myNEO Therapeutics

A wholly owned subsidiary of
Arcturus Therapeutics Holdings Inc.

ONE PLATFORM, ENDLESS POSSIBILITIES

Turning immunogenic insights into clinical assets

Corporate deck

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COMPANY SNAPSHOT

AI-driven Technology Company

Technology Superiority

- ImmunoEngine: N°1 immunogenic antigen selection platform
- 350+ novel highly expressed cancer targets identified

Robust IP Position

- 3 technology patent applications (2 granted)
- 3 product patent applications

Strong Pipeline

- 3 CTA/IND filings in 2025
- Strong preclinical & clinical validation
- IVD-ready, ISO 13485 & FDA QSAR compliant
- MHRA approved
- Multiple programs in development: CRC, TNBC & PAAD

Deals & Collaborations

- Unique products already led to several $20M+ asset deals

PIPELINE OVERVIEW

PARTNER	DISEASE	THERAPY	PRE-CLINICAL	PHASE 1	PHASE 2
CureVac (BioNTech)	NSCLC	Off-the-shelf mRNA			
CureVac (BioNTech)	Undisclosed	Off-the-shelf mRNA			
University of Liverpool	NSCLC	Personalized DNA			
Undisclosed EU partner	Solid tumors	Personalized DNA			
Undisclosed US partner	Solid tumors	Personalized MVA			
Etherna	COVID-19	Off-the-shelf mRNA			

PROGRAM	DISEASE	THERAPY	PRE-CLINICAL	PHASE 1	PHASE 2
CAMYO-CRC	MSS-CRC	Off-the-shelf mRNA			
CAMYO-TNBC	TNBC	Off-the-shelf mRNA			
CAMYO-PAAD	PAAD	Off-the-shelf mRNA			
PRIMYO	Solid tumors	Personalized mRNA			

KEY PUBLICATIONS

PARTNERS & COLLABORATORS

CUREVAC · Johnson & Johnson · UNIVERSITY OF LIVERPOOL · HOOKIPA PHARMA · odimma · abera

N°1 Immunogenic Antigen Selection

3 CTA/IND Filings in 2025

$20M+ Asset Deals Completed

TECHNOLOGY SUPERIORITY

Most Exhaustive Antigen Prioritization Engine

Whole genome discovery
> novel target exploration

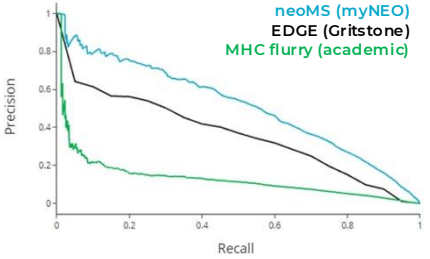
ImmunoEngine prioritization
> top immunotherapy candidate selection
(working towards ISO13485 & FDA QSAR compliance)

Leveraging the WGS information of both tumor and healthy cells, enables discovery in the **dark genome**

> Novel and more cancer-specific targets are core to therapy development for lowly mutated (cold) solid tumors

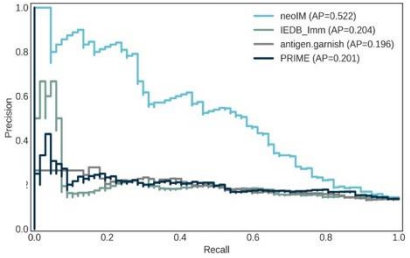
Best-in-class presentation prediction algorithm

neoMS: PCT/EP2021/069341



First-in-class immunogenicity prediction algoritm

neoIM: PCT/EP2021/078639



FOR BIOLOGICS, VACCINE & T-CELL THERAPEUTICS DEVELOPERS

Powering Immune-driven Discovery

myNEO – Personalized neoantigen discovery

AI-powered, IVD-ready personalized neoantigen discovery for onco immunotherapeutic modalities

myCONSTRUCT – Construct design

Computational construct design enhancing expression and functional performance

mySHARED – Shared MHC-bound target discovery

AI-powered discovery of shared MHC-bound targets for off-the-shelf immunotherapeutic modalities.

myRNA – Codon optimization

Advanced codon optimization engine improving stability and translational efficiency.

mySURFACE – Surfaceome target discovery

AI-powered identification of surface antigens for biological therapeutic modalities.

myADA – ADA risk prediction

Anti-Drug Antibody risk prediction enabling rational, data-driven biologics engineering.

mySELF – Autoimmune target discovery

AI-powered discovery enabling rational design of autoimmune disease therapeutic modalities.

myEPITOPE – Immunogenicity screening

Accurate epitope immunogenicity prediction derisking preclinical validation.

myPATHOGEN – Infectious target discovery

AI-powered discovery of pathogen-derived targets for infectious disease therapeutic modalities.

myINSIGHTS – Large data analysis

Large dataset analysis supporting biomarker identification, response prediction, and decisions.

