

## Sichun Yang, Ph.D. (biophysics)

### Assistant Professor

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### Biography

Dr. Sichun Yang started his biophysical research at the University of California San Diego after receiving B.S. and M.S. in Physics from China. He obtained a Ph.D. in Biophysics from UCSD on September 9<sup>th</sup>, 2006. His PhD research with Dr. Herbert Levine and Dr. Jose Onuchic (both now at Rice) focused on protein folding and protein-protein assembly, from the perspective of computer simulation and statistical mechanics. In 2006-2010, Dr. Yang carried out his postdoctoral research with Dr. Benoit Roux at the Department of Biochemistry and Molecular Biology at the University of Chicago. He began to bridge computation and experiment and demonstrated that combining computer simulation and synchrotron X-ray scattering is ideally positioned to study the structural dynamics of bimolecular complexes (PNAS, 2010). This work has been featured in a *News & Views* article (Nature, 2010). In collaboration with Dr. Geof Greene at UChicago, Dr. Yang began to work on the molecular biophysics of estrogen receptor (ER), a key molecule in breast cancer biology, and had received a prestigious *idea award* from the Department of Defense.

Dr. Yang joined the School of Medicine at Case Western Reserve University in 2010. Since then, he has been focusing on basic and translational studies of estrogen receptor (ER), ranging from fundamental biophysics to drug discovery. With a recent 5-year NIH R01 support (as well as DoD, ACS and CTSC), he has developed a powerful integrated multi-biophysical platform, termed iSPOT (i.e., the integration of Small-angle scattering, hydroxyl radical footprinting, and docking simulation). We have provided a principle-of-principle demonstration on well-studied molecular systems and more importantly, a realistic application to solving a first mediate-resolution structure of ER, a key molecule in breast cancer biology. Also, Dr. Yang has been actively researching the folding of an intrinsically disordered domain of the ER to understand the role of such a protein folding phenomena in cancer activation. His contribution in algorithms and methods development (e.g., Fast-SAXS-pro, protection factor analysis, and iSPOT) leads to collaboration with computational and experimental biophysicists here at Cleveland and other parts of the globe.