Molecular Replacement: Past, Present And Future

Airlie McCoy[1]

[1]N/A

ajm201@cam.ac.uk

It is remarkable that the first review of the 'molecular replacement' phasing method for macromolecules was published 50 years ago and just a year after the Protein Data Bank was established [Crystallography: Protein Data Bank. Nature New Biology 233, 223 (1971); Rossmann, The Molecular Replacement Method. New York: Gordon & Breach (1972)]. What began as a niche method for exploiting the phase information inherent to non-crystallographic symmetry and/or different crystal forms has evolved into the predominant phasing method in macromolecular crystallography, regardless of crystal form or whether similar structures are present in the Protein Data Bank. The evolution of molecular replacement has seen advances in its speed and sophistication, driven by the passion of crystallographers to answer ever more elaborate biological questions as quickly as possible, and has been facilitated by computational progress that would delight the pioneers. In this personal view, I will explore how molecular replacement became the most versatile of macromolecular phasing methods, the current best practice, and make some predictions for its future.