The broad focus of our research is on pre-mRNA splicing regulation and the importance of alternative splicing in generating transcriptomic diversity unique to our species.

We study mechanisms of alternative splicing regulation using a combination of computational and experimental (mostly molecular biology) methods. We also study the potential link between DNA packaging and splicing, and are interested in the effects nucleosomal positioning, specific histone modifications and other epigenetic characteristics have on pre-mRNA processing.

An increasing body of evidence indicates that transcription and splicing are coupled and it is accepted that chromatin organization and DNA modification regulate transcription. Little is known, however, about the cross-talk between chromatin structure and splicing. We continue to examine how RNA polymerase II and DNA modifications mediate cross-talk between chromatin structure and splicing (see Schwartz et al., Nature Structural and Molecular Biology, 2009). We also study splicing-related genetic diseases like the neurodegenerative disease Familial Dysautonomia and the link between splicing and various cancer types (lung and colon cancer, for example) using molecular and computational methods. Finally, we study the role splicing plays in microRNA (miRNA) regulation as well.
Research Fields

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Diagram a: pre-mRNA, RNAPII, exon, nucleosome

Diagram b: cap, pre-mRNA, 5'SS, 3'SS, RNAPII, exon, nucleosome