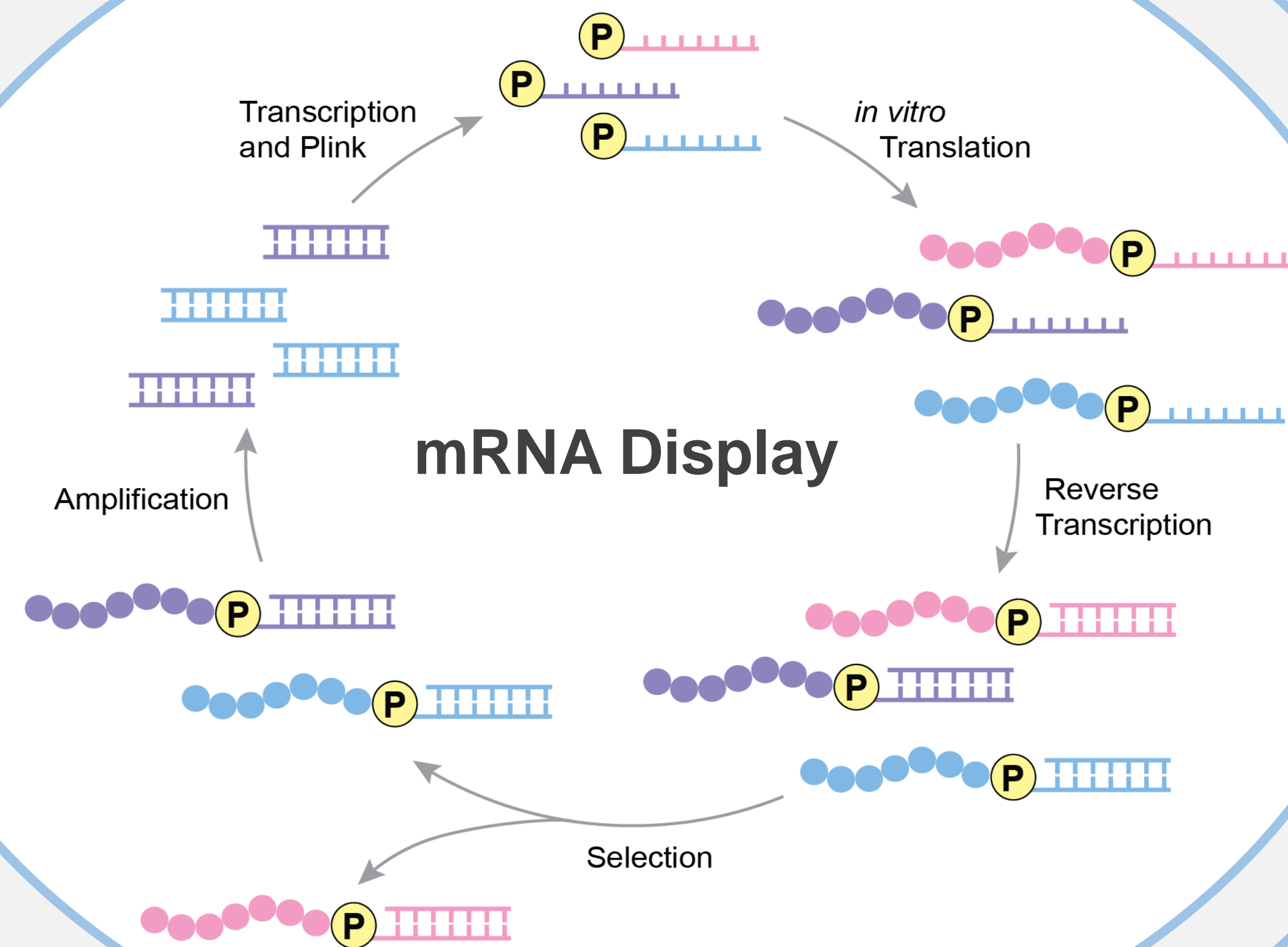
