Stellingen

behorende bij het proefschrift

Dynamics of Protein Ubiquitination upon Proteasome Modulation
A Quantitative Mass Spectrometry Approach

1. Proteins which do both increase in abundance and are more ubiquitinated upon proteasome inactivation are not by definition targets for proteasome-dependent degradation (this thesis).

2. dsRNA-mediated knockdown of proteasome subunits Prosalpha5, Prosbeta6 and RPN11 is a recommendable method to interfere with proteasome functioning (this thesis).

3. Compared to USP14 and UCHL5, RPN11 is the major player in deubiquitination-mediated proteasome-dependent protein degradation (this thesis).

4. UCHL5 is the major proteasome-bound DUB that responds to cellular stress (this thesis).

5. Major cellular events, such as ecdysone hormone signaling, could still result in only minor global proteome dynamics (this thesis).

6. Reminiscent of a ubiquitin cloud, the local concentration of substrate-attached ubiquitin molecules, rather than the linkage between them, might be an important determinant of proteasomal delivery (Richard Yau and Michael Rape).

7. It appears that most proteins will experience ubiquitination at some point in their cellular lifetime (David Komander).

8. Ubiquitination alone is not sufficient to target proteins for degradation.

9. A main bottleneck in proteomics is the downstream biological analysis of highly multivariate quantitative protein abundance data generated using mass-spectrometry-based analysis (Jürgen Cox)

10. The use of proteomics in the clinic is the future of personalized medicine

11. Absence of evidence is not evidence of absence (Carl Sagan)