

# Data Collection using Cryo-cooling Technique and Reducing the Damage by Freezing Samples to Collect High-intensity Protein Data using Cryocrystallography

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**Abstract**—*It is noteworthy that we have solved a good no. of protein structure (at in-house facility comprising RU300 Rotating Anode Generator, mar345dtb Imaging Plate, mar300 scanner and low temperature device from oxford system) nearly to atomic resolution.*

*The low resolution technique would be used to get an overview and identify interesting regions and then incorporating the high resolution technique to zoom in and look at details pertaining to different techniques. In this context there are limitations related to radiation damages caused by high intensity beam from the Generator. Reducing the damage by freezing samples would allow investigations of structure but the dynamic part is of course not accessible any more. We are working to reduce the damages caused by high intensity beam by innovating different techniques in this direction.*