

Propositions belonging to the thesis

A QUEST TO REVEAL NOVEL PLAYERS IN NUCLEOTIDE EXCISION REPAIR

From proteomics to mechanistic insights

1. Although discovered more than 50 years ago, NER is still full of surprises. *This thesis*
2. Quantitative proteomics is a powerful tool enabling identification of novel NER players and thereby paving the path for new mechanistic insights. *This thesis (Chapter 2, 3 and 4)*
3. Describing new roles for an old ally: next to its roles in post-replication repair pathways, the newest NER factor HLTf facilitates the removal of the incised damage-containing DNA fragment and the progression of DNA repair synthesis. *This thesis (Chapter 3)*
4. FACT (facilitate chromatin transcription) subunit Spt16 does not only facilitate chromatin transcription but also the recruitment of UVSSA to lesion-stalled RNA Polymerase II. *This thesis (Chapter 4) and Dinant, C. et al., (2013)*
5. Fluorescently-labelled photolyases, well-preserved gems with a fresh remake, enable DNA damage detection and repair in living cells and thereby open up new possibilities. *This thesis (Chapter 5)*
6. The discovery of CRISPR/Cas9 marks the beginning of a new era in genome editing.
7. The high level of scientific collaboration during crisis situations such as COVID-19 should also be the norm for regular science, not the exception.
8. Replication studies are equally important as the innovative ones, especially considering that a high number of biomedical studies cannot be reproduced. *Errington, T.M. et al., (2014)*
9. Every biologist should be taught basic data science skills to be able to analyze data in a reproducible way.
10. Publication of negative results would not only save time and resources for those addressing similar research questions but also greatly help against publication bias.
11. To scoop or to get scooped, that is the question: this seems to represent the current status in science.