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Correction to "Single-Molecule Protein Unfolding in Solid State Nanopores"

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Pages 9289 and 9291. The first line of eq 2 should read as follows:

$$P_{\mathrm{fpt}}(t_{\mathrm{d}}) = \frac{d\ \mathrm{e}^{-(d-vt)^2/4Dt}}{2t\sqrt{\pi Dt}}$$

The corresponding cumulative distribution function, which is useful for fitting, is

$$\mathrm{CDF}(t_{\mathrm{d}}) = \frac{1}{2}\left(\mathrm{e}^{dv/D}\ \mathrm{erfc}\left(\frac{d+vt}{2\sqrt{Dt}}\right) + \mathrm{erfc}\left(\frac{d-vt}{2\sqrt{Dt}}\right)\right)$$

The difference in the probability distribution function results in a small change in the fit parameters in Table 1. The revised values appear in the "Biased Diffusion" entries in the new Table 1, provided here. We also note that there were two typographical errors in the original Table 1. In the column reporting the fit parameters for the data in Figure 2A in the full paper, the amplitudes for the biased diffusion fits should have been $a_1 = 0.27 \pm 0.04$ and $a_2 = 0.73 \pm 0.04$. The differences in the physical parameters resulting from fitting to the alternative formula were inconsequential. The conclusions of the paper remain the same. The proteins' translocation times cannot be explained by biased diffusion. The long event times and observed excluded volumes are consistent with unfolded and looped translocations being halted at points of electrostatic balance that we call stall points.

Table 1. Excluded Volumes and Sojourn Time Distribution Fit Parameters[a]

	Figure 2A	Figure 2B	Figure 2C	Figure 2F	Figure 3A	Figure 3B	
Fit	βLGa 0 M urea	βLGa 5 M urea	βLGa 8 M urea	DNA 0 M urea	βLGa 8 M urea	HPr 8 M urea	units
Excluded Volume	$\Lambda_{1a} = 7.1 \pm 0.15$	$\Lambda_{1a} = 7.3 \pm 0.1$	$\Lambda_{1a} = 8.24 \pm 0.13$	$\Lambda_1 = 34.9 \pm 0.2$	$\Lambda_{1a} = 7.5 \pm 0.2$	$\Lambda_{1a} = 6.8 \pm 0.1$	nm^3
	$\Lambda_{1b} = 8.6 \pm 0.7$	$\Lambda_{1b} = 8.7 \pm 0.2$	$\Lambda_{1b} = 9.8 \pm 0.9$	—	$\Lambda_{1b} = 9.5 \pm 0.8$	$\Lambda_{1b} = 8.3 \pm 0.6$	nm^3
	$\Lambda_{2a} = 11.1 \pm 1.7$	$\Lambda_{2a} = 10.8 \pm 2.7$	$\Lambda_{2a} = 12 \pm 5$	$\Lambda_2 = 41.9 \pm 0.8$	$\Lambda_{2a} = 12.3 \pm 2.1$	—	nm^3
	$\Lambda_{2b} = 17.6 \pm 1.4$	$\Lambda_{2b} = 17.4 \pm 2.1$	$\Lambda_{2b} = 16 \pm 5$	$\Lambda_3 = 9.6 \pm 0.1$	—	—	nm^3
	$d = 20$	$d = 20$	$d = 20$	$d = 950$	$d = 20$	$d = 20$	
Biased Diffusion	$a_1 = 0.26 \pm 0.04$	$a_1 = 0.27 \pm 0.04$	$a_1 = 0.086 \pm 0.007$	$a_1 = 0.21 \pm 0.01$	$a_1 = 0.27 \pm 0.05$	$a_1 = 0.27 \pm 0.05$	—
	$D_1 = 0.24 \pm 0.02$	$D_1 = 0.33 \pm 0.03$	$D_1 = 0.10 \pm 0.01$	$D_1 = 134. \pm 5.$	$D_1 = 0.20 \pm 0.02$	$D_1 = 0.20 \pm 0.02$	$\mathrm{nm}^2/\mu\mathrm{s}$
	$v_1 = 0.253 \pm 0.003$	$v_1 = 0.300 \pm 0.004$	$v_1 = 0.201 \pm 0.002$	$v_1 = 16.19 \pm 0.03$	$v_1 = 0.256 \pm 0.004$	$v_1 = 0.256 \pm 0.004$	$\mathrm{nm}/\mu\mathrm{s}$
Biased Diffusion	$a_2 = 0.74 \pm 0.04$	$a_2 = 0.73 \pm 0.05$	$a_2 = 0.914 \pm 0.013$	$a_2 = 0.79 \pm 0.01$	$a_2 = 0.73 \pm 0.05$	$a_2 = 0.73. \pm 0.06$	—
	$D_2 = 0.47 \pm 0.05$	$D_2 = 0.55 \pm 0.08$	$D_2 = 0.43 \pm 0.01$	$D_2 = 144 \pm 2$	$D_2 = 0.40 \pm 0.07$	$D_2 = 0.40 \pm 0.07$	$\mathrm{nm}^2/\mu\mathrm{s}$
	$v_2 = 0.091 \pm 0.003$	$v_2 = 0.094 \pm 0.003$	$v_2 = 0.042 \pm 0.001$	$v_2 = 13.33 \pm 0.02$	$v_2 = 0.097 \pm 0.003$	$v_2 = 0.097 \pm 0.003$	$\mathrm{nm}/\mu\mathrm{s}$
Activated Barrier/ Exponential	$b_1 = 190 \pm 16$	$b_1 = 180 \pm 7$	$b_1 = 66 \pm 4$	—	$b_1 = 195 \pm 2$	$b_1 = 137 \pm 1$	—
	$t_1 = 53 \pm 4$	$t_1 = 56 \pm 2$	$t_1 = 33 \pm 4$	—	$t_1 = 230 \pm 3$	$t_1 = 113 \pm 2$	$\mu\mathrm{s}$
	$b_2 = 158 \pm 17$	$b_2 = 89 \pm 7$	$b_2 = 160 \pm 3$	—	—	—	—
	$t_2 = 177 \pm 11$	$t_2 = 210 \pm 10$	$t_2 = 322 \pm 7$	—	—	—	$\mu\mathrm{s}$

[a]Excluded volume distributions were fit with enough (2−4) Gaussian components to give flat residuals. Protein sojourn time distributions were fit to both the biased diffusion model (a, D, v) and to the activated barrier crossing model (b, t). Subscripts on the parameters correlate to the cluster labels in Figure 2. The errors are fitting errors.

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