Nucleating Agent Crystallophore Induces Instant Protein Crystallization

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SUPPORTING INFORMATION

Movie S1: Evolution of the HEWL–TbXo4 mix over time. The first sequence was recorded after 3 min when microcrystals started to appear and sediment at the bottom of the SAXS capillary. The solution was pushed forward every 10 s by the syringe pump to refresh the sample exposed to the X-ray beam symbolized by the yellow rectangle. The second sequence at 12 min after the mix shows increased microcrystal formation and sedimentation (MP4)

Movie S2: Sequence of 150 SAXS images (1 image every 10 s) illustrating the appearance and intensification of diffraction rings with a mix consisting of 100 mg/mL HEWL, 10 mM TbXo4, 400 mM NaCl, and 50 mM Na acetate (pH 4.5) (MP4)

Movie S3: Sequence of 180 SAXS images (1 image every 10 s) illustrating the appearance and intensification of diffraction rings with a mix consisting of 75 mg/mL HEWL, 10 mM TbXo4, 400 mM NaCl, and 50 mM Na acetate (pH 4.5) (<u>MP4</u>)

Table S1: Lysozyme data acquisition by 3D ED and integration statistics of individual nanocrystals.

Data set	1	2	3	4	5
Wavelength (Å)	0.02508				
Camera length (mm)	1285				
Exposure (s/frame)	0.125				
Δφ (°/frame)	0.1835				
Number of frames	206	253	208	252	175
ϕ_{total} (°)	37.8	46.4	38.2	46.2	32.1
Data processing					
Space group	P4 ₃ 2 ₁ 2				
Unit cell dimensions	a=b=78.5	a=b=78.5	a=b=78.3	a=b=78.8	a=b=78.5
	c=38.9	c=38.8	c=38.7	c=37.0	c=38.9
Resolution (Å)	35.0 - 3.32	27.8 - 3.21	55.4 - 3.41	24.9 - 3.21	78.5 - 4.01
	(3.52 - 3.32)	(3.40 - 3.21)	(3.62 - 3.41)	(3.33 - 3.21)	(4.25 - 4.01)
No. reflections	5521 (870)	7546 (1172)	5048 (767)	5834 (379)	2650 (415)
No. unique reflections	1394 (219)	1566 (338)	1132 (173)	1427 (109)	667 (104)
Completeness (%)	69.5 (68.9)	71.0 (70.7)	61.6 (61.3)	67.2 (49.8)	57.1 (56.8)
R _{sym}	0.518 (1.991)	0.564 (1.505)	0.698 (1.992)	0.451 (1.385)	0.713 (0.995)
R _{meas}	0.596 (2.275)	0.635 (1.687)	0.792 (2.256)	0.513 (1.626)	0.826 (1.151)
l/σl	2.54 (0.88)	2.44 (0.77)	2.04 (0.62)	3.38 (0.84)	1.55 (1.09)
CC _{1/2}	0.891 (0.425)	0.905 (0.408)	0.909 (0.293)	0.921 (0.438)	0.733 (0.550)

Figure S1: A) SAXS profile averaged over images 135 to 150 highlighting powder diffraction ring positions as a function of q and 20. Miller indices of Bragg peaks correspond to tetragonal microcrystals with cell parameters of a = b = 79.0 Å and c = 38.3 Å. B) Image 150 showing the superposition of diffuse scattering from the solution and powder diffraction signals from microcrystals. q-values corresponding to resolution rings are indicated.

