Multi-crystal Anomalous Diffraction for Low Resolution Macromolecular Phasing

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Anomalous diffraction experiment from single crystal is one of most commonly used methods for macromolecular phasing. Here we show an alternative way for anomalous phasing with anomalous diffraction data extracted from multiple crystals. Our study demonstrates that multi-crystal anomalous data can significantly benefit low resolution phasing in both heavy atom substructure determination as well as electron density maps interpretation at low resolution. We propose that the multi-crystal strategy may help solve crystal structures of large macromolecular complexes and membrane proteins which are prone to be damaged by X-ray radiation.