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PERSONALIZED ANTIGEN DISCOVERY

myNEO

Identification of neoantigens for personalized immunotherapies

Neoantigen Discovery

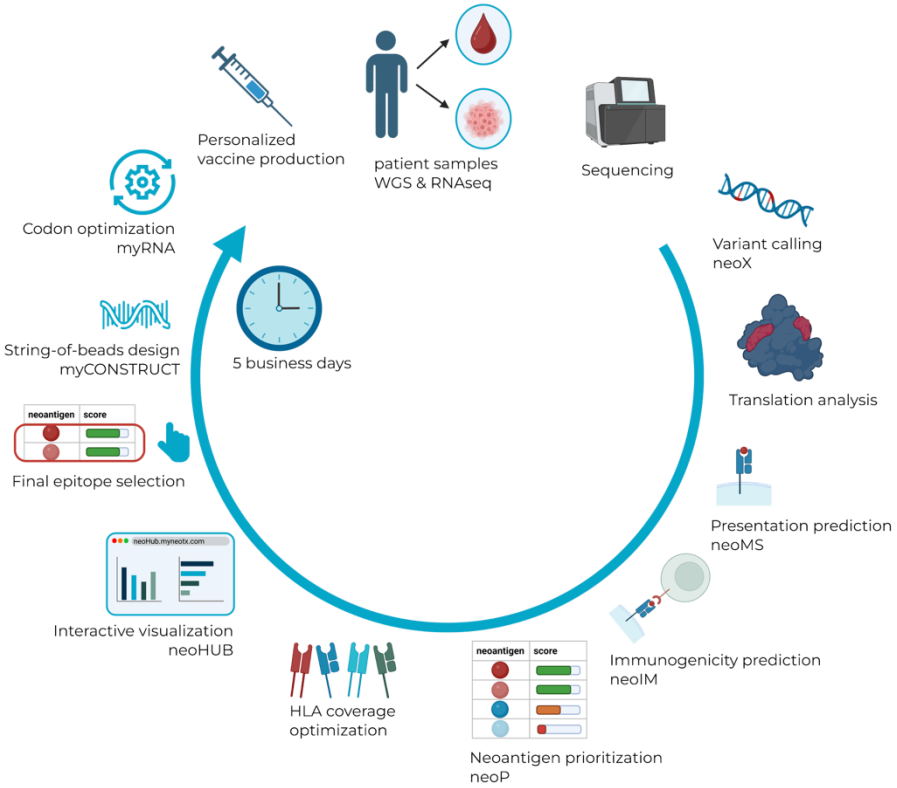
Cancer immunotherapies require highly immunogenic, tumor-specific targets - yet current discovery approaches fall consistently short:

- **Coding mutations only** → most approaches ignore the dark genome, missing a vast landscape of immunogenic targets
- **Predicted neoantigens underdeliver** → many computationally identified neoantigens fail to trigger meaningful T-cell responses in practice
- **Personalized therapies don't scale** → patient-specific approaches remain too slow and costly to deploy broadly across oncology indications

WHERE WE COME IN

myNEO leverages the ImmunoEngine to deliver 25–50% more actionable targets - personalized, whole genome targets inaccessible to conventional pipelines.

Our Solution



5 DAYS

From sequencing data to neoantigen selection & product design

REGULATORY FAVORED

IVD-ready
ISO13485 compliance
FDA QSAR compliance
MRHA approved

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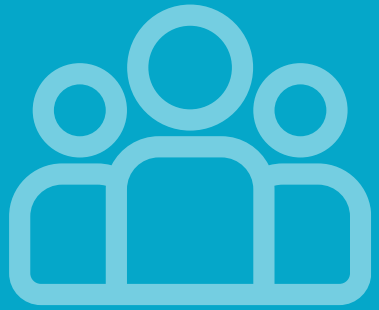


MHC-BOUND ANTIGEN DISCOVERY

mySHARED

Identification of shared tumor antigens for off-the-shelf immunotherapeutic strategies

