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Radiation damage at cryotempreatures - application to redox systems

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Abstract content

Protein crystallography has been the most successful technique for determining 3D structures from protein molecules. However, the technique has several disadvantages including the need of a crystalline sample, radiation damage and a static, averaged on time and space, resulting model. Radiation damage is unavoidable and is one of the limiting steps to estimate phases by anomalous methods. Protein crystals are usually diffracted at 100 K to reduce the rate of radiation damage inflicted by the X-rays. However, despite the use of cryotechniques diffracted intensity fades with increasing dose and a dose to half intensity, $D\frac{1}{2}$, of 43 MGy has been experimentally established. Another consequence of radiation-matter interactions is specific damage; as the dose increases residues are damaged in a reproducible order (breakage of disulfide bonds, decarboxylation of aspartates and glutamates, OH group lost from tyrosines). At room temperature radical scavengers have been shown to mitigate both global and specific damage, presumably by intercepting radicals created in the surrounding medium [2]. In this work we test the effectiveness of radiation damage at cryotemperatures where the motion of these radicals will already be impeded and we present an approach to describe catalytic mechanisms in redox enzymes by taking advantage of radical formation during X-ray irradiation of protein crystals.

Summary

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