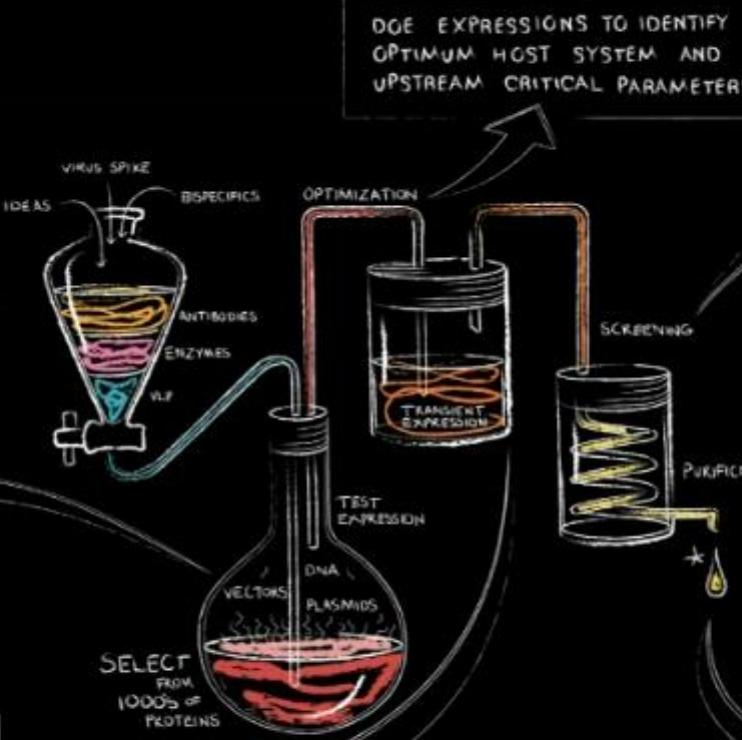
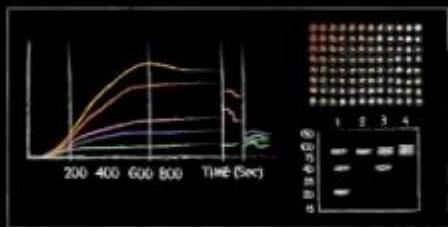


