DICKERSON BIOCHEMISTRY SEMINAR SERIES

"Structure of pre-miR-31 reveals an active role in Dicer processing"

Prof. Sarah Keane

University of Michigan Department of Chemistry, Program in Biophysics

As an essential post-transcriptional regulator of gene expression, microRNA (miR) levels must be strictly maintained. The biogenesis of many, but not all, miRs is mediated by trans-acting protein partners through a variety of mechanisms, including remodeling of the RNA structure. The intrinsic structural properties of RNAs can provide an additional layer of regulation. miR-31 functions as an oncogene in numerous cancers and interestingly, its biogenesis is not known to be regulated by protein binding partners. We determined the solution structure of the precursor element of miR-31 (pre-miR-31) to investigate the role of distinct structural elements in regulating Dicer processing. We found that the presence or absence of mismatches within the helical stem do not strongly influence Dicer processing of the pre-miR. However, both the apical loop size and structure at the Dicing site are key elements for discrimination by Dicer. Interestingly, our NMR-derived structure reveals the presence of a triplet of base pairs that link the Dicer cleavage site and the apical loop. Mutational analysis in this region suggests that the stability of the junction region strongly influence both Dicer binding and processing. Our results enrich our understanding of the active role that RNA structure plays in regulating Dicer processing.

Friday, January 20 at 3:30pm

Mani L. Bhaumik Collaboratory, Dongwon Yoo Seminar & Conference Hall (Young Hall 4222)

More information: marla@chem.ucla.edu

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