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Date: Monday, November 2, 2015
Time: 14:00 – 15:00
Venue: C210, Center Bldg., Level C

"Structural studies of histone variants in chromatin"

Abstract:

Chromatin plays pivotal roles in packaging of genomic DNA within the nucleus. The nucleosome is the fundamental unit of chromatin, and is involved in the epigenetic regulation of DNA metabolism in eukaryotes. Four core histones, H2A, H2B, H3, and H4, are protein components of the nucleosome, and a histone octamer, containing two of each histone, H2A, H2B, H3, and H4, wraps about 150 base-pairs of DNA. Canonical histones are incorporated into chromatin during the S-phase of the cell cycle. In addition to canonical histones, many histone variants are identified as non-allelic isoforms in higher eukaryotes. In contrast to canonical histones, production of histone variants is not restricted at the S-phase, and tissue/cell type-specific production has been reported, suggesting that histone variants may have their specific functions in chromatin organization. To understand the contribution of histone variants in the functional chromatin architecture, we have determined the three-dimensional structures of nucleosomes containing histone variants by X-ray crystallography, and have studied their biophysical, biochemical, and biological functions [1-4]. Here, I will present our current results and discuss how histone variants contribute to the organization of the functional chromatin landscape.

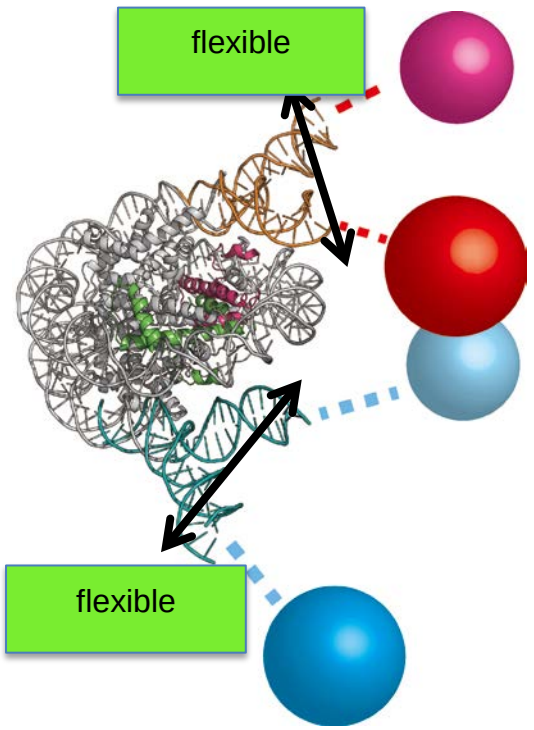

Fig. 1. Structure and dynamics of a nucleosome affect the higher order folding of chromatin.

References:

1. Arimura et al., Scientific Reports, 3, 3510 (2013).
2. N. Horikoshi et al., Acta Cryst, D69, 2431-2439 (2013).
3. H. Tachiwana et al., Nature, 476, 232-235 (2011).
4. H. Tachiwana et al., Proc Natl Acad Sci USA, 107, 10454-10459 (2010).