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Scavengers and pH: two approaches to reduce radiation damage on protein crystalline samples.

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Abstract content

Macromolecular X-ray crystallography is the experimental technique which allows to obtain atomic-detailed structural models of macromolecules in crystalline state. Radiation damage is an inherent problem in this technique. The consequences of radiation damage can be from obtaining models with altered atoms, incomplete amino acid residues, or even no model at all. In this work we analyzed two strategies to deal with radiation damage, specifically in the breaking of disulfide bonds, using hen egg white lysozyme (HEWL) crystals as a model. Both strategies attempt to eliminate the effects of the solvated electrons, one of the first free radicals generated within the macromolecular crystal. The first strategy was the use of complex molecules with heavy atoms as electron scavengers and the second strategy was the change in the pH of the crystallization solution, allowing hydrated electrons to react with protons. Our results suggest that the molecules evaluated here do not protect HEWL crystals from radiation damage. On the other hand the change in pH shows some preliminary positive results which need to be further analysed.

Summary

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