Screenshots der Präsentation vom 16.07.2024

YOUR GMP "READY" PROTEIN

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



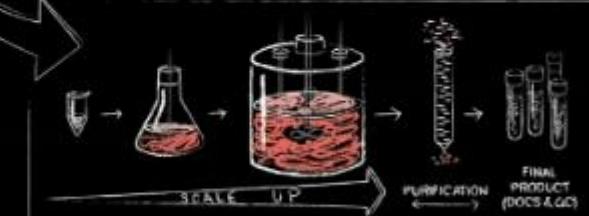
KEMP
PROTEINS
QUALITY EXPRESSED

DOWNSTREAM
PROCESS
OPTIMIZATION

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

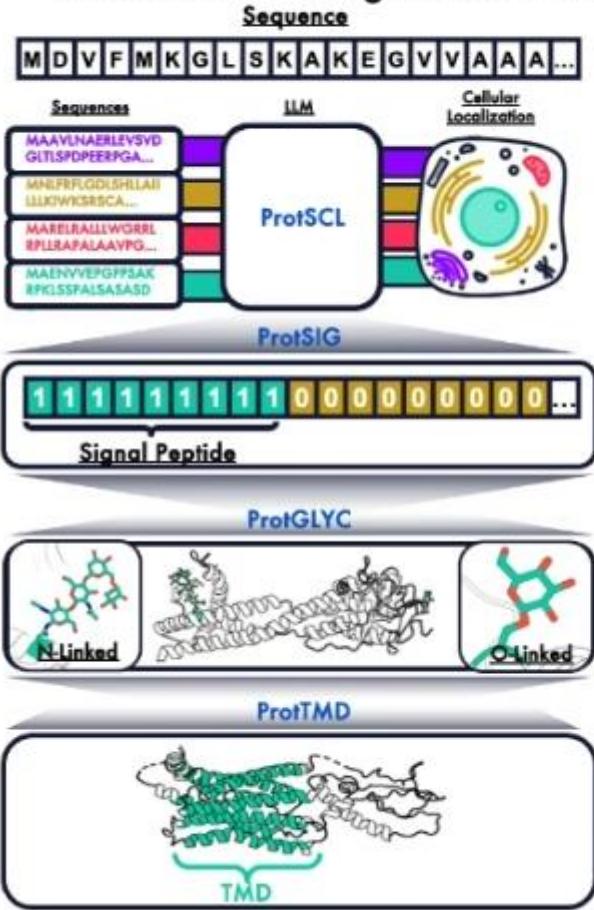
DOWNSTREAM
PROCESS DEVELOPMENT
IS AN ITERATIVE PROCESS

SUPPORT DOSSIER FROM
KEMP PROTEINS

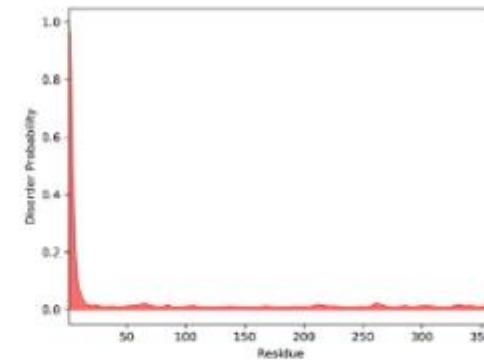
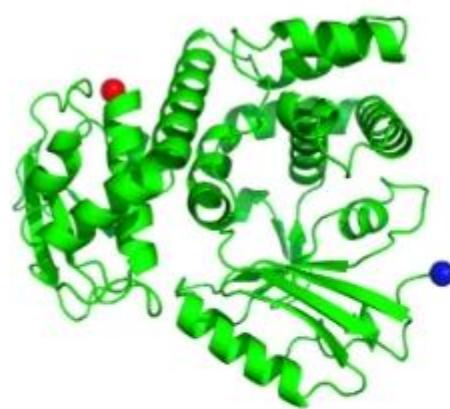
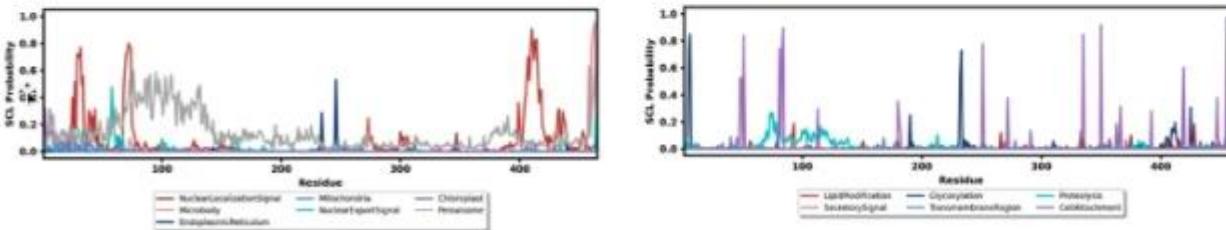


