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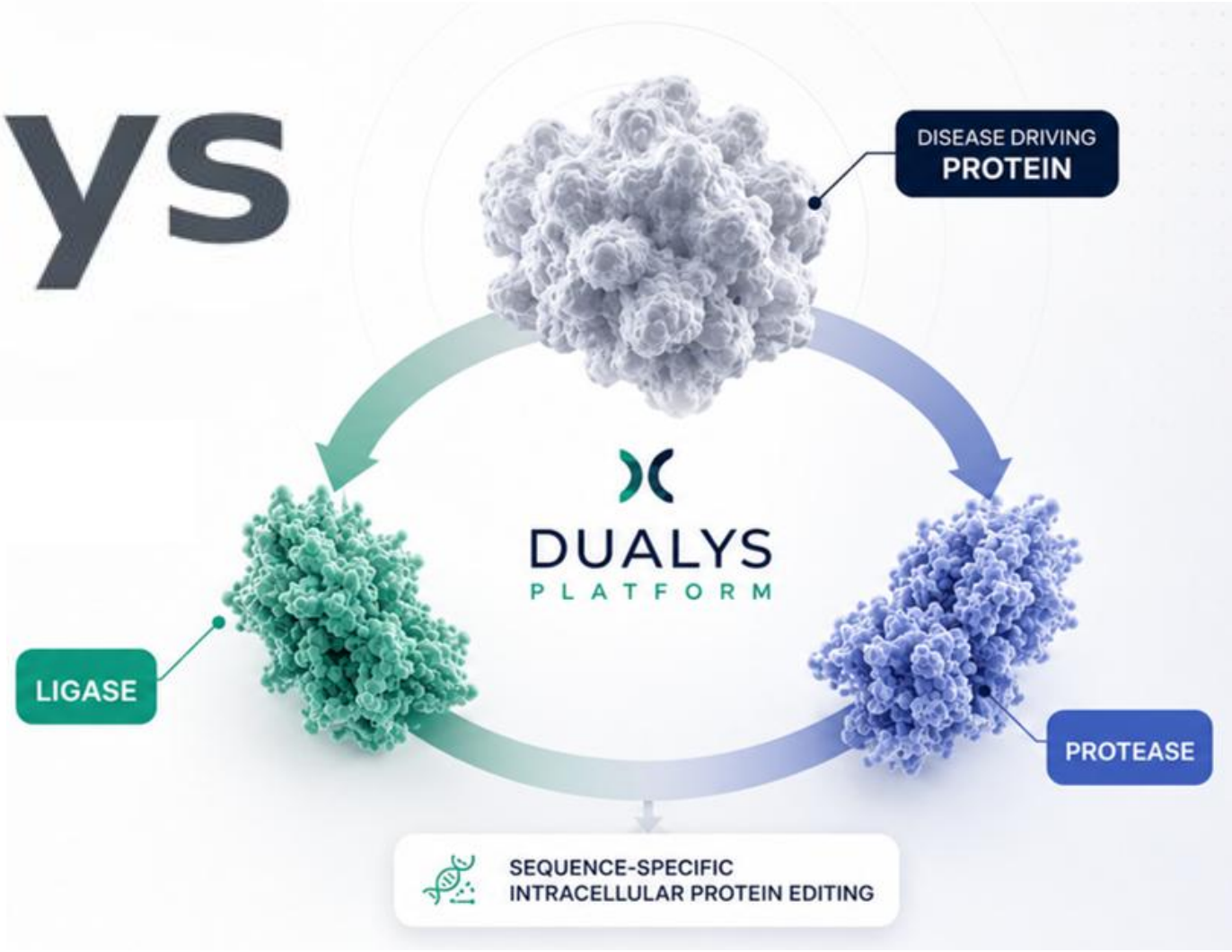
CRISPR for Proteins



The Problem Nobody Has Solved

Diseases are often caused by proteins that current modalities can't affect

THE APPROACH	WHY IT FAILS
Pills (small molecules) *The standard first approach for most diseases*	These proteins have no pocket or crevice for a pill to grab onto — there's nothing to bind.
Antibodies *Precise, but built to work outside the cell*	The target hides deep inside the cell, in the nucleus — antibodies can't get in to reach it.
Gene & RNA-based drugs *Newer, experimental technologies*	These can only knock the target down partway, and carry real safety and delivery risks.

Cap3 solves this differently: it doesn't try to bind the target at all — it cuts it out of the cell completely.

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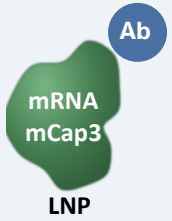
"Think CRISPR for Proteins"

A programmable bacterial enzyme built to cut the proteins driving these cancers — proteins nothing else can reach.



1

DELIVER

A tumor-targeted nanoparticle carries the therapy straight into cancer cells.

