

Welcome

Written by Administrator

Saturday, 07 July 2007 09:54 - Last Updated Tuesday, 25 October 2016 10:07



Alternative splicing is a mechanism by which more than one mRNA transcripts are generated from the same mRNA precursor. Recent findings suggest that almost all the human genes undergo alternatively spliced, and we demonstrated that humans contain the highest level of alternative splicing. Alternative splicing can be specific to tissue type, environment or developmental stage. Splice variants have also been implicated in various diseases including cancer. Detection of these variants will enhance our understanding of the complexity of the human genome and provide disease-specific and prognostic biomarkers. Our group has made seminal contributions to our understanding of the complexity in genomic expression through alternative mRNA splicing and the involvement of this process in genetic disorders and cancer.

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.

We are currently seeking highly motivated individuals who want to join us. Please contact us at

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The Edmond J. Safra Center for Bioinformatics

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