

Kemp Proteins provides a full-continuum of gene-to-protein production services from discovery (mg) to pre-GMP (G)



The Protein Person's
Protein People



The Protein Problem Solvers

Location: Frederick, MD

Staff: ~40 employees (50% w/ Advanced Degrees)

Project Management: 4 Dedicated PMs

Facility: 15,000 sq ft modern lab space

Quality Expressed: ISO9001, ISO13485, AAALAC



Reimagining Bioservices



who are KEMP PROTEINS

Kemp Proteins is a US based Bioservices company focused on expressing, purifying and characterizing proteins for use in life sciences

our AIM:

To create value for our clients through a coordinated continuum of unsurpassed quality, communication, efficiency, and satisfaction from design concept through process development to final manufacturing

Presentation ToC

Understanding The Global Hypothetical Proteome

Proteins Expression at Kemp in Various Platforms

Flexibility is Critical - all expression systems assessed

Solutions for Cell Line Development

Hybridoma Development and Screening

Analytical Services

Rapid Small Scale Expression & Purification

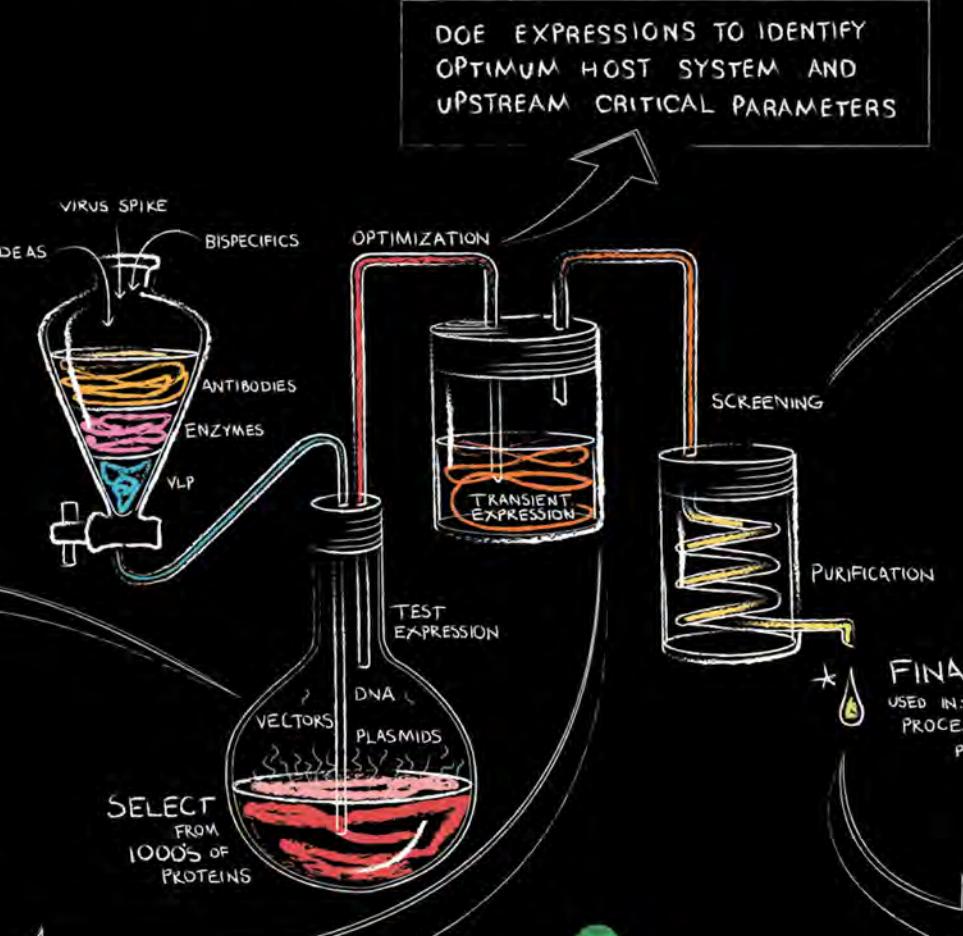
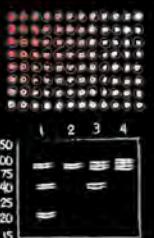
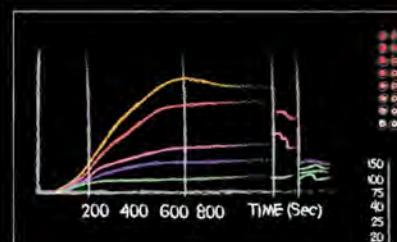
CASE STUDIES: mAB and Multispecifics

CASE STUDY: Critical Reagents

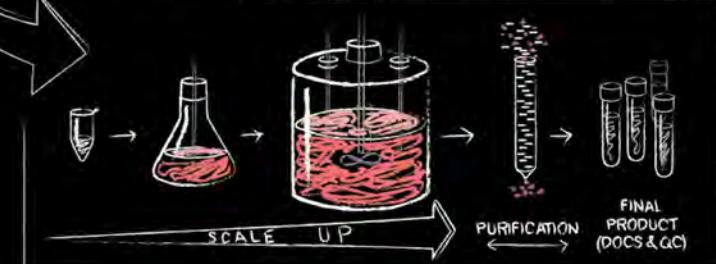
CASE STUDY: Target Proteins

YOUR GMP "READY" PROTEIN

COLLABORATIVE DISCOVERY
WHAT IS THE PROTEIN?
WHAT INFO IS AVAILABLE?
WHAT IS THE USE?
WHAT QUANTITY IS REQUIRED?



KEMP
PROTEINS
QUALITY EXPRESSED

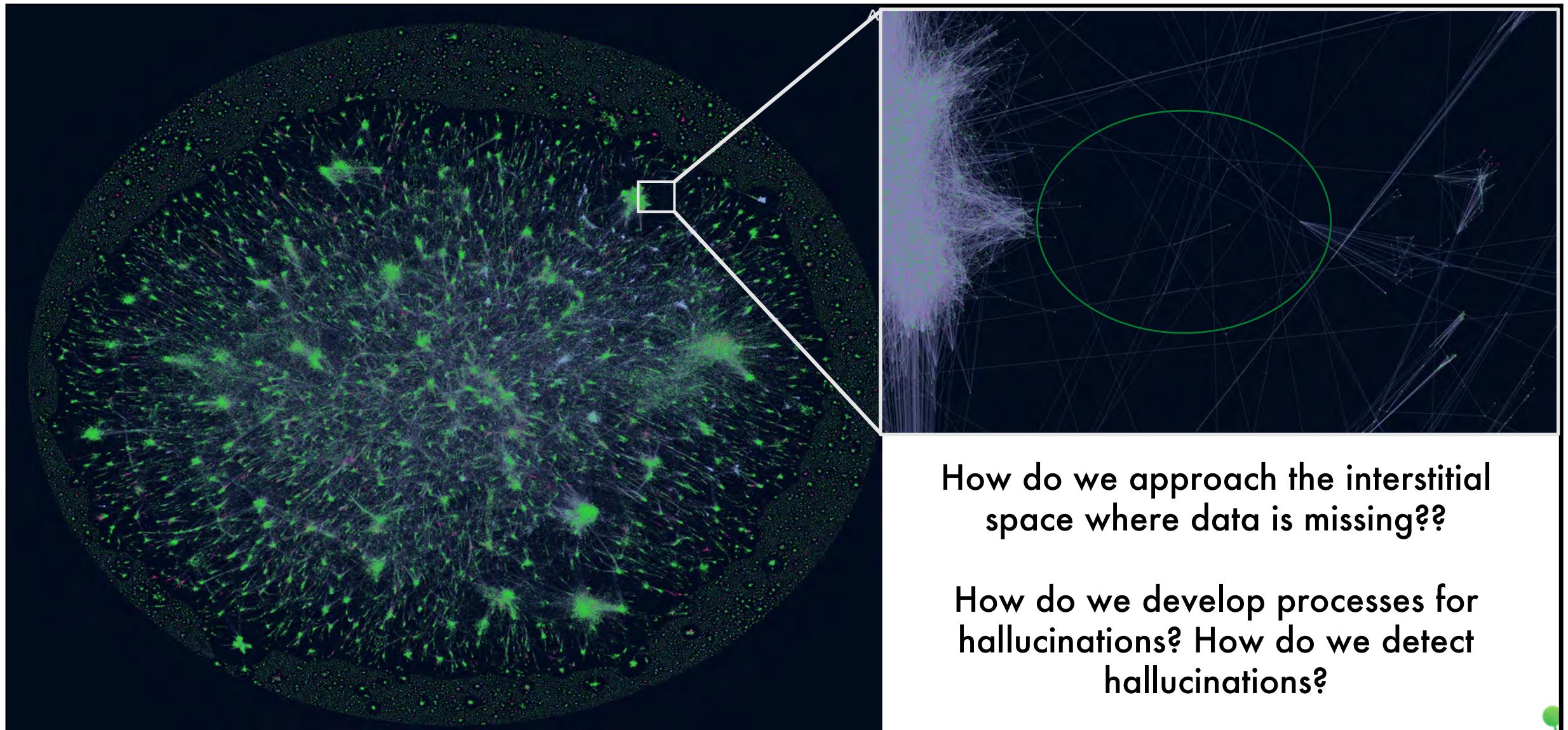


DOWNSTREAM PROCESS OPTIMIZATION

- CLARIFICATION
- ULTRA/DIA FILTRATION
- VIRAL INACTIVATION?
- BIND/ELUTE
- VIRAL INACTIVATION?
- POLISH
- VIRAL FILTRATION?
- ULTRA/DIA FILTRATE FORMULATE

DOWNSTREAM PROCESS DEVELOPMENT IS AN ITERATIVE PROCESS

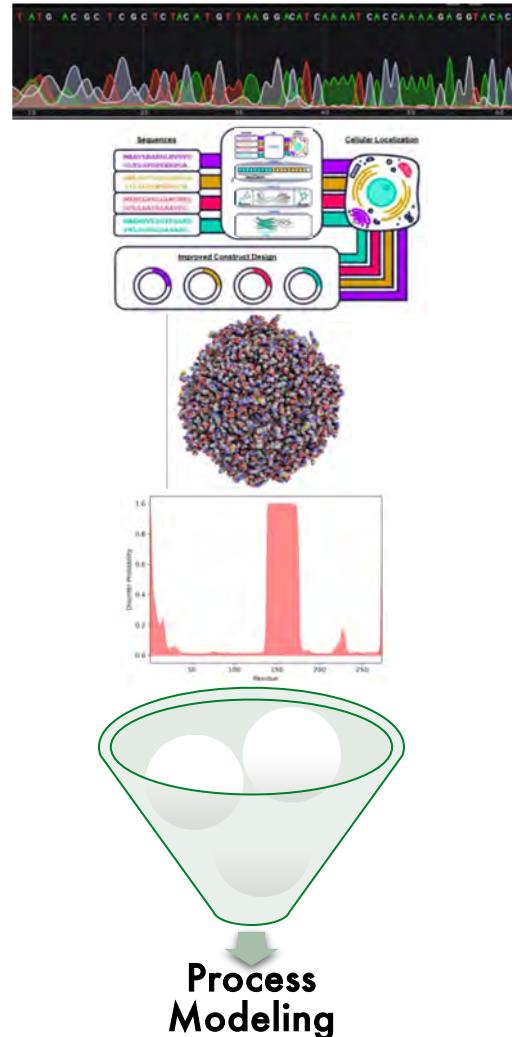
The Global Hypothetical Proteome



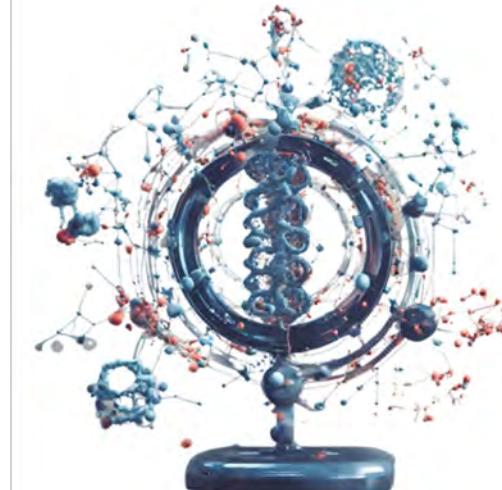
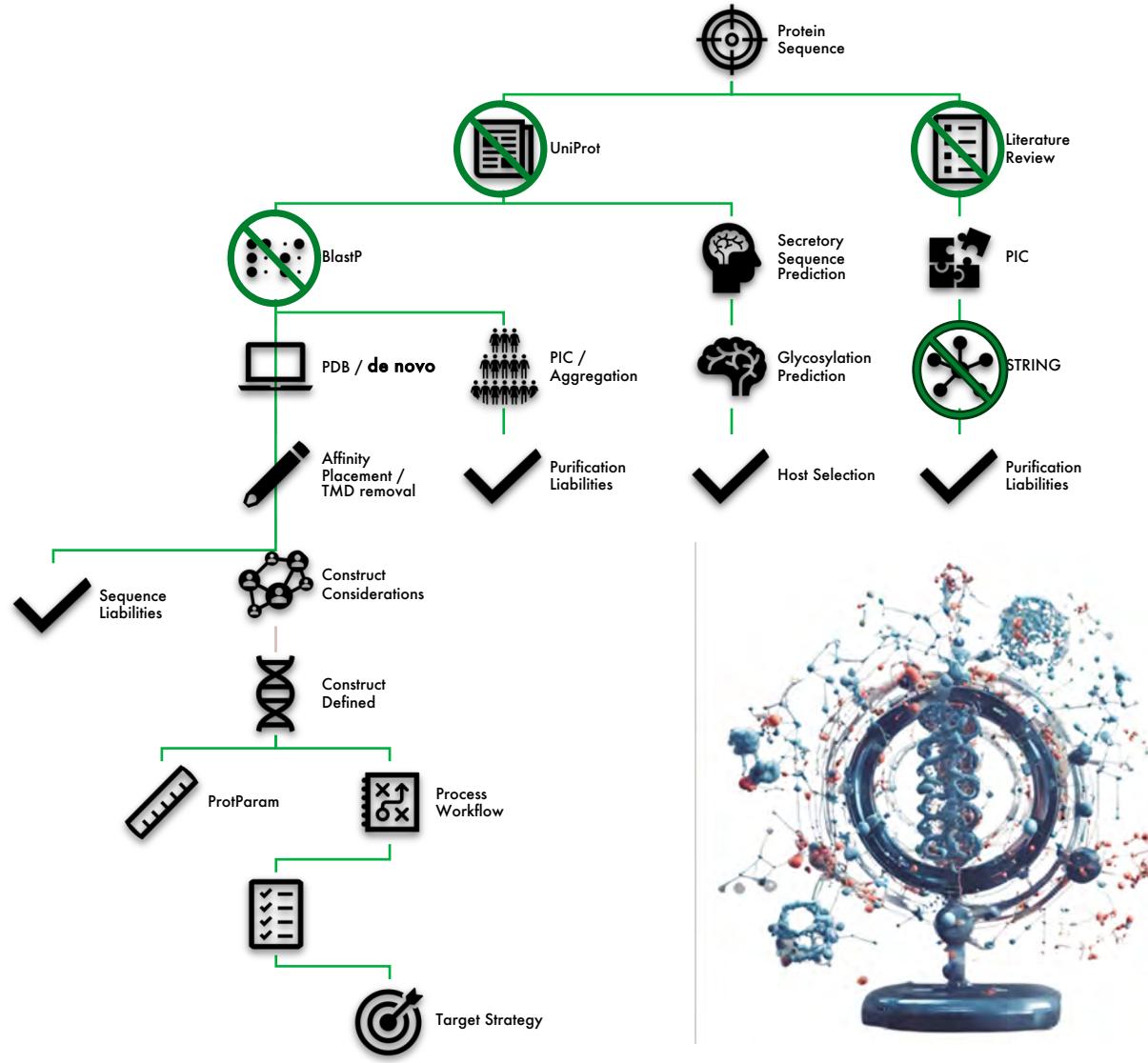
How do we approach the interstitial
space where data is missing??

