Comparing NMR and X-ray protein structure: Lindemann-like parameters and NMR disorder

E. Faraggi
RIS, LLC

Disordered protein chains and segments are fast becoming a major pathway for our understanding of biological function, especially in more evolved species. However, the standard definition of disordered residues: the inability to constrain them in X-ray derived structures, is not easily applied to NMR derived structures. We carry out a statistical comparison between proteins whose structure was resolved using NMR and using X-ray protocols. We start by establishing a connection between these two protocols for obtaining protein structure. We find a close statistical correspondence between NMR and X-ray structures if fluctuations inherent to the NMR protocol are taken into account. Intuitively this tends to lend support to the validity of both NMR and X-ray protocols in deriving biomolecular models that correspond to in-vivo conditions. We then establish Lindemann- like parameters for NMR derived structures and examine what order/disorder cutoffs for these parameters are most consistent with X-ray data and how consistent are they. Finally, we find critical value of L = 4 for the best correspondence between X-ray and NMR derived order/disorder assignment, judged by maximizing the Matthews correlation, and a critical value L = 1.5 if a balance between false positive and false negative prediction is sought. We examine a few non- conforming cases, and examine the origin of the structure derived in X-ray. This study could help in assigning meaningful disorder from NMR experiments. Intuitively this tends to lend support to the validity of both NMR and X-ray protocols in deriving biomolecular models that correspond to in-vivo conditions. We then establish Lindemann- like parameters for NMR derived structures and examine what order/disorder cutoffs for these parameters are most consistent with X-ray data and how consistent are they. Finally, we find critical value of L = 4 for the best correspondence between X-ray and NMR derived order/disorder assignment, judged by maximizing the Matthews correlation, and a critical value L = 1.5 if a balance between false positive and false negative prediction is sought. We examine a few non- conforming cases, and examine the origin of the structure derived in X-ray. This study could help in assigning meaningful disorder from NMR experiments.

[l] A. Keith Dunker, Pac. Symp. Biocomput **3**, 473 (1998).