PROTiQSM: Novel Generalizable ML Tools

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



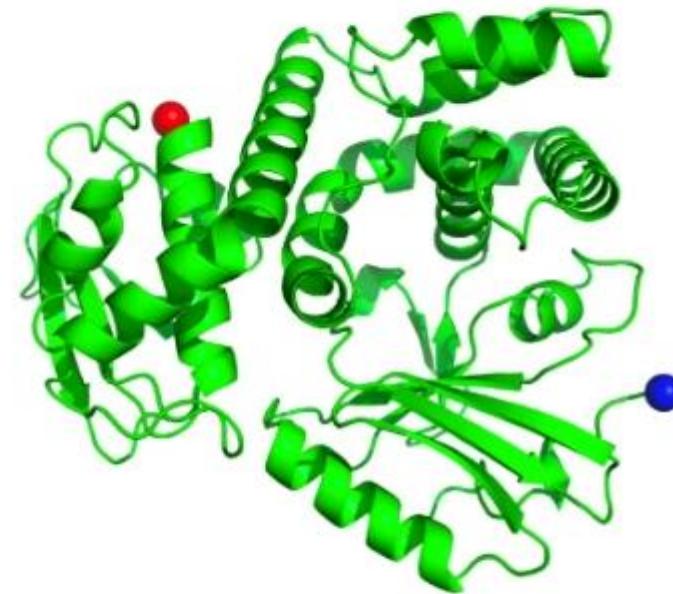
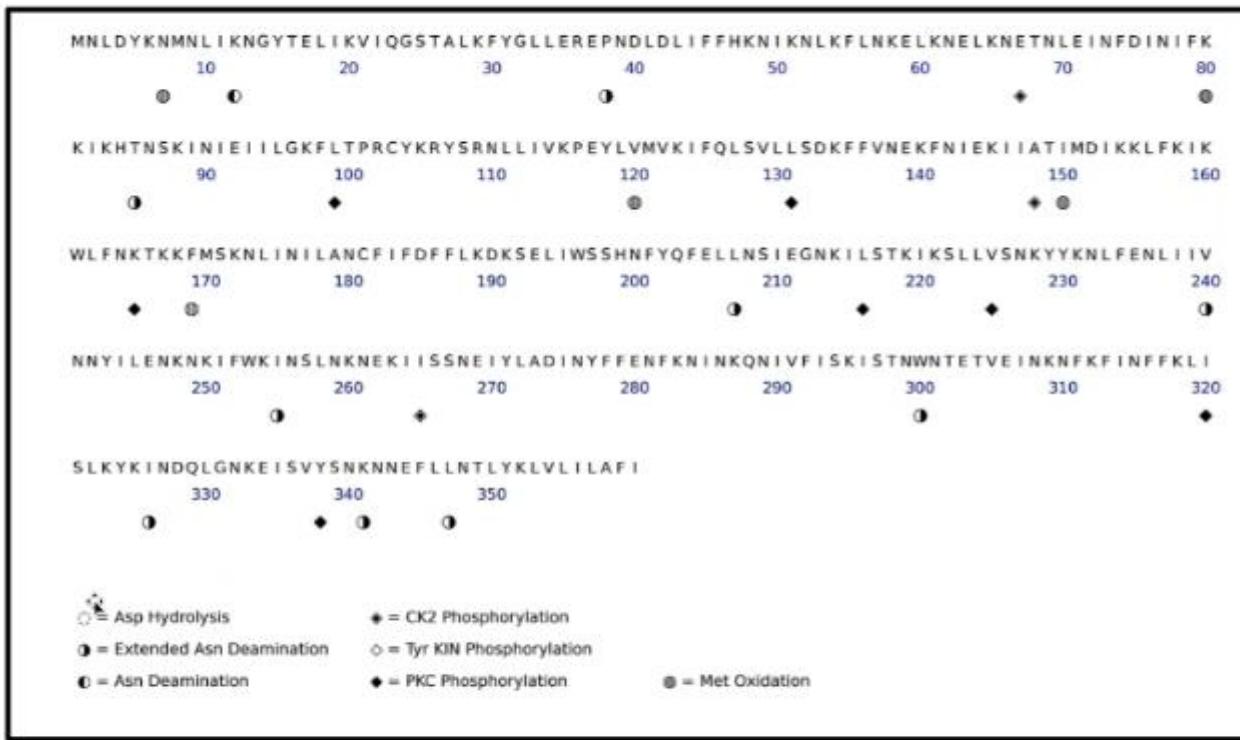
Probability of PTMs and localizations based from sequences