How do we develop processes for
hallucinations? How do we detect
hallucinations?

ML: Understanding Nodes to Gain Insight into the Unknown

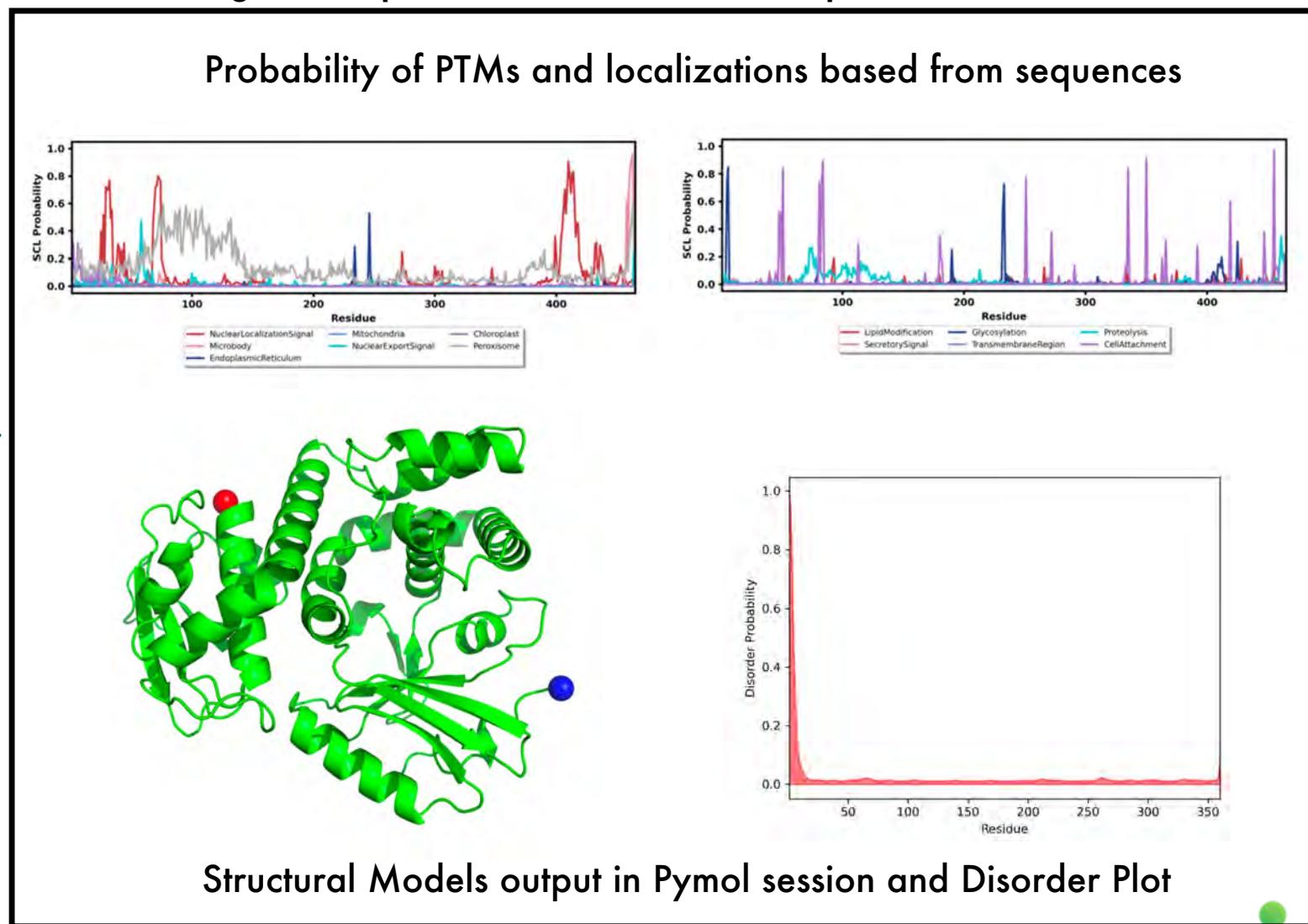
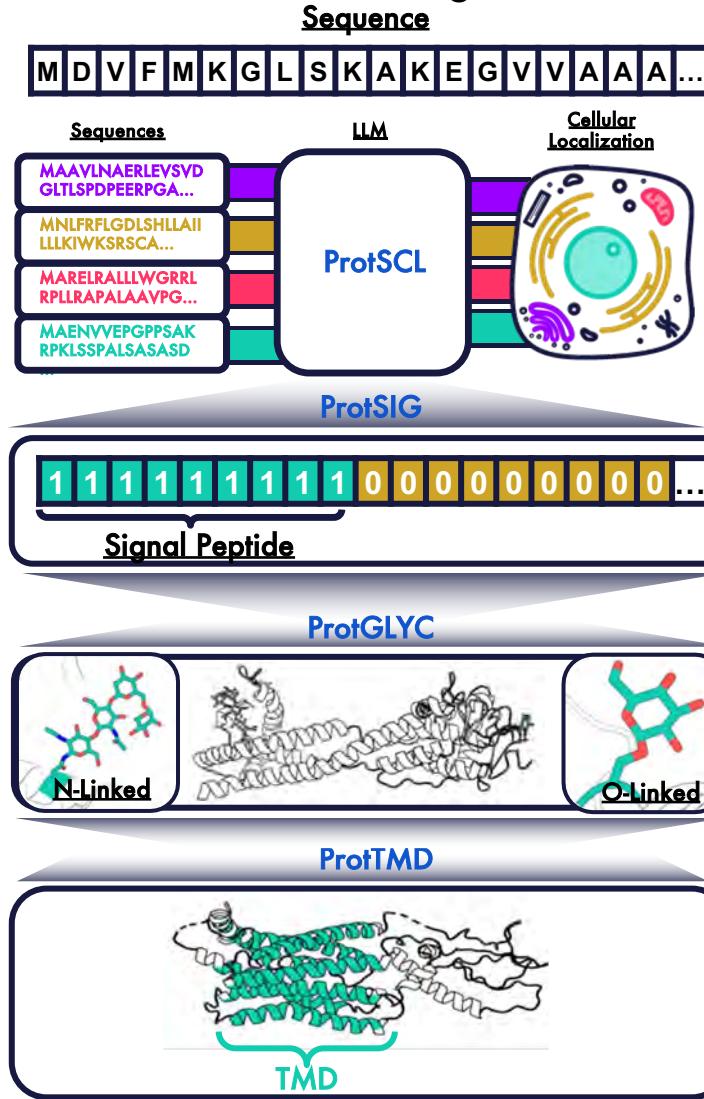


Sequence
ML Tools
Structural Modeling
Disorder Prediction
Feasibility Score

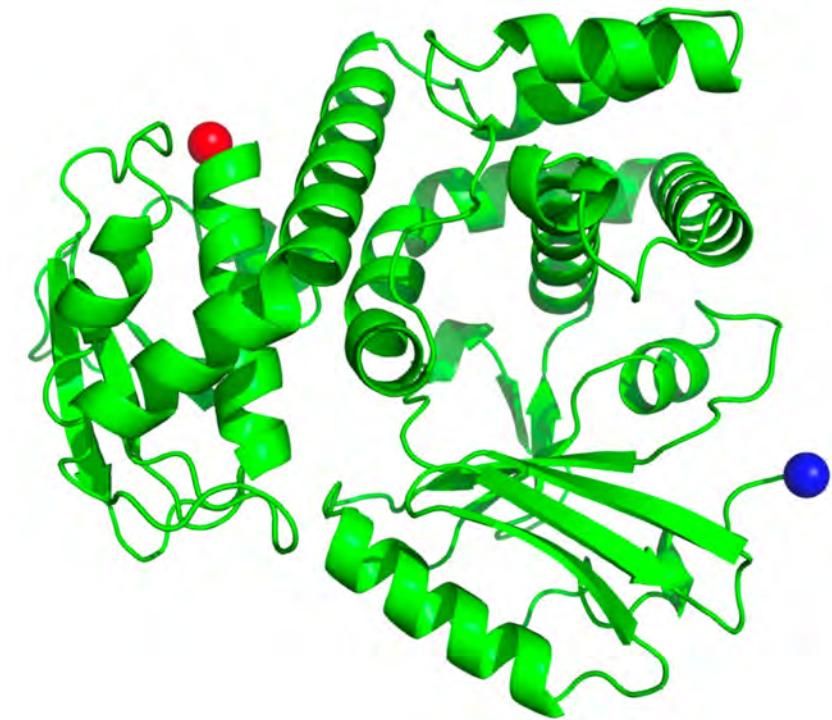
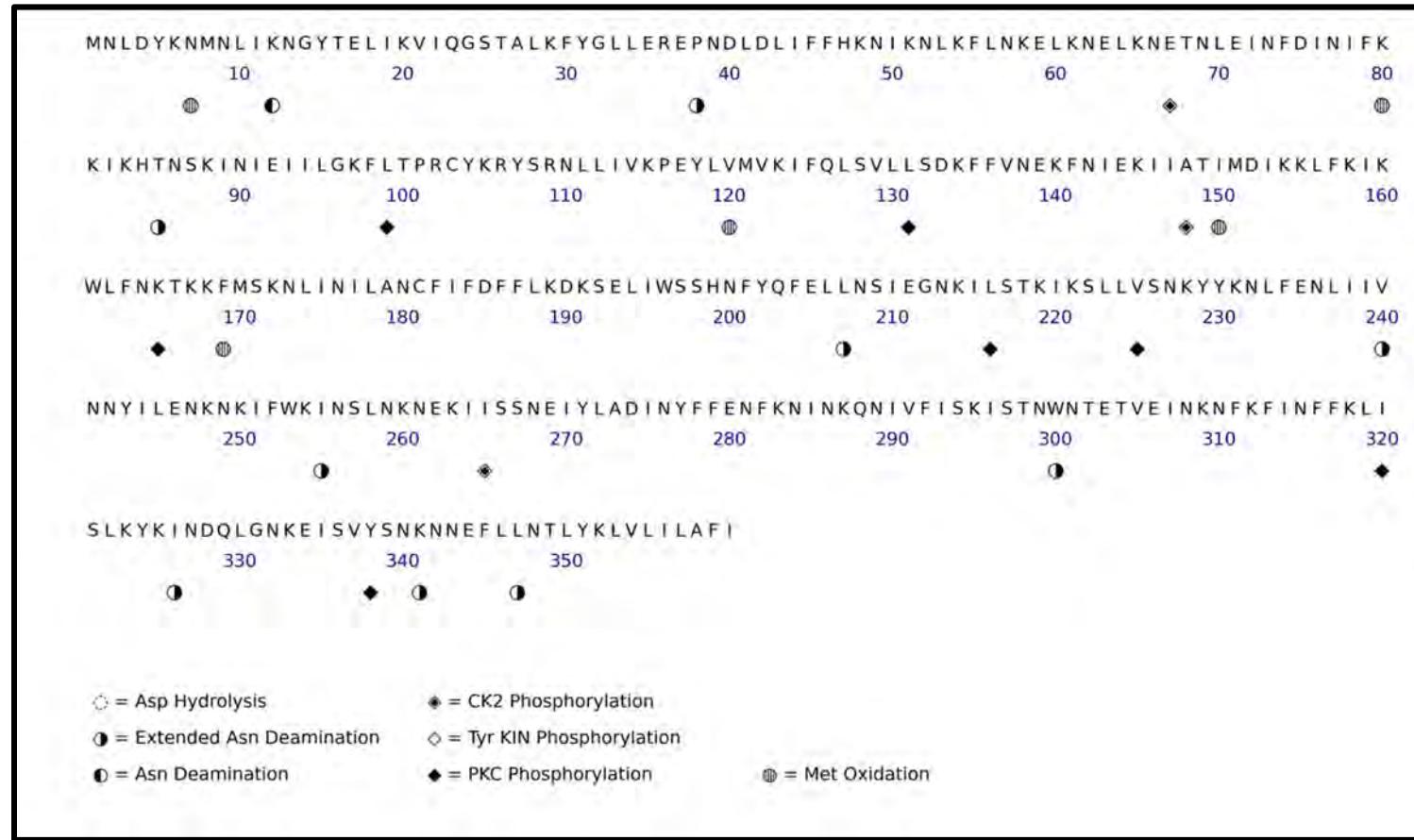


PROTiQSM: Novel Generalizable ML Tools

Machine Learning based Bioinformatic Tools designed to predict features from sequence alone