Shared Antigen Discovery

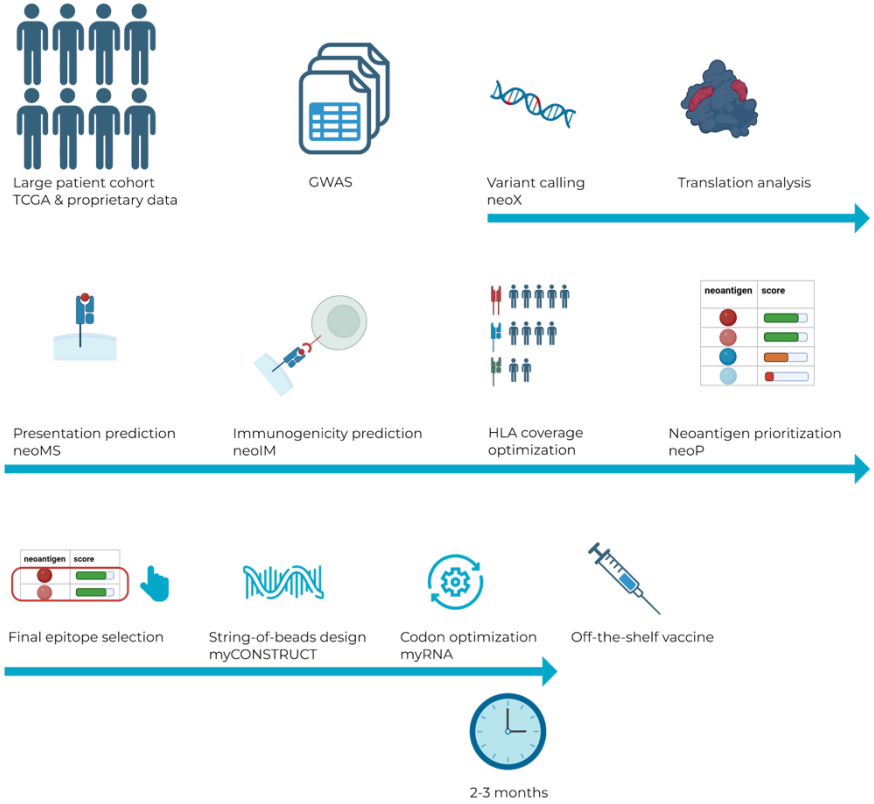
Cancer immunotherapies require immunogenic, highly abundant, and shared targets - yet current discovery approaches fall consistently short:

- **Coding mutations only** → most approaches ignore the dark genome, missing a vast landscape of immunogenic targets
- **Predicted neoantigens underdeliver** → many computationally identified neoantigens fail to trigger meaningful T-cell responses in practice
- **Low patient population coverage** → most tumor-associated antigens have a small population coverage excluding larger patient populations from treatment and requiring pre-selection
- **Multi-antigen targeting is limited** → current known tumor-associated antigens are few in numbers increasing immune-escape risk

WHERE WE COME IN

myNEO leverages the ImmunoEngine to deliver more, better, and novel shared, whole genome targets inaccessible to conventional pipelines.

Our Solution



	mySHARED	State of The Art
Full mutation inventory	✓	✗
Dark genome unlocked	✓	✗
MHC-I presentation prediction	✓ ✓	✓
MHC-II presentation prediction	✓	✗
CD4 immunogenicity prediction	✓	✗
CD8 immunogenicity prediction	✓ ✓	✓
Actionable neoantigens	✓ ✓	✓

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SURFACE TARGET DISCOVERY

mySURFACE

Identification and prioritization of transmembrane targets for biologics through AI-driven discovery

