



Correction to “Local Isotropic Diffusion Approximation for Coupled Internal and Overall Molecular Motions in NMR Spin Relaxation”

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The original version of Figure 66 is incorrect; the corrected figure is shown below. In addition, the sentence “The experimental data are fit in the fast-exchange limit with a population of the B state of 0.68, yielding an average $\tau_m = 5.29$ ns and $S^2 = 0.13$ ” (p 11126) should read “The experimental data are fit in the fast-exchange limit with $S^2 = 1$ (by construction, eq 21) and a population of the B state of 0.67 and $k_2 = 1.6 \times 10^9$ s⁻¹, yielding an average

$\tau_m = 5.19$ ns.” The population of 0.68 reported in the caption to Figure 7 also should be 0.67. No conclusions of the paper are affected by these corrections.

ACKNOWLEDGMENTS

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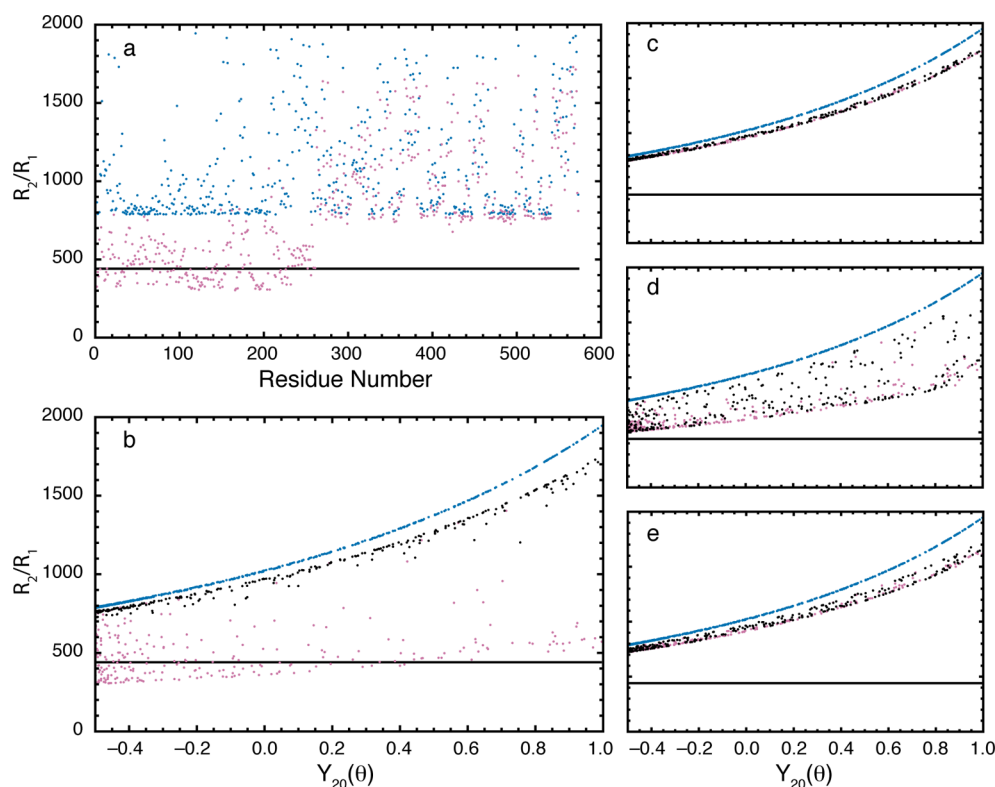


Figure 6. Calculated relaxation rate constants for enzyme I. The R_2/R_1 ratio is shown as a function of k_2 , the rate constant for transitions from closed to open conformations. (a, b) The R_2/R_1 ratio is shown versus (a) the residue sequence position or (b) $Y_{20}(\theta) = (3 \cos^2 \theta - 1)/2$, in which θ is the polar angle of the N–H bond vector in the principal axis coordinate system of the open conformation for $k_2 = 10^8$ s⁻¹. Results are also shown as in panel b for (c) $k_2 = 10^6$ s⁻¹, (d) $k_2 = 10^{10}$ s⁻¹, and (e) $k_2 = 10^{11}$ s⁻¹. Other parameters are the same as those for Figure 5 and are given in Methods. In all panels, the horizontal black line and the blue symbols are the calculated results for the closed and open conformations, respectively. In panel (a) the reddish-purple symbols are the calculated results for the exchanging system. In the other panels, reddish-purple symbols are for residues in the outer domain (residues 1–269) and black symbols are for residues in the core inner domain (residues 270–573).

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