# Framework to Design mRNA Sequences to Control Co-Translational Folding 

ID\# 2015-4330
technology readiness level

## Seeking

Investment | Licensing | Research

## Keywords

- co-translational protein folding
- synonymous codon mutations
- codon optimization
- optimized mRNA sequences
- heterologous protein production


## Researchers

## Edward O'Brien

Assistant Professor, Department of Chemistry in the Eberly College of Science

Office of Technology Management Contact Long, Melissa
mkl137@psu.edu
814-865-5730

## Application \& Market Utility

High-quality proteins are required for commercial/academic applications. This method provides a way to rationally design mRNA sequences based on the folding kinetics of nascent protein. It predicts its own success or failure through mathematical modeling without actually carrying out an experiment, thus reducing costs and time. Applications include: Biotechnology companies that supply high-quality proteins to academic labs and other industries. Pharmaceutical companies that produce functional proteins to design monoclo $\neg$ nal antibodies or for therapeutic purposes.

## Next Steps

Seeking research collaboration and licensing opportunities.

Invent Penn State is a Commonwealth-wide initiative to spur economic development, job creation, and student career success. Invent Penn State blends entrepreneurship-focused academic programs, business startup training and incubation, funding for commercialization, and university-community collaborations to facilitate the challenging process of turning research discoveries into valuable products and services that can benefit Pennsylvanians and humankind. Learn more at invent.psu.edu.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