MYSURFACE - FOR BIOLOGICS DEVELOPERS

Surface Target Discovery

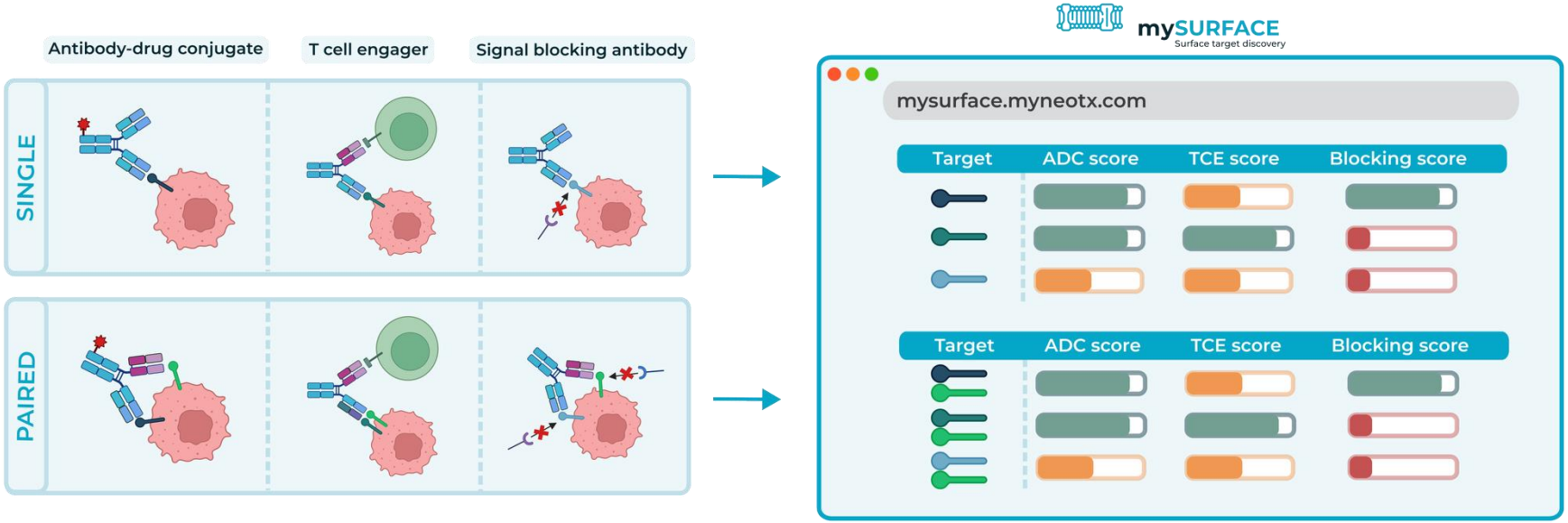
Surface proteins represent one of the richest target classes in oncology, yet remain significantly underexploited.

- **High relevance** → ~70% of approved drugs target transmembrane proteins
- **Low diversity** → <30 targets used by approved oncology biologics
- **Rising complexity** → multi-target biologics are increasing in development
- **Untapped space** → ~30% of all proteins are transmembrane

WHERE WE COME IN

mySURFACE enables systematic identification and prioritization of surface targets and target combinations for biologics development

Our Solution



Key Features

01

Agentic AI

- Literature automation
- PubMed database
- AI synthesis & consensus

02

Structural accessibility

- Accessibility along sequence
- Glycosylation motifs
- 3D protein structure

03

Target relevance

- Literature-derived evidence
- Known Abs, ADCs
- Cancer relevance

04

Internalization & shedding

- Internalization and shedding motifs
- Literature evidence

05

Tumor specificity

- Bulk RNA expression
- Expression in normal
- Clonality scRNAseq
- IHC in normal

06

Co-expression

- Retrieve relevant co-expressed genes
- In bulk and scRNAseq
- Associated ligands from literature

07

Target prioritization

- Application-specific scoring
- ADC, TCE, blocking score
- Paired target score

08

Flexibility

- Plug-in of additional public and proprietary datasets

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IMMUNOGENICITY SCREENING

myEPITOPE

Analyzing immuno-genomic datasets to deliver actionable insights across biomarker discovery, response prediction, trial design, and cross-dataset interpretation.

Immunogenicity Screening

Epitope-level understanding is essential for immunological characterization

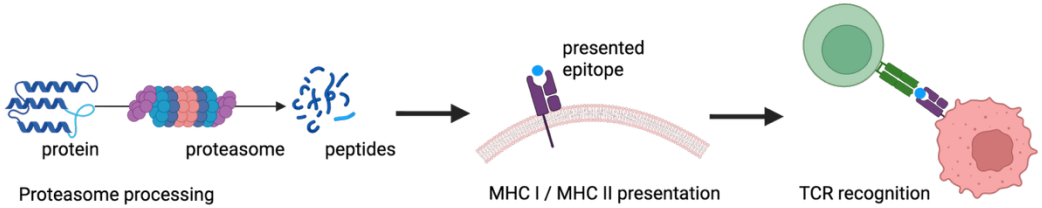
- **Epitope mapping** → identification of relevant epitopes
- **Epitope characterization** → Analysis of epitope properties
- **Immunological relevance** → understanding epitope-driven immune responses

WHERE WE COME IN

myEPITOPE enables epitope mapping and characterization to support immunological analysis and therapeutic development

Our Solution

	myEPITOPE Immunogenicity screening	State of The Art
Identification of MHC I and MHC II presented peptides	✓	✓
CD4+ T cell response prediction	✓	✗
CD8+ T cell prediction	✓	✗
HLA agnostic	✓	✗