PROTiQSM: Sequence Liabilities Prediction

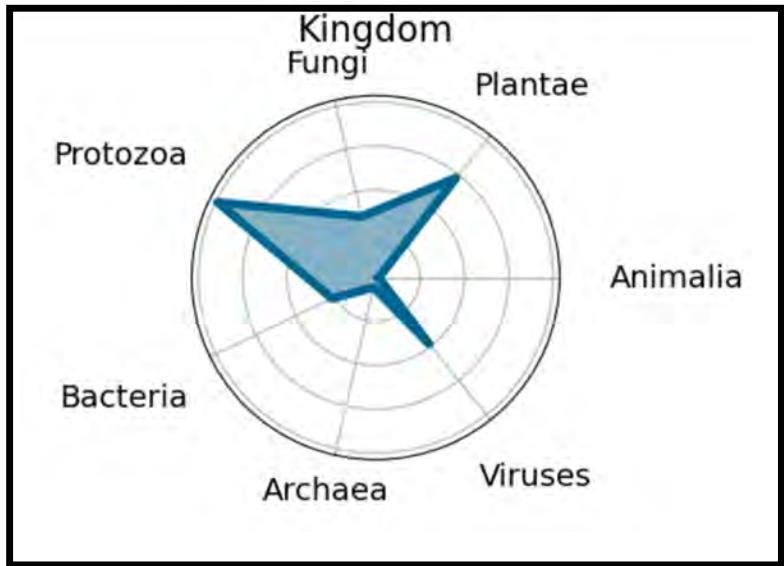


RoseTTAFold Model + Gromacs Energy Minimization

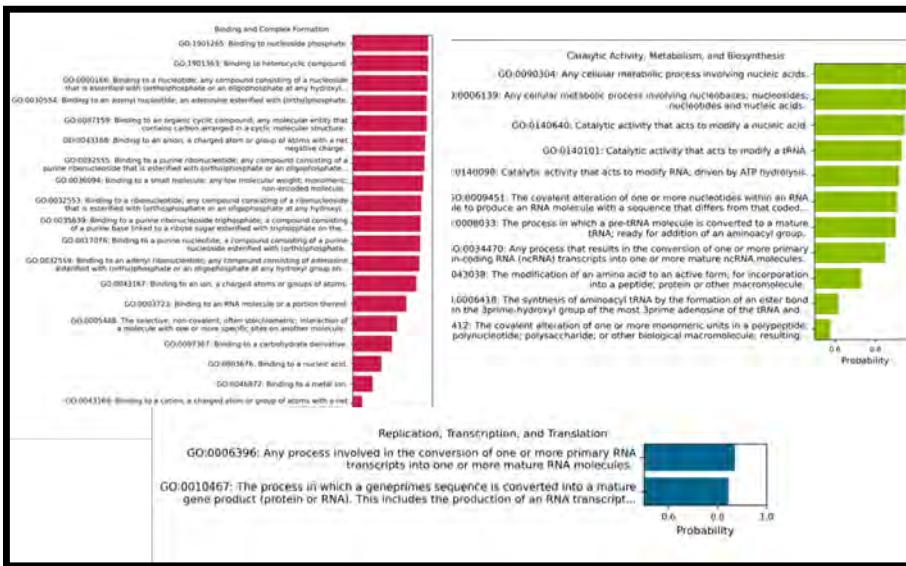
The sequence is processed through the generalizable ML tools to identify and sequences liabilities as a function of recombinant expression host. Not shown here are proteolytic liabilities as a function of recombinant host

PROTiQSM: FAUNA

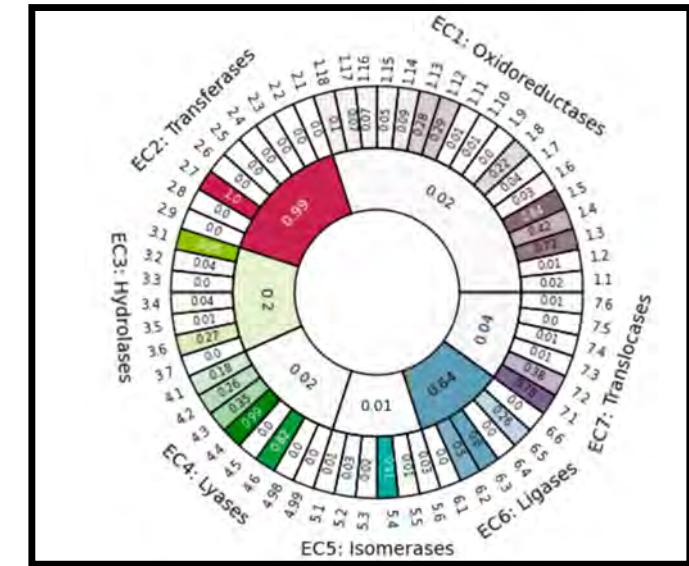
Kingdom Prediction & GO / Enzyme Classifiers



ProtFAUNA Kingdom -
assigns probabilities that a given
sequence belongs to a Kingdom



ProtFAUNA GO -
assigns probabilities that a given
sequence satisfies GO terms



ProtFAUNA EC -
assigns probabilities that a
given sequence belongs to
an Enzyme Commission

PROTiQSM: FAUNA Report



Report Date: 22 March 2024

Client: FNL – Alpha-Twist and Beta-Turns

Client Contact: Carter A. Mitchell

About ProtIQSM
Decades of research enabled the creation of extensive databases that provide a foundation for our work. We have localized this information to combine this knowledge with expertise from our own experts, providing our clients with a cutting edge system for designing proteins that may face challenges during initial protein development. This system ProtIQSM, provides a report document between Client and Kemp Proteins regarding a Protein Development.

Following initial discussions and review of the data provided by ProtIQSM, our client Services Agreement as part of the project initiation and expression of the protein sequence.

Kemp Proteins
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240-629-8924

ProtIQSM is owned and trademarked by Kemp Proteins. It was built in strategic Licensing and AI consulting opportunities exist for ProtIQSM, contact us if you would like to learn more.

The information in this report is for research purposes only and it is understood by the reader that Kemp Proteins makes no representation or warranty, either express or implied, as to the suitability of the protein sequences generated, nor does Kemp Proteins guarantee specific results. All content on this report is the property of Kemp Proteins until such time that a client enters into commercial arrangements for rights to the information contained in this report agree to indemnify and hold harmless Kemp Proteins from use of the information contained in this report.

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Data input into a LLM Summarizer:

FAUNA EC Final Analysis:

"... the evidence isn't strong enough to confidently classify any section of this sequence as part of an enzymatic domain based on the traditional threshold."

FAUNA GO Final Analysis:

"... the protein seems to be crucial for RNA metabolism and protein synthesis, likely localizing to the cytoplasm or specific organelles like the mitochondria where these processes occur."

FAUNA Host Suggestion: Choice of Organism

- *E. coli*, *Saccharomyces cerevisiae*, and *Pichia pastoris* might be preferred due to simple PTM patterns and potentially lower maintenance costs. –

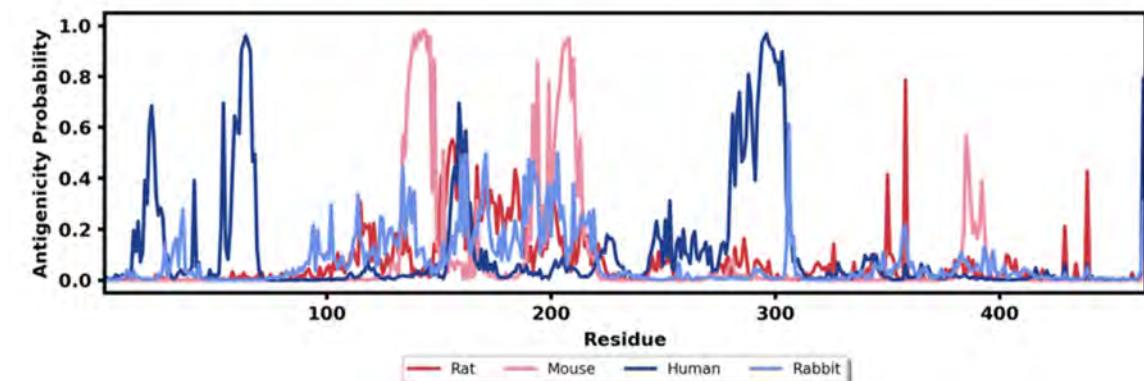
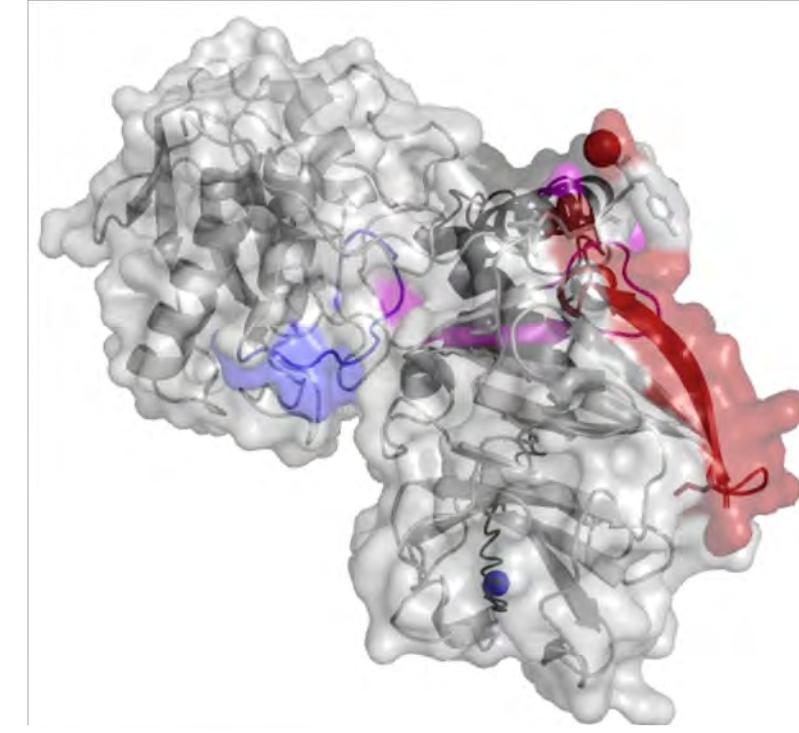


PROTiQSM: Antigenicity Scoring Function

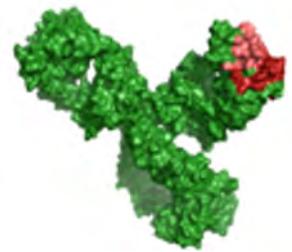
The Antigenicity Score is generated from analysis of known interactions taken from the literature and curated databases that include structural information when available.

Current rules include:

- >10 residues < 40 residues
- Sequence Identity $\geq 55\%$; Similarity $\geq 65\%$
- Solvent accessible, noninteraction regions
- Identification of preferred immunization animal as a function of sequence homology including
 - 1) Mouse
 - 2) Rat
 - 3) Human
 - 4) Rabbit
 - 5) Camelid



Antibody Expression at Kemp in Various Platforms



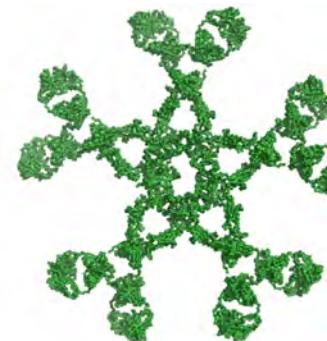
- Full-Length mAB
 - Grafted
 - Isotype Switching
 - Variables provided



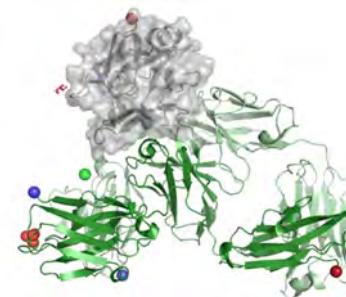
- VHH
 - Bacterial
 - Mammalian



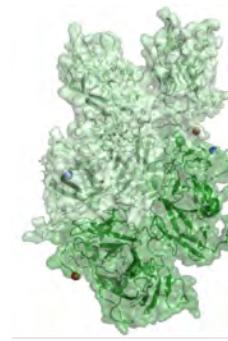
- scFv
 - Bacterial
 - Mammalian
 - Refolded if needed



- IgM
 - Pentameric
 - Hexameric



- BiS
 - KiH
 - Reductive Pairing
 - Common Light
 - DVD-IgG, Charge Repulsion
 - Cross mAB, etc

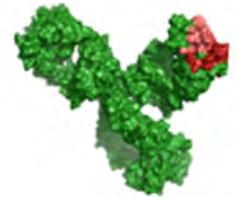


- Fc-Fusion
 - Common engineering mode

Proteins Expressed at Kemp in Various Platforms

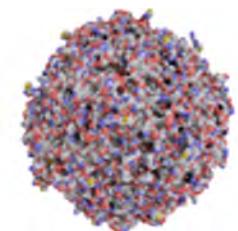
- **Antibody Class of Molecule**

- Full-Length - AB Fragments
- Multi-specific Antibodies
- Nanobodies – VHH & scFv
- IgM



