Zbignew Dauter Selected to Receive the 2017 ACA Patterson Award
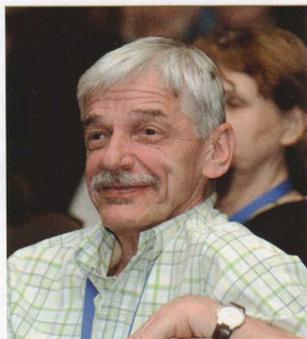
For over 30 years, Zbignew Dauter has been one of the leading proponents of the use of synchrotron radiation for advancing the methodology and speed of macromolecular crystal structure determination and for enhancement of the quality of the results. Zbigniew Dauter's career has been centered at synchrotron beamlines, including those at the EMBL Outstation in Hamburg, at the National Synchrotron Light Source at Brookhaven and at the Advanced Photon Source at Argonne, where he has played a significant role in supporting users at these facilities. More importantly, in the larger picture, he has been an innovative developer of methodology with highly influential studies on the use of anomalous diffraction in structure determinations and in biomolecular structure analysis at true atomic resolution. He has strongly influenced the development of phasing methods based on native anomalous scatterers. He has analyzed many structures at exceptional resolution and detail that provided new insights in biological chemistry.

Dauter's work on utilizing anomalous scattering, has helped to develop methods for phasing using both light atoms such as sulfur and phosphorus, and also halogen atoms. Sulfur is intrinsic to most proteins, and advances in instrumentation and software have enabled phasing of more and more complicated structures. He is among the leaders in this area, with an emphasis on obtaining high quality diffraction data at what are referred to as 'non-heroic x-ray wavelengths' i.e. without resorting to the longer wavelengths where these light atoms' anomalous scattering are set to increase but at the 'cost' of sample absorption and where the experiment has the challenge, in the ideal, of working in vacuo. Zbigniew Dauter has also pioneered the application of phosphorus anomalous scattering to solve nucleic acid structures. In a separate development one of his most important contributions was the introduction of fast soaks of macromolecular crystals with high concentrations of halide ions (Br- and I-) for phasing by anomalous dispersion. This latter method has been adopted by many subsequent investigators to solve novel macromolecular structures, including ones intransient to other methods.

He is a sought-after lecturer and workshop instructor, and indeed he has assisted even the most experienced crystallographers in their work through his insights presented in his keynote and plenary lectures. Along with his colleagues he applies his crystallographic exptertise to indentify / correct errors in published macromolecular crystal structures. His extraordinary depth of understanding also comes to the fore in his longstanding work as a Section Editor of the biological crystallography section (D) of *Acta Crystallographica*, where he handles papers expeditiously and provides substantial insight. He is, as well, very much involved in advisory committees for synchrotron facilities. Zbigniew is also an extraordinary teacher. He has answered the call to take part in numerous workshops on data collection where he has left an indelible imprint on the minds of emerging crystallographers. He has also delivered many plenary lectures at international conferences where, in his inimitable style, he both educates and entertains.

Zbigniew is an exceptionally productive scientist working in diverse areas of crystallography; indeed he is one of the very rare examples of a crystallographer who has published in all the sections of *Acta Crystallographica*. Zbigniew Dauter embodies the positive spirit of scientific research at all levels, in depth and in breadth, and fulfils the vision of the ACA Patterson Award *To recognize and encourage outstanding research in the structure of matter by diffraction methods, including the methodology of structure determination and/or innovative application of diffraction methods.*

Selection Committee: John R Helliwell (Chair), A. Brunger, W. Hendrickson, A. Sarjeant, Ton Spek, J. Britten, M. Nespolo, Vivian Stojanoff

Helen M. Berman Selected as Receipient of the 1st ACA David Rognlie Award

Helen Berman received her PhD in Chemistry in 1967 from the University of Pittsburgh under the direction of George Jeffrey, and stayed on for postdoctoral training as a National Institutes of Health Trainee. In 1969, she joined the Fox Chase Cancer Center, where her research program focused on nucleic acid crystallography. In 1989, she joined the faculty at Rutgers, The State University of New Jersey, where she is now a Board of Governors Professor of Chemistry and Chemical Biology. At Rutgers, she studied collagen and protein-nucleic acid complexes in addition to nucleic acids, and at the same time developed structural databases and ontologies.

Helen has been a champion for open access to scientific information since the concept of data sharing was in its infancy. Beginning in 1971, she played an influential role in the initiation and early development of the Protein Data Bank (PDB), first operated by Brookhaven National Laboratory. For nearly five-decades she has been committed to ensuring that the PDB archive has been a resource created by, and for, the community. As head of the Research Collaboratory for Structural Bioinformatics (RCSB), Helen became the Director of the PDB in 1998, and developed the RCSB PDB into a vital and key resource for biology and education (*rcsb.org*). The primary reference for the RCSB PDB (*Nucleic Acids Research, 2000, 28: 235-242*) has been cited over 20,000 times and was included in Nature's 2014 list of the 100 most-cited papers as tracked by the *Web of Science*. Today, she serves the RCSB PDB as Director Emerita and Associate Director.

In 2003, Helen formed the Worldwide PDB with groups in the UK and Japan to ensure that a single PDB archive woiuld continue to be freely and publicly available to the global community (*wwpdb.org*). Her passion for making structural data accessible and understandable by a broad community has driven the development of other bioinformatics resources,