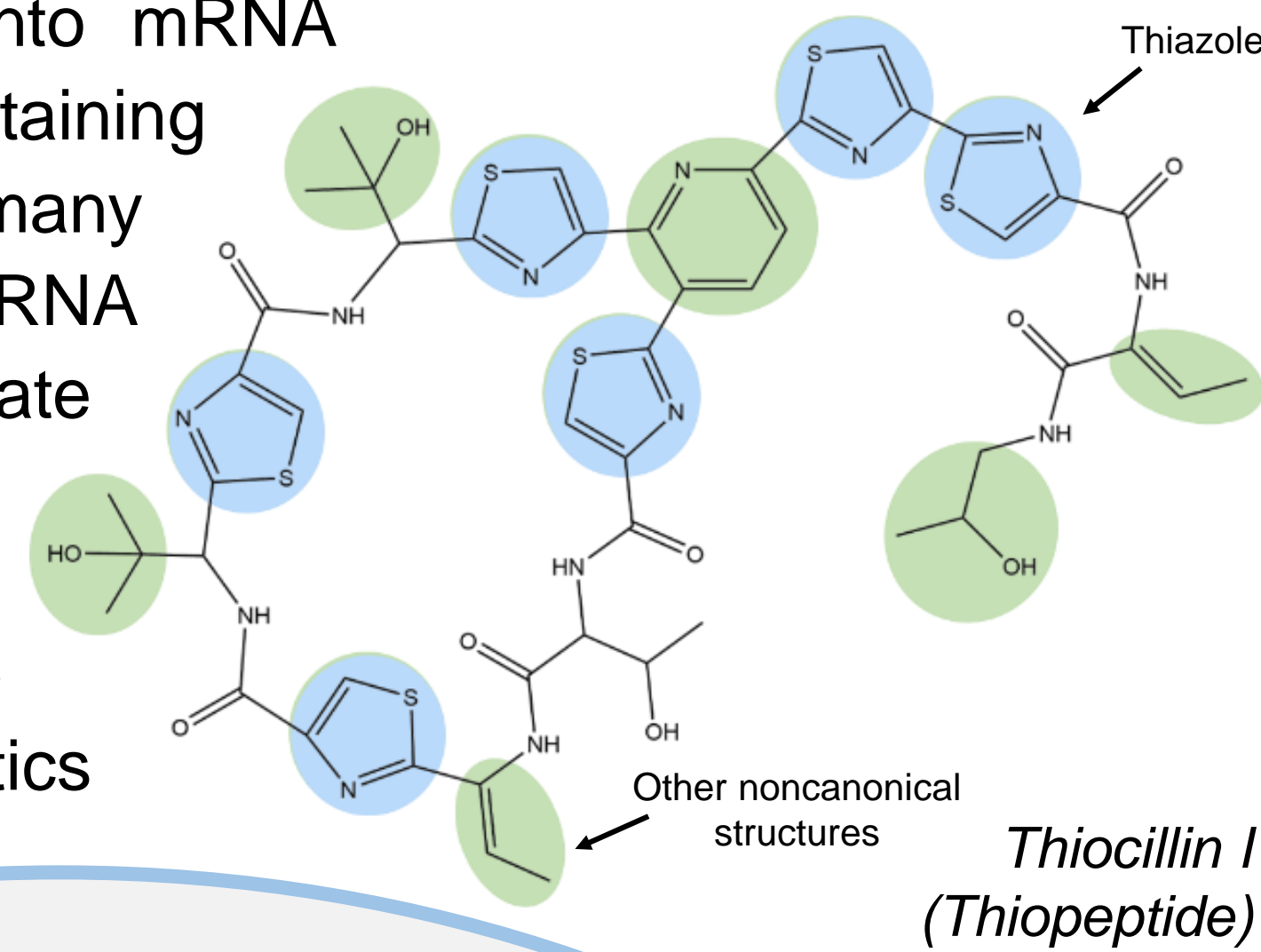