- **Virus Related Proteins and Particles**

- Viral Glycoproteins
- Virus-Like Particles
- Nanoparticles



- **Multi-protein Complexes**

- E3 ligases with targets

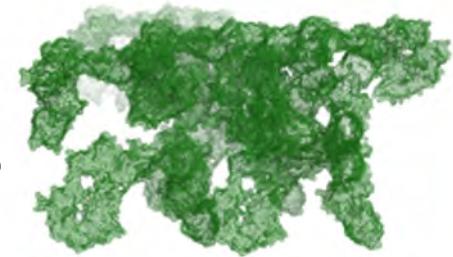
- **Toxins**

- Ricin, Botox, CtXB



- **Membrane Proteins**

- GPCRs
- Extracellular Domains
- Soluble TM mutants



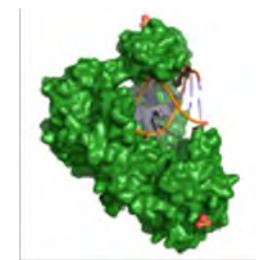
- **Immunologic Proteins / Hormones**

- Hormones
- Interleukins
 - IL27, IL23, IL13, IL15



- **Enzymes**

- DNA pol
- Methyltransferases

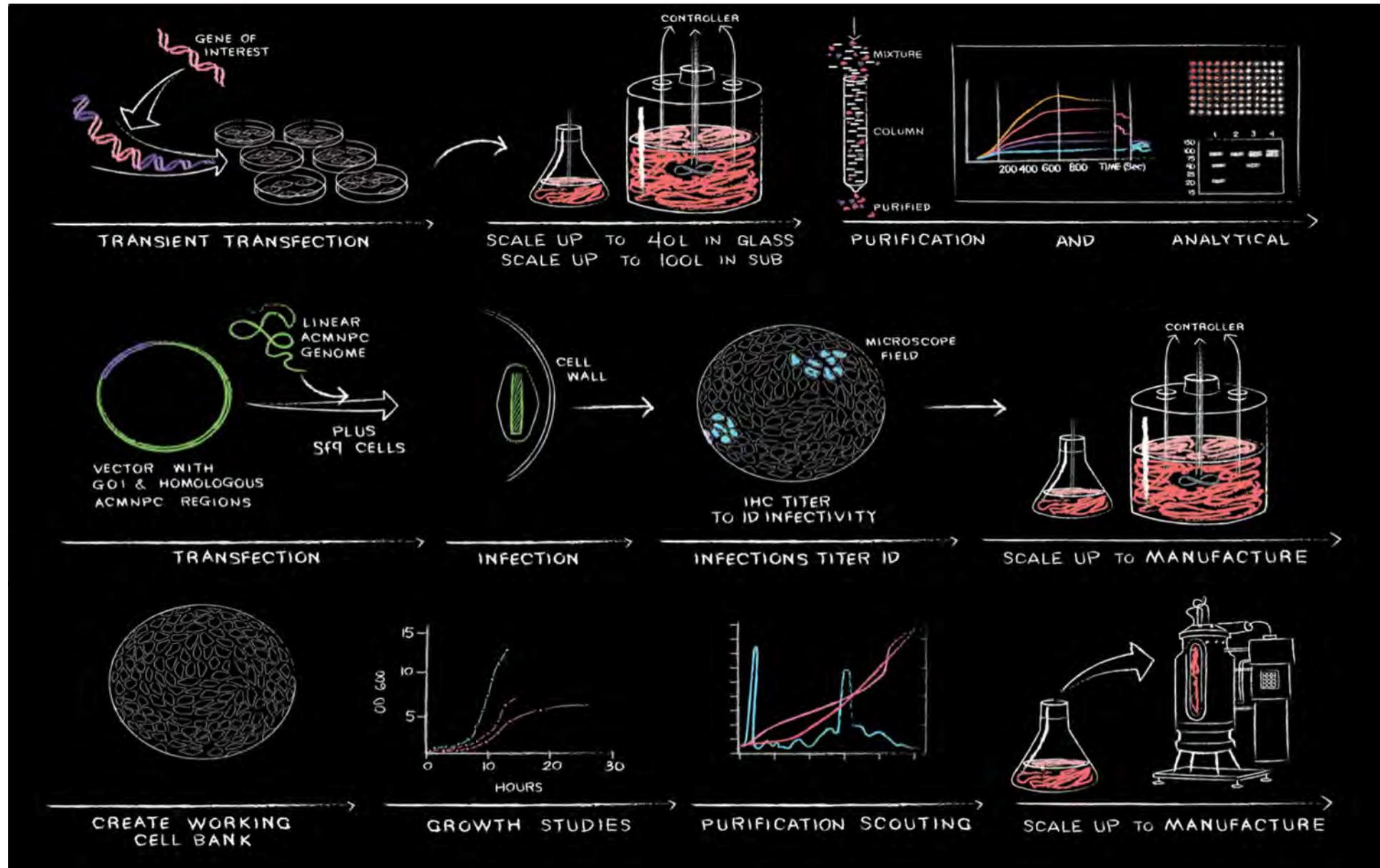


- **Cytoskeletal Elements**

- Dystrophin SILAC / unlabeled¹

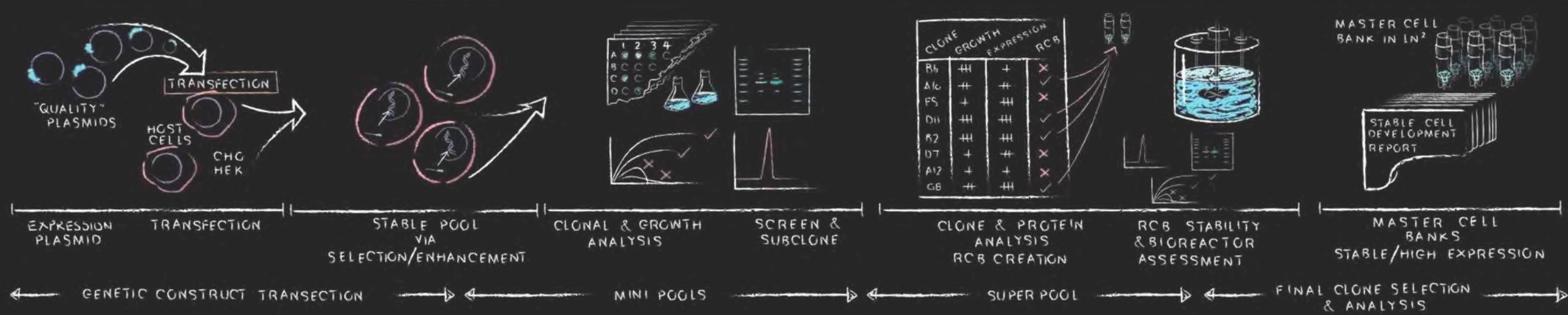
Flexibility is Critical - all expression systems assessed

Mammalian:
0.5 mL - 100L
HEK, CHO
PEI & BacMam
96 x 50 mL



Plants in 2024*

Solutions for Cell Line Development



- **Integration Mode**

- IP and License Flexibility
 - Linear random integration
 - Client Requested Modes

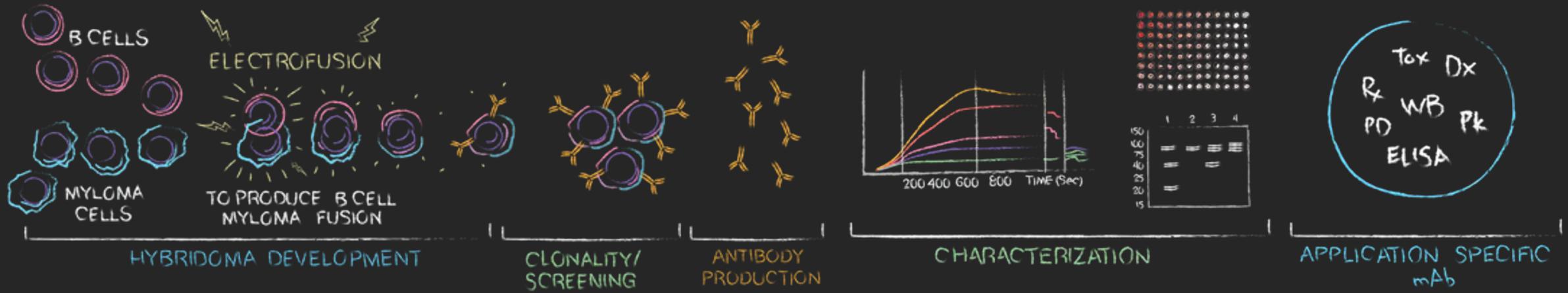
- **Expression Host w/ Random Integration**

- CHO, HEK, NS0, S2, Yeast

- **Equipment**

- ClonePIX and CloneSelect Imager
- Celigo High Content Imager
- BLI for Titer Assessment
- Flex2 Bioprofile
- Full Suite of Analytical Equipment

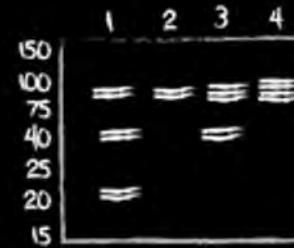
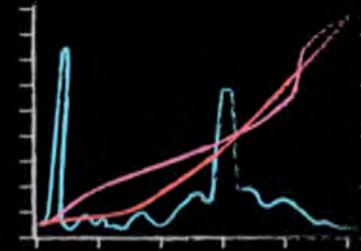
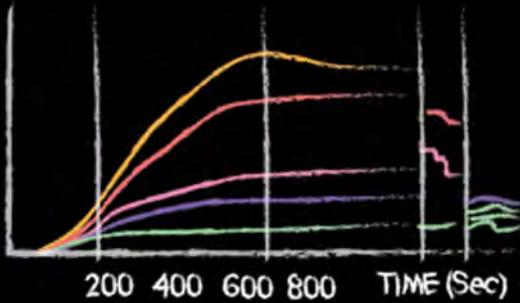
Hybridoma Development and Screening



Internal antigen production decreases TAT and increases success

- **Type of Molecule**
 - mAB, Anti-ID, ADA
 - Tx / Dx, Molecular Tool, & Release
- **Immunization Strategies**
 - Proteinaceous / Peptide
 - Particle / Cell-Based
 - DNA – gene gun
- **Recombinant Conversion**
 - Isotype switching
 - Species grafting
 - Fab and Fab2' generation
 - Gain control over your critical reagents
 - Process Development and Manufacturing

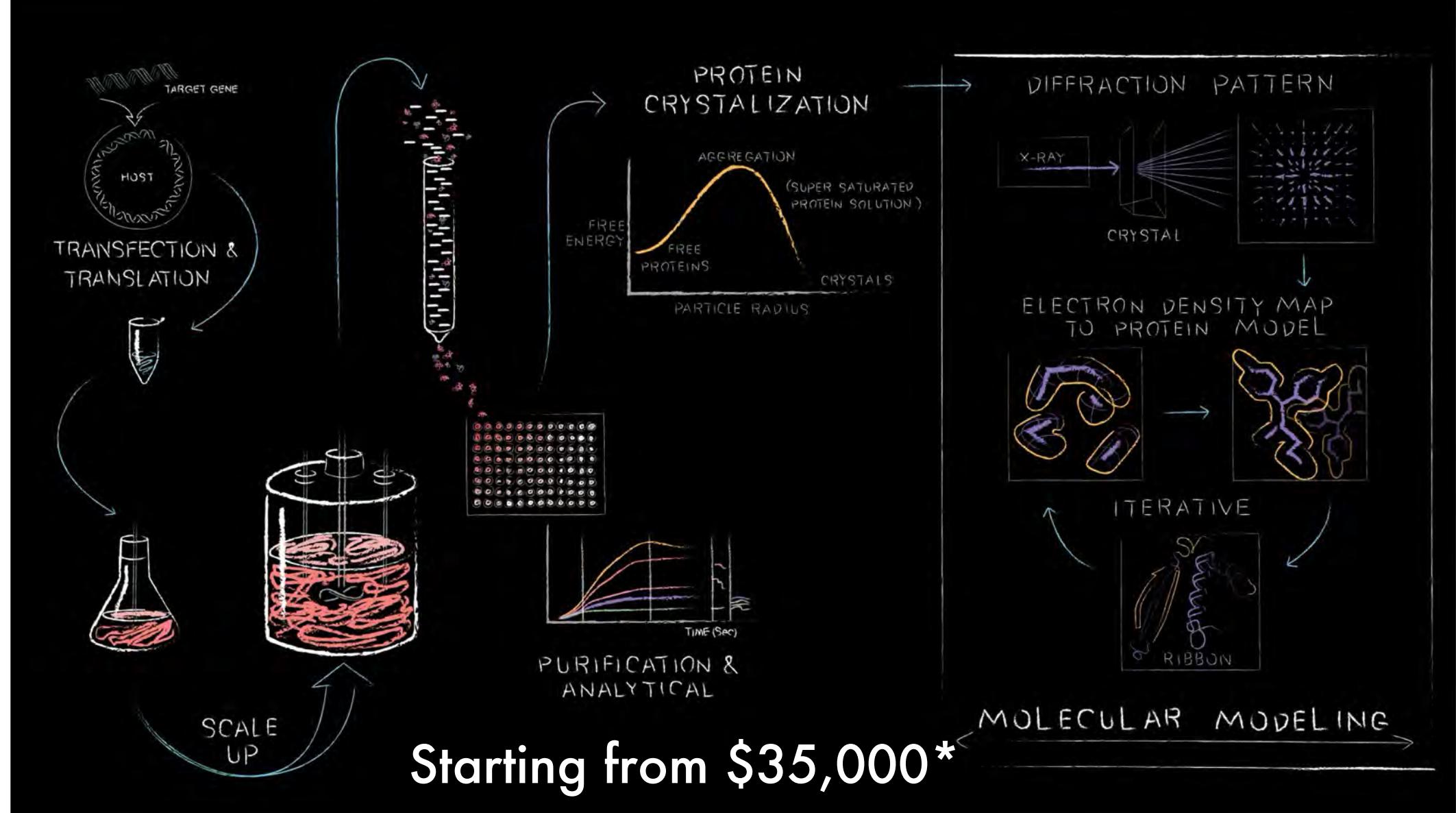
Analytical Services



- Affinity Characterization (SPR/BLI)
 - Relative affinity
 - Matched pair confirmation
 - Binning and k_{off} rates via Octet
- Assays
 - ELISA Standard or Development
 - Western Blot
 - Stability Assays (Non-GLP)
 - Enzymatic assays
 - BioBurden USP <61>
 - Sterility USP <71>
 - Osmolality USP <785>
 - Endotoxin <85> CapeCod and EndoSafe
 - HCP and HCD
- Biochemical Characterization
 - aSEC & SEC-MALS
 - TEM / SEM*
 - DLS
 - DSF
 - aHIC, aIEX, & RP-HPLC
- Mass-Spec Services*
 - Protein ID
 - Intact Mass Protein Analysis
 - Post-Translational Modifications
 - *De novo* Sequencing
- Sequencing*
 - Hybridoma Sequencing

*Local third party preferred provider for quick TAT with internalization plans in the future

