



iSEQ seminar series

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A real-ome or an imagin-ome? Are lncRNAs functional?

Venue: Merete Barker Auditoriet, The Lakeside Theatres

Time: 4 December 2013 at 12.00 – 13.00

Abstract:

The discovery of thousands of long noncoding loci in the human genome was unexpected. Much work is required, however, to determine whether, in general, lncRNAs contribute greatly to human biology or whether each makes only a minor contribution to overall organismal fitness.

Our evolutionary studies have shown that mammalian lncRNAs are mostly under very weak selection. This indicates either that they are rarely functional, or else that their patches of functional sequence are very short.

Our experimental research has focused on a handful of conserved mammalian lncRNAs and, somewhat to our surprise, we have identified cellular functions for each and every one.

This talk will focus on this evolutionary and lab-based work, and will look to what studies are still required to show convincingly what proportion of these enigmatic loci have fundamental functions.

Refreshments:

Sandwiches will be provided. Therefore, please email Anne Hedemand (anneh@hum-gen.au.dk) before 3 December, if you would like to participate.