Key Features

01

Immunogenic potential

Immunogenicity quantification and maximization

02

Actionability

Prioritization of highly actionable epitopes

03

Presentation context

For MHC class I and MHC class II contexts

04

Risk assessment

Immunogenicity risk assessment

05

Compatibility

Compatible with animal models incl mice

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ADA RISK PREDICTION

myADA

Identification and prioritization of immunogenic and tolerogenic self-antigens using AI-driven immunogenicity prediction

ADA Risk Prediction

Immunogenicity screening is critical during biologic drug development

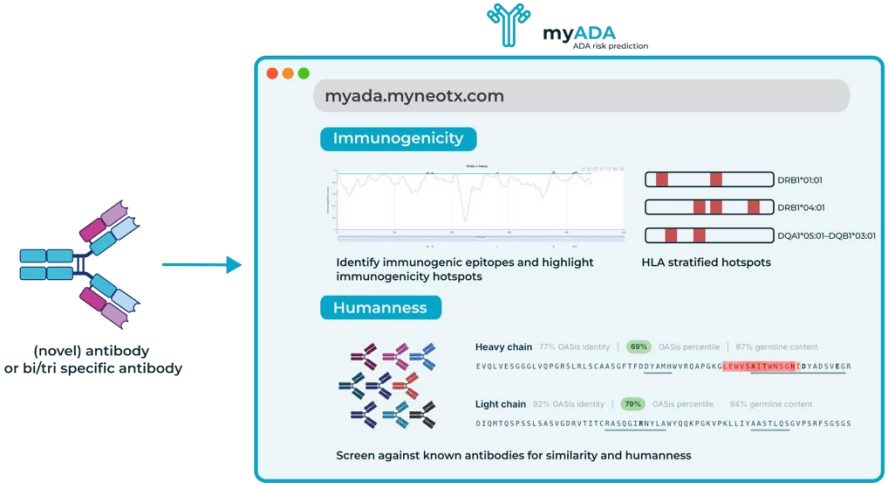
- **ADA risk assessment** → anti-drug antibody responses impact biologic safety and efficacy
- **T cell driven response** → identification of immunogenic regions is essential
- **Population impact** → immunogenicity must be assessed across patient populations

WHERE WE COME IN

myADA enables in silico assessment of immunogenicity risk to support biologic design and development

Our Solution

- **ADA risk assessment** → predicts likelihood of T-cell–dependent ADA responses
- **Hotspot identification** → identifies CD4+ T cell epitope clusters
- **Humanness profiling** → evaluates similarity to known antibodies
- **Lead optimization support** → supports candidate selection and re-engineering



Key Features

01

In silico ADA-risk assessment

Powered by advanced MHC class II epitope immunogenicity modeling, myADA predicts the likelihood of T-cell–dependent ADA responses early in biologic design.

02

Immunogenic hotspot identification

myADA pinpoints high-impact CD4+ T-cell epitope clusters across antibody sequences, enabling rapid detection of regions that drive immunogenicity risk.

03

Lead selection and re-engineering

Support candidate prioritization and sequence optimization through hotspot re-engineering, population-level impact assessment, and humanness profiling.

04

Humanness profiling

Evaluation of similarity to known antibodies

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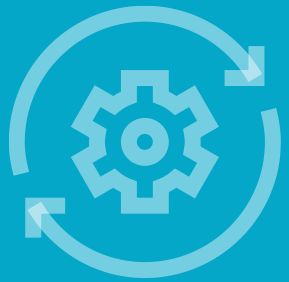


CONSTRUCT & CODON OPTIMIZATION

myCONSTRUCT & myRNA

Design and optimization of multi-epitope RNA therapeutics using integrated construct engineering and constraint-aware codon optimization.

