# SFB 960-/BZR – Kolloquium

## 16. Oktober 2018, 17.00 Uhr
## Neubau Biologie H53

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*Architectural principles of metabolic regulation by Hfq and Crc in Pseudomonas aeruginosa*

In *Pseudomonas aeruginosa* the RNA chaperone Hfq and the *c*atabolite *r*epression *c*ontrol protein (Crc) act in conjunction as translational regulators during *c*arbon *c*atabolite *r*epression (CCR), whereas the regulatory RNA CrcZ functions as a decoy to abrogate Hfq/Crc mediated translational repression[1]. Biochemical and biophysical approaches indicated that Crc and Hfq form an assembly in the presence of RNAs containing A-rich motifs, and that Crc interacts with both, Hfq and RNA[2]. Cryo-EM studies revealed the architecture of the Hfq/Crc/RNA complex, which disclosed for the first time how an interacting protein can augment translational repression by Hfq. Moreover, it will be discussed how these insights on Hfq/Crc/CrcZ mediated regulation can be harnessed to increase Hfq-dependent antibiotic susceptibility of *Pseudomonas aeruginosa.*

[1]Sonnleitner, E. and Bläsi, U. (2014) Regulation of Hfq by the RNA CrcZ in *Pseudomonas aeruginosa* Carbon Catabolite Repression. *PloS Genet.* 10, e1004440.

[2]Sonnleitner, E., Wulf, A., Campagne, S., Pei, X.P., Wolfinger, M., Forlani, G., Prindl, K., Abdou, L., Resch, A., Allain, F., Luisi, B.F., Urlaub, H., and Bläsi, U. (2018) Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in *Pseudomonas aeruginosa*. *Nucl. Acids Res.* 46:1470-1485.

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