Kemp & HWI Now Offering Gene to Structure Services



Rapid Small Scale Expression & Purification

DNA Synthesis

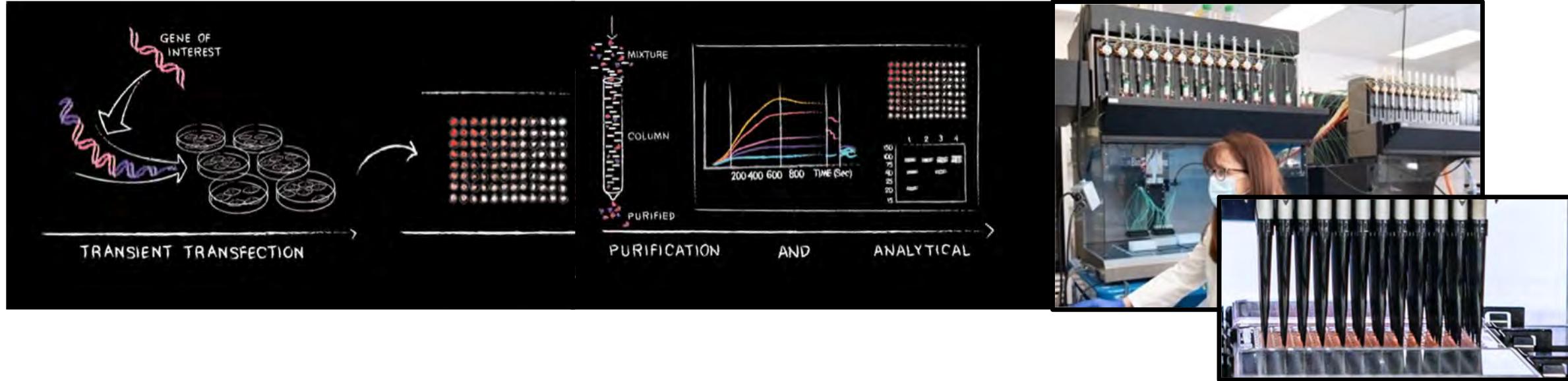
Plasmid

Expression

Purification

QC

QA



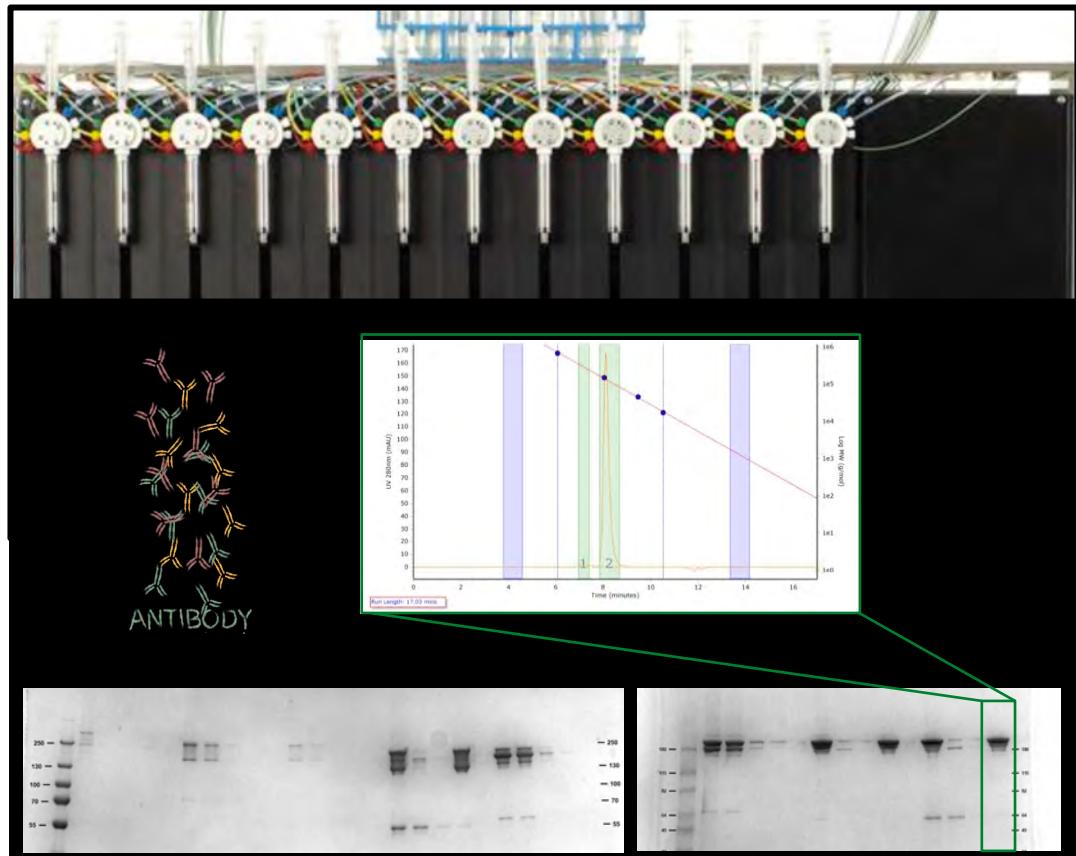
ML Derived Sequence Assessment

- 24–96 purifications from 0.5 mL - >1L
- Flexible expression & purification modalities
- Quick TAT ~15-20 days to get 100's protein variants and associated data (plasmids provided)

Final Deliverables:

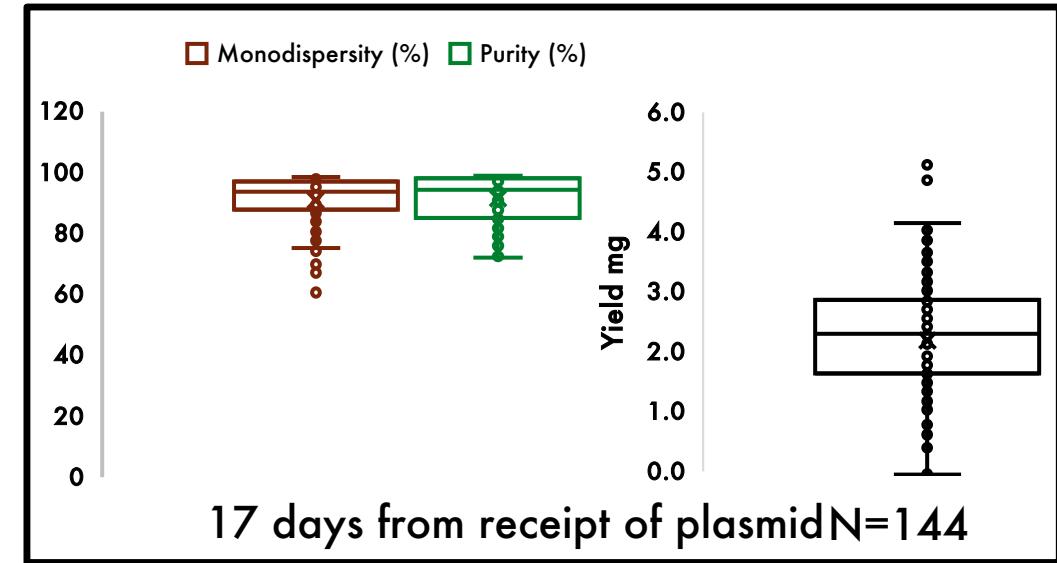
- Go / No-Go on Constructs
- Customizable QC packages to feed into ML models
- ng to >100 mg of purified protein buffer exchanged

CASE STUDY: 144 Multispecifics



ML Derived Sequence Assessment

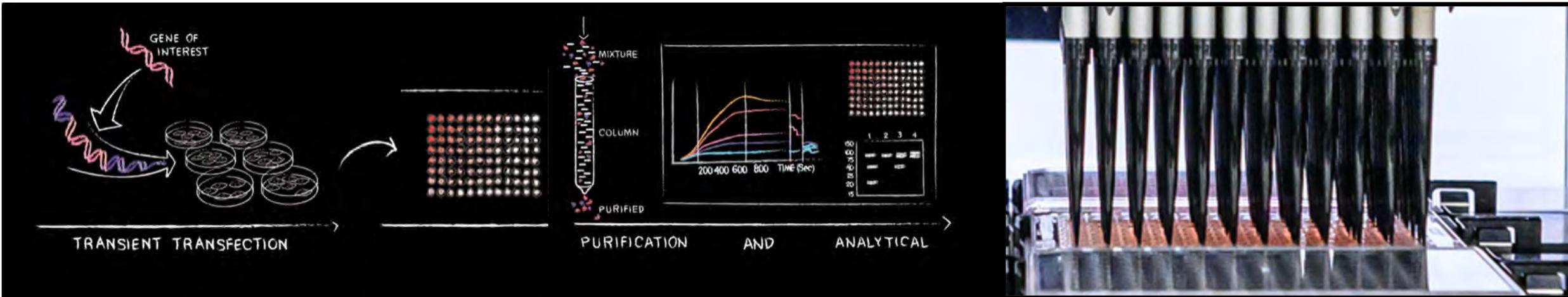
- 144 expressions in CHO system
- Scalable Affinity Capture
- 17 day TAT (DNA Provided)



Developability and Lead Identification:

- Identified:
 - Hc point mutations affecting DSP.
 - Lc sequences that decreased titer
- Results used to dev the next round

Test Case: 377 ML Derived mAB



Average	0.196
STDEV	0.11
MIN	0.020
MAX	0.927
Sample Size	377

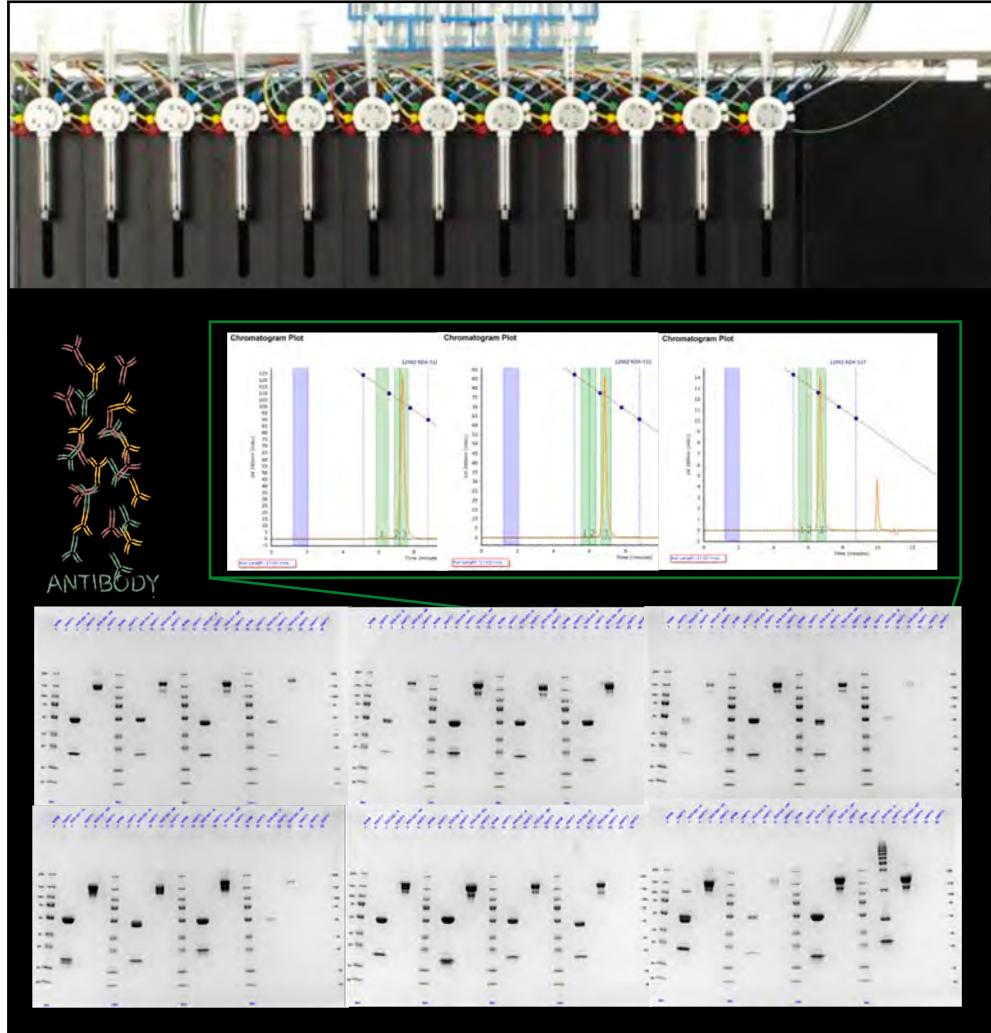
ML Derived Sequence Assessment

- ~220 sequences ordered
- 4 weeks for plasmid
- 4 weeks for expression, purification, QC, Shipping

Final Deliverables:

- Protein in 4 replicate plates
- aSEC, Spectrophotometry, DLS, and SDS-PAGE

CASE STUDY: 48 Rabbit mAB Dx



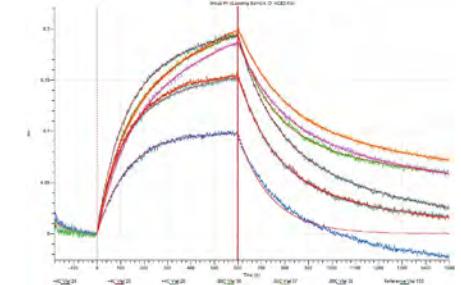
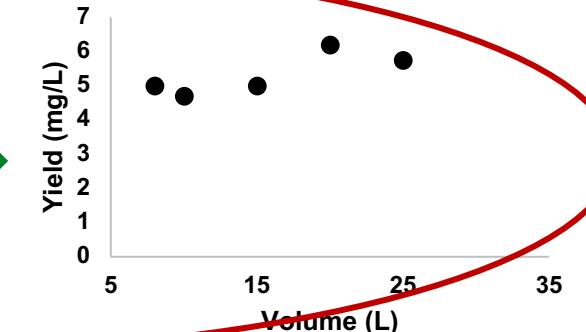
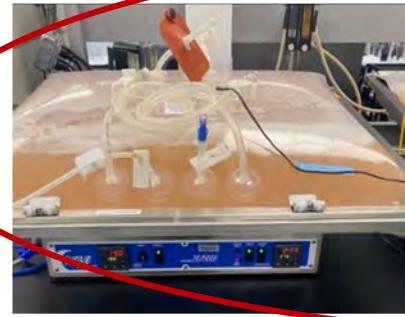
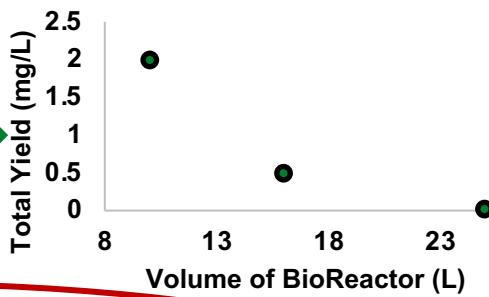
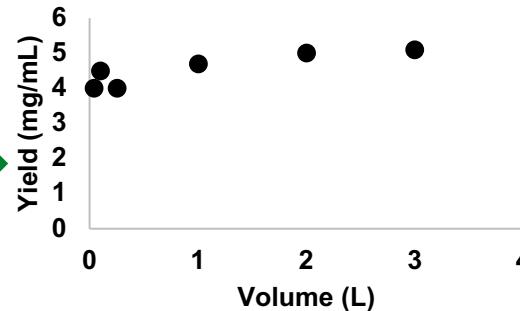
	Volume Shipped (mL)	Yield Shipped (mg)	Initial Volume (mL)	Conc. (mg/mL)	Initial Yield (mg)	% Agg	% Monomer	% Purity
Average	7.31	5.53	7.93	0.76	6.00	3.46	92.97	94.93
STDEV	0.12	4.89	0.00	0.67	5.30	4.51	8.28	6.05
min	7.00	0.23	7.93	0.03	0.24	0.00	66.58	64.60
max	7.50	19.03	7.93	2.61	20.66	21.66	99.84	98.00

