Despite decades of research, the mechanism used by the mRNA splicing machinery to precisely identify short exonic islands within the vast intronic ocean remains to a large extent obscure. Our group has recently made several major discoveries pertaining to splicing unit recognition. Firstly, we demonstrated that nucleosome positioning and DNA methylation mark the exon-intron structure (*Schwartz et al., Nature SMB, 2009; Schwartz and Ast, EMBO 2010; Gelfman et al., Genome Research 2013. Gelfman and Ast, Epigenomics 2013*
). Secondly, we found that during the evolution of warm-blooded organisms two exon-intron GC content architectures had developed, and that these relate to two different modes through which the splicing machinery recognizes exons and introns (
Amit et al., 2012, Cell Reports
). Our current research focuses on two aspects of splicing unit recognition: (
i
) we will illuminate the role that DNA methylation plays in the correct selection of exons and (
ii
) we plan to identify the elements that contribute to splicing unit recognition in GC-rich and GC-poor environments and how the two differ.