

# BIOLS SEMINAR SERIES

## 北京生命科学研究院精品讲座

报告时间：2014年4月22日（星期二）下午14:00

报告地点：中国科学院生物物理研究所生物物理所9501会议室

报告题目：Structural insights into H1 bound nucleosome and CENP-C bound centromeric nucleosome as revealed by NMR.

报告人：Dr. Yawen Bai. Senior Investigator. Laboratory of Biochemistry and Molecular Biology, National Cancer Institute, NIH.

欢迎广大科研人员和研究生光临！



Dr. Yawen Bai received his Ph.D. in biophysics from the University of Pennsylvania Medical School in 1994. He did his Ph.D. work in Walter Englander's lab, where he developed the native-state hydrogen exchange method to detect partially unfolded states of proteins. Then he completed his postdoctoral training in Peter Wright's lab at the Scripps Research Institute, where he studied protein folding using multi-dimensional NMR methods. He joined the Lab of Biochemistry of NCI, NIH as an independent investigator in 1997, and became a senior investigator in 2006.

Prof. Bai's research group is interested in understanding the basic principles that control the dynamic folding/unfolding processes of protein and chromatin using biophysical approaches. The failure of proteins to properly fold can impact their activity and/or stability, while the folding and compaction of DNA is critical for the regulation of gene expression and cell function. Defects in either of these processes can contribute to the development of many diseases, including cancer. Thus, an understanding of the fundamental mechanisms involved in protein and chromatin folding processes is critical for the advancement of cancer research, and for the discovery of potential treatment options.

### Key Publications:

- 2014. The catalytic subunit of the SWR1 remodeler is a histone chaperone for the H2A.Z-H2B dimer. *Mol. Cell.* 53: 498-505.
- 2013. A conserved mechanism for centromeric nucleosome recognition by centromere protein CENP-C. *Science.* 340: 111-3.
- 2013. Structural insights into the histone H1-nucleosome complex. *Proc. Natl. Acad. Sci. U.S.A.* 110: 19390-5.
- 2011. Architecture of the high mobility group nucleosomal protein 2-nucleosome complex as revealed by methyl-based NMR. *Proc. Natl. Acad. Sci. U.S.A.* 108:12283-8.
- 2011. Structure of the budding yeast *Saccharomyces cerevisiae* centromeric histones Cse4-H4 complexed with the chaperone Scm3. *Proc. Natl. Acad. Sci. U.S.A.* 108:E596.
- 2011. Structural basis for recognition of centromeric histone variant CenH3 by the Scm3 chaperone. *Nature.* 472: 234-237.
- 2009. Characterization of the tail domain of histone H3 in nucleosome in condensed nucleosome arrays by NMR and hydrogen exchange, *J. Am. Chem. Soc.* 131:15104-15105.
- 2008. Structure of chaperone Chz1 complexed with histones H2A.Z-H2B. *Nat. Struct. Mol. Biol.* 15, 868.
- 2007. Structure Biology: Analysis of protein-folding cooperativity. *Nature.* 445, E16-E17.
- 2005. A protein folding pathway with multiple intermediates at atomic resolution. *Proc Natl. Acad. Sci. USA.* 102: 5026-31.
- 1995. Protein folding intermediates: native-state hydrogen exchange. *Science.* 269: 192-7.

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