Rabbit mAB Down selection Campaign

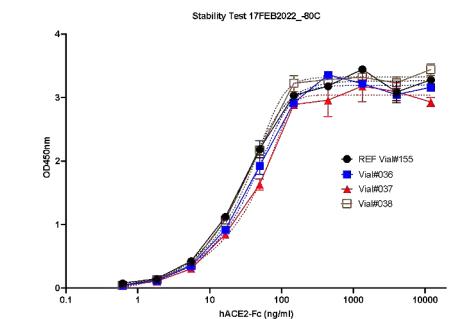
- 48 mAB with 2 plasmid pairs
- 200 mL expression in client qualified HEK293
- Expression, Purification, QC, and Ship 24 days
- Materials provided to client for down selection
- Final scale 1G from start to finish 3.5 month

Case Study: Scale Up of the Upstream Process

Sf9-Derived Process to hit gram scale



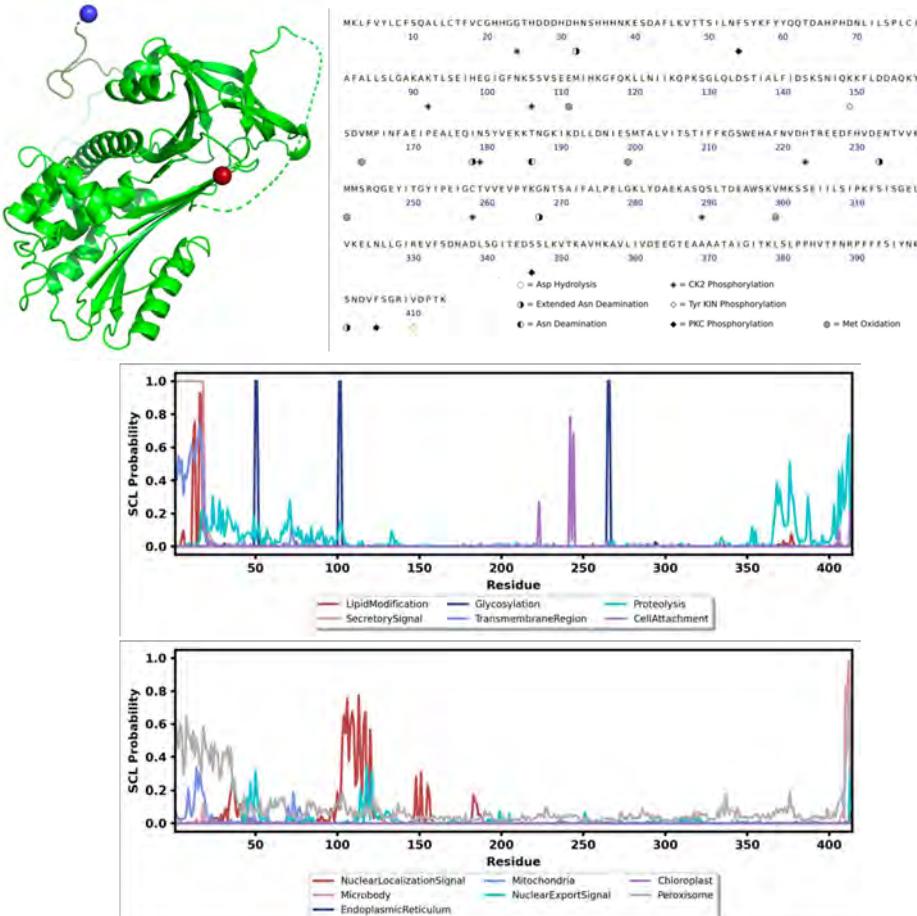
BLI: $K_d = 22.125 \text{ nM}$



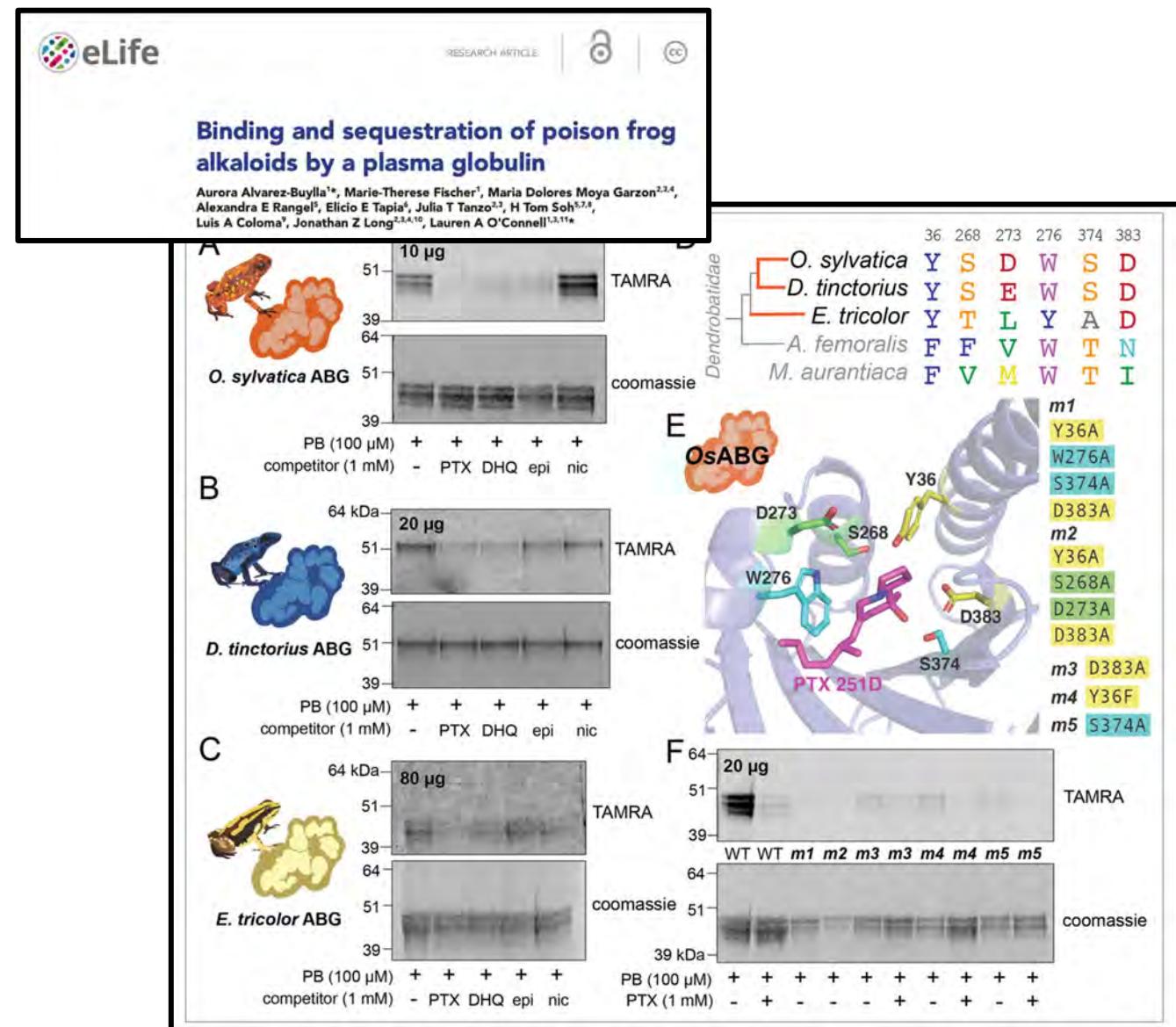
ELISA: $K_d = 32.127 \text{ nM}$

Case Study: Killer Frogs

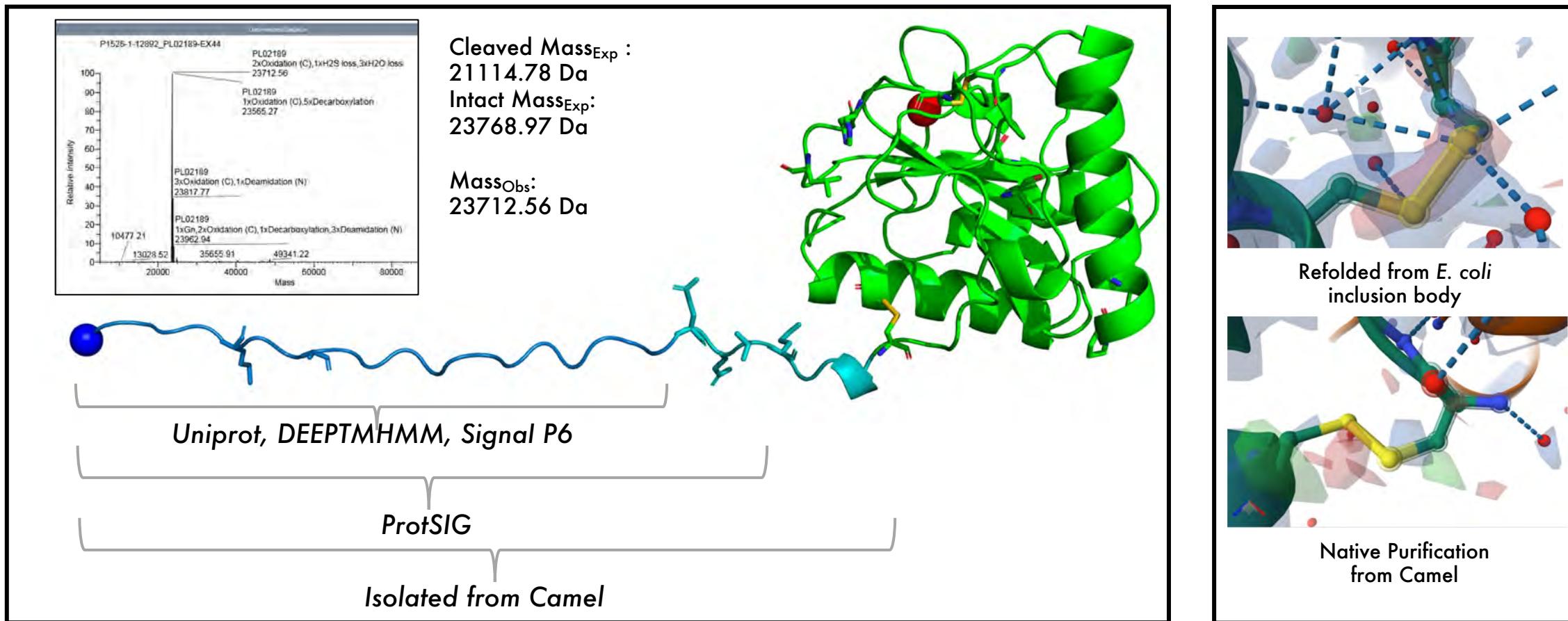
ML Based Bioinformatic Tools:
Secreted insect expression with predicted glycosylation



Structural Search returned <42% identity

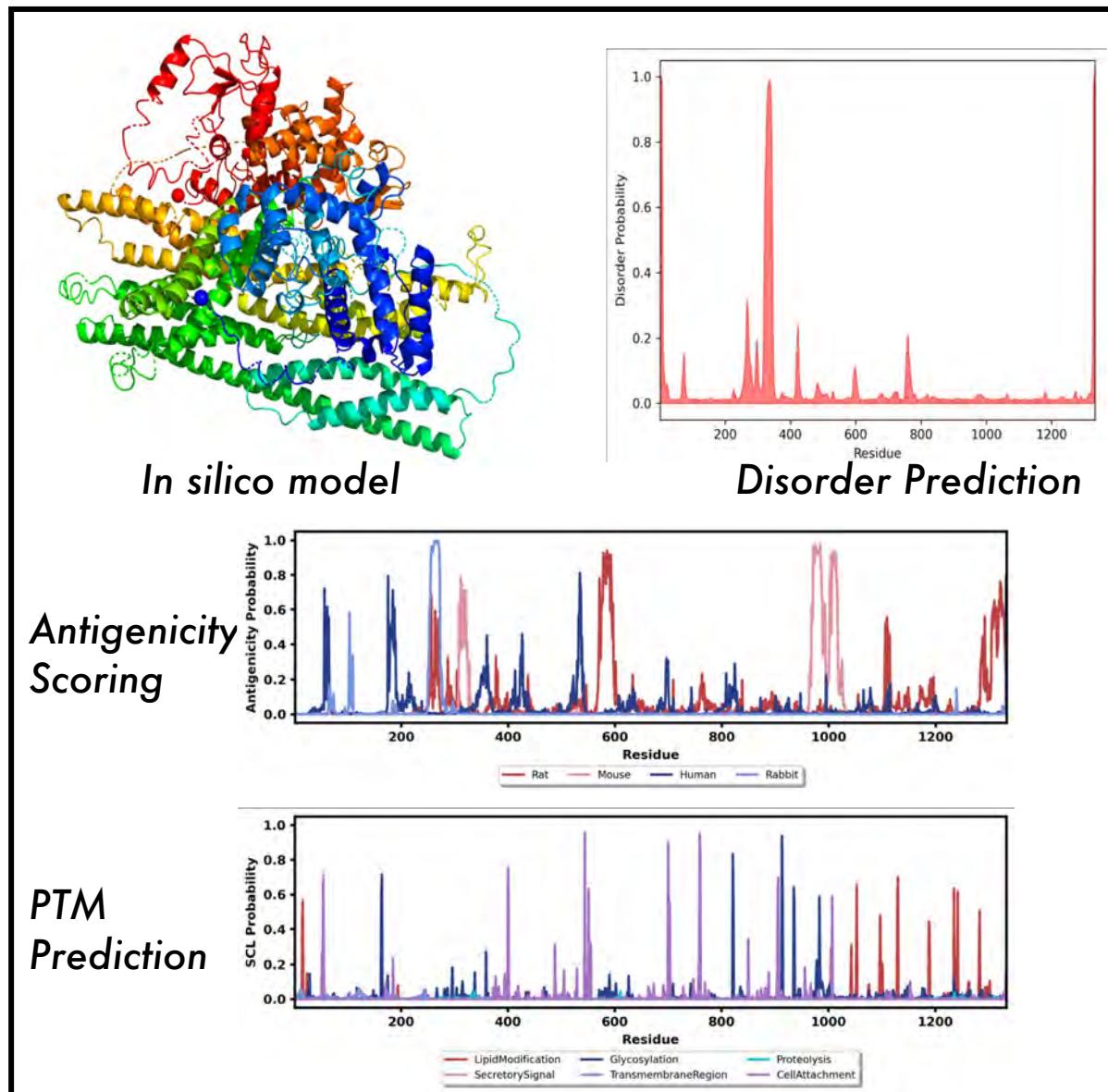


Case Study: Curious Targeting Sequence



- Characterized protein involved in immune response was analyzed through various means.
- Discrepancies with the secretory sequence between literature, predictions, and crystal structures.
- Native expression in HEK293 resulted in 100% intact protein – NO CLEavage of SS.
- Experiments currently underway to learn how to better predict these liabilities in the future.

