**MSc thesis project at the University of Copenhagen to develop a new method to screen novel RNA-protein complexes (RNA-decoder)**

*Would you like to participate in the development of a new method that will allow answering numerous biological problems? Are you interested in uncovering the non-coding genome? If you like challenges, this is your opportunity!*

**Background:** The minority of eukaryotic DNA codes for proteins. Despite this, non-coding DNA regions are also actively transcribed by RNA polymerase II into long non-coding RNAs (lncRNA). Knowledge about the regulatory function of lncRNA transcripts is still limited. These transcripts form protein-RNA complexes to modulate different activities, such as epigenetic regulation or nuclear organization. However, screening which proteins are bound to a specific RNA transcript (whether coding mRNA or lncRNA) is challenging.

**Aim:** In this project you will focus in developing a promising new method to screen novel RNA-protein complexes. Through the application of the developed method, you will be able to uncover the functional differences between RNA-protein complexes in coding and lncRNA transcripts and study how the protein composition changes as cells are exposed to different conditions.

**Methods:** To solve which proteins are bound to a specific RNA transcript, you are going to develop a completely new technique – *RNA-decoder* – which relies on DNA barcoding and RNA immunoprecipitation followed by sequencing (RIP-Seq). In this method, ***CRISPR-based genomic engineering*** is used to prepare a library of yeast *S. cerevisiae* strains. In the library each individual strain combines one different protein marked with a common tag, with two unique barcodes inserted in its genome, one within a coding region, and the other at a non-coding region. After pooling the entire library, RNAs associated with all yeast proteins carrying the tag are pulled down by ***RNA immunoprecipitation***. The unique barcodes connecting the identities of proteins and specific RNAs are then detected by ***high-throughput cDNA sequencing***. Subsequent ***bioinformatics analyses*** will reveal the specific proteins associated with specific RNA transcripts. The advantage of such approach is that it does not rely on mass spectrometry and therefore avoids challenges that it implies.

**Site of research:** The work will be carried out in in Sebastian Marquardt´s lab at Copenhagen University (<https://plen.ku.dk/english/research/molecular_plant_biology/nct/>). Marquardt lab is located at the Department of Molecular Plant Biology. The MSc thesis will be supervised jointly by Assistant Professor Desire Garcia Pichardo (Copenhagen University) and Academy Research Fellow Matti Turtola (University of Turku, Department of Life Technologies). Part of the research project can also be carried out in University of Turku at the Department of Life Technologies.

**If you are interested, please contact Matti Turtola for further information (matti.turtola@utu.fi).**