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Rapid and High Resolution Ambient Temperature Structure Determination at Turkish Light Source

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Determining the high-resolution biomacromolecular structure is crucial for understanding protein function and dynamics. Serial crystallography is a new structural biology technique, but it is constrained fundamentally by the need for large samples or by the need for quick access to the scarce X-ray beamtime. The key challenge in serial crystallography continues to be obtaining a large number of sufficiently large, well-diffracting crystals while minimizing radiation damage. As an alternative, we provide the plate-reader module designed for determining the structure of biomacromolecules utilizing a 72-well Terasaki plate at a home X-ray source. We also provide the first lysozyme structure identified at ambient temperature from the Turkish Light Source (Turkish DeLight). The entire dataset, which had a resolution of 2.39 and was 100% complete, was collected in 18.5 minutes. The ambient temperature structure sheds important light on the structural dynamics of the lysozyme when combined with our earlier cryogenic structure (PDB ID: 7Y6A). Turkish DeLight offers reliable and quick analysis of biomacromolecular structure at ambient temperature with minimal radiation damage.

Primary authors: Dr DEMIRCI, Hasan (Koc University); Ms YILMAZ, MERVE (Koc University); Mr GÜL, Mehmet (Koc University)

Presenters: Ms YILMAZ, MERVE (Koc University); Mr GÜL, Mehmet (Koc University)

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