



The Physics of Soft and Biological Matter

P.11 New insight into the structure and function of Hfq carboxyl terminus

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Accumulating evidence indicates that assemblies of essential components of RNA metabolism are localized on the cytoplasmic membrane of the bacterial cell, and that this cellular compartmentalization plays important roles to process RNAs. These assemblies include Hfq, the RNA chaperone protein, which is involved in the post-transcriptional control of protein synthesis by virtue of its interactions with several small regulatory RNAs. Structurally, Hfq possesses two domains. The N-terminal domain folds as a five strongly bent β -sheets within individual protomers to assemble into a typical toroidal hexameric ring with a continuous β -sheet. The C-terminal flexible domain, which represents about one-third of the protein, seems intrinsically unstructured and most of 3D structures of Hfq lack C-terminal region. While the RNA binding core of Hfq lies within its Nterminal domain, the function of the flexible domain is controversial and remains largely unknown. We recently showed that this C-terminal region is responsible for the self-assembly of the protein into long fibers and that this property is associated with the ability of Hfq to localize within organized cellular structures in the vicinity of the membrane. Our progress toward studying the architecture of these ordered fibrillar ultrastructures formed by Hfq C-terminal domain will be presented during this meeting.