Protein Science “Best Paper” Awards to Youngil Chang and Liam Longo

This year the Protein Society is introducing *Protein Science* “Best Paper” awards which are intended to recognize outstanding contributions of junior investigators.

At the end of each year two “best papers” which have appeared in *Protein Science* will be selected, and a junior author from each article will be invited to give a talk at the following Annual Protein Society Symposium.

The inaugural winners are Youngil Chang from the group of Chiwook Park at Purdue University, and Liam Longo from the group of Michael Blaber at Florida State University.

Youngil Chang received Bachelor’s degrees in Biology and in Chemistry as well as a Master’s degree in Chemistry from Seoul National University in Korea. He is currently pursuing a degree in pharmacy at Atlantic University in Florida.

Youngil’s “best paper”¹ describes a simplified proteomics approach to discover protein-ligand interactions. Differing from traditional affinity-based capture approaches, the new method does not require any labeling or immobilization of the test molecule. It depends on the principle that the binding of a ligand will stabilize a protein of interest and suppress its unfolding in urea, which they monitored by a short pulse of proteolysis (pulse proteolysis). Proteins showing a different degree of unfolding in the presence of the ligand are identified by SDS PAGE followed by mass spectrometry.

The second award winner, Liam Longo, started work in the Blaber laboratory as an undergraduate and is pursuing his Ph.D. in molecular biophysics. He is currently working on a number of different projects including the design of proteins from prebiotic amino acids to understand aspects of the origins of proteins in abiogenesis. Another study employs solid-state NMR to study the aggregation properties of proteins with engineered sequence symmetry. On completing his Ph.D., Liam wants to focus on protein folding and design and then pursue a career in academia.

Liam’s *Protein Science* “best paper”² addresses the question as to whether there is a compromise between protein foldability and protein function (the “foldability-function tradeoff hypothesis”). To test whether function is accommodated at the expense of foldability, fibroblast growth factor-1 (FGF-1) was subjected to a comprehensive ϕ -value analysis at each of the 11 turn regions. Because of its three-fold symmetrical structure, FGF-1 is a particularly attractive subject for the study as it allows direct comparisons between symmetry-related regions of the protein, some of which are associated with function and some that are not.

On behalf of *Protein Science* and the Protein Society, we warmly congratulate Liam Longo and Youngil Chang for this well-deserved recognition and look forward to their presentations at the Boston Symposium.

Background Information

It is the intention of the Protein Society and *Protein Science* to continue these awards on an annual basis.

All articles published within a given calendar year will be candidates for the awards. Every submitted manuscript will be considered and no nomination statement is required. At the same time, if authors submitting a manuscript feel that it will be a strong candidate for a “best paper” award, they are very welcome to include a brief note in the submission letter explaining why the contribution is especially worthy of consideration.

Brian W. Matthews
Editor

REFERENCES

1. Chang Y, Schlebach JP, VerHeul RA, Park CW (2012) Simplified proteomics approach to discover protein-ligand interactions. *Protein Sci* 21:1280–1287.
2. Longo L, Lee J, Blaber M (2012) Experimental support for the foldability-function tradeoff hypothesis: Segregation of the folding nucleus and functional regions in fibroblast growth factor-1. *Protein Sci* 21:1911–1920.

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