Case Study: Critical Reagent of Notorious BIG



The AAPS Journal (2023) 25:12
https://doi.org/10.1208/s12248-022-00776-0

RESEARCH ARTICLE

Development and Validation of a Western Blot Method to Quantify Mini-Dystrophin in Human Skeletal Muscle Biopsies

Catherine I. Soderstrom¹ · Jennifer Larsen¹ · Carolina Owen¹ · David Gifondorwa² · David Beidler³ · Florence H. Yong⁴ · Patricia Conrad¹ · Hendrik Neubert⁵ · Steven A. Moore⁶ · Mohamed Hassanein³

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The AAPS Journal (2023) 25:12

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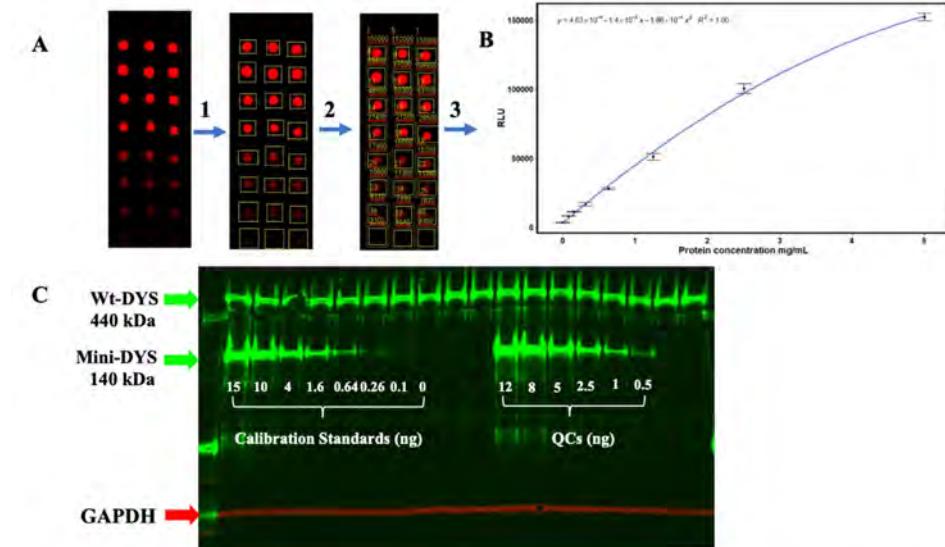


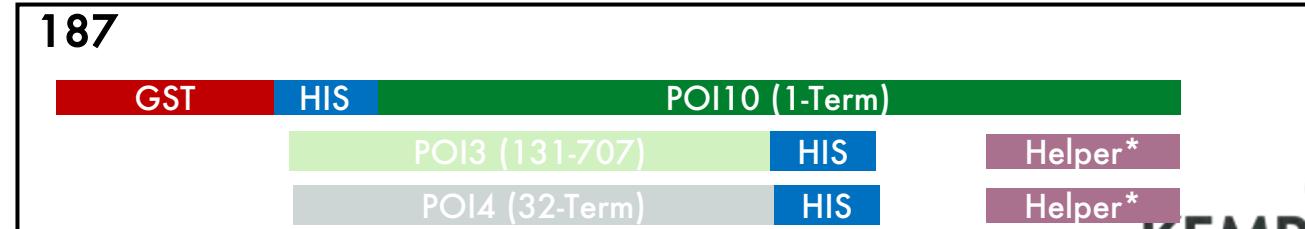
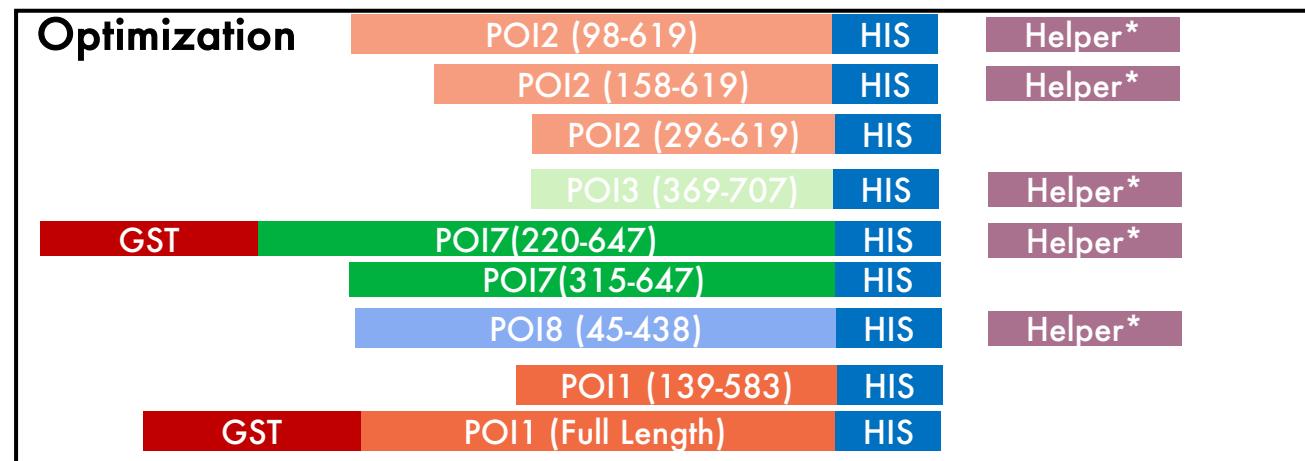
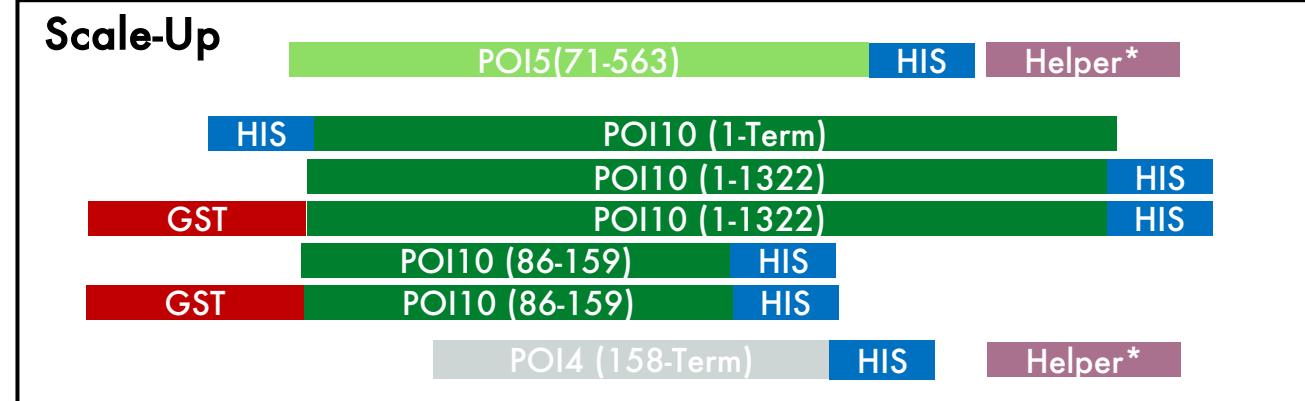
Fig. 1 Quantitation of dystrophin using mini-dystrophin STD curve. A representative scheme of a validation run. **A** Image acquisition and quantitation of total protein from tissue extracts using dot-blot followed by **B** construction of standard curve. **C** An image of a WB

gel showing the wt-DYS, mini-DYS standard curve, quality controls (QCs) detected through the green fluorescent channel (800 nm), and protein normalization with GAPDH using the 700 nm channel (in red) is shown

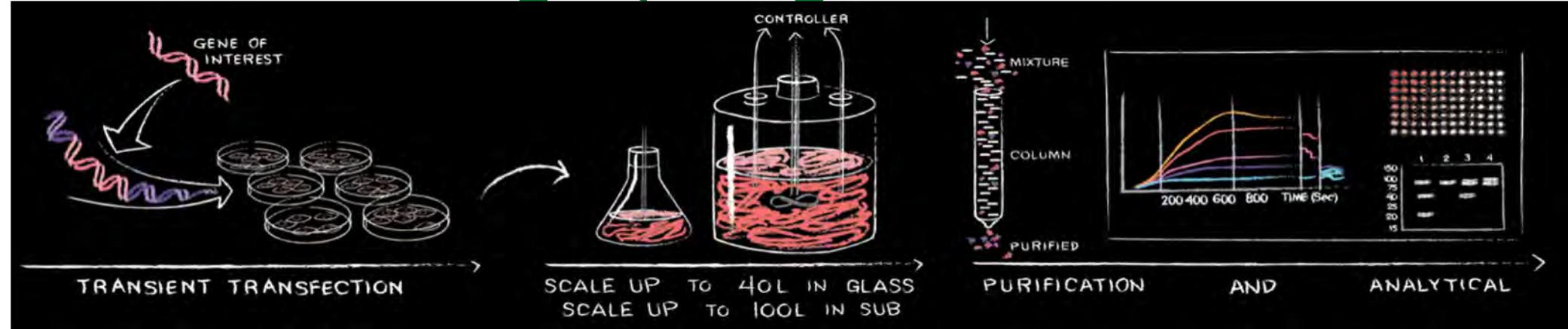
Case Study: Insect Expression of Critical Targets

Selection, Optimization, Scale, and ...

Insert	POI in Eluate	Expected MW
POI5(71-563)-His6; Helper*	Yes	56.2 kDa + 19.1 kDa
GST-3c-POI7(220-647)-His6; Helper*	Maybe	76.1 kDa + 19.1 kDa
POI7(315-647)-His6	Low	38.2 kDa
His6-POI10	Yes	254.8 kDa
His6-GST-3c-POI10	No	281.6 kDa
POI10(1-1322)-His6	Yes	150.9 kDa
GST-3c-POI10(1-1322)-His6	Yes	177.6 kDa
POI10(86-159)-His6	Yes	9.1 kDa
GST-3c-POI10(86-159)-His6	Yes	35.8 kDa
Insert	POI in Eluate	Expected MW
POI1(139-583)-His6	In FT	49.6 kDa
POI2(98-619)-His6; Helper*	Low	58.5 kDa + 19.1 kDa
POI2(158-619)-His6; Helper*	Yes Degrade?	51.7 kDa + 19.1 kDa
POI8(45-438)-His6; Helper*	Low SOL	45.7 kDa + 19.1 kDa
Insert	POI in Eluate	Expected MW
GST-3c-POI1-HIS6; Helper*	Low Yield	98.6 kDa + 19.1 kDa
POI2(296-619)-His6	FT	36.4 kDa
POI3(131-707)-His6; Helper*	ND	65.9 kDa + 19.1 kDa
POI3(204-707)-His6; Helper*	FT	57.6 kDa + 19.1 kDa
POI3(369-707)-His6	Inef Cap	38.5 kDa
POI4(His32-C-term)-His6; Helper*	NO	65.2 kDa + 19.1 kDa
POI4(158-C-term)-His6	YES	31.6 kDa



Mammalian Antigen/Target Protein: Case Studies



Requests:

Construct design, synthesis and midi-scale production Single step affinity purification for three unrelated programs

Expression Host: HEK293

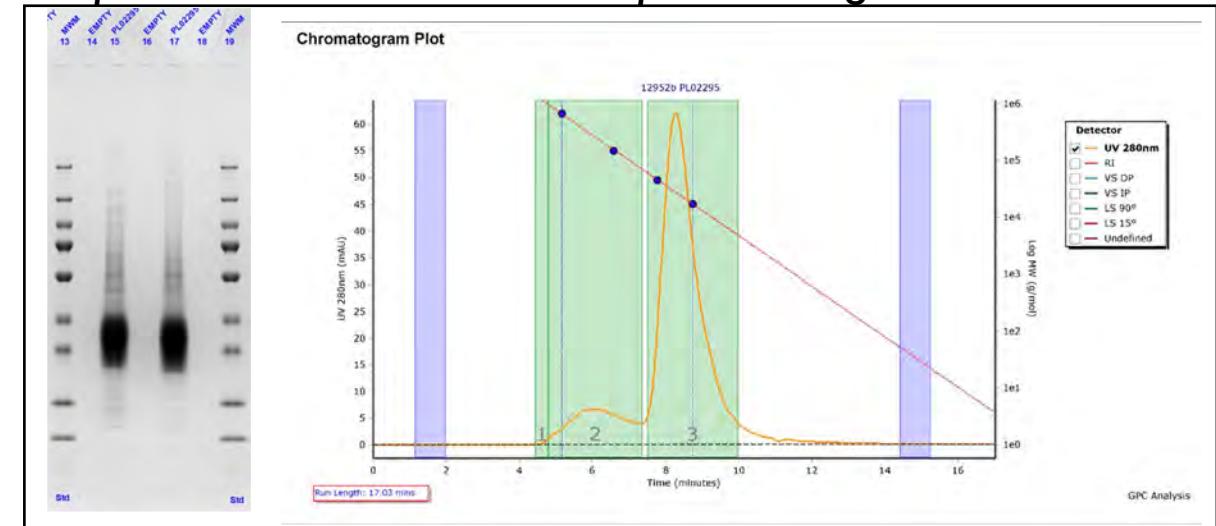
Scale: 30–100mL

of Proteins: 82

Request Period: Q1FY2024

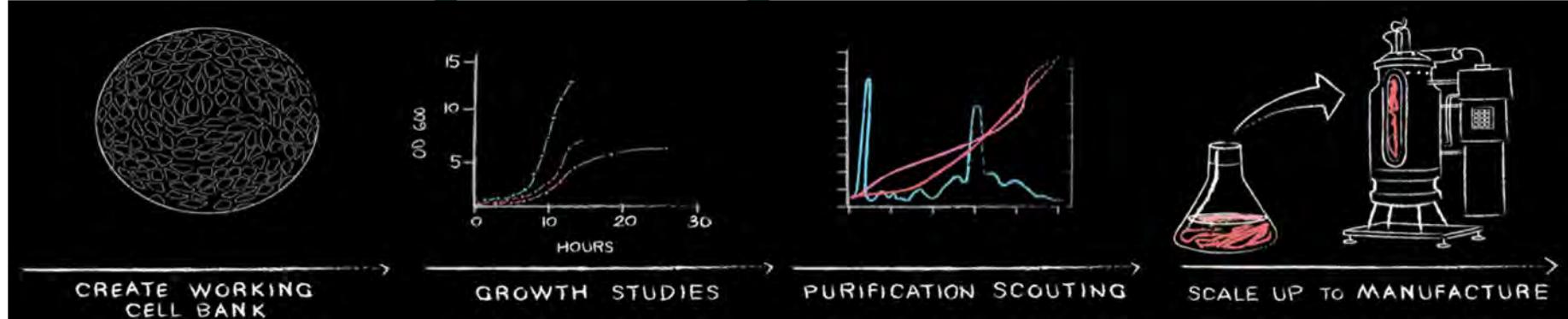
Protein Types: Antigens – Virus-derived

Representative data from one protein target



	Yield (mg)	Purity %	Agg%	TAT (Days)
Average	1.84	74.69	5.54	66.71
STDEV	1.77	35.36	5.00	24.45
Total Number				82.00

