



**FOR IMMEDIATE RELEASE**

**Date: March 15, 2018**

**Contact:**

Raluca Cadar  
The Protein Society  
Phone: (844) 377-6834  
E-mail: [rcadar@proteinsociety.org](mailto:rcadar@proteinsociety.org)

---

**THE PROTEIN SOCIETY ANNOUNCES ITS 2018 AWARD RECIPIENTS**

---

**CANYON COUNTRY, CA** – The Protein Society, the premiere international society dedicated to supporting protein research, announces the winners of the 2018 Protein Society Awards, which will be conferred at their 32<sup>nd</sup> Annual Symposium (July 9 - 12, 2018, Boston, Massachusetts). Plenary talks from the recipients are scheduled throughout the 3.5-day event\*.

**The Carl Brändén Award**, sponsored by Rigaku Corporation, honors an outstanding protein scientist who has also made exceptional contributions in the areas of education and/or service to the field. The 2018 recipients of this award are Professors **Jane and Dave Richardson** (Duke University). Jane and Dave have been involved in many groundbreaking developments through the years, including solving two of the first 20 protein crystal structures (Staph nuclease & Cu,Zn superoxide dismutase); early work in what is now called structural bioinformatics: (beta bulges, Greek key folds, helix caps, etc.); developing the ribbon drawing, still widely used to represent 3D protein folds both on the page and in 3D graphics -- the hand-drawn TIM barrel ribbon schematic was Picture of the Day on Wikipedia Nov 19, 2009 (<http://commons.wikimedia.org/wiki/User:Dcrjrsr>); pioneering early protein de novo design in the 1980s with Betabellin and Felix; pioneering interactive 3D macromolecular graphics for small personal computers with the Mage/kinemage system, first used as digital supplements at the launch of Protein Science, then for the Branden & Tooze textbook, and later online with KiNG; developing the method of all-atom contact analysis, which adds explicit hydrogen positions to analyze packing inside and between macromolecules. It diagnoses and helps correct local modeling problems in protein and RNA structures. They were also involved in developing and updating the MolProbity validation web service, now used by most crystallography labs, within the Phenix software system, at deposition to the worldwide Protein Data Bank, and in crystallography courses; and are currently developing new validation methods suitable in the 2.5-4Å resolution range, for crystallography and especially for modern cryoEM.

**The Christian B. Anfinsen Award**, sponsored by The Protein Society, recognizes technological achievement or significant methodological advances in the field of protein science. The recipient of this award in 2018 is **Professor Yifan Cheng** (University of California, San Francisco). Yifan is considered one of the world's top few experts in high-resolution cryo-EM. He has been involved in various groundbreaking technological developments that greatly advanced single particle cryo-EM and its application in studying integral membrane proteins. He has also been involved in the structural studies of TRP channels. In particular, Dr. Cheng has been involved in the determinations

of TRPV1 ion channel, the first atomic structure of an integral membrane protein determined by single particle cryo-EM, and the determination of the atomic structure of TRPV1 in lipid nanodisc, the first membrane protein atomic structure in a lipid bilayer by single particle cryo-EM. These studies had major impact on structural biology of membrane proteins, and methods developed in these studies are now widely used in structural studies of a broad range of integral membrane proteins.

**The Dorothy Crowfoot Hodgkin Award**, sponsored by Genentech, is granted in recognition of exceptional contributions in protein science which profoundly influence our understanding of biology. The 2018 recipient is **Professor Susan Marqusee** (University of California, Berkeley). Dr. Marqusee, a biophysical chemist whose work focuses on protein folding and dynamics, is one of the world's top experimental scientists in the field of protein folding. Her work has led to the most complete characterization of a protein energy landscape and provided a rigorous and unprecedented detailed analysis of the diffusion of a folding protein on this energy surface, testing in this manner key models of protein folding. She is known for many contributions, including the first de novo design of a short peptide that folded into a specific structure (alpha helix), the application of novel hydrogen exchange methods to measure rare partially-structured conformers, and the mechanical manipulation of single-protein molecules. Her work has produced the most detailed view of the energy landscape of a protein. Her work impacts areas of biology ranging from deciphering the effects of genome variation to the mechanism of protein misfolding pathologies.

