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Supporting information for article:

Identification of grown-in dislocations in protein crystals by digital X-ray topography

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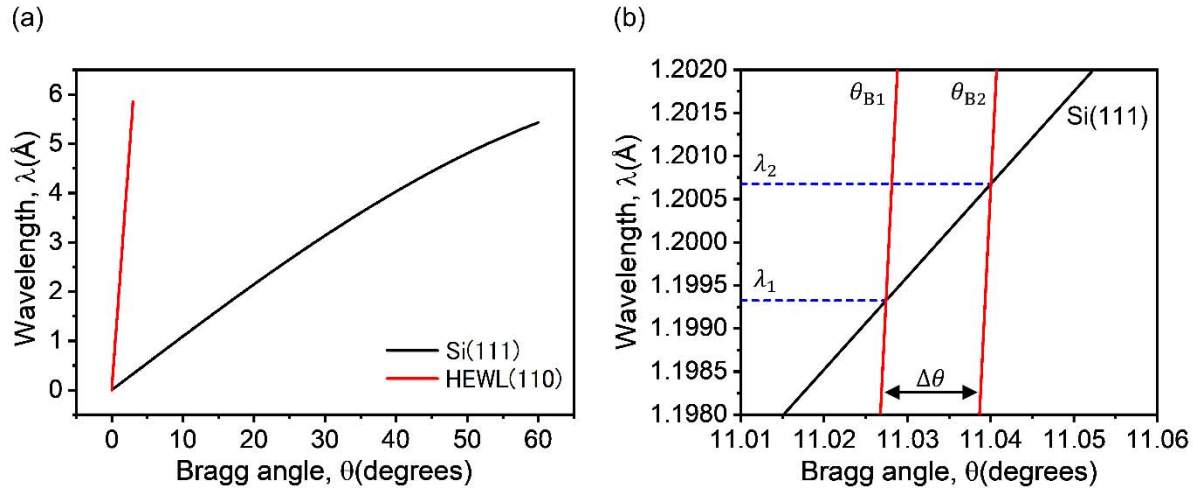

Figure S1 The (+*n*, –*m*) setting for Si(111) and HEWL(110) as first and second crystals. (a) DuMond diagram when the crystal planes are parallel, giving no reflection from the HEWL crystal. (b) DuMond diagram when the HEWL crystal is rotated by 10.41314º (θ_{B1}) and 10.42503º (θ_{B2}) corresponding to the reflection with 1.19932 Å (λ_1) and 1.20068 Å (λ_2), respectively. The reflected beam shows up where the Bragg condition is satisfied locally. In order to obtain the reflection of the whole crystal, the rotation with the angle of 1.18897×10^{-2}º ($\Delta\theta$) of the HEWL crystal is necessary even if the crystal is perfect.

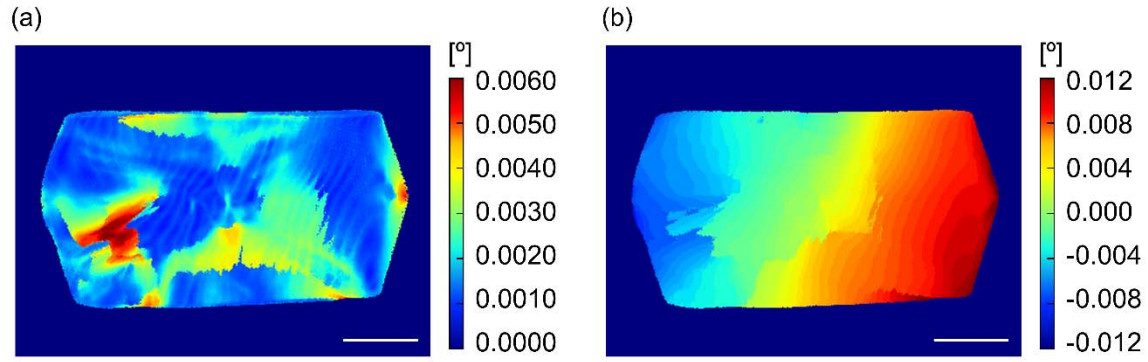

Figure S2 Mapping of (a) rocking curve width (full-width at half maximum), and (b) intensity-angular distribution taken with $\bar{4}40$ reflection. The region without dislocations have a slightly broaden in (a). Both mappings are not good agreement with the dislocation image. The scale bar represents 500 μm.

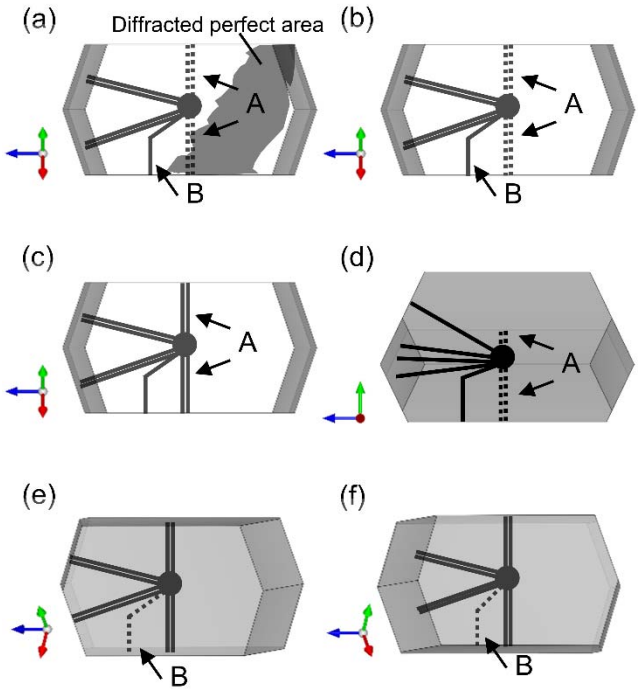

Figure S3 Schematics of crystal morphology corresponding to the X-ray topographic images of Figure 4. The solid lines and broken lines are the appeared and disappeared dislocations, respectively. The axes with red, green and blue colour are *a*, *b* and *c* axes, respectively. All images are prepared with VESTA software (Momma & Izumi, 2011).

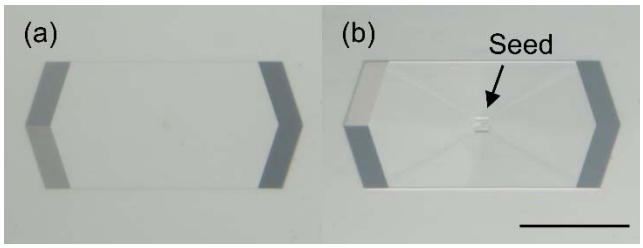

Figure S4 Typical optical micrographs of the grown HEWL crystals from a seed crystal. (b) is taken by changing the angle of the reflecting mirror of (a). The seed crystal and the sector boundaries are clearly observed in (b).