# How electrostatic interactions drive nucleosome binding of RNF168 & PSIP : structural studies and their implications for rational drug design

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# STELLINGEN

Behorend bij het proefschrift

## HOW ELECTROSTATIC INTERACTIONS DRIVE NUCLEOSOME BINDING OF RNF168 & PSIP1

1. The basic helix residues R57, R63 and R67 are essential in the binding of RNF168$^{RING}$ to the nucleosomal acidic patch.

   *This thesis, chapter 2*

2. The geometric arrangement of positive charges surrounding the canonical arginine anchor is the cause of specificity in acidic patch binding by RING domains.

   *This thesis, chapter 3 & 4*

3. Through the addition of charged residues to a peptide, the nature of a complex can be shifted from a specific binding mode to an encounter complex.

   *This thesis, chapter 2*

4. Through the addition of charged residues to a peptide, the nature of a complex can be shifted from a specific binding mode to an encounter complex.

   *This thesis, chapter 3 & 4*

5. The side chain alkylation of cysteine offers the possibility to identify functional groups that exceed the binding affinity of trimethyllysine for PSIP1.

   *This thesis, chapter 4*

6. Formation of encounter complexes results in limited to no observed CSPs in NMR titration experiments.

*This thesis, chapter 4*
*& Schilder, J. and M. Ubbink (2013)*

7. The publication and sharing of structural models of protein complexes allows for iterative refinement based on positive as well as negative results and allows to obtain vital information on biological systems that is yet inaccessible.

*This thesis, chapter 1*

8. Modification of peptides derived from protein-protein interactions is a promising strategy to develop inhibitors of these interactions.

*This thesis, chapter 3 & 4*

9. The complexity and size of nucleosome-protein complexes necessitates integration of various biophysical data by computational approaches for understanding of structure-function relationships

*This thesis, chapter 1*

10. The amount of experimental data needed in integrative structural biology is inversely correlated to advancements in computational capacities.

11. By opposing the *status quo* in scientific publishing, Alexsandra Elbakyan and Aaron Swartz contributed more to science than the author of this thesis ever could.