BIOCHEMISTRY. For the article "Enzyme structure and dynamics affect hydrogen tunneling: The impact of a remote side chain (I553) in soybean lipoxygenase-1," by Matthew P. Meyer, Diana R. Tomchick, and Judith P. Klinman, which appeared in issue 4, January 29, 2008, of *Proc Natl Acad Sci USA* (105:1146–1151; first published January 23, 2008; 10.1073/pnas.0710643105), the authors note that in Table 1, the values given for the calculated Arrhenius parameters and the input parameters appeared incorrectly. The parameters were calculated incorrectly due to a sign inversion. Because the trends remain the same, this error does not affect the conclusions of the article. The corrected table appears below.

Table 1. Summary of empirical and computed Arrhenius parameters

SLO mutant	Experimental Arrhenius parameters			Calculated Arrhenius parameters*		Input parameters[†]	
	$E_a(H)$, kcal/mol	$E_a(D) - E_a(H)$, kcal/mol	A_H/A_D	$E_a(D) - E_a(H)$, kcal/mol	A_H/A_D	r_0, Å	Ω_{Gating}, cm^{-1}
WT	2.1 ± 0.2[‡]	0.9 ± 0.2[‡]	18 ± 5[‡]	1.0[§]	15[§]	0.66[§]	292[§]
Ile$^{553} \rightarrow$ Val	2.4 ± 0.5	2.6 ± 0.5	0.3 ± 0.2	3.1	0.4	1.24	64
Ile$^{553} \rightarrow$ Leu	0.4 ± 0.7	3.4 ± 0.6	0.3 ± 0.4	3.4	0.2	1.43	56
Ile$^{553} \rightarrow$ Ala	1.9 ± 0.2[‡]	4.0 ± 0.3[‡]	0.12 ± 0.06[‡]	4.0[§]	0.11[§]	1.79[§]	47[§]
Ile$^{553} \rightarrow$ Gly	0.03 ± 0.04	5.3 ± 0.7	0.027 ± 0.034	5.2	0.027	2.55	38

*Calculated by treating the hydrogen wave functions as Morse oscillators. The significance of these calculations is the trends in parameters, not their absolute magnitude.

[†] r_0 is the initial distance that hydrogen would have to transfer between the donor and acceptor (prior to gating). Ω_{gating} is the frequency of the gating mode.

[‡] Data from ref. 15.

[§] Data from ref. 16.

CELL BIOLOGY. For the article "The Dam1 ring binds microtubules strongly enough to be a processive as well as energy-efficient coupler for chromosome motion," by Ekaterina L. Grishchuk, Artem K. Efremov, Vladimir A. Volkov, Ilia S. Spiridonov, Nikita Gudimchuk, Stefan Westermann, David Drubin, Georjana Barnes, J. Richard McIntosh, and Fazly I. Ataullakhanov, which appeared in issue 40, October 7, 2008, of *Proc Natl Acad Sci USA* (105:15423–15428; first published September 29, 2008; 10.1073/pnas.0807859105), the authors note that due to a printer's error, Fig. 1B *Inset* appeared incorrectly. The corrected figure and its legend appear below.
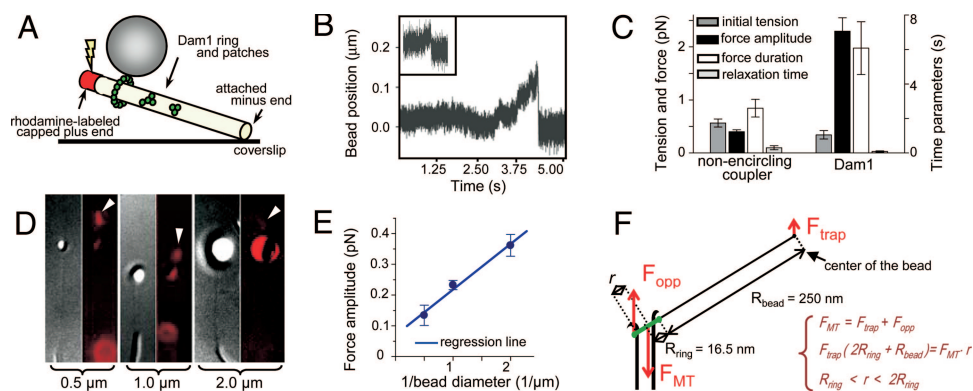

Fig. 1. Quantitative analysis of the force-transducing attachments. (*A*) A schematic of the experimental system. Position of beads bound to the GDP-MT walls was followed with QPD before and after induction of MT disassembly. (*B*) Unprocessed QPD records of representative signals from a Dam1-coated bead in the presence of soluble Dam1 and a streptavidin-coated bead (*Inset*) relative to the center of the laser trap. (*C*) Mean values for the four parameters that describe force signals (see ref. 9 for details). (*Left*) 0.5-μm streptavidin-coated beads assayed with biotinylated MTs ($n = 35$). (*Right*) Wild-type Dam1-coated beads with soluble Alexa488–Dam1 ($n = 26$). (*D* and *E*) Force measurements carried out with streptavidin-coated beads: 0.5 μm ($n = 45$), 1 μm ($n = 81$; includes data from ref. 9), 2 μm ($n = 35$). Photos show DIC images of representative beads attached to MT walls and their fluorescence images (red) taken during dissolution of the rhodaminated GMPCPP caps (arrowheads). Graph shows median values for force amplitudes for these beads. Trap stiffness, ≈ 0.008 pN/nm. (*F*) Drawing (not to scale) of the forces from MT depolymerization and the laser trap. The fulcrum is at ring's edge on the bead-distal side of the MT; because of the ring's tilt, F_{MT} is likely to act slightly off the MT axis, so its lever arm r is defined by a range. The bead (not shown) is 15 times larger than the ring, so a