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Supporting information for article:

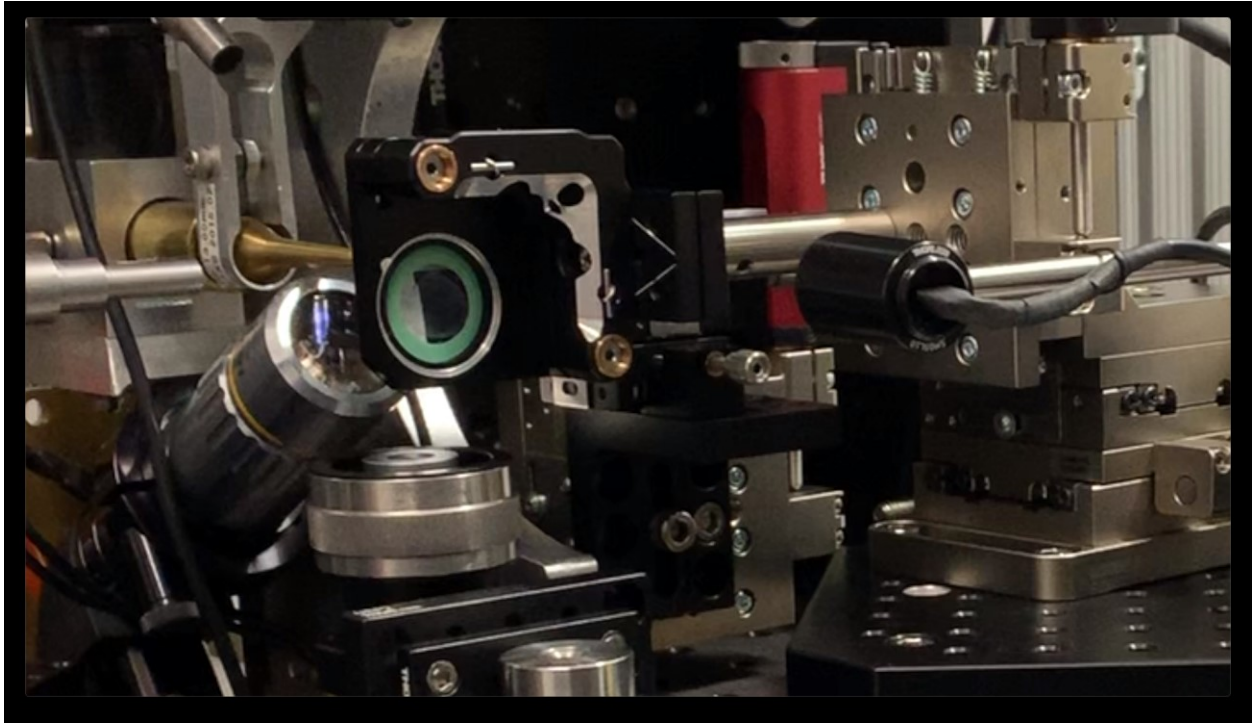
An Automated Platform for *in Situ* Serial Crystallography at Room Temperature
An Automated Platform for *in Situ* Serial Crystallography at Room Temperature

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Table S1 Data processing and structural refinement

Dataset/PDB ID	G3 Pfr 100K/6uvb	G3 Pfr/6uv8	G3 @ 785 nm	Pa497 dark	Pa497 @ 785 nm
Space group	P4 ₂ 2 ₂	P4 ₂ 2 ₂	P4 ₂ 2 ₂	C222 ₁	C222 ₁
Unit cell (Å)	108.8, 108.8, 68.7	108.8, 108.8, 67.9		154.7, 163, 427.2	
Molecular mass/asymmetric unit (kDa)	21	21	21	460	460
Crystallization devices	-	22	10	15	12
Exposure time per frame (µs)	5 s/1° frame	22	8	22	8
Frames used/collected = index rate (%)	100/100 = 100	802/4,055 = 19.8	175/1,120 = 15.6	261/2,627 = 9.9	151/2,762 = 5.5
Spots measured	-	586,816	85,518	730,280	420,917
Spots merged/spots per frame	62,940/629	577,282/720	84,140/481	716,508/2,745	398,212/2,637
Unique reflections/redundancy	9,394/6.7	11,702/49.3	11,160/7.5	98,518/7.3	90,979/4.4
Harmonic/spatial overlap deconvolutions	-	2,794/165	2,228/40	19,584/1,069	23,383/733
Resolution/high resolution bin (Å)	2.95/3-2.95	2.7/2.8-2.7	2.8/3.0-2.9	3.0/3.1-3.0	3.0/3.1-3.0
Completeness/high resolution bin (%)	98.9/100	99.1/94.2	89.4/45.4	95.1/80.3	85.6/79.7
X-ray bandwidth in FWHM ¹ (%)	Single wavelength	2.7	5.6	3.4	4.7
$\langle F \rangle / \sigma(F)$ /high resolution bin	30.2/1.0	24.3/11.3	9.7/8.2	10.5/11.0	21.7/23.6
R_{merge} (%)	3.3	22.2	22.7	21.9	9.9
$R_{1/2}$ (%) / $CC_{1/2}$	-	8.7/0.9868	24.4/0.7918	22.0/0.6641	18.2/0.5059
$R_{\text{work}}/R_{\text{free}}$ (%)	25.8/30.3	21.1/26.1	-	-	-
Bond length/angle rmsd (Å/°)	0.008/1.248	0.015/1.606	-	-	-
Favored/allowed/disallowed Ramachandran (%)	96.1/3.3/0.55	91.8/8.2/0.0	-	-	-

