



## Jane (Shelby) Richardson

Science Talent Search Finalist 1958  
MacArthur Fellow 1985

Of the 635 MacArthur Foundation “genius” grants made to date, less than 30 percent have been awarded in the hard sciences, and only one has been given in the field of crystallography – in 1985 to Jane (Shelby) Richardson. Now a renowned biophysicist, Richardson early interest was in astronomy. By junior high she was grinding mirrors for her own telescope and in 1958 became a Science Talent Search finalist with a project that tracked the orbit of a small Russian satellite that had captured the attention and imagination of people around the world - Sputnik. Her Science Talent Search experience is marked by memories of roaming the halls at night “talking about shared intellectual passions.”

Following high school, her interests shifted from astronomy, math and physics to philosophy. “One thing I really appreciated was the tolerance and vision that let me keep my scholarship even though I switched to a major in philosophy partway through college; that was the perspective I got excited about at the time, and it turned out to have a very useful payoff in my later career in biophysics.”

After completing her philosophy major at Swarthmore College and doing graduate work at Harvard, she landed a job in a lab at MIT and was introduced to inorganic chemistry. At MIT she met her future husband, David Richardson, and joined him in his work on protein structures. Today they are both professors of biochemistry at Duke University Medical Center where their research continues to unravel the mysteries of how, why and by what rules proteins create their unique 3D structures.

Richardson and her husband have worked together for nearly forty years and were among the first to do protein crystallography and protein *de novo* design. According to Richardson, “The aim of our research is to understand the three-dimensional structure of proteins and how that structure is formed. Our methods are the study and comparison of the known structures, and especially the *de novo* design of new model proteins and their synthesis and characterization. We also develop new tools, where needed, for the representation and modeling of macromolecules.”

These tools include:

- ribbon drawings for showing overall folds (through which Richardson became an accomplished and widely published illustrator),
- kinemages (for “kinetic images”) and the associated Mage 3D computer graphics program,
- the Reduce and Probe programs for improving the actuality and accuracy of structure determinations.

“A good scientist is completely open-minded but ceaselessly critical of every assumption. ... Protein design is a good way for students, trainees, and all of us to ask very fundamental questions about why certain sequences form the specific structures they do, because starting all over again from scratch can make you stumble over your wrong assumptions even if you didn't know they were there.”