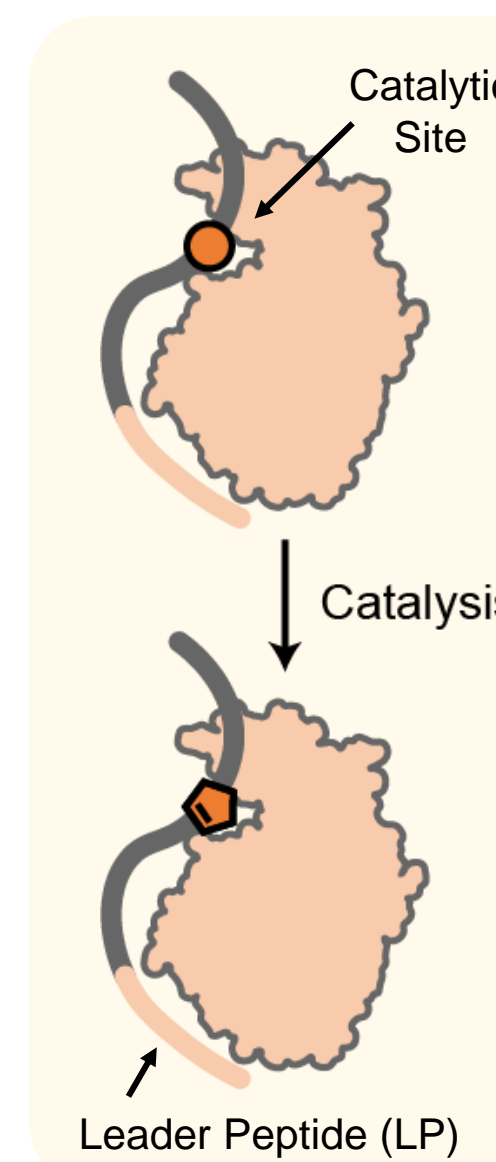
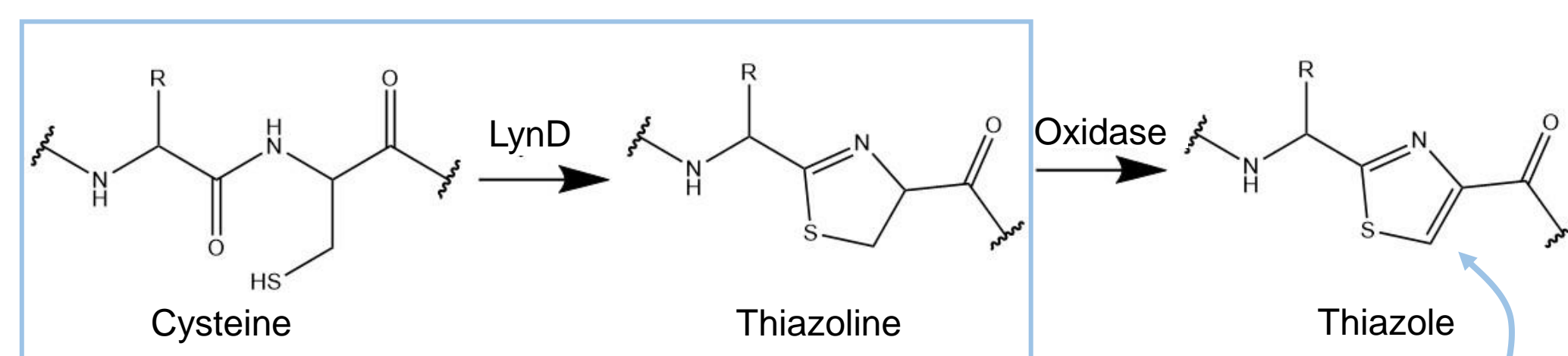
Introduction