Structural Models output in Pymol session and Disorder Plot



PROTiQSM: Sequence Liabilities Prediction

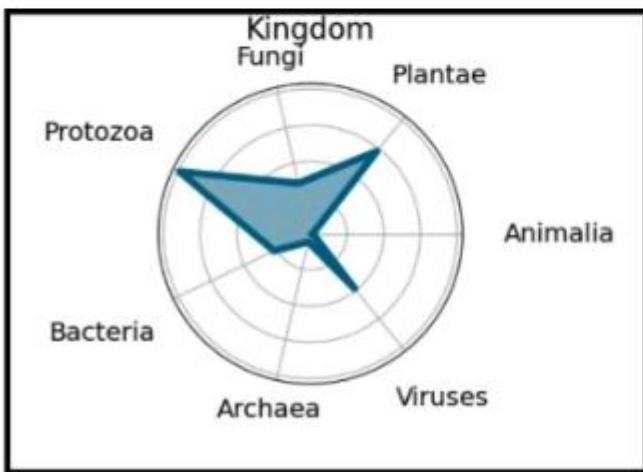


RoseTTAFold Model + Gromacs
Energy Minimization

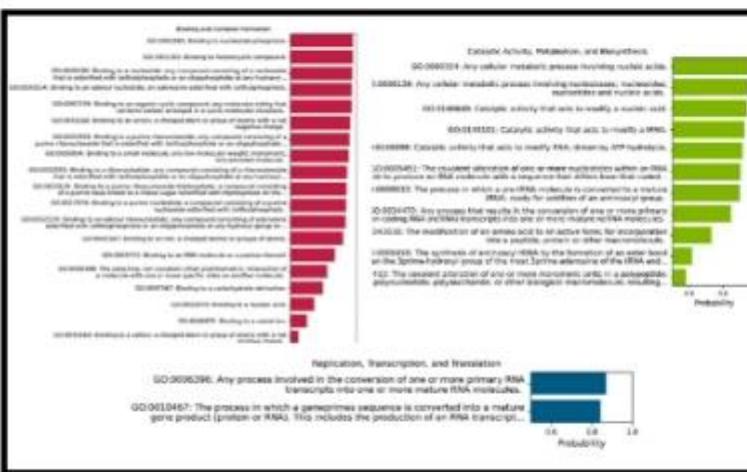
The sequence is processed through the generalizable ML tools to identify and sequences liabilities as a function of recombinant expression host. Not shown here are proteolytic liabilities as a function of recombinant host

PROTiQSM: FAUNA

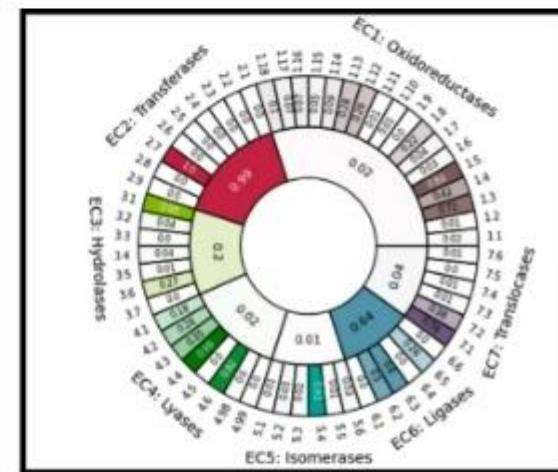
Kingdom Prediction & GO / Enzyme Classifiers



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

KEMP PROTEINS

PROTi

Report Date: 22 March 2024

Client: FNL – Alpha-Twist and Beta-Turns

Client Contact: Carter A. Mitchell

About ProtiQ™
Decades of research enabled the creation of extensive databases that provide a about the structure and action of various proteins. We have localized this information learning process to combine this information with knowledge from our own experts, provide our clients with a cutting edge system for designing proteins that may challenges during initial protein development. This system ProtiQSM, provides a report design 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 se