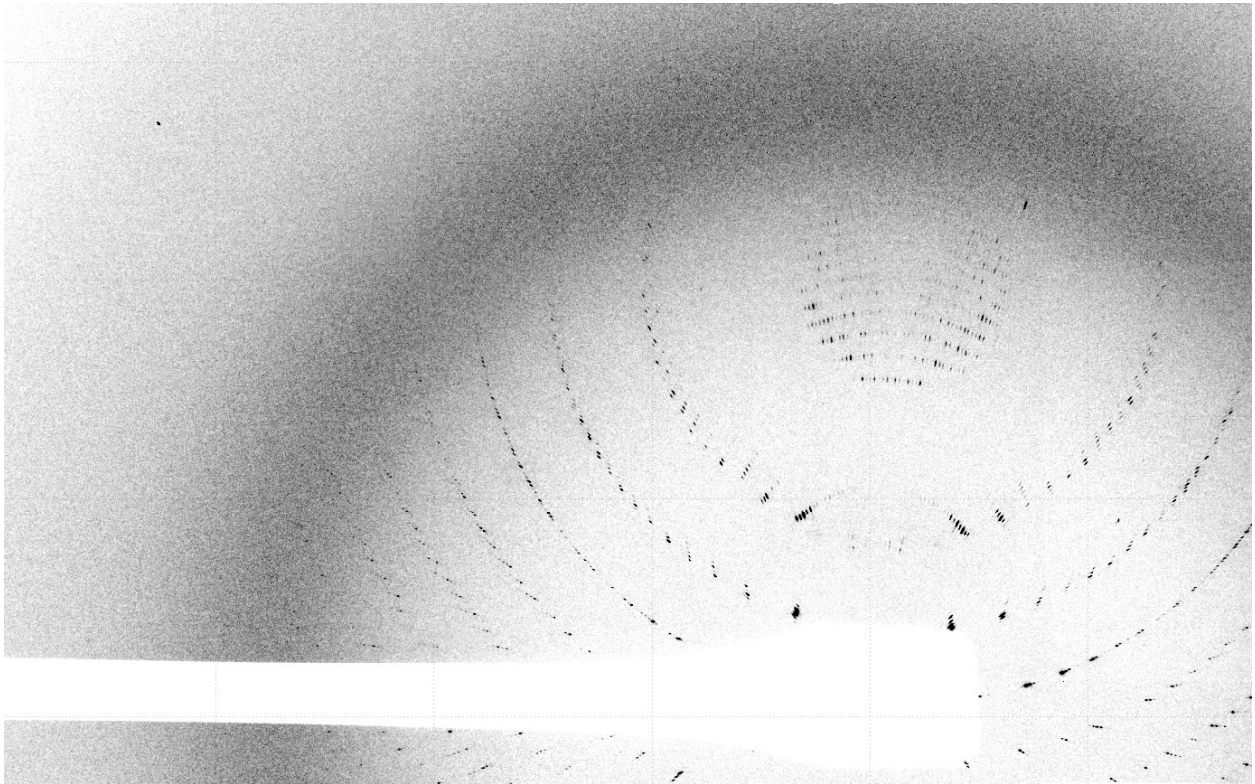
¹Full width at half maximum



Movie S1. Optical scanning. Crystals grown on a quartz chip (green circle) are being scanned under infrared light. The room light should be off if the crystals are photosensitive during a normal operation. See Fig. 1 legend for detail.



Movie S2. Simulated data collection for X-ray diffraction. The targeted Pa497 crystals are translocated into the X-ray beam (white circle of 30 μm in diameter) in a pre-programmed sequence according to a crystal ranking. An X-ray pulse is fired at each stop.



Movie S3. Laue diffraction patterns from Pa497 crystals. A portion of the Laue images at random orientations are shown. Each diffraction image is obtained from a fresh volume of a crystal.