Structural Radiation Damage Seen at Atomic Resolution - Broken Disulfide Bonds.

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Radiation damage is an inherent problem in protein X-ray crystallography and recently the process was shown to be highly specific, exhibiting features such as cleavage of disulphide bonds, decarboxylation of acidic residues, increase in atomic B-factors and increase in unit cell volume [1-4].

We have compared two trypsin structures at atomic resolution (1.00 and 0.95 Å), from which the data is collected at a third generation synchrotron (ESRF) at two different beamlines, ID14-EH4 and SNBL [5]. Both trypsin structures exhibit broken disulphide bonds, and particularly the bond from Cys191 to Cys220 is very sensitive to synchrotron radiation. The data set collected at the most intense beam line (ID14-EH4) shows increased structural radiation damage in terms of lower occupancies for cysteine residues, more breakage in the six disulphide bonds and more alternate conformations. It appears that high beam intensity and not only the total X-ray dose is most harmful to protein crystals.

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