RCB – Colloquium

Tuesday, February 24th, 2026, 2 p.m.
H 53

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"New insight into mRNA surveillance and translation initiation"

Post-transcriptional regulation is highly versatile and adaptable in exploiting cellular time and space. RNA-binding proteins play a key role in the regulation of spatial and temporal changes in protein synthesis through control of transport, translation and decay of mRNA. Deregulation and failed coordination of these mechanisms contribute to the pathophysiological development and conditions.

Transcriptome-wide high-resolution maps of RNA-protein contacts allow us to study how these interactions control mRNA fate [Hafner & Landthaler et al., Cell 2010; Rybak-Wolf et al., Cell 2014]. Different next generation sequencing approaches are being applied to examine the function of RNA-binding proteins in mRNA biogenesis, translation and decay [Murakawa et al. Nature Communications 2015].

In addition, we have developed a UV crosslinking and oligo(dT) purification approach to identify the mRNA-bound proteome using quantitative proteomics. We use this method to monitor dynamic changes of the mRNA-protein interactome to capture differentially binding proteins as a consequence of intra- and extra-cellular signals. [Milek et al., Genome Research 2017].

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