



## Microarrays in Non-Coding RNAs Profiling

Guest Editor:

**Prof. Dr. Shizuka Uchida**

Center for RNA Medicine,  
Department of Clinical Medicine,  
Aalborg University, Frederikskaj  
10B, 2. (Building C), DK-2450  
Copenhagen SV, Denmark

Deadline for manuscript  
submissions:

**closed (30 April 2018)**

### Message from the Guest Editor

Dear Colleagues,

The presence of non-coding RNAs (ncRNAs) is firmly fixed in various fields to overturn the previous concepts of junk DNA and transcriptional noise. Many ncRNAs have been shown to be functional as in the case of microRNAs and more recent long non-coding RNAs. It is predicted that the number of ncRNAs well surpasses that of protein-coding genes as organisms become more complex. Given such complexity, it is suggested that ncRNAs could be a key to decipher yet unknown mechanisms of physiological processes and disease status. Although the emergence of next generation sequencing (NGS) technology revolutionized the way genomics and transcriptomics studies are conducted, the past generation technology microarray still outperforms NGS for its specificity and ease of data analysis. In this Special Issue, we would like to revisit the power of microarrays in ncRNAs profiling to facilitate further functional studies of exciting molecules that hold more functions to be discovered.

