

P037 RNA-aptamers binding the dsRBD

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The double-stranded RNA-binding domain (dsRBD) is an RNA-binding motif found in many proteins involved in RNA processing and localization. The seventy amino acids long dsRBD recognizes double-stranded RNA. *In vitro*, it was not possible to show that a dsRBD can specifically recognize a substrate RNA whereas *in vivo* data demonstrates specific RNA interaction. For example adenosine deaminases that act on RNA (ADARs) are able to recognize and deaminate their substrates selectively. ADAR mediated editing can lead to codon changes in mRNAs and consequently to changes in the protein sequence. A more general dsRNA-binding protein is *Xenopus laevis* RNA-binding protein A (Xlrpba), which acts as an hnRNP with chaperone activity. To determine whether individual dsRBDs are capable of discriminating amongst different RNA molecules, SELEX experiments (Systematic Evolution of Ligands by Exponential enrichment) with the second dsRBD of either protein and a pool of approximately 10^{15} RNAs with randomized sequences, were performed. Selected RNAs were examined for their binding capacities to dsRBDs. For the best binding RNAs their minimal binding region was determined and folding predictions were confirmed by structure mappings. It can be concluded that the best binding RNAs are highly structured, containing stacked double-stranded regions, which are often interrupted by mismatches and bulges. Currently we are testing the biological effects of these aptamers on editing and cleavage by *dicer*.