Most of the protein coding genes of higher eukaryotes contain introns which have to be removed from primary transcripts to make mRNA which can be used as a template for protein synthesis. This crucial step in the pre-mRNA processing is carried out by the spliceosome, a complex ribonucleoprotein machine formed from small ribonucleoprotein particles (snRNPs). snRNPs biogenesis is a complex process composed of several steps which take place in both the cytoplasm and the nucleus. Spliceosome assembly is highly dynamic and tightly regulated and pre-mRNA splicing depends not only on the sequence of the pre-mRNA itself but also on the nuclear context, such as the chromatin modifications.

How do cells regulate where and when the spliceosome would be assembled? What determines which introns will be spliced? These are fundamental, yet unanswered, biological questions. In this work we analyzed the formation of splicing machinery in the context of the cell nucleus from several different points of view.

First, we investigated the unexpected connection between splicing factor U1-70K and the survival of motor neurons (SMN) complex which is a major player in the snRNP biogenesis pathway. We revealed that U1-70K interacts with the SMN complex and that this interaction is crucial for the stability of nuclear gems, small non-membrane organelles associated with neurodegenerative diseases.
Secondly, we explored the role of an SR-like protein RNA binding motif 39 (RBM39) in the regulation of alternative splicing of the vascular endothelial growth factor (VEGF) gene. We showed that RBM39 is a part of the early spliceosomal complex where it interacts with proteins U1-70K and U2AF35.

Finally, we characterized the interactions of the histone acetylation reader protein Brd2 with acetylated chromatin in vivo.