Kemp Proteins
ProtiQ@kempproteins.com
240-829-8224

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The information in this report is for research purposes only and it is understood by the re experimental in nature and as such Kemp Proteins makes no representation or warranty, e the stability of the protein sequences generated, nor does Kemp Proteins guarantee spec report may contain links to third-party websites or content and Kemp Proteins does not a party websites, products, or services. All content on this report is the property of Kemp Prote of Kemp Proteins until such time that a client enters into commercial arrangements for right of the information contained in this report agree to indemnify and hold harmless Kemp Prote 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. -

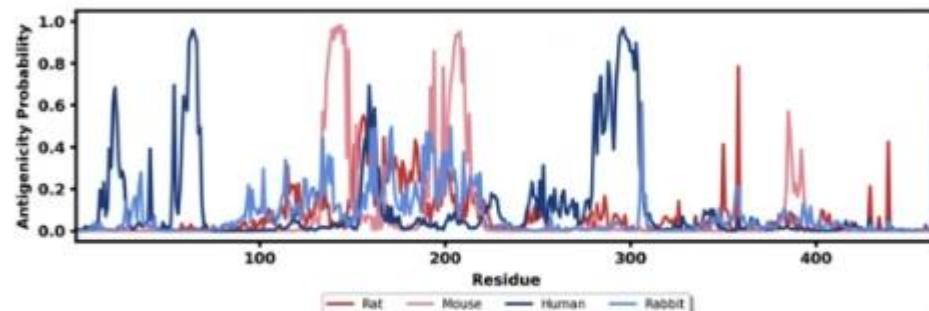
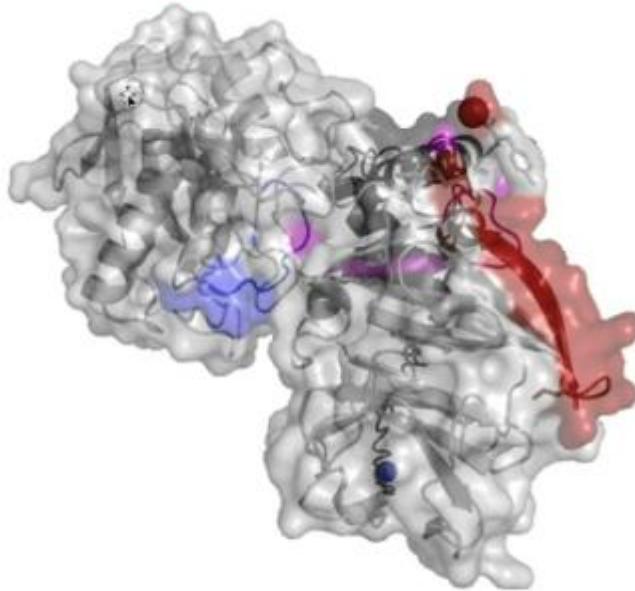


PROTiQSM: Antigenicity Scoring Function

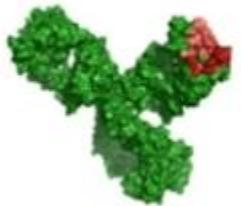
The Antigenicity Score is generated from analysis of known interactions taken from the literature and curated databases that include structural information when available.

Current rules include:

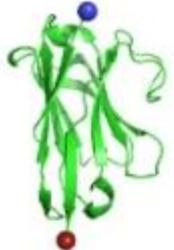
- >10 residues < 40 residues
- Sequence Identity ≥55%; Similarity ≥65%
- Solvent accessible, noninteraction regions
- Identification of preferred immunization animal as a function of sequence homology including
 - 1) Mouse
 - 2) Rat
 - 3) Human
 - 4) Rabbit
 - 5) Camelid



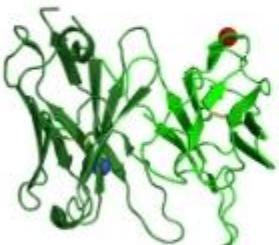
Antibody Expression at Kemp in Various Platforms