**The Emil Thomas Kaiser Award**, sponsored by The Protein Society, recognizes a recent, highly-significant contribution to the application of chemistry in the study of proteins. The 2018 recipient is **Professor Michael Rosen** (University of Texas SW Medical School). Dr. Rosen has been a leader in deciphering how macromolecular phase separation organizes eukaryotic cells through formation of biomolecular condensates, compartments that concentrate proteins and RNA without a surrounding membrane. Of greatest current impact is his seminal work on liquid-liquid phase separation in cells and how the resulting membrane-less organelles participate in fundamental cellular physiology. His group showed that diverse multivalent molecules, including natural and engineered multidomain proteins, intrinsically disordered proteins and nucleic acids, undergo phase separation in vitro and in cells, forming distinct structures with unique functions. Further, they demonstrated how covalent modifications can control the formation and dissolution of condensates and provided initial models to explain condensate composition. Dr. Rosen's work has important implications for protein chemistry, biophysics and cell biology, and for human diseases such as neurodegeneration and cancer.

**The Hans Neurath Award**, sponsored by The Hans Neurath Foundation, seeks to honor individuals who have made a recent contribution of exceptional merit to basic protein research. In 2018, the Hans Neurath Awardee is **Professor David Baker** (University of Washington). Dr. Baker's scientific achievements have put him at the forefront of many disciplines in computational protein science over the past decade. Some of these achievements have included: Advances in de novo protein design and protein structure prediction of thousands of proteins of

unknown structure using Rosetta atomistic modeling and evolutionary couplings; atomistic refinement of x-ray crystallographic structures, which has been packaged in the most popular software suite for x-ray crystallography, PHENIX; and reproducible design of stable, atomically accurate, small proteins, which may be used as binders and inhibitors. These breakthroughs required many additional technical advances in modeling and experimental characterization, and they reduce to practice what was for many decades the holy grail of protein science: fundamental understanding of the determinants of protein structure and stability that leads to consistent predictive capabilities, including the ability to design protein shapes and functions as desired.

**The Stein & Moore Award**, sponsored by The Protein Society, is named for Nobel laureates Dr. William Stein and Dr. Stanford Moore. The award is given to recognize eminent leaders in protein science who have made sustained high impact research contributions to the field. The 2018 recipient is **Professor Raymond Stevens** (University of Southern California). Dr. Raymond Stevens has pioneered the development of membrane protein structural biology technologies including nanoliter crystallization robotics, nanoliter imaging, micro-expression and screening of constructs, thermal stability analysis, and the fusion partner tool chest that led to the ground breaking seminal work on the structures and mechanistic understanding of the G protein-coupled receptor superfamily. His latest and quite possibly most impactful endeavor is to create the first atomic model of the human body that can be used for testing drugs without any risk to patients' health. He founded six biotechnology companies focused on structure-based drug design and was involved in the development of several marketed drugs to treat a number of different human diseases. Dr. Stevens also founded two research institutes - iHuman Institute in Shanghai, China and Bridge Institute in Los Angeles, CA.

**The Protein Science Young Investigator Award**, named for the academic journal of the Society, recognizes a scientist within the first 8 years of an independent career who has made an important contribution to the study of proteins. The 2019 recipient is **Professor Brandon Ruotolo** (University of Michigan). Dr. Ruotolo, Associate Professor of Chemistry, has made continual and substantive contributions to our understanding of protein structure in the absence of bulk solvent, performing pioneering ion mobility-mass spectrometry measurements on model peptide, protein and multi-protein complex systems that have illustrated the level of conformational memory retained by biopolymers in the gas phase. Dr. Ruotolo is also responsible for the creation of new measurement technologies that have furthered our understanding of protein biophysics and structure. Most recently, Dr. Ruotolo has spearheaded the development of collision induced unfolding for the rapid analysis of protein complex structure and stability and demonstrated the utility of such experiments for applications ranging from conformationally-selective inhibitor screening to the characterization of biotherapeutics.

---

*Delegates, exhibitors, sponsors and the press can learn more about the 32<sup>nd</sup> Annual Symposium at The Protein Society website <http://www.proteinsociety.org/page/annual-symposium> or by calling (844) 377-6834.*

*\*Dr. David Baker will not be able to attend this year's Symposium, but he will present a talk at the 2019 Annual Symposium in Seattle, Washington.*

###

The Protein Society is the leading international Society devoted to furthering research and development in protein science. Founded in 1986, the purpose of the Society is to provide international forums to facilitate communication, cooperation, and collaboration regarding all aspects of the study of proteins. In support of these goals, the Society publishes *Protein Science*, the premier journal in the field, hosts an annual international symposium, and facilitates the education of early-career protein scientists across all lines of discipline. The Protein Society members represent a wide spectrum of academic, industry, governmental, and non-profit institutions from more than 50 countries around the world. Media inquiries can be directed to Raluca Cadar, Executive Director at 844.377.6834.