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**Effects of Crystal Twinning on the Ability to Solve a Macromolecular Structure Using Multi-Wavelength Anomalous Diffraction**

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ABSTRACT: The crystal structure of gpD, the capsid-stabilizing protein of bacteriophage lambda, was solved by multi-wavelength anomalous diffraction (MAD) for a selenomethionine (SeMet) derivative of the protein at 1.8 Å resolution, using crystals in space group P2(1). Subsequent analysis showed that the crystals of both the original protein and the SeMet derivative were pseudo-merohedrally twinned with a twinning fraction approximately 0.36, owing to the near-identity of the a and c axes. An analysis of the crystal structure solution is presented and the utility of twinned crystals for solving the structure using MAD and of different phasing strategies is discussed; the results obtained with several software packages are compared.