*i*SEQ lunch seminar series

Wednesday 30 March 2016 at 12.00 – 13.00

Dr Sander Granneman
Centre for Systems and Synthetic Biology,
University of Edinburgh.

Talk:
Unravelling the role of RNA decay in shaping gene expression profiles during stress adaptation.

Abstract:
By rapidly rewiring their transcriptional program to adapt to environmental changes, microbes can thrive in hostile environments. Typically, the adaptation process is largely attributed to the activity of transcription factors. Yet it is becoming increasingly clear that post-transcriptional regulation, such as RNA decay, is instrumental in shaping gene expression profiles. Little is known, however, about the contribution of RNA decay factors and the signaling pathways that regulate this process.
Our aim is to obtain mechanistic insights into the role of RNA decay factors in stress adaptation. In order to address this, we have developed a vastly improved UV cross-linking and cDNA analysis method (CRAC) that enables us to measure the dynamics of protein-RNA interactions *in vivo* at very short (minute) time-scales. With the kinetic CRAC approach (χCRAC) we have been able to, for the first time, quantitatively measure the dynamics of protein-RNA interactions *in vivo* at minute time-point resolution. Our χCRAC-studies on RNA decay factors as well as RNA polymerase II revealed detailed insights into the kinetics of gene expression changes and suggested that RNA decay may contribute to stress adaptation by ensuring a balanced expression of stress-responsive genes. Results from these studies will be presented.

Venue:
Merete Barker Auditory, The Lakeside Theatres, Aarhus University, Bartholins Allé 3, 8000 Aarhus C.

Refreshments:
Sandwiches will be provided. Therefore, please email Anne Hedemand (anne@biomed.au.dk) no later than 29 March 2016, if you would like to participate.

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