21.1.8. Future

During the 1990s, the field of protein model validation matured rapidly (MacArthur *et al.*, 1994; EU 3-D Validation Network, 1998; Laskowski *et al.*, 1998) and further fundamental breakthroughs seem unlikely at present (although it would be highly desirable to be able to calculate and compare the information content of experimental data and models alike). In contrast, work on the validation of nucleic acid models (Schultze & Feigon, 1997) and hetero-entities (Kleywegt & Jones, 1998) has only just begun. In addition, there is still scope for further development of validation methods that use both the atomic model and the crystallographic data. In addition, the increasing number of structures that are solved at (near-)atomic resolution may lead to an adjustment of some validation criteria, *e.g.* of 'ideal' geometric target values, rotamer libraries *etc.* Also, validation of model aspects typically associated with very high resolution studies (refined occupancies, alternative conformations, anisotropic ADPs, H atoms) is still poorly developed. An increased understanding and appreciation of factors that determine model quality (and knowledge of how to measure them) will be important for the development of more automatic methods for protein structure determination. This in turn will enable 'black-box' high-throughput protein crystallography to become a reality, at least for 'run-of-the-mill' structures.

Acknowledgements

The author gratefully acknowledges the many useful discussions about validation with Alwyn Jones (Uppsala), Axel Brunger (Yale), Eleanor Dodson (York), Randy Read (Cambridge), Carl-Ivar Brändén (Stockholm), the members of the EU-funded 3-D Validation Network and many other colleagues in the field. This work was supported by the Swedish Foundation for Strategic Research (SSF), its Structural Biology Network (SBNet) and the EU-funded 3-D Validation Network.

references