



iSEQ lunch seminar series

Talk:

Deciphering gene expression with genomics: from transcriptional complexity to ribosome dynamics.

Speaker:

Vincent Pelechano, PhD, Staff Scientist. European Molecular Biology Laboratories.

Venue: Jeppe Vontillius Auditory, The Lakeside Theatres

Time: 4 March 2015 at 12.00 – 13.00

Abstract:

Gene expression is the fundamental process whereby information stored in the genome is expressed to control cellular identity and plasticity. Here I will discuss how, applying novel genome-wide approaches, we can obtain valuable insights into both transcription and translation regulation.

We have extensively characterized transcriptome architecture as well as its functional impact. By simultaneously sequencing both the 5' and 3' ends of each RNA molecule, we have showed that the complexity of overlapping transcript isoforms had been greatly underestimated. Hundreds of isoforms of coding and non-coding RNAs alike are transcribed, even in a genetically homogeneous population of cells. Most genes harbour alternative isoforms with varying regulatory signals and interactions with RNA binding proteins. In addition we explore how this heterogeneity can lead to divergent posttranscriptional fates and cellular phenotypes.

Moving downstream on the gene expression process, we show that co-translational 5'-3' mRNA decay is a general and evolutionary conserved process that produces an *in vivo* footprinting of the ribosome position from yeast to human. By measuring the relative abundance of 5'P mRNA degradation intermediates, we obtain a genome-wide drug-free measurement of ribosome dynamics, identify codon-specific ribosome pausing events and overcome previous limitations caused by the use of translation inhibitors.

In conclusion, we believe that by combining novel experimental and computational strategies to study gene expression, we can bring new insights into the basic molecular understanding of this fundamental process.

Refreshments:

Sandwiches will be provided. Therefore, please email Anne Hedemand (anne@biomed.au.dk) no later than 3 March 2015, if you would like to participate.