Computational, biochemical, and NMR-driven structural studies on histone variant H2A.B

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Propositions

1. The H2A.B-H2B dimer has the canonical histone-fold core in solution.
   This thesis, Chapter 3
2. The H2A.B-H2B dimer has higher thermostability compared to the canonical H2A-H2B dimer, due to reduced electrostatic repulsion between the two histones.
   This thesis, Chapter 3
3. The H3 N-terminal tail has increased flexibility and is less DNA-bound in the H2A.B nucleosome compared to canonical nucleosome.
   This thesis, Chapter 4
4. The acidic patch of the canonical nucleosome is acidic at physiological pH condition.
   This thesis, Chapter 5
5. With ILV labeling strategy and methyl TROSY experiments, NMR is a unique technique to study nucleosome dynamics and nucleosome-protein interactions in solution.
   Schutz & Sprangers, PNMRS, 2020, 116, 56-84.
6. The N-terminus of H2A.B is an RNA binding module.
   Soboleva et al., PLoS Genet, 2017, 13, e1006633.
7. Consistency regarding protein names is indispensable for efficient literature searching.
8. *In silico* protein modeling will eventually be the leading force in protein studies, and wet lab experiments will become second line support when needed.
9. We don't know the things we don't know.
10. We think we know the things we know.