Macromolecular crystallography - how to minimize the effect of radiation damage on the quality of diffraction experiment

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Radiation decay is usually the biggest contribution to the error of structure factor determination in the X-ray diffraction experiment. Other sources of error, like non-uniform exposure, detector artefacts, and hardware imperfections, play less significant roles in well-functioning synchrotron stations. Precise measurements of the X-ray intensities are critical for SAD and MAD experiments. The radiation decay correction applied in HKL-3000 and some other programs exploits data redundancy to correct 3D-integrated reflections in standard X-ray experiments. The best strategies for the experiments conducted on macromolecular crystals and the benefits of radiation decay correction for SAD experiments will be discussed in detail.