Construct & Codon Optimization

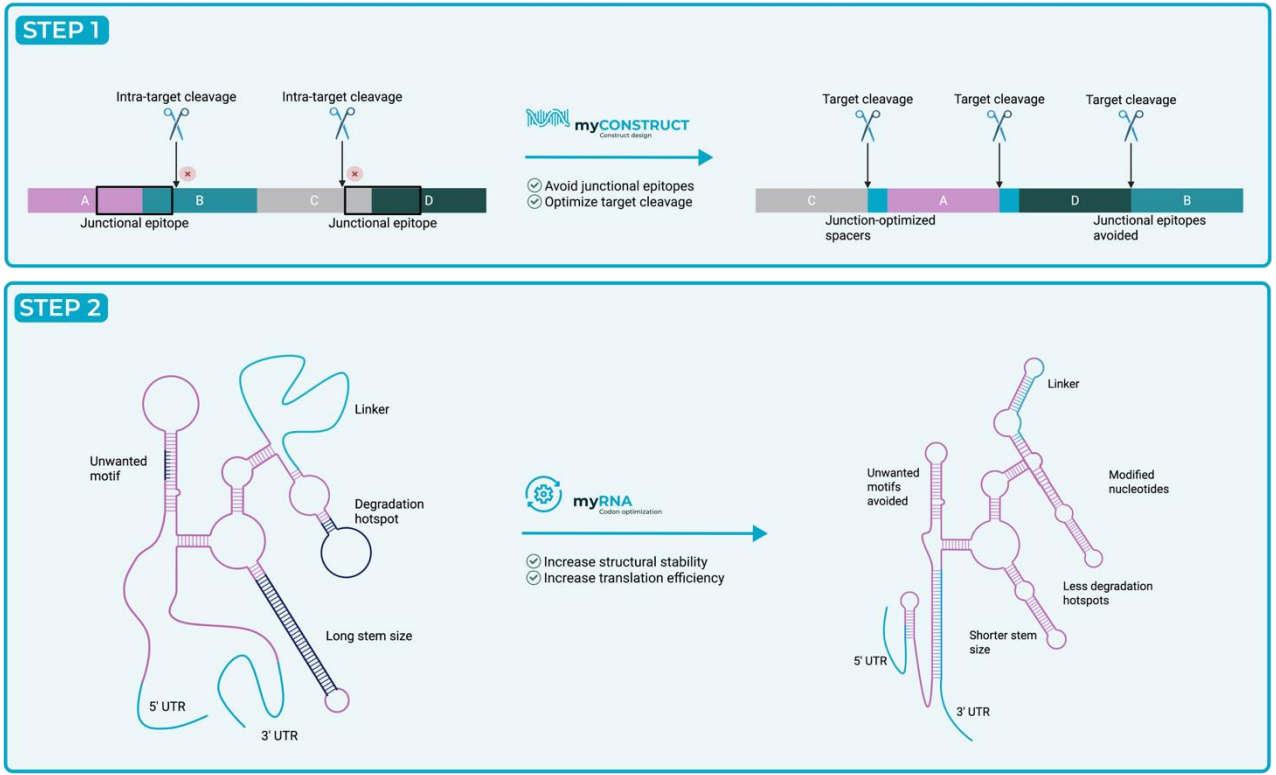
From optimized peptide constructs to optimized mRNA sequences for multi-epitope therapeutics

- **Construct design challenge** → combining multiple epitopes while avoiding unintended immunogenic junctions
- **Sequence optimization need** → ensuring efficient expression and structural stability of mRNA
- **Multi-step process** → design and optimization can be performed on both construct and mRNA level
- **Flexibility in design** → project-specific customizations and multi-species support

WHERE WE COME IN

myCONSTRUCT and myRNA enable computational design and optimization of multi-epitope constructs and their corresponding mRNA sequences

Our Solution



Key Features myCONSTRUCT

01

Junction Scoring

Score all junctions between epitope pairs

- High penalty scores for junctions with predicted presented and immunogenic junctional epitopes
- Cleavage predictions
- Junction-optimized spacers

02

Construct Optimization

Run optimization algorithm to obtain multiple construct designs with minimized impact of potential junctional epitopes & optimized cleavage

03

Construct Selection

From the set of optimized constructs, select diverse optimized constructs for experimental validation

Key Features myRNA

01

Dual optimization

Optimize both stuctural stability & codon usage

02

Sequence refinement

Progressive candidate refinement

03

Region preservation

Locked regulatory regions

04

Multi-epitope support

Supports multi-epitope constructs

05

Degradation avoidance

Avoids degradation hotspots

06

Motif avoidance

Avoids undesired sequence motifs

07

Structure control

Control over mRNA stem size

08

Modified nucleotides

Supports incorporation of modified nucleotides

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AUTO-IMMUNE TARGET DISCOVERY

mySELF

Identification and prioritization of immunogenic and tolerogenic self-antigens using AI-driven immunogenicity prediction