→

2

CLEAVE

Inside the cell, the enzyme finds and cuts the cancer-driving protein at a site unique to the tumor.

→

3

DEGRADE

The cell clears away the pieces — the protein driving the cancer is gone for good.

First-in-class: a programmable enzyme that cuts the cancer-driving protein directly — no binding pocket required.

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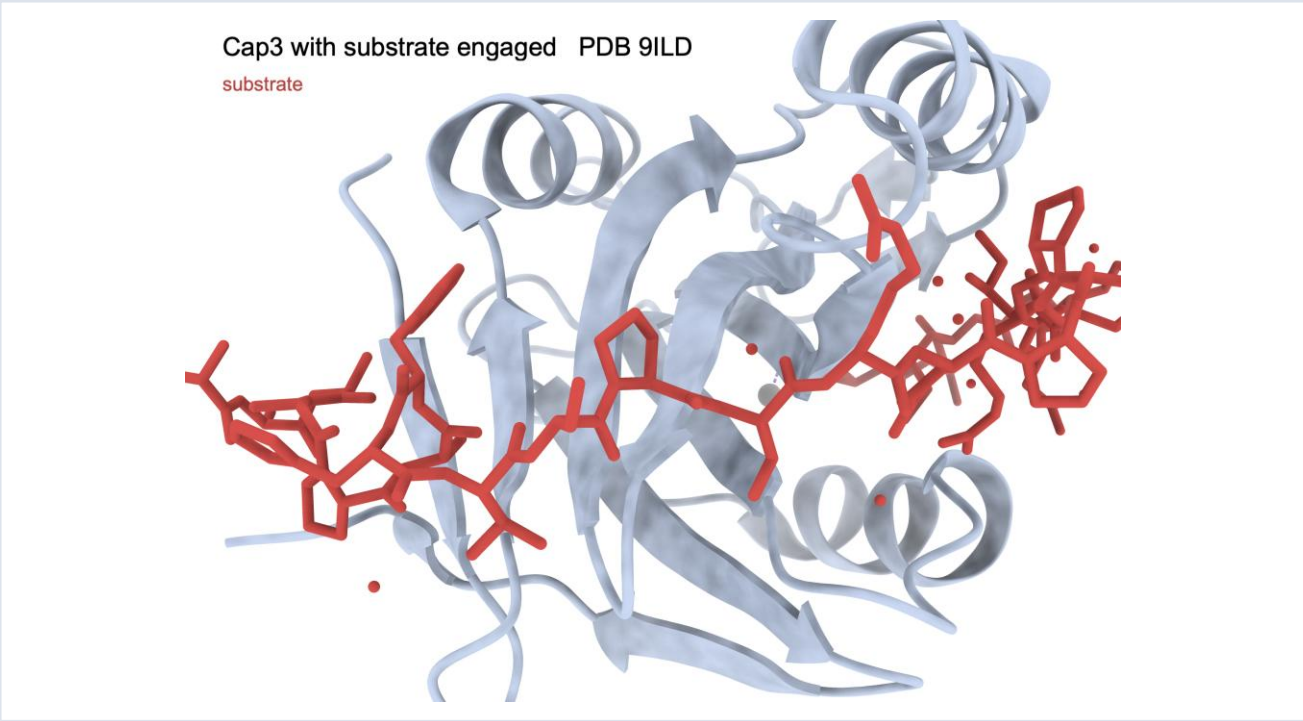
A Programmable Protein-Cleaving Enzyme

Bacterial Enzyme — a zinc protease that reads a 14-residue sequence and cuts it.



The red chain is a substrate peptide threaded through the enzyme's groove, with the catalytic zinc at the centre.

Unlike an inhibitor, which must occupy a pocket and stay there, a protease destroys its target and moves on — one enzyme, many substrate molecules.

That makes targets accessible which have no druggable pocket at all: transcription factors, fusion oncoproteins, scaffolding proteins.

The engineering question is which 14 residues it reads.

All results are structure prediction. No biochemical validation to date — the enabling experiment is defined and costed.