Bacterial Antigen/Target Protein: Case Studies



Representative data from one protein target – Native Purification

Requests:

Construct design, synthesis and pilot-scale production Single step affinity purification for three unrelated programs “Get what you get”

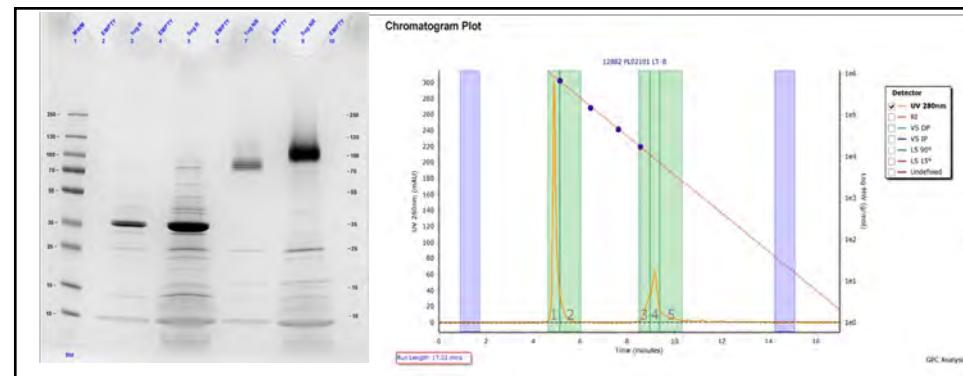
Expression Host: *E. coli*

Scale: 1 L

of Proteins: 7 unrelated proteins

Request Period: Q3FY2023

Protein Types: Potential Antigens – Microbial derived; unstudied and no prior literature



Target	Yield (mg)	Purity %	Aggregation %
1	5.24 mg	56%	14%
2*	N/A	N/A	N/A
3	12.77 mg	82%	58.60%
4	0.05 mg	~50%	N/A
5	11.47 mg	72.20%	N/A
6	0.705	67.70%	N/A
7	10.17 mg	82.50%	65.65%

*No Expression

Microbial and Mammalian Target Assessment

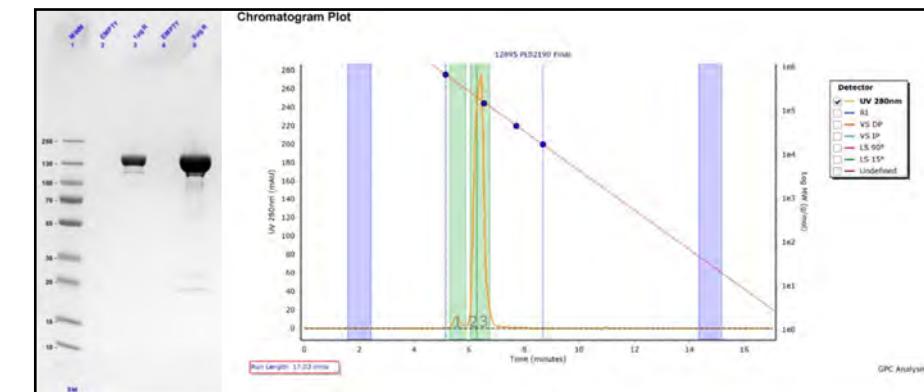


Requests:
 Construct design, synthesis and pilot-scale production Single step affinity purification for 6 unrelated programs
 Constructs have different affinity designs and formats to maximize the likelihood of success and decrease over all TAT.

Expression Host: E. coli & Mammalian
Scale: 1 L
of Proteins: 6 unrelated proteins
Request Period: Q3FY2023
Protein Types: Target proteins for C>

Representative data from one protein target

Plasmid IDs	Description	Exrepssion System	Yield (mg)	Purity	Agg%
PL02190	1044 AA Enzyme	Mammalian	30.68	>98%	3.71%
PL02194/PL02199	343 AA Enzyme	Mammalian	0.468	>90%	N/A
PL02195/PL02196	412 AA Enzyme	Mammalian	N/A	N/A	N/A
PL02193	343 AA Enzyme	E coli	N/A	N/A	N/A
PL02192/2191	433 AA Enzyme	Mammalian	0.802	76.60%	10.32
PL02195-PL02198	412 AA Enzyme	Mammalian	4.376	96.60%	12.78



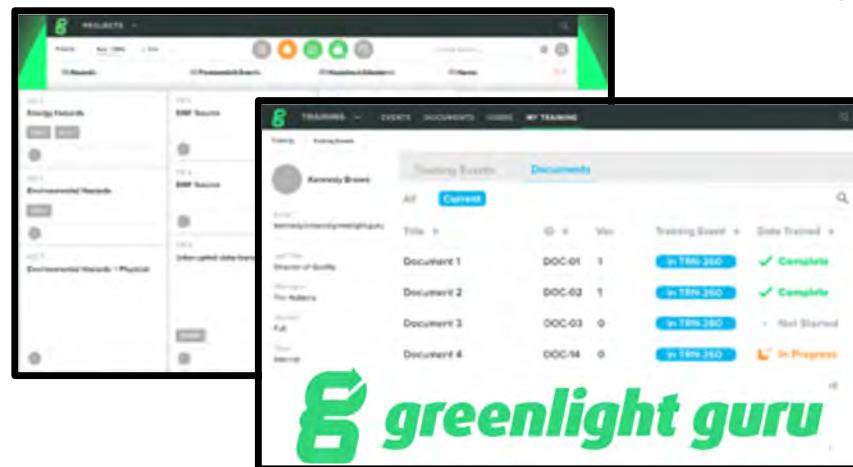
Additional Tools for Project Management & QA/QC

Every program is reviewed upon completion to grade each department on Quality and TAT – We STRIVE for continual improvement!



Jira Software

For Project Tracking



greenlight guru

For QMS Management

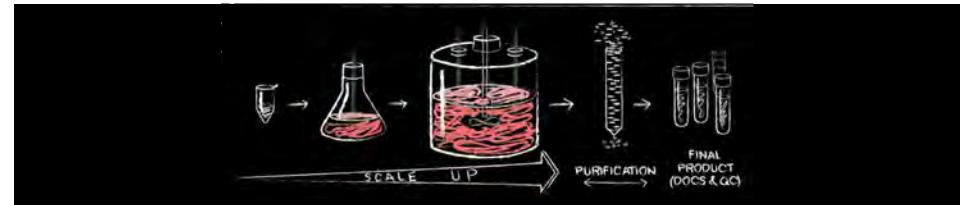
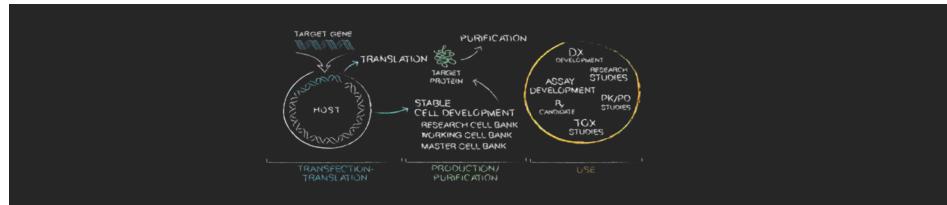
Gantt Charts for Current Timelines



Secure File Transfers – Client Data is Safe

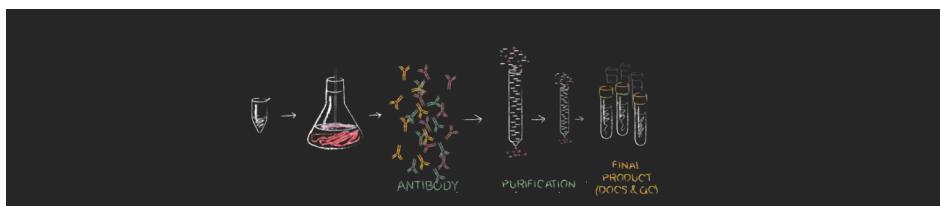


Range of Complementary Services



Protein Expression & Purification:

- Gene-to-Protein Services
- Flexible Expression Systems
- Expression Scale mL – 250 L

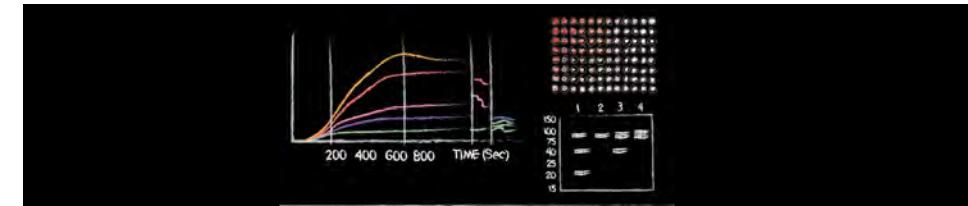


Antibodies, Nanobodies, and BiS:

- Custom Ab and anti-ID Development
- mAb and Multi-specific Production
- Hybridoma-to-Recombinant Conversion

Production:

- USP & DSP Development Services
- Biomanufacturing

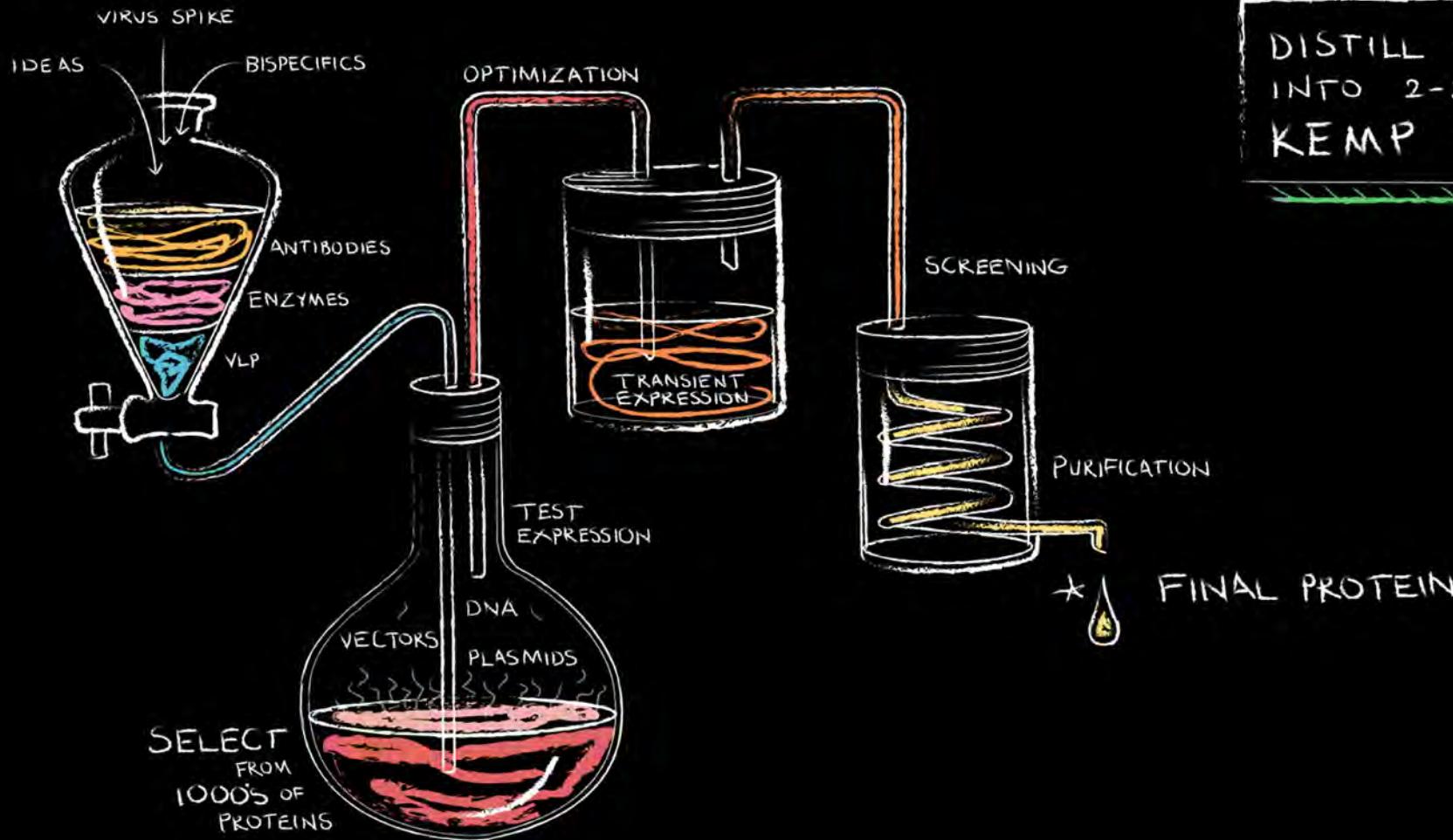


Analytical & Assay:

- Biophysical Characterization
- Analytical Chromatography
- Stability Studies
- Assay Development



Kemp Proteins' Q³: Quality Expressed¹, Quality Purified², Quality by Design³



DISTILL 1000's OF PROTEINS
INTO 2-3 TARGETS USING
KEMP PROTEINS HTP

USED IN:
PROCESS DISCOVERY
ASSAY DEVELOPMENT
PHASE 1 PHASE 2 PHASE 3
CLINICAL DEVELOPMENT

SUPPORT DOSSIER FROM
KEMP PROTEINS



solutions@kempproteins.com