Visualization of biomolecular strctures by WAXS and MD

W. He[1], Y. L. Chen[2], Serdal Kirmizialtin[3], Lois Pollack[4]

[1]New York University [2]Cornell University, [3]New York University Abu Dhabi, [4]Cornell University

wh1165@nyu.edu

Solution wide-angle X-ray scattering (WAXS) has exhibited its promising potential for characterizing conformational states of biomolecular structures with increasing accuracy at near-native conditions. WAXS probes structural information about biomolecules and their variations. However, the extraction of this hidden information is nontrivial and the accurate interpretation of the solution scattering data is prevented by the low resolution of the data. Here, we integrate WAXS with all-atom molecular dynamics (MD) simulations to investigate the solution structure of macromolecules, including DNA and RNA. This WAXS-MD strategy achieved excellent agreement between measured and simulated WAXS profiles and allows insights into the structural dynamics on the atomic scale which is inaccessible in experiment. From computer simulations and machine learning based analysis, we built correlation maps to visualize the relationship between well-defined features in the scattering profiles and real space characteristics of macromolecules. Notably, our analysis reveals that double stranded RNA (dsRNA) displays a marked insitu structural bending induced by G-tract-specific (i.e. GGG sequence dependence) cations binding, and tandem uracils (UUU) of RNA triple helices perform unique function in stabilizing their tertiary structure. Though demonstrated for nucleic acids duplex and triplex, our general approach can be applied to solve flexible single stranded RNA (ssRNA) in solution and can extend to study dynamic systems containing both protein and RNA partners.

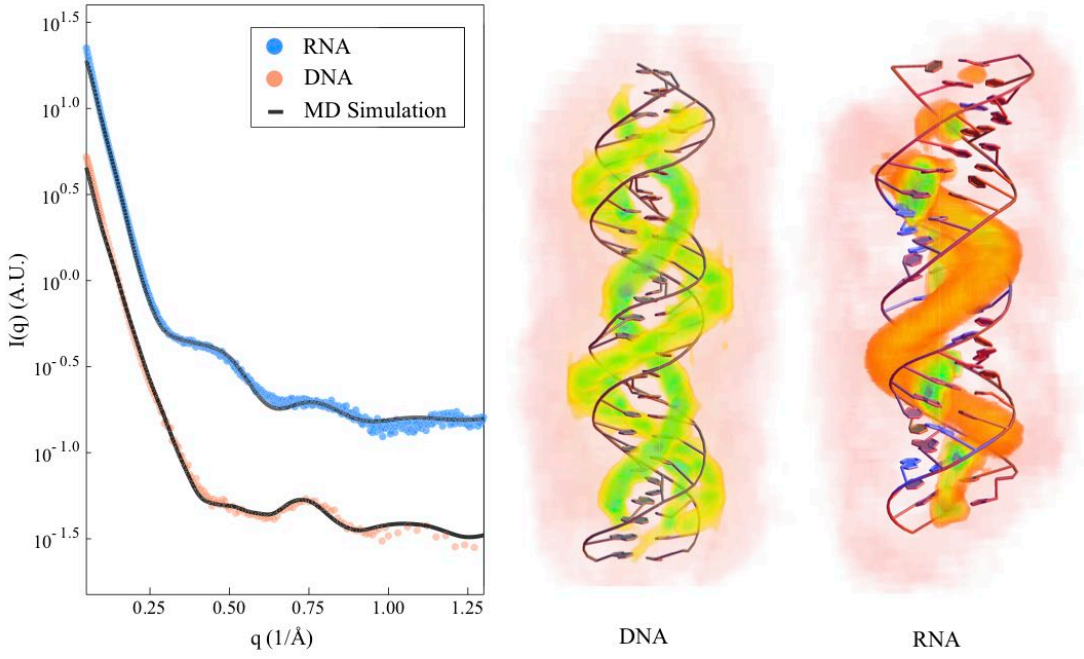

Figure 1