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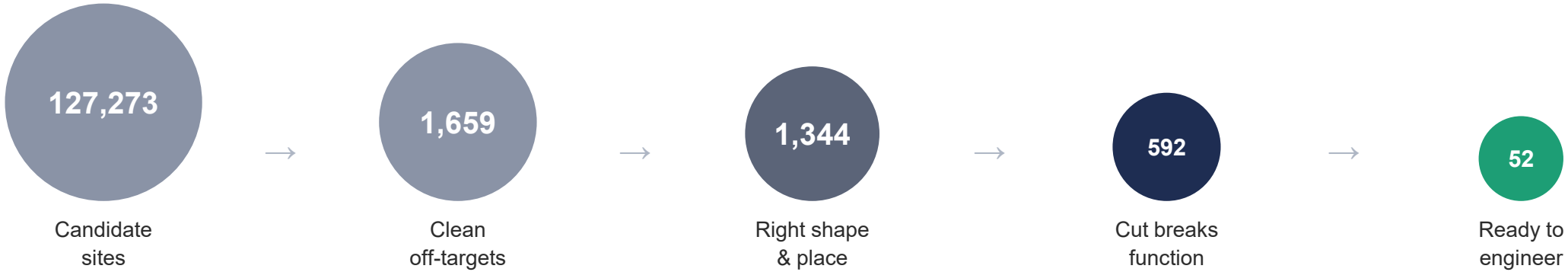
The Engine, Start to Finish

The same pipeline runs for every target we touch. This is one full pass through it.

STAGE 1 · FIND THE TARGET



PICK ONE TARGET

STAGE 2 · ENGINEER THE ENGINEER THE ENZYME

111

Natural enzyme scaffolds screened against the target

→

AI

Computational redesign scores and selects the variant

→

10/10 vs 0/10

Cuts the target, ignores the near-identical decoy ($p = 10^{-5}$)

One engine, any target: 127,273 candidates in, one validated, selective enzyme out.

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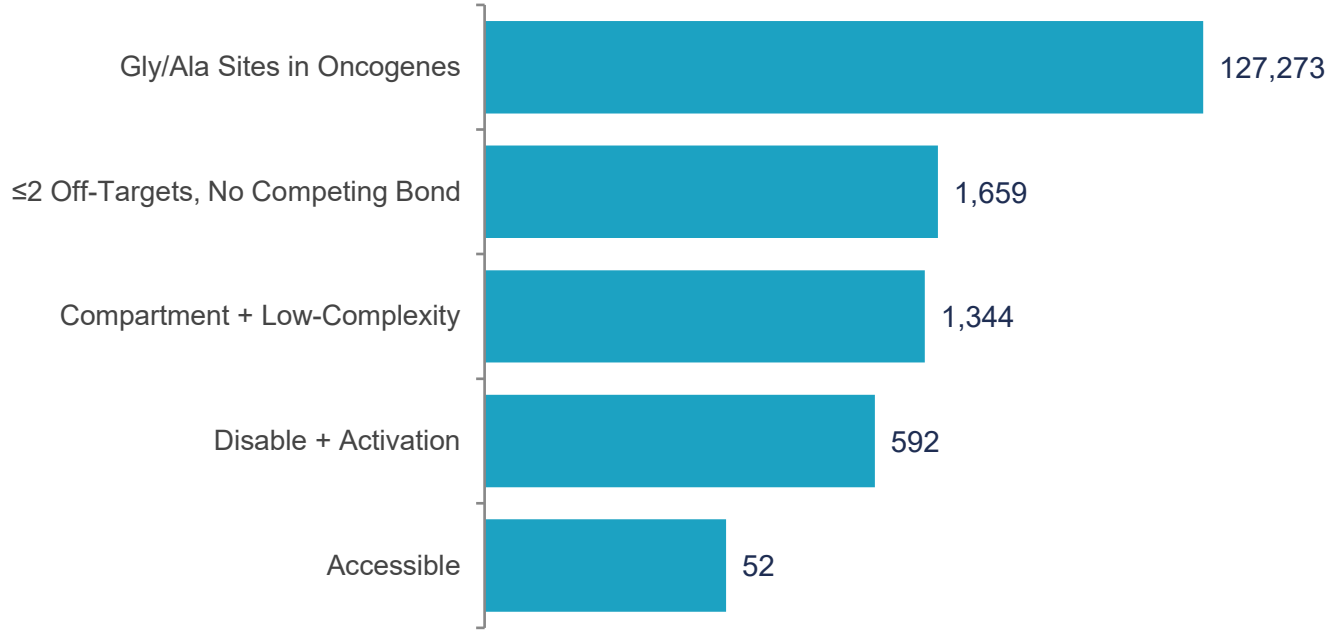
A Target-Selection Engine, Not a Target List

127,273 candidate bonds reduced to 52 by gates the field has not articulated.



FOUR MECHANISTIC GATES, APPLIED BEFORE CHEMISTRY

Compartment — the site must face cytosol or nucleus.

Composition — the groove needs side chains, not a floppy Gly/Ser stretch.

Disable — the cut must destroy function, not trim a tail.

Activation — the cut must not release an autoinhibited catalytic module.

The Activation gate is the differentiated insight: cutting BRAF 387, CARD11 504, RPS6KB1 458, or MAP3K14 136 converts a proto-oncogene into a driver. It removes 387 sites automatically — and it is not in anyone's published workflow.

