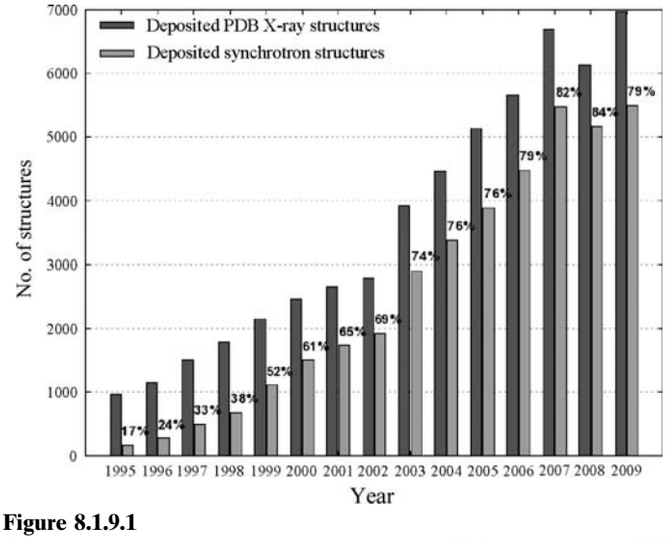

Figure 8.1.9.1
Synchrotron structures deposited in the PDB *versus* all PDB deposited structures (from http://biosync.rcsb.org/BiosyncStat.html) as of December 2009, *i.e.* a majority of all determined macromolecular crystal structures are now synchrotron-radiation derived.

discovery [for an early description see Bugg *et al.* (1993), for an example of pharmaceutical company collaboration see the Industrial Macromolecular Crystallography Association (IMCA) Collaborative Access Team at APS in Chicago (http://www.imca.aps.anl.gov/) and for a recent European perspective see *e.g.* Maclean *et al.* (2006).]

8.1.8.6. Radiation damage

The successes of these sources in macromolecular crystallography have been spectacular, so much so that provision of such beamlines now accounts for ~40% of the APS and ESRF insertion-device sectors. Nevertheless, X-radiation damage has been a continuing concern not least as the 'cutting edge' of capability to study ever-smaller crystals and ever-larger unit cells at synchrotron-radiation sources has been improved and optimized. A notable development has been a series of International Workshops on X-ray Damage to Crystalline Biological Samples. Most of these workshops have resulted in special issues of the *Journal of Synchrotron Radiation* (Volume 9 part 6, Volume 12 part 3, Volume 14 part 1 and Volume 16 part 2). The latest of these has a mini-review by Garman & Nave (2009).

8.1.9. Concluding remarks

SR and crystallography are now intricately intertwined in their scientific futures and in facilities provision (see *e.g.* Helliwell, 1998; Dauter, 2006; Fig. 8.1.9.1). Jiang & Sweet (2004) have given a systematic analysis of the impact of SR on macromolecular crystallography capabilities.

The new XFELs have produced very novel possibilities for 3D structure determination not only of non-crystallizable proteins but also whole cells (Neutze *et al.*, 2000; Miao *et al.*, 2001; Sayre, 2008; Shapiro, 2008). Whilst these approaches have attracted controversy, they represent a bold new push of X-ray diffraction methods towards widening capabilities in important frontiers in structural biology and structural cellular biology.

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