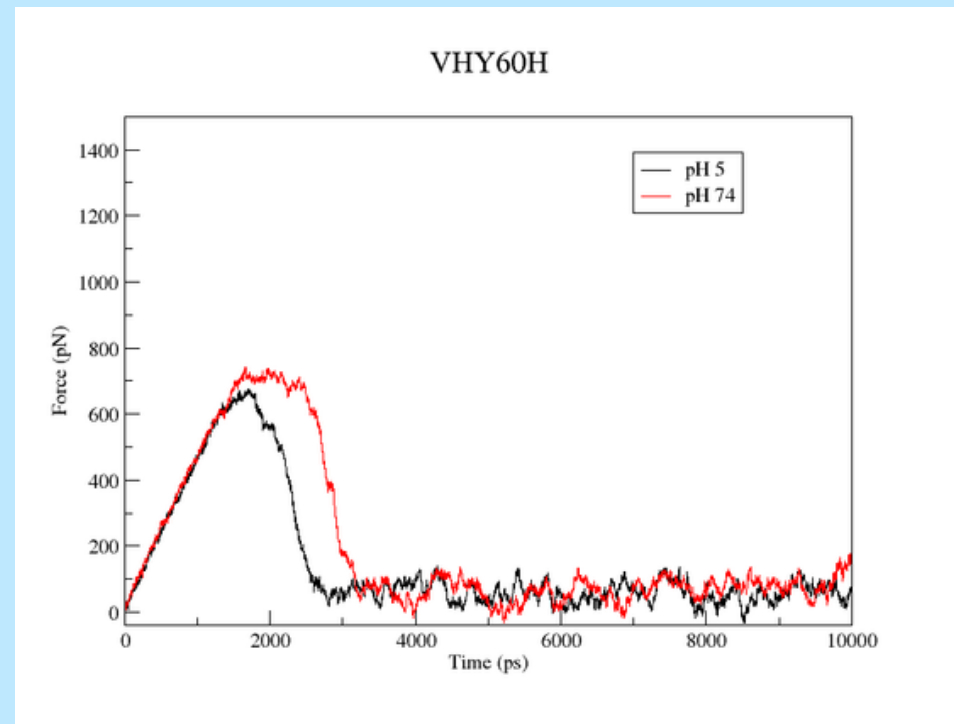
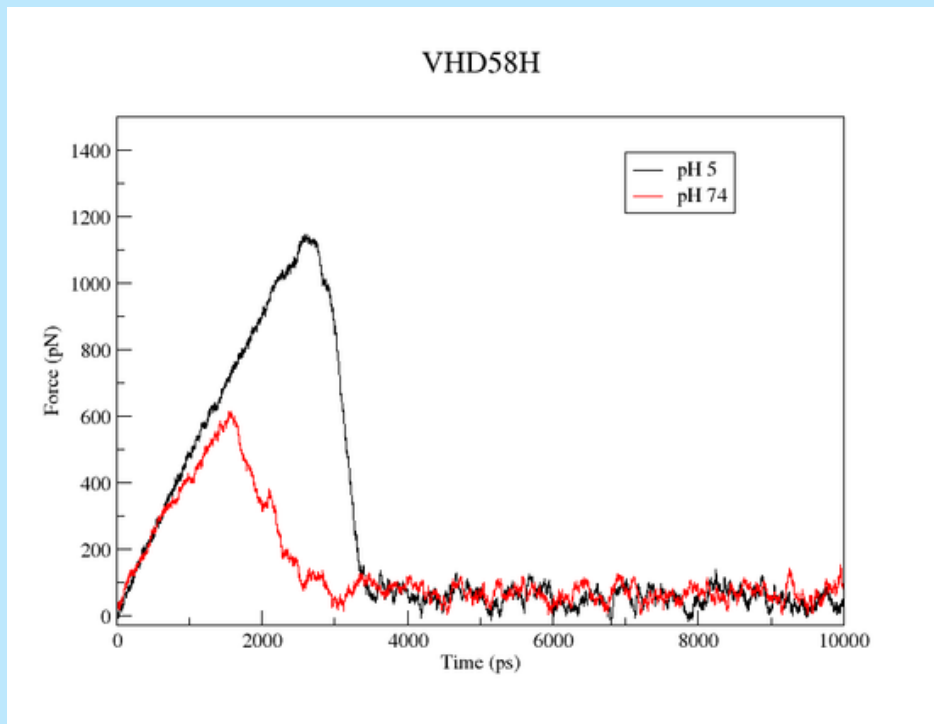
THE IDEAL ANTIBODY-DRUG-CONJUGATED (ADC) CANDIDATE



- Monospecificity
- High-affinity
- High-productivity
- Low immunogenicity
- High payload content
- Low self-aggregation

Differential binding mode at different pH to promote Ab recycling and prevent its sequestration.

RESULTS



In-silico analysis revealed pH-dependent conditional binding profiles for several mutants. Some show slower dissociation at acid pH (5.8H), other slower at physiological pH (6.0H). Such behavior translates to better performance in antibody recycling and targeting the oncologic microenvironment.

OUTLOOKS

- In-vitro validation of found mutants by Bio-Layer-Interferometry (OCTET).
- Design de-novo Ab against selected epitopes
- Consolidation of AI infrastructures for Ab generation based on existing candidates.

REFERENCES

- Krapp LF, Abriata LA, Cortés Rodríguez F, Dal Peraro M. PeSTo: parameter-free geometric deep learning for accurate prediction of protein-binding interfaces. *Nat Commun.* 2023 Apr 18;14(1):2175. doi: 10.1038/s41467-023-37701-8. PMID: 37072397; PMCID: PMC10113261.
- Chowdhury R, Allan MF, Maranas CD. OptMAVEN-2.0: De novo Design of Variable Antibody Regions against Targeted Antigen Epitopes. *Antibodies (Basel).* 2018 Jun 30;7(3):23. doi: 10.3390/antib7030023. PMID: 31544875; PMCID: PMC6640672.