Auto-immune Target Discovery

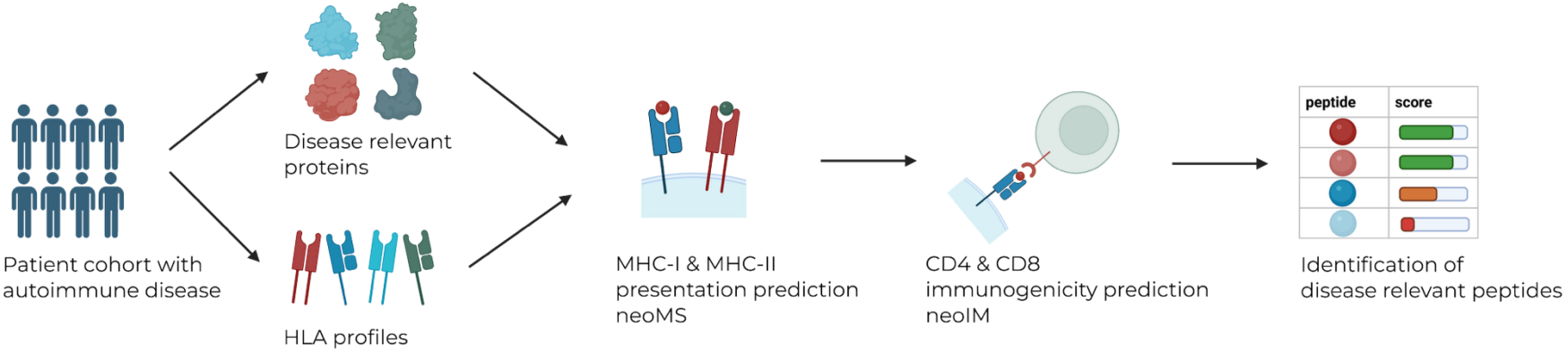
Understanding and quantifying self-antigen immunogenicity is key to autoimmune disease and tolerance design

- **Self-antigen immunogenicity** → drives autoimmune disease and immune tolerance mechanisms
- **T cell-driven response** → requires understanding of both CD8 and CD4 contexts
- **Need for prioritization** → identifying biologically relevant epitopes remains challenging

WHERE WE COME IN

mySELF quantifies and prioritizes immunogenic self-antigens to support autoimmune target discovery and tolerance-oriented design

Our Solution



Key Features

01

Self-antigen identification

Identifies self-derived peptides with high immunogenic potential across CD8 and CD4 contexts.

02

Full MHC-I & MHC-II modeling

Models antigen presentation across both MHC class I and II to capture comprehensive T-cell recognition.

03

Immunogenic Profiling

Characterizes immunogenic patterns across proteins to reveal biologically relevant regions.

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INFECTIOUS DISEASE TARGET DISCOVERY

myPATHOGEN

Identifying conserved, immunogenic pathogen epitopes through AI-guided antigen selection, immunogenicity ranking, and population coverage optimization.

Infectious Disease Target Discovery

Identification of potent pathogen epitopes for vaccine design

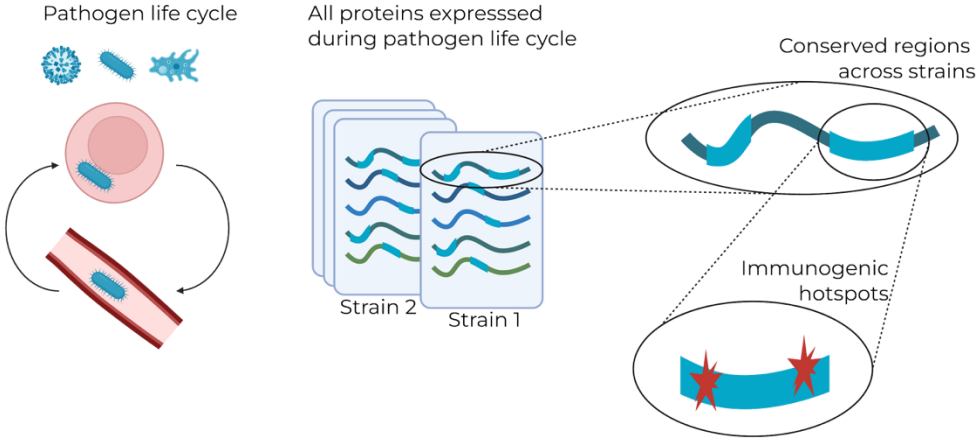
- **From sequence data to vaccine targets** → Converting pathogen proteomes into actionable CD4 and CD8 epitope candidates
- **Designed to reduce escape risk** → Conservation analysis prioritizes targets in robust regions less likely to be lost through mutation
- **Optimized for real populations** → HLA-aware hotspot identification supports target selection for the intended patient population
- **Focused on true immunogenic relevance** → Integrates presentation and immunogenicity signals beyond binding prediction alone
- **Pathogen-agnostic** → Applicable across viral, bacterial, parasitic, and other infectious disease settings

WHERE WE COME IN

myPATHOGEN helps turn broad pathogen diversity into robust, population-relevant CD4 and CD8 vaccine targets.

