

Interpretation of RNA cryo-EM maps of various resolutions

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RNA cryo-EM is a fast advancing field. It has solved RNA structures yet unsolved by x-ray crystallography such as the tetrahymena ribozyme and has pushed the boundaries of cryo-EM by resolving small molecules; down to 28kDa. We are now able to propose atomic models of RNA, guided by cryo-EM maps, ranging from 10Å resolution to below 3Å. However, these models should not be viewed as equal as various features of RNA, in particular the backbone, are resolved in a resolution-dependent manner. We have analyzed published and unpublished cryo-EM maps of RNA to systematically address the resolvability of various RNA features at different resolutions. Finally, we have explored RNA as a model system to examine the charge-dependent manner of electron scattering; revealing a key difference between interpreting x-ray and cryo-EM maps and the limitations and potential applications enabled by the charge-dependent nature of electron scattering.