Abstract:

mRNA display is a powerful high-throughput screening technique used to identify potential therapeutics from diverse libraries of peptides.¹ Natural products provide insights into therapeutically relevant moieties that may be incorporated into mRNA display peptide libraries. For example, thiazoles are amide isosteres with beneficial drug-like properties that are found in many natural products.^{2,3} LynD, the cyclodehydratase enzyme in aesturamide biosynthesis,⁴ may be integrated into mRNA display to develop thiazole-containing libraries, but LynD must tolerate many diverse substrates to function with mRNA display. By exploring the substrate tolerance of LynD, more diverse mRNA display screening libraries may be created, expanding the potential of peptide-based therapeutics in drug discovery.



LynD to Incorporate Thiazoles:



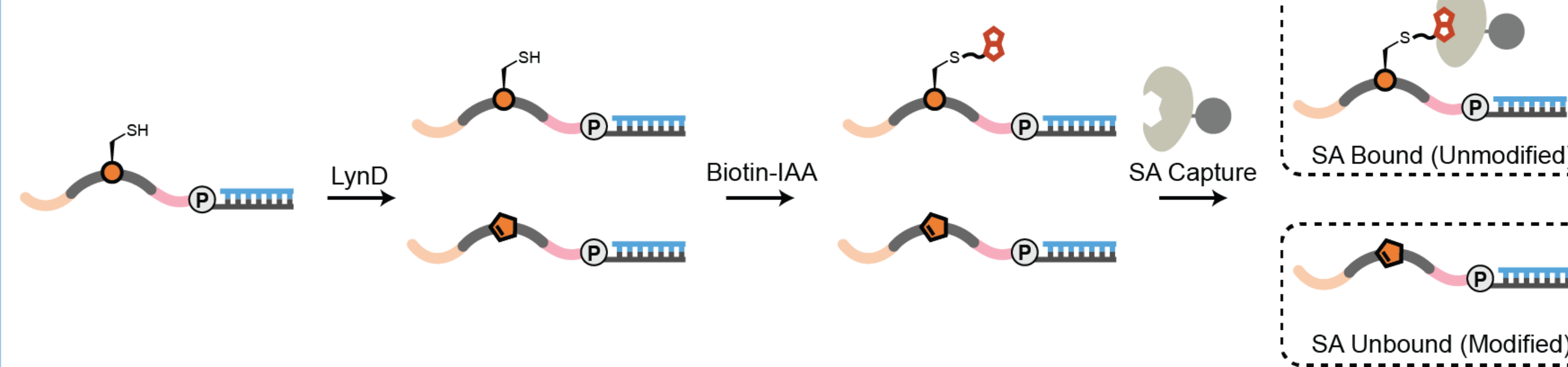
- Amide Isostere
- Planar
 - Reduced H-bonding

Will LynD modify libraries in mRNA Display?

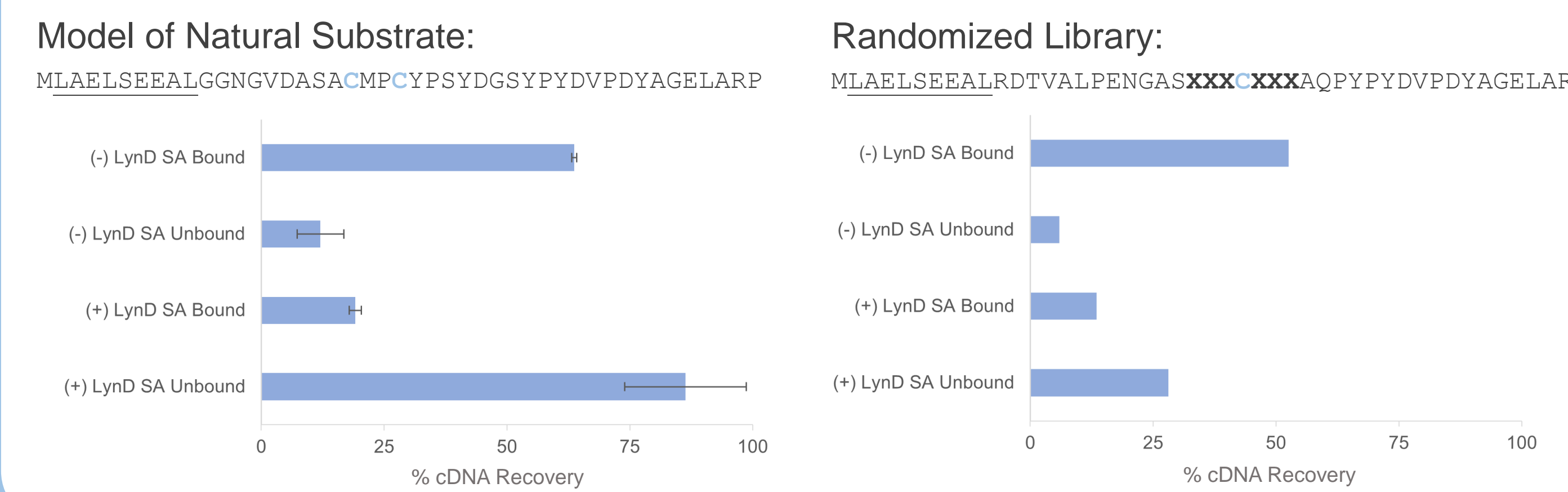
- RNA Library
- Affix puromycin (P) to 3' end of mRNA
- In vitro translation
- Ribosomes
 - Elongation factors
 - Amino acids
 - tRNAs
 - tRNA synthetases

Assay Development

Assay Design:

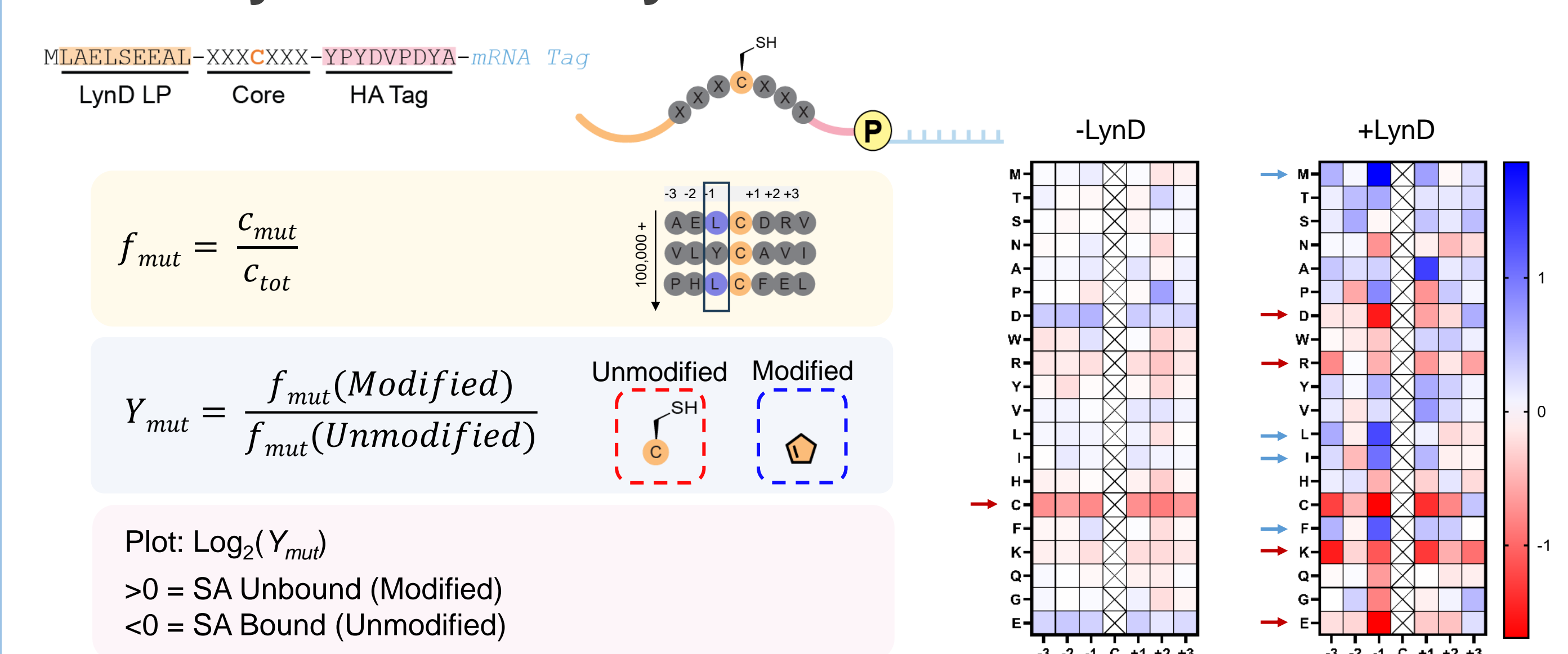


Assay Validation through qPCR Quantification:

