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AcrB et al.: Obstinate contaminants in a picogram scale. One more bottleneck in the membrane protein structure pipeline

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Table 2

Crystallographic data processing & refinement

Data collection	AcrB crystal from GluP condition
X-ray source and wavelength	SLS, PX06SA, 0.9000 Å
Detector	MAR CCD 225 mm
Space group	<i>H32</i>
Unit-cell dimensions (Å)	146.53, 146.53, 515.02
Resolution	35 – 4.2 Å
Observations; unique reflections	66936; 14936
Mosaicity	0.93°
$I/\sigma(I)$; R_{merge}^*	8.8 (1.3); 0.102 (0.561)
Completeness (%)	94.8 (74.6)

$$* R_{\text{merge}} = \frac{\sum_{hkl} \sum_j |I_{j,(hkl)} - \langle I(hkl) \rangle|}{\sum_{hkl} \sum_j I_{j,(hkl)}}$$

Note. Statistical values in parentheses correspond to the highest resolution shell.