Our Solution

- **Genome-wide association studies** → linking pathogen genetic variation to phenotypes such as virulence, drug resistance, or immune evasion
- **Conservation analysis** → prioritization of immunogenic epitopes within conserved regions
- **Presentation prediction** → identification of surface-presented epitopes in populations infected with different strains
- **Immunogenicity prediction** → identification of presented epitopes recognized by immune cells
- **myCONSTRUCT** → next-generation string-of-beads design (optional)
- **myRNA** → next-generation codon optimization (optional)



Key Features

01

Identification

Identification of highly conserved and immunogenic epitopes across pathogens strains

02

Target prioritization

AI-guided antigen selection and conservation-driven target prioritization

03

Presentation

Population-aware presentation prediction for CD4 and CD8 target discovery

04

Immunogenicity

Immunogenicity ranking to focus on epitopes most likely to drive relevant immune responses

05

Downstream support

Support for downstream construct and RNA design workflows

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LARGE-SCALE DATA ANALYSIS

myINSIGHTS

Analyzing immuno-genomic datasets to deliver actionable insights across biomarker discovery, response prediction, trial design, and cross-dataset interpretation.

Large-scale Data Analysis

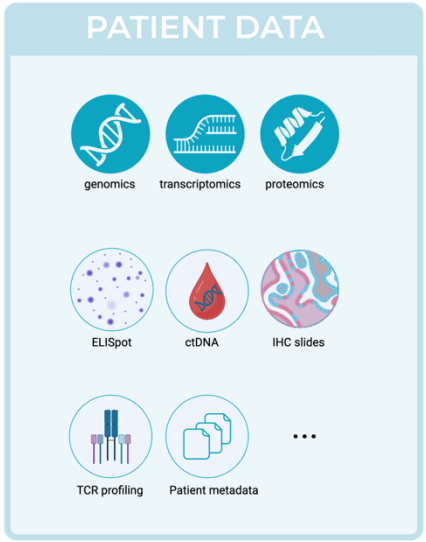
Translational research requires integration and interpretation of complex patient-level datasets

- **Multi-omics integration** → integrates sequencing, clinical, and experimental datasets
- **Biomarker discovery** → identify predictors of clinical response and treatment outcome
- **Patient stratification** → enables data-driven grouping of patients
- **Response prediction** → supports prediction of treatment response

WHERE WE COME IN

myINSIGHTS enables interactive translational data analysis and interpretation to accelerate clinical decision-making

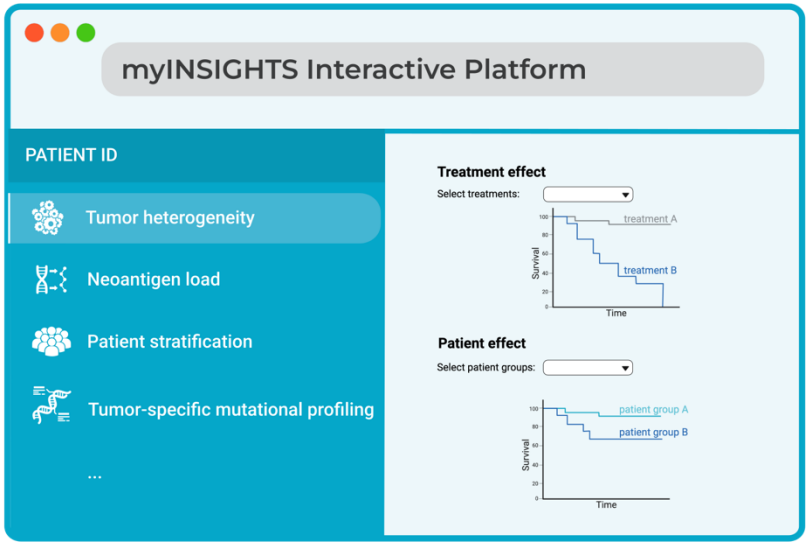
Our Solution



myINSIGHTS
Large-scale data analysis

AI-driven multi-parametric analysis:

- Multi-omic integration
- Digital genomic twin comparison
- Biomarker discovery
- Translational data analysis



Key Features

01

Multi-omics data integration

Integrate complex patient-level datasets including omics, TCRseq, ELISpot, ICS, MSD 30-plex, IHC, immunophenotyping, and NanoString into one translational analytics framework.

02

Biomarker and response insight

Identify pre-treatment and early-response biomarkers, uncover correlates of clinical outcome, and support therapy response prediction through AI-driven multi-parametric analysis.

03

Clinical decision support

Enable patient stratification, tumor profiling, ctDNA monitoring, cross-dataset interpretation, and trial design optimization to guide data-driven translational decisions.