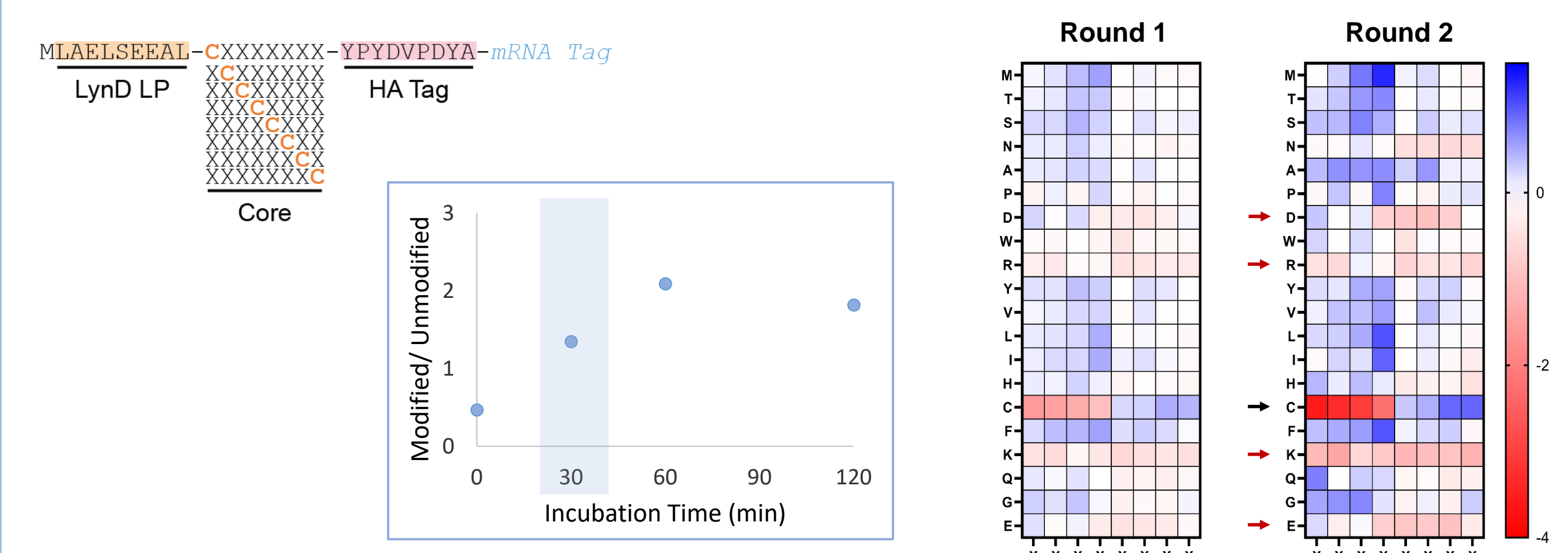


Substrate Tolerance

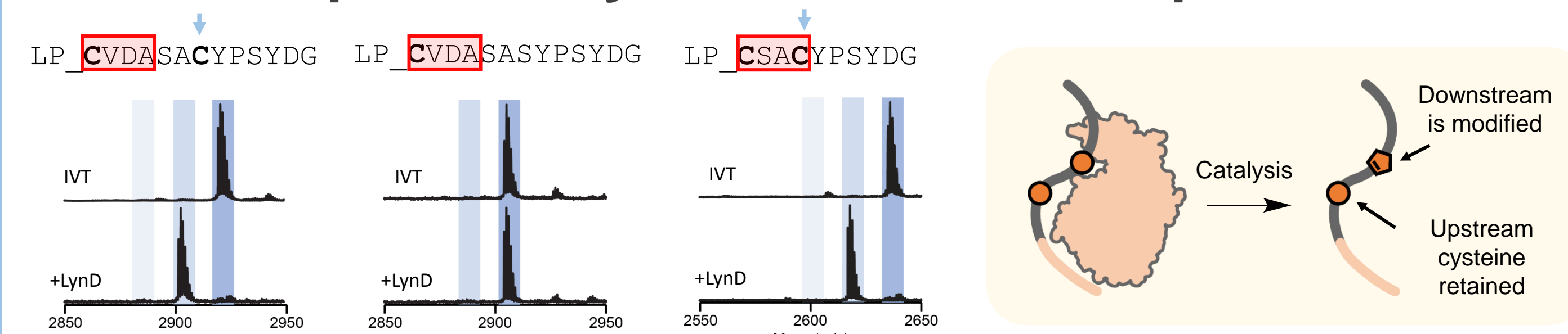
Fixed Cysteine Library NGS Results:



Expanded Library Initial NGS Results:

