My research interests have always been focused on understanding how molecules affecting our everyday life work and interact with each other. Since enzymes, proteins, DNA, and RNA, and their ligands, drugs, cofactors, and metal ions, are all extremely tiny entities invisible to the naked eye, I use crystallographic methods to bring them alive. In a crystal, molecules associate themselves following a regular pattern in three-dimensions, so that impinging extremely energetic light on them will cause it to diffract. The diffracted rays produce an image that is recorded and mathematically converted to atom types, bond lengths, bond angles, and non-covalent bonding interactions. Since the level of resolution achieved with this methodology is the atom, powerful X-ray light, the kind produced at a synchrotron source like SLAC, is employed.

My fifteen years experience, first in single-crystal small-molecule crystallography (molecules of less than hundred atoms), and then in macromolecular crystallography, had taught me how difficult the road to a successful crystal structure determination can be. Obtaining good quality crystals for X-ray diffraction analysis is paramount: your subject could never crystallize! Yet, tremendous advances in recent years, with the inception of automation and platforms dedicated for protein crystallography, have endowed researchers new tools to tip the balance towards achieving the goal of a successful crystal structure determination.

Now, as part of the Stanford ChEM-H Macromolecular Structure Knowledge Center, I will continue focusing my studies on crystals, and, therefore, I am welcoming you to join our community.