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The X-ray crystallography phase problem solved thanks to *AlphaFold* and *RoseTTAFold* models: a case-study report. Corrigendum

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A figure in the article by Barbarin-Bocahu & Graille [(2022), *Acta Cryst.* D**78**, 517–531] is corrected.

In the article by Barbarin-Bocahu & Graille (2022) the labels in Fig. 5(*b*) are incorrect. The corrected Fig. 5 is given below.

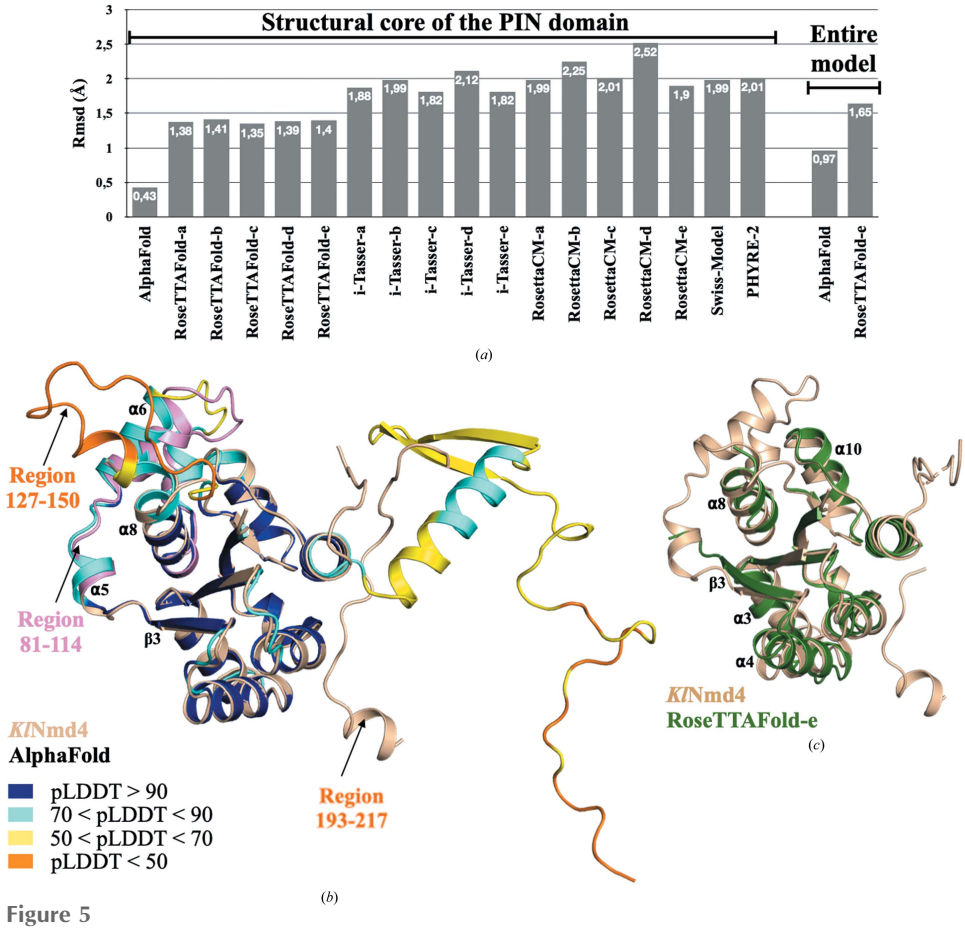

Figure 5
Comparison of the crystal structure of KlNmd4 with the various models. (*a*) Graph depicting the r.m.s.d. values between the C^{α} atoms of the KlNmd4 crystal structure and of the different models, either truncated (identified as 'structural core of the PIN domain') or intact ('entire model'). (*b*) Superposition of the full-length KlNmd4 *AlphaFold* model onto the KlNmd4 crystal structure (beige). The full-length KlNmd4 *AlphaFold* model is colored according to the pLDDT values. The region 81–114 of the KlNmd4 crystal structure is highlighted in pink. (*c*) Superposition of the KlNmd4 crystal structure (beige) and the truncated KlNmd4 *RoseTTAFold*-e model (dark green).

References

Barbarin-Bocahu, I. & Graille, M. (2022). *Acta Cryst.* D**78**, 517–531.