

Atomic Structure of the SARS-CoV-2 Pseudoknot in Solution

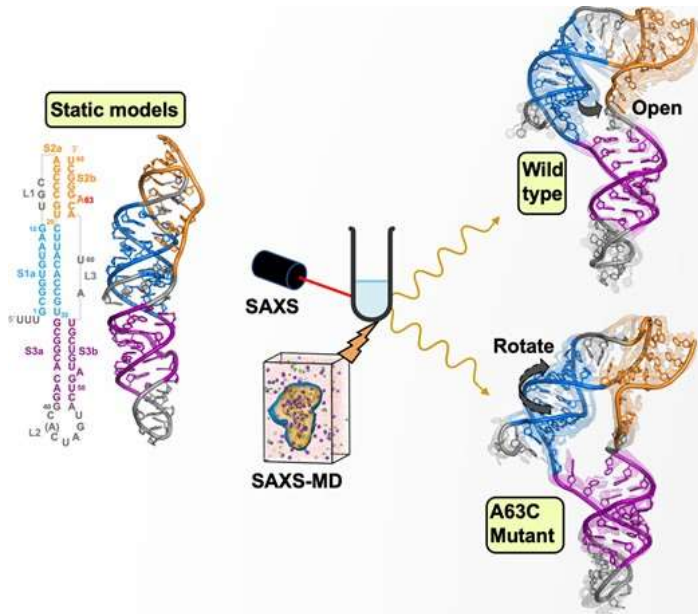


Figure shows the structures of the static models (left), in solution (top right), and mutated (bottom right).

W. He, J. San Emeterio, M.T. Woodside, S. Kirmizialtin, L. Pollack, *Nucleic Acids Research* Vol 51, Issue 20, pages 11332-11344 (2023)

This work was performed in part at NSLS-II

National Synchrotron Light Source II

Scientific Achievement

Scientists determined the solution-based molecular structure of the SARS-CoV-2 virus "pseudoknot," a section of the virus that is essential in creating proteins required for virus replication.

Significance and Impact

The study provides a more accurate structure of the SARS-CoV-2 pseudoknot, a possible COVID-19 drug target due its role in viral expression of proteins essential for replication.

Research Details

- Previous structural models are not consistent and come from frozen or constrained samples rather than samples in solution, which are more physiologically relevant.
- Researchers used small-angle X-ray scattering (SAXS) at the LiX beamline at NSLS-II to study the structure in solution and found that the profile did not match profiles computed from previously solved static structures.
- The group used their SAXS data to feed molecular dynamics simulations, to clarify the dynamic structures of the SARS-CoV-2 pseudoknot in solution.