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



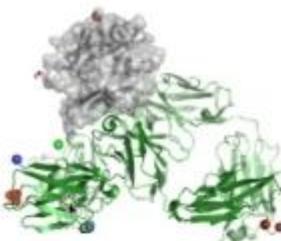
- VHH
 - Bacterial
 - Mammalian



- 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

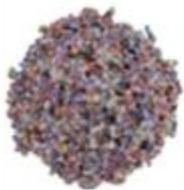
Proteins Expressed at Kemp in Various Platforms

- **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**

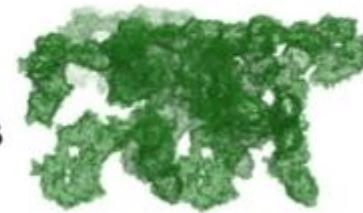


- E3 ligases with targets

- **Toxins**

- Ricin, Botox, CtXB

- **Membrane Proteins**



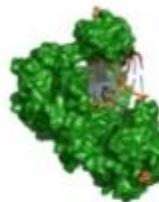
- GPCRs
- Extracellular Domains
- Soluble TM mutants

- **Immunologic Proteins / Hormones**



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

- **Enzymes**



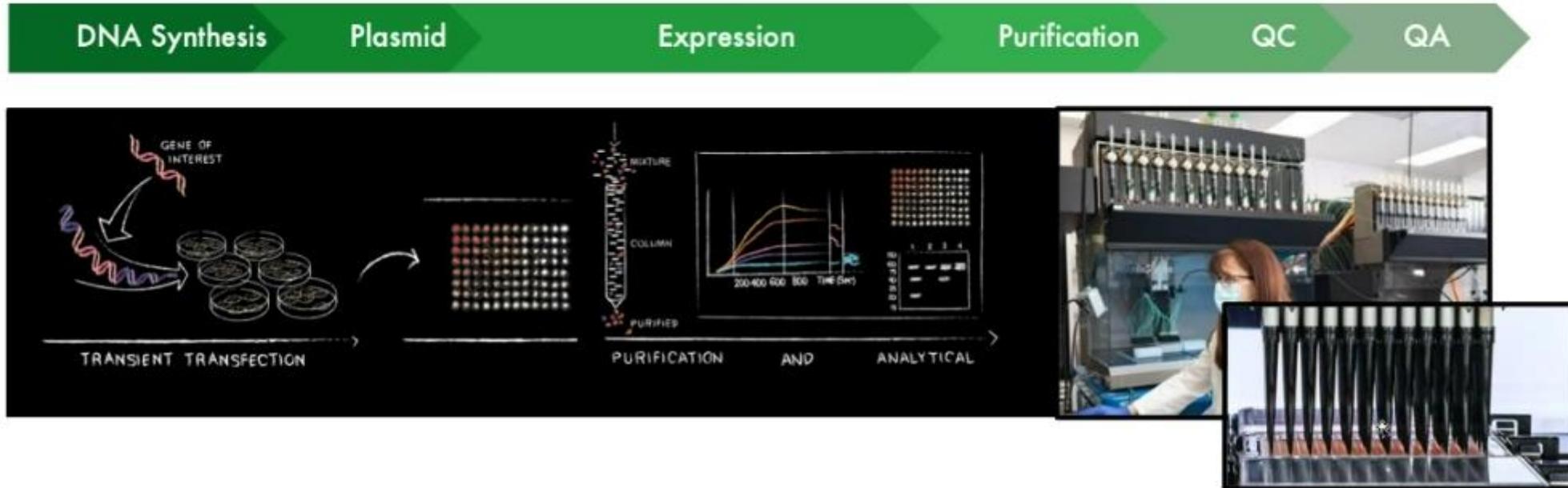
- DNA pol
- Methyltransferases

- **Cytoskeletal Elements**



- Dystrophin SILAC / unlabeled¹ KEMP

Rapid Small Scale Expression & Purification



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