A Comparison of Gas Stream and Plunge Cooling in Macromolecular Cryocrystallography

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Macromolecular structure determination via diffraction is commonly carried out at cryogenic temperature. Crystals are typically cooled via plunging into liquid cryogens or placing directly into a cold gas stream. Here we compare these two approaches using two different crystal forms of thermolysin. We find that fast plunge cooling of ~300 μm crystals into liquid nitrogen yields higher mosaicities than gas stream cooling using the vial mounting approach (Farley et al., 2014). In some cases low mosaicities can also be achieved by plunging slowly through the cold gas layer above the liquid nitrogen. The observed effects are more pronounced for a cryosolution of DMF (10% contraction) than for a cryosolution of D-xylose (3% contraction). The results are consistent with a model in which non-homogeneous cooling-induced strain is amplified by faster cooling of greater contracting materials (Kriminski et al., 2003).