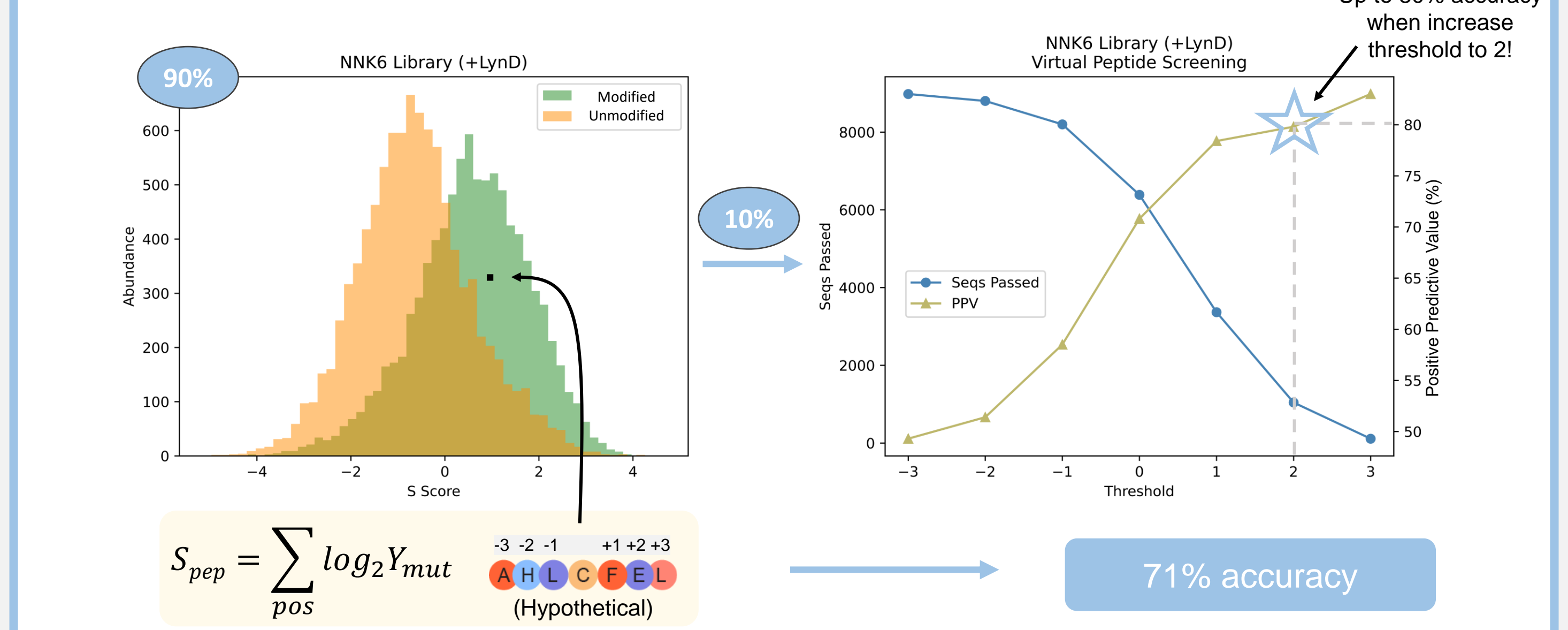


Leader Peptide to Cysteine Distance Dependence:

