Guidelines for de novo phasing using multiple small-wedge data collection. Corrigendum

Seiki Baba, a Hiroaki Matsuura, b Takashi Kawamura, a Naoki Sakai, b Yuki Nakamura, a Yoshiaki Kawano, b Nobuhiro Mizuno, a Takashi Kumasaka, a Masaki Yamamoto b and Kunio Hirata * a

a Protein Crystal Analysis Division, Japan Synchrotron Radiation Research Institute, 1-1-1 Kouto, Sayo, Hyogo 679-5198, Japan, and b Life Science Research Infrastructure Group, RIKEN SPring-8 Center, 1-1-1 Kouto, Sayo-Cho, Sayo-gun, Hyogo 679-5148, Japan. *Correspondence e-mail: kunio.hirata@riken.jp

A figure in the article by Baba et al. [(2021), J. Synchrotron Rad. 28, 1284–1295] is corrected.

The x-axis ranges (0–120) shown in Fig. 2 on p. 1290 of the article by Baba et al. (2021) are incorrect. The correct figure with the x-axes in the range 0–200 is published here.

Figure 2
Correlation between the number of data merged for each dose and \( CC_{\text{map}} \) for (a) \( \lambda = 1.4 \ \text{Å} \), (b) \( \lambda = 1.7 \ \text{Å} \). Mean values of the correlation coefficient \( CC_{\text{map}} \) derived from the phase determinations for ten randomly selected merged sub-datasets were plotted against the number of sub-datasets.

References