Charge-flipping structure solution from powder diffraction data: the protein perspective

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Since the publication of the charge-flipping algorithm [1], the method has received widespread interest. Although originally developed with the focus on single crystal data, the structure solution algorithm was applied with especial vigour to more the specialized fields of modulated structures [2] and powder data [3,4].
The algorithm is extremely successful solving large structures containing substantial vacancies, the very first results being achieved on large volume, low symmetry fullerene structures.
What are the chances of solving proteins using this method? An overview and outlook on these fascinating new developments will be given.

References

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