



Supplementary Figure S1

Figure S1. X-ray data collection and structure determination of the crystals prepared by the current apparatus. **a.** HEW lysozyme crystals grown in the protein association control cell. **b.** The crystal mounted on a litholoop cooled at 100 K. The crystal was shortly soaked in the circulating solution added by 30% (v/v) ethylene glycol prior to the flash frozen. **c.** An X-ray diffraction image with the closed-up view indicating the higher shell limit of the diffraction spots over at 1.1 Å resolution. **d.** A sigma-A weighted electron density map (at 1.3 Å resolution, contoured at 1σ) superposed on the refined X-ray structure. **e.** The solved X-ray structure of the HEW lysozyme.