



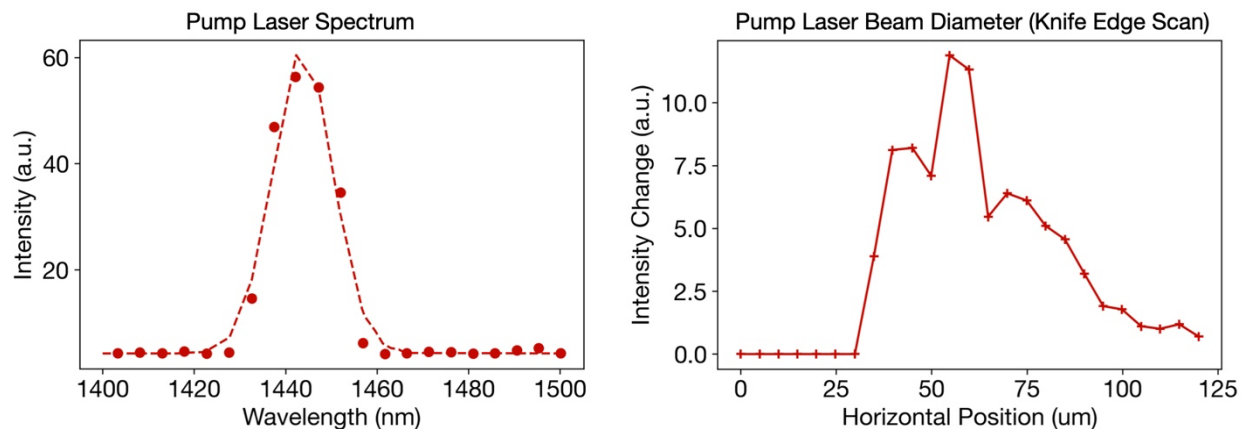
# Mapping protein dynamics at high spatial resolution with temperature-jump X-ray crystallography

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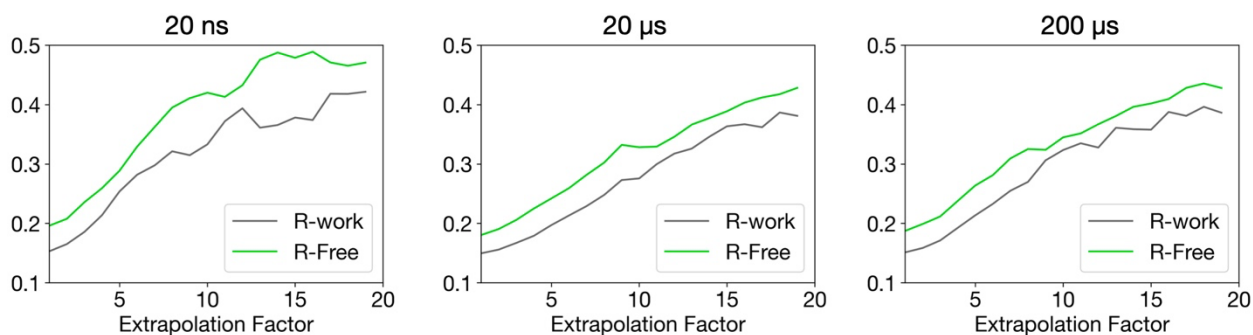
## **Supplementary Figures**

Supplementary Fig. 1: Pump laser parameters

Supplementary Fig. 2: R-factors from extrapolated structure factor refinement



**Supplementary Figure 1. Pump laser parameters.** Measurements of pump laser spectrum and beam size (horizontal knife edge scan). The spectrum has a peak at approximately 1443 nm with a bandwidth (FWHM) of approximately 16 nm. The results of a knife edge scan reveal the beam to have an approximate diameter (FWHM) of 50  $\mu\text{m}$ . We note these values represent our best estimations, due to the non-gaussian shape of the plotted data. Nevertheless, the IR beam diameter is much larger than that of the X-ray beam, which is approximately 1.5  $\mu\text{m}$ .



**Supplementary Figure 2. R-factors from extrapolated structure factor refinement.** Final R-factors following extrapolated structure factor refinement were plotted as a function of extrapolation factor ( $N$  as described in Eq. 2) for the three pump-probe time delays for apo lysozyme structures. Both R-work and R-free increased with extrapolation factor for all three datasets.