

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 $\sim 300\ \mu\text{m}$ 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).

Farley, C., Burks, G., Siegert, T. & Juers, D. H. (2014). *Acta Cryst. D* **70**, 2111-2124.

Kriminski, S., Kazmierczak, M. & Thorne, R. E. (2003). *Acta Cryst. D* **59**, 697-708.