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Capturing high temperature protein conformations for low-temperature study using ultra-fast cooling DAVID MOREAU, HAKAN ATAKISI, ROBERT THORNE, Cornell University — protocols for cooling biomolecular crystals for x-ray cryocrystallography are poorly controlled, leading to crystal-to-crystal and within-crystal non-isomorphism. Furthermore, cooling times below the protein-solvent glass transition of .1 s provide ample time for biological temperature conformations to depopulate and shift. To address these issues, methods and apparatus for cooling biomolecular crystals at rates approaching 100,000 K/s have been developed. These cooling rates are sufficient to eliminate ice formation on cooling without use of cryoprotectants, and to quench additional high-temperature conformations for low-temperature study. Time scales for conformational relaxation can be characterized using variable cooling rates. Possible extension of these methods to maximize conformational quenching will be discussed.

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