One of the reasons why pathogenic bacteria are so successful is their ability to survive (and even thrive) in hostile environments. To achieve such rapid adaptation, these pathogens remodel their transcriptome within minutes of stress imposition. Clearly, transcription factors determine which genes are expressed under environmental insults, however, it is becoming increasingly evident that a substantial amount of regulation also occurs post-transcriptionally. Post-transcriptional regulators, such as non-coding RNAs (ncRNAs) and RNA-binding proteins (RBPs), are now recognized as key players in controlling adaptive responses in pathogenic bacteria. By directly binding to mRNAs, these molecules can shape gene expression profiles by modulating mRNA translation and/or degradation rates.

Research in the Granneman lab focusses on elucidating the role of RBPs and ncRNAs in controlling rapid adaptive responses in pathogenic bacteria and yeast. Although a large number of RBPs proteins and ncRNAs have been identified, for the vast majority their function remains unclear. To fill this gap, we are using state-of-the-art systems biology approaches, such as kinetic CRAC (χCRAC), CLASH and quantitative proteomics. Detailed characterization of these post-transcriptional regulatory systems may uncover new avenues for improving treatment of infections and/or reveal new targets for antimicrobial drug development.

The lab has two MRC-funded full-time post-doctoral positions available to work on post-transcriptional regulation in MRSA (Methicillin Resistant Staphylococcus aureus).

Researchers with experience in next generation sequencing technologies or quantitative mass-spectrometry are particularly encouraged to apply.

To learn more about the projects and how to apply, please go to the University of Edinburgh vacancies website: **https://www.vacancies.ed.ac.uk; Vacancy Refs: 042618 and 042619**

For informal inquiries, please contact Sander Granneman (**sgrannem@ed.ac.uk**)

Relevant publications:

1. van Nues, R., Schweikert, G., de Leau, E., Selega, A., Langford, A., Franklin, R., Iosub, I., Wadsworth, P., Sanguinetti, G. & Granneman, S. Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress. *Nat Commun* **8,** 12 (2017).
2. Tree, J. J., Granneman, S., McAteer, S. P., Tollervey, D. & Gally, D. L. Identification of bacteriophage-encoded anti-sRNAs in pathogenic Escherichia coli. *Mol. Cell* **55,** 199–213 (2014).
3. Webb, S., Hector, R. D., Kudla, G. & Granneman, S. PAR-CLIP data indicate that Nrd1-Nab3-dependent transcription termination regulates expression of hundreds of protein coding genes in yeast. *Genome Biol.* **15,** R8 (2014).
4. Kudla, G., Granneman, S., Hahn, D., Beggs, J. D. & Tollervey, D. Cross-linking, ligation, and sequencing of hybrids reveals RNA-RNA interactions in yeast. *Proc. Natl. Acad. Sci. U.S.A.* **108,** 10010–10015 (2011).
5. Granneman, S., Kudla, G., Petfalski, E. & Tollervey, D. Identification of protein binding sites on U3 snoRNA and pre-rRNA by UV cross-linking and high-throughput analysis of cDNAs. *Proc. Natl. Acad. Sci. U.S.A.* **106,** 9613–9618 (2009).