Propositions - Stellingen

Keep in touch

The role of cohesin and CTCF in organizing the human genome

1. Loss of cohesin or CTCF affects chromatin structure in different ways (This thesis).

2. NIPBL influences transcription in two ways; directly due to its binding to the promoters and indirectly by loading of cohesin complexes which then regulate genes by chromatin insulation and chromosomal long-range interactions (This thesis).

3. The chromatin fiber is organized in topological domains (This thesis and Dixon JR. et al., Nature 2012).

4. Several observations have led to the proposal that CTCF might act as "master weaver" of the genome via recruitment of cohesin to facilitate long-range interactions (This thesis and Phillips JE. et al., Cell 2009).

5. The different genomic binding pattern of NIPBL and cohesin is in contrast with observations in mouse embryonic stem cells (mouse ES) that report colocalization of cohesin with NIPBL (This thesis and Kagey MH. et al., Nature 2010).

6. All genomes in a population of cells can be expected to fold according to the same probabilistic rules, yet every single cell likely has a different genome structure. (Holwerda S., de Laat W., Front Genet. 2012).

7. Cohesin functionally behaves as a tissue-specific transcriptional regulator, independent of CTCF binding (Schmidt D. et al., 2011).

8. Although the focus on CTCF-mediated chromatin loops is an important first step in understanding the higher order structure of chromatin domains, it is highly likely that other types of chromatin looping interactions exist, which may involve additional proteins (Espinoza CA., Ren B., Nat Genet, 2011).

9. "A person who never made a mistake never tried anything new." (Albert Einstein)

10. "It's easier to resist at the beginning than at the end." (Leonardo da Vinci)

11. "It is something unpredictable but in the end it is right. I hope you had the time of your life." (Good Riddance -Time of Your Life, Green day 1997)