Output: 52 sites across 37 genes, each with mechanism, off-target count, degron routing, and accessibility attached — reproducible from sequence in minutes.

All results are structure prediction. No biochemical validation to date — the enabling experiment is defined and costed.

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Androgen Receptor: The Lead Program

The largest market on our list — and a clear, testable question that takes it to in vivo proof.

THE OPPORTUNITY

~300,000 new patients per year — castration-resistant prostate cancer

~35,000 deaths per year in the same population

~37% 5-year relative survival, distant-stage disease

Current standard of care: ADT + ARPI (abiraterone, enzalutamide, apalutamide, darolutamide), docetaxel, PARP inhibitors, Lu-177-PSMA — sequenced lines, not a cure. A durable, mechanistically distinct option changes that conversation.

THE EXPERIMENTAL PLAN

What This Program Is Built to Prove

- AlphaFold3 + Bolt-2 modeling is complete — the next step is the bench, not further modeling
- The central question: whether cleaving the C-terminal fragment (293–920) is sufficient to disable the receptor, given it retains TAU-5, the DNA-binding domain, and the ligand-binding domain — exactly what our in vitro assays are designed to answer
- Six prior AR sites already screened in this programme sharpened the design behind this one
- One computationally identified off-target (CACNA1C) tracked through validation

AR is where the platform meets its biggest market — with a specific, well-defined experiment standing between us and in vivo proof.

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Three Ways This Becomes a $1B+ Company

The engine doesn't just produce our own pipeline — it's a platform other companies will pay to use. Each path can generate $100M+ on its own.

OWN & OUT-LICENSE

Advance, Then Exit the Asset

Take owned programs like AR to a real value inflection point (in vivo proof) then out-license or sell. The standard biotech playbook: upfront payments, milestones, and royalties on a validated asset.

PLATFORM LICENSING

License the Engine Itself

Pharma and biotech partners have their own undruggable targets. License them the target-selection engine to pursue those targets, capital-efficient, recurring, and scalable without us running every program.

CO-DEVELOPMENT

Share the Risk, Share the Upside

Partner on shared targets from the discovery stage, splitting cost and risk in exchange for splitting the economics. Faster path to revenue than developing everything alone.

This is a platform business, not a single-asset bet: the same engine can pay for itself three different ways.

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The Team

Andrew Zorn, Ph.D.

•Biotech founder/operator (CEO) with experience building platform and asset-focused companies
•Led therapeutic programs, pharma/CVC partnerships, and major non-dilutive funding efforts
•Background in business strategy, BD, and venture creation
•Deep expertise in platform design, early pipeline development, and company scaling

Scott McMenemy, Ph.D.

•15 years of BD leadership in biopharma
•Specialist in creating, scaling, and commercializing R&D tools, biologics discovery platforms, and end-to-end drug discovery services
•Led global strategic partnerships and accelerated platform adoption across biotech and pharma
•Biotech founder/operator
•Cell and Developmental Biologist-Immunomodulatory imide drug (IMiD) teratogenicity

Aaron Whiteley, Ph.D.

•Inventor of the Cap2–Cap3 programmable ligase/protease system
•Assistant Professor of Biochemistry, University of Colorado Boulder
•Research focuses on molecular evolution of innate immune signaling
•Recognized for foundational work in immune biochemistry and protein engineering
•Recipient of the NIH Director's New Innovator Award and multiple major early-career honors

Timothy Whitehead, Ph.D.

Scientific Advisor / Collaborator —Protein Design

- Professor, Chemical and Biological Engineering, CU Boulder
- Leads computational protein design and directed evolution for the platform
- Expert in translating functional prediction into engineered scaffolds

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Pre-Seed SAFE Financing

TARGET RAISE

$700K

Validate the mechanistic hypothesis in AR-driven prostate cancer — our lead program — while advancing 2–4 additional targets to initial in vitro proof-of-concept.

STRETCH GOAL

$1.5M

Enter IND-enabling studies and bring additional targets to proof-of-concept.

Clear Milestones — *In Vitro & In Vivo*

- ✓ Intracellular processing and preparation of the therapeutic protease
- ✓ Nuclear localization
- ✓ Identifiable cleavage of the AR target site
- ✓ Significant change in biomarkers
- ✓ Tumor growth inhibition
- ✓ In vitro proof-of-concept across 2–4 additional priority targets

Terms: a SAFE note with a 20% discount and a $5.0M valuation cap — a standard, founder-friendly instrument for this stage.

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Thank You

We're building CRISPR for proteins, a way to reach and remove the disease-driving proteins nothing else can touch. The same platform can unlock cancer treatments that don’t exist yet.

PARTNER WITH US

Have an undruggable target of your own? Bring it to us. This is what the engine was built to find out.

INVEST WITH US

This round funds the proof that takes us from computational evidence to a validated result in living cells.

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