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Reconstructing three-dimensional protein crystal intensities from sparse unoriented two-axis X-ray diffraction patterns. Corrigendum

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A figure in the article by Lan, Wierman, Tate, Philipp, Elser & Gruner [*J. Appl. Cryst.* (2017), **50**, 985–993] is corrected.

The color code of the curves in Fig. 3 on p. 989 of the article by Lan *et al.* (2017) is incorrect. The correct code (as shown in Fig. 1) is as follows:

Topmost (black) curve: local (n_c, n_f) = (60, 150)
Second from top (blue) curve: local (n_c, n_f) = (60, 100)
Third from top (red) curve: standard, n = 40
Bottom (green) curve: local (n_c, n_f) = (40, 60)

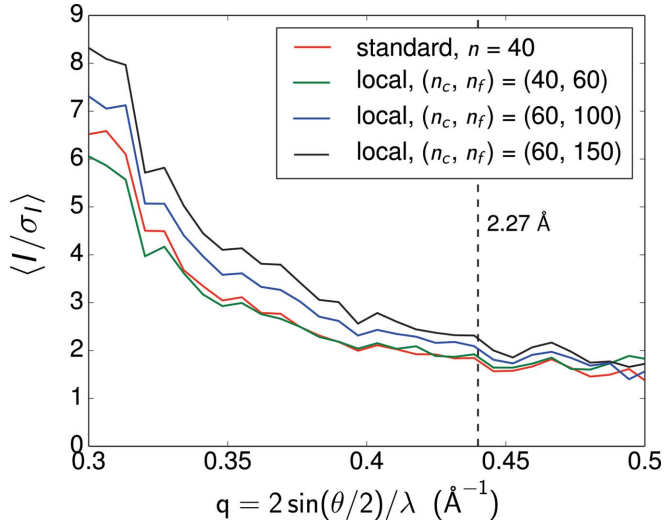

Figure 1
The corrected version of Fig. 3 of Lan *et al.* (2017). The average signal-to-noise ratio of the integrated reflections from the converged intensity maps at different stages of the reconstruction. The increase of $\langle I/\sigma_I \rangle$ at high q indicates the reconstruction of high-resolution peaks. The 2.27 Å resolution determined by CC* is marked by the black dashed line.

References

Lan, T.-Y., Wierman, J. L., Tate, M. W., Philipp, H. T., Elser, V. & Gruner, S. M. (2017). *J. Appl. Cryst.* **50**, 985–993.