

***Protein Science* Best Paper Awards to
Tatsuya Niwa, Qingping Xu and Matthew Biancalana**

Each year the Protein Society selects two papers in *Protein Science* for special recognition.

For 2019 the first such paper is “Translation-coupled protein folding assay using a protease to monitor the folding status”,¹ and the Best Paper awardee is Tatsuya Niwa [Fig. 1(A)].

The second award-winning paper is “Structures of single-layer β -sheet proteins evolved from β -hairpin repeats”² and the two co-equal first authors, Qingping Xu [Fig. 1(B)] and Matthew Biancalana [Fig. 1(C)], are both recognized as Best Paper awardees.

On behalf of the Protein Society and *Protein Science*, congratulations to all three awardees for their outstanding research contributions.

The award-winning work of Dr. Niwa addresses two of the longest-standing questions in protein science. First, how does the amino sequence of a protein dictate its native structure and, second, how is the native structure achieved in the cell, where correct protein folding is hampered by intermediate aggregate formation? Dr. Niwa began working in this area at the University of Tokyo with Professor Hideki Taguchi and has continued at the Tokyo Institute of Technology. As a student he started a comprehensive analysis of protein aggregation and folding using a reconstituted cell-free protein synthesis approach called PURE system, developed by Professor Takuya Ueda. He plans to continue these studies in the future. As he explains, “I am also interested in ‘abnormal proteins’, such as intrinsically-disordered proteins and the proteins that can form liquid-liquid phase separation... These ‘special’ proteins may extend the conception of proteins. Ultimately, I would like to aim to find the answer to the question ‘What is a protein?’.”

According to Professor Taguchi “Tatsuya is a really talented and dedicated biochemist, who started his career with me and Professor Takuya Ueda at the University of Tokyo. Tatsuya conducted an epoch-making analysis of global folding and chaperone effects using a reconstituted cell-free translation system during his Ph.D. project. This work by Tatsuya opened up a new field in my lab. The translation-coupled folding assay is based on the assumption that soluble fractions following centrifugation are folded, but the soluble fractions include nonnative structures. The paper selected for a best paper award tackled the long-standing problem in the assay by adding a protease to monitor the folding status. Tatsuya literally led the research in both experiments and data analysis. I would like to emphasize that Tatsuya now has an amazing ability to analyze big data. The award encourages Tatsuya a lot for the future of his career”.

The two co-recipients of the second Best Paper award, Qingping Xu and Matthew Biancalana, were brought together not so much through being in the same location as by a common research interest. Qingping obtained his undergraduate education in physics at Anqing Normal University, Anhui, China, and took his Ph.D. in biochemistry at the University of Oklahoma under the guidance of Ann West. He has determined many protein structures and worked on understanding their functions through worldwide collaborations at the Joint Center for Structural Genomics consortium at Stanford, led by Ian Wilson. Qingping currently works at the Argonne

National Laboratory, where he develops software to help synchrotron users collect better data, and continues his research in protein structure and function.

Matthew Biancalana then picks up the thread: “I began my research career working in Shohei Koide's lab at the University of Chicago, where I studied the fundamental structural and dye-binding properties of amyloid fibrils. We skirted many of the technological difficulties of working with fibrils directly by using the β -sheet rich model protein Outer surface protein A (OspA). The research was compelling and inventive, and sparked my fascination with protein structure.

I subsequently conducted my Ph.D. at the University of Cambridge in Alan Fersht's group. In the course of this research, I stumbled across a structure solved by Qingping Xu that bore several similarities to the OspA variants I had worked with as an undergrad. I reached out to Qingping and we forged a long-distance collaboration to describe and analyze this unusual class of single-layer β -sheet proteins (SLBPs). Amazingly, it would take us nearly a decade to finally bring the complete story together and publish in *Protein Science*”.

Background Information

All articles published in *Protein Science* are candidates for the Best Paper awards. No nomination statement is required. At the same time, if authors submitting a manuscript feel that it will be a strong candidate for the 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. Niwa T, Uemura E, Matsuno, Y, Taguchi H (2019) Translation-coupled protein folding assay using a protease to monitor the folding status. *Protein Sci* 28:1252-1261.
2. Xu Q, Biancalana M, Grant JC, Chiu H-J, Jaroszewski L, Knuth MW, Lesley SA, Godzik A, Elsliger M-A, Deacon AM, Wilson IA (2019) Structures of single-layer β -sheet proteins evolved from β -hairpin repeats. *Protein Sci* 28:1676-1689.

Figure Legends

Figure 1: Award winners: (A) Tatsuya Niwa. (B) Qingping Xu. (C) Matthew Biancalana.