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Structural basis for the fast maturation of pcStar, a photoconvertible fluorescent protein. Erratum

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Keywords: fluorescent proteins; photoconvertible; pcStar; crystal structure; maturation mechanism.

Several corrections are made to the article by Zheng *et al.* [(2025), *Acta Cryst.* D**81**, 181–195].

The following corrections are made to the article by Zheng *et al.* (2025).

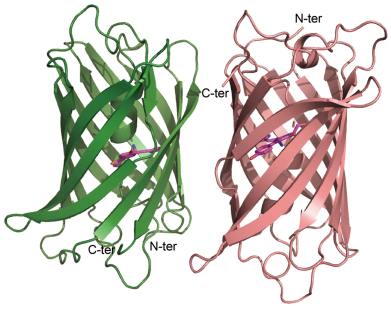
In the caption to Fig. 5, the references to parts (*a*) and (*b*) were incorrect. The correct caption should read as follows:

> Molecular-dynamics simulation analyses of mEos3.2 and pcStar. (*a*, *b*) The dynamic changes of secondary structure in pcStar (*a*) and mEos3.2 (*b*). The regions close to residues 54–61 are highlighted in red boxes. AA is an abbreviation for amino acids. (*c*) R.m.s.f. of each amino acid in mEos3.2 and pcStar, with residues 73–76 and 163–167 framed in blue rectangles. (*d*) R.m.s.f. of each atom in the chromophore of mEos3.2 and pcStar. (*e*–*h*) Chromophore torsion profiles: conformational changes of rotatable bonds in the chromophores throughout MD simulation. Probability densities of the torsion for rotatable bonds are shown for mEos3.2 (*e*, *g*) and pcStar (*f*, *h*). Colour-coded rotatable bonds correspond to (*d*).

In Section 3.5, the references to the Supplementary Figures are corrected. The first paragraph of Section 3.5 should read as follows:

> Identical to as in mEos2, a hydrogen-bond network is formed around the chromophore in both mEos3.2 and pcStar, with the involvement of direct hydrogen bonds from Thr58, Arg66, Trp89, Arg91, Asn105 and Ser142 and a solvent-mediated hydrogen bond from Glu140 (Supplementary Figs. S4*a*–S4*c*). Additionally, the indole side chain of Trp89 is stacked edge-to-face with the cyclized imidazolinone ring and the imidazole side chain of His194 is stacked face-to-face with the chromophoric phenol ring, thereby sandwiching the chromophore by π–π interactions (Supplementary Figs. S4*d*–S4*f*).

In Section 4, an incorrect reference to the Supplementary Figures was made. The fourth paragraph of Section 4 should read as follows:



> As for the possible mechanism linked to this decline in R_g revealed in our structures, we noticed some trivial but probably significant secondary-structural inconsistencies outside the β-barrel between pcStar and mEos3.2 (Figs. 2*b*, 5*a* and 5*b*). Although a few such conformational discrepancies occur in regions far away from the mutational sites, in particular N166G and D28E, a possible cause-and-effect relationship may exist between them. In principle, a mutation occurring in a protein may propagate its impact to a distant region, which has recurringly been observed in several structures of GFP-like proteins (Kim *et al.*, 2015; Pakhomov *et al.*, 2020). According to this

rationale, N166G and D28E might play an important role in the secondary-structural rearrangement, which in turn affects the packing of the β-barrel scaffold and imposes tighter restraints on the chromophore in pcStar, thereby effectively limiting its mobility.

References

Zheng, S., Shi, X., Lin, J., Yang, Y., Xin, Y., Bai, X., Zhu, H., Chen, H., Wu, J., Zheng, X., Lin, L., Huang, Z., Yang, S., Hu, F. & Liu, W. (2025). *Acta Cryst.* D**81**, 181–195.