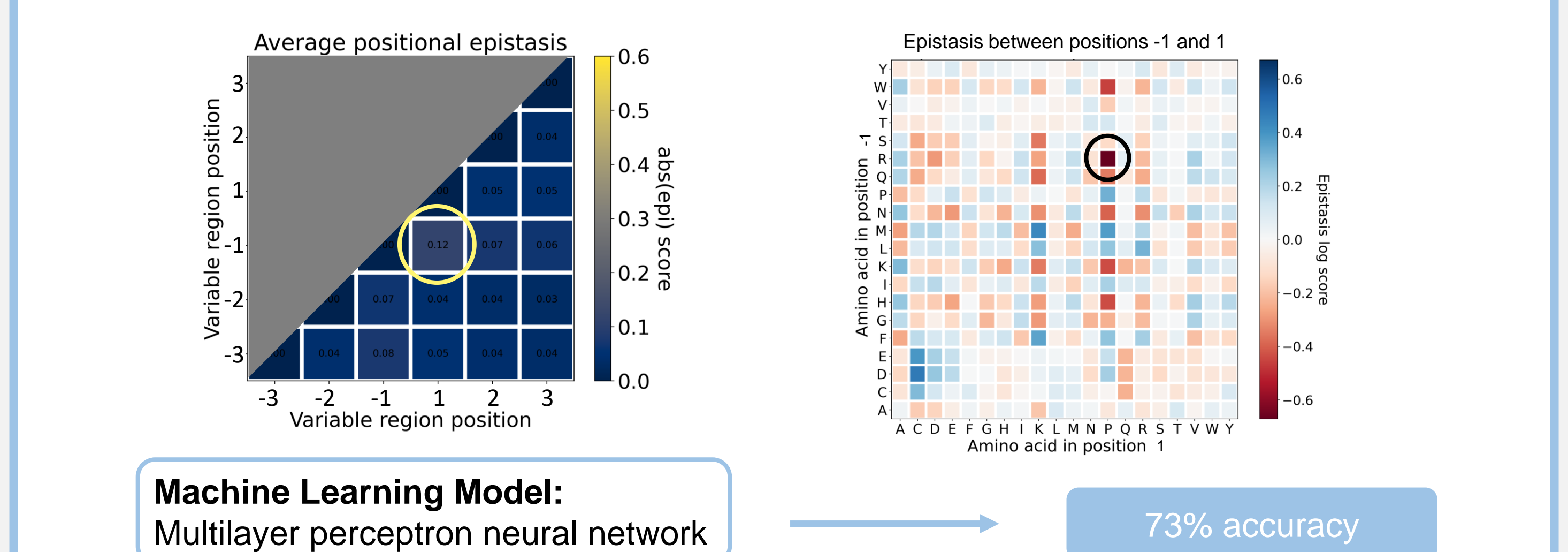


Computational Analysis

S-Score Predictive Model:



Machine Learning Model for Epistatic Interactions:



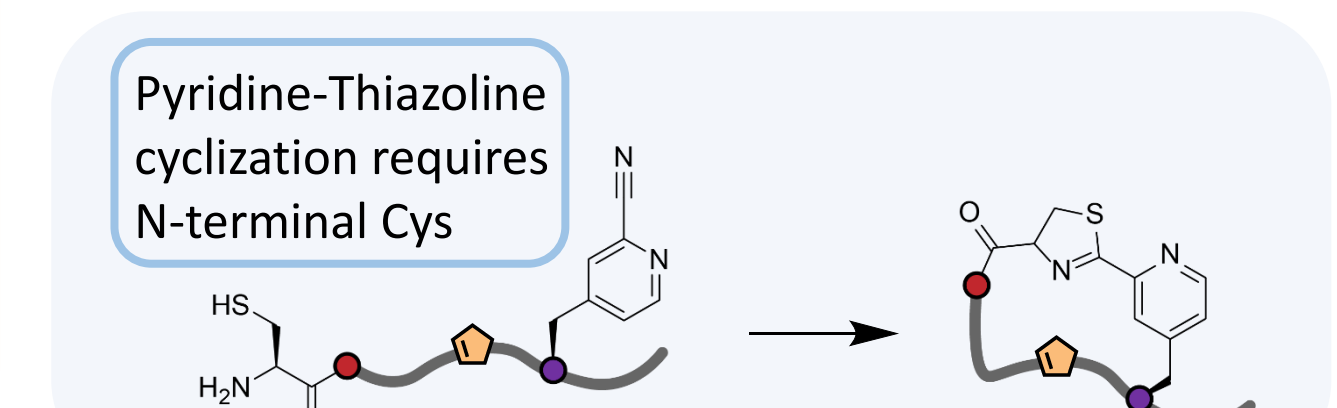
Conclusions

Summary:

- Validated LynD in mRNA display
- Determined high substrate tolerance!
 - Dislikes charged residues at -1 position
 - Prefers hydrophobic at -1 position
 - Low overall epistasis
- Developed model to predict LynD substrates with >70% accuracy
- Showed Cys distance from leader peptide dependence

Future Directions:

- Additional rounds of display for machine learning model
- Incorporate cyclization method into thiazoline library
- Run selection with library



References & Acknowledgements

This work was completed in collaboration with Henry Dieckhaus in Dr. Brian Kuhlman's laboratory and Jarrett Pelton in Dr. Albert Bowers' laboratory.

- Iskandar, S. E.; Haberman, V. A.; Bowers, A. A. Expanding the Chemical Diversity of Genetically Encoded Libraries. *ACS Comb. Sci.* **2020**, *22*, 712, DOI: 10.1021/acscmb.0c00179
- Siodlak, D.; Stas, M.; Broda, M. A.; Bujak, M.; Lis, T. Conformational properties of oxazole-amino acids: Effect of the intramolecular N-H...N hydrogen bond. *J. Phys. Chem. B* **2014**, *118*, 2340–2350, DOI: 10.1021/jp4121673
- Wipf, P.; Fritch, P. C.; Geib, S. J.; Sellen, A. M. Conformational studies and structure-activity analysis of lissoclinamide 7 and related cyclopeptide alkaloids. *J. Am. Chem. Soc.* **1998**, *120*, 4105–4112, DOI: 10.1021/ja973580h
- Koehnke, J.; Mann, G.; et al. Structural analysis of leader peptide binding enables leader-free cyanobactin processing. *Nat. Chem. Biol.* **2015**, *11*, 558–563, DOI: 10.1038/nchembio.1841

