Curriculum Vitae for Sichun Yang

Contact Information

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Research Interests

Our research is focused on the assembly and function of nuclear hormone receptors by employing an integrated computational and experimental approach. Another area is on computational prediction of protein-protein interactions and experimental validation via a P-factor analysis. Our group is actively involved in the development of SAXS-based methods and software packages for structural studies of complex-forming macromolecules.

Awards

NSF-sponsored ICAM Fellowship, University of California San Diego 2005
Peking University Research Innovation Award, Peking University 2001

Selected Publications

Ravikumar, K., Huang, W., and Yang, S. "Coarse-grained simulations of protein-protein association: An energy landscape perspective," *Biophys. J.*, 10.1016/j.bpj.2012.07.013, (2012). (Highlighted as a cover article)

Khurana, S., Chakraborty, S., Zhao, X., Liu, Y., Guan D., Lam M., Huang, W., Yang, S., and Kao, H. "Identification of a novel LXXLL motif in alpha actinin 4 (ACTN4) spliced isoform that is critical for its interaction with estrogen receptor alpha and co-activators," *J. Biol. Chem*., submitted, (2012).

Yang, S. and Roux, B. "EROS: Better than SAXS!," *Structure* 19 (1), 3-4 (2011)

Yang, S., Blachowicz, L., Makowski, L., and Roux, B. "Multidomain assembled states of Hck tyrosine kinase in solution," *Proc. Natl. Acad. Sci. USA* 107 (36), 15757–15762 (2010) [Featured in a *News & Views* article in *Nature* (2010), and highlighted again in a Commentary in *Nature Chemical Biology* (2012)].

Yang, S., Parisien, M., Major, F., and Roux, B. "RNA structure determination using SAXS data," *J. Phys. Chem. B.* 114 (31), 10039-10048 (2010).

Yang, S., Park, S., Makowski, L., and Roux, B. "A rapid coarse residue-based computational method for X-ray solution scattering characterization of protein folds and multiple conformational states of large protein complexes," *Biophys. J.* 96 (11), 4449–4463 (2009).

Yang, S., Onuchic, J. N., Garcia, A. E., and Levine, H. "Folding time predictions from all-atom replica exchange simulations," *J. Mol. Biol.*372 (3), 756–763 (2007).