

Opportunities to communicate results from challenging, non-routine macromolecular structures in open access, online journals

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Many of the most biologically interesting macromolecular crystallographic structural projects also prove to be quite challenging, yet the majority of life science journals provide little encouragement or opportunity to provide full details of non-routine methods for 3-D structure determination and/or refinement. In addition, many of the peer-reviewers in these journals lack sufficient knowledge regarding the effects and limitations on structural results from crystallographic pathologies such as low data resolution or completeness, severe radiation damage, high data anisotropy, poor phasing signal, partial merohedral twinning, pseudosymmetry, incorrect sequence assignment and over-optimistic ligand identification. Reviewers are also often not familiar with up-to-date crystallographic software and methods for data processing, structure phasing, refinement and validation, and thus question the results presented and often require extensive justification for the crystallographic methods used. Recent positive experiences with open access, online journals, especially one that publishes the reviewer letters and author comments, will be presented as a model for not only the publication of results but also the edification of editors, peer reviewers and readers in modern crystallographic methods.