

## CORRECTION

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Cite this: *J. Mater. Chem. B*, 2025, 13, 9294

DOI: 10.1039/d5tb90102b

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## Correction: Charge engineering controls cooperative assembly and loading in protein host–guest complexes

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Correction for 'Charge engineering controls cooperative assembly and loading in protein host–guest complexes' by Zhiheng Wang et al., *J. Mater. Chem. B*, 2025, <https://doi.org/10.1039/D5TB01202C>.

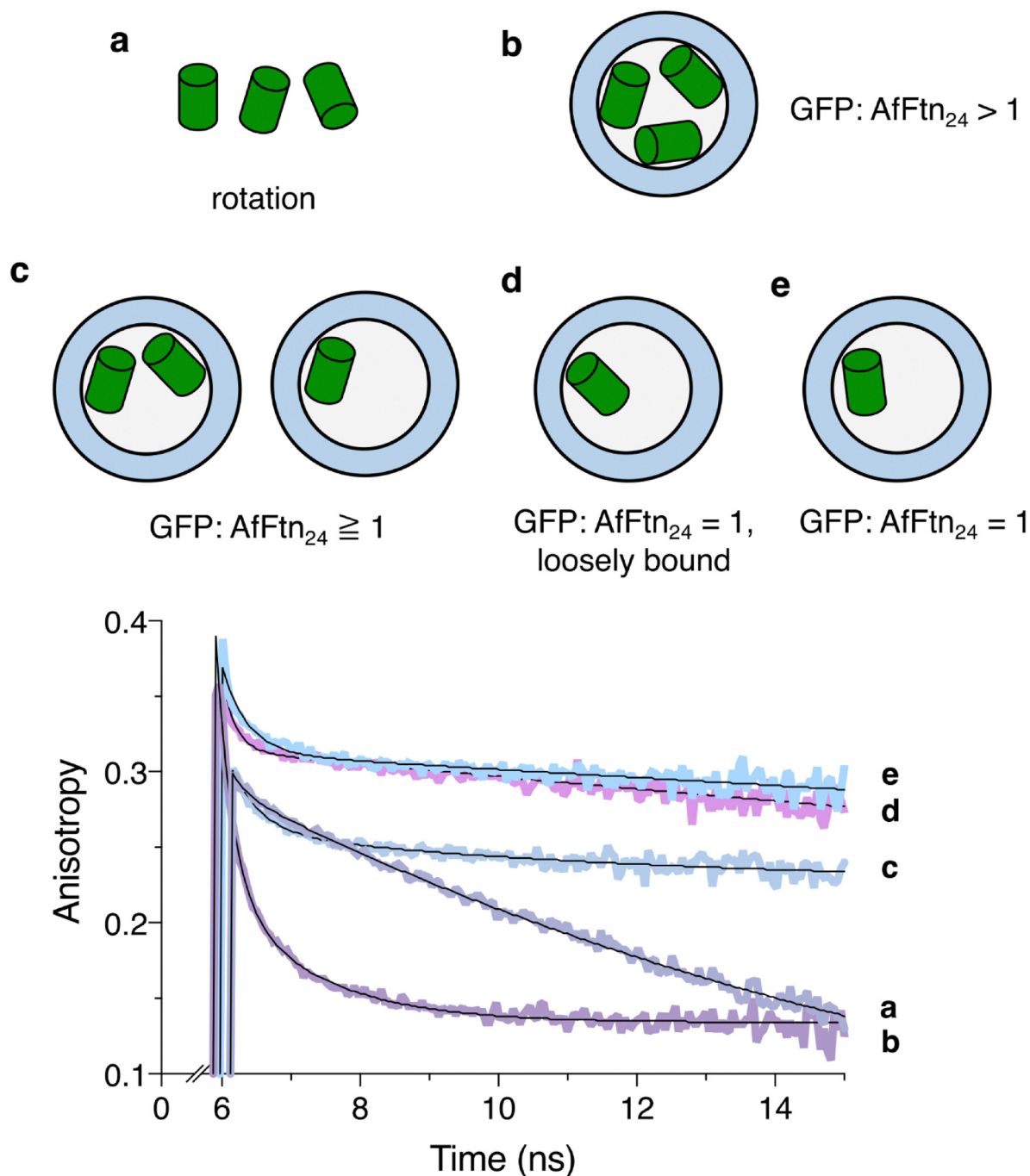
The authors regret that an incorrect version of Fig. 5 was included in the originally published article. The correct version of Fig. 5 is shown below.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

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**Fig. 5** Time-resolved fluorescence anisotropy of AfFtn–GFP. (a) GFP(+36) in the low ionic strength buffer, pH 7.6. The observed decay time (12.1 ns) is consistent with the rotational diffusion of GFP. (b) SEC-purified AfFtn–GFP(+36) at pH 7.6. (c) SEC-purified AfFtn–GFP(+36) at pH 5.8. From the fits, three decay times were obtained and associated with instrument response, homoFRET, and rotation. (d) AfFtn–GFP(+36) assembly at pH 7.6, 500 mM NaCl. (e) AfFtn–GFP(+36) assembly at pH 7.6, 175 mM NaCl. In (d) and (e), both anisotropy decays were fit biexponentially with only instrument response and rotation diffusion of the assembly with no homoFRET observed. This suggested that a 12-to-1 complex was formed under both conditions. The  $t = 0$  was set by the timing of the excitation laser pulse, and the data acquisition started around 6 ns. Each experiment was conducted in triplicate, and the sum files were plotted. In all samples, [GFP] = 1  $\mu$ M. In each case, the anisotropy was fit with a multiexponential model equation (see Methods). Conditions and fitted fluorescence anisotropy parameters with uncertainties are summarized in ESI,† Table S1.