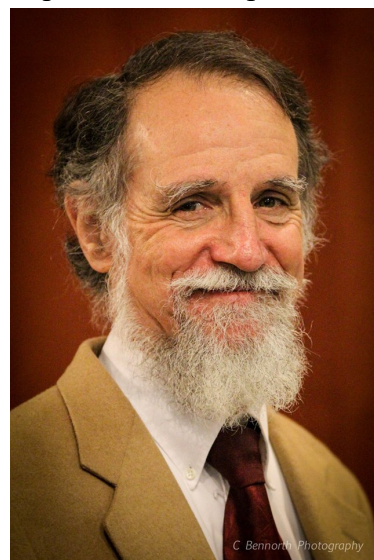


Andrew J Howard

I'm a structural biologist.

I joined the faculty at IIT in 1996 after twelve years as a researcher in three small companies on the East Coast. As a structural biologist, I use a physically sophisticated experimental tool, X-ray crystallography, to probe the three-dimensional structures of large molecules—mostly proteins, but sometimes nucleic acids. By determining these structures, my colleagues and I are able to determine what these molecules do and how they do it. This answers some questions in basic biology, and it enables the production of pharmaceutical and industrial products that depend on the knowledge of these structures. We can also use our knowledge of these structural realities to understand how some substances, including illegal drugs, can exert harmful effects on people.

Most researchers focus either on developing and refining methods, or on applying those methods to tackle new problems. My emphasis is on methods development, because in that way I'm able to use my knowledge of both Life Science and Physical Science. Between 1996 and 2004 I spent much of my time at the Advanced Photon Source (APS) at Argonne National Laboratory, building and operating a facility within the APS at which researchers could use X-ray crystallography as a tool in designing new ethical pharmaceuticals. Since then I've been developing methods and using them on campus, although I continue to do experiments at the APS.



Current Project

My current research focus involves revisiting and reanalyzing existing three-dimensional structures determined via X-ray crystallography. The purpose of these revisits is to apply up-to-date tools and my knowledge of how proteins are held together to these known structures so that the final models of these structures can more faithfully reflect the realities that the crystallographic experiments indicate. I'm developing new tools to highlight the reliability of particular parts of these structures, including the water molecules that are closely bound to the protein or nucleic acid molecules. Some of my work involves helping a small company called DeNovX develop better ways of growing protein crystals and demonstrating that these crystallization tools are useful.

What do you think?

If we understood more fully how illegal drugs damage the human body, would we be closer to finding a solution to drug abuse? How do we decide whether the models of the structures we study are really reliable? Can our knowledge of 3-D structures speed up the development of better drugs and vaccines to combat scourges like COVID-19, pathogens that have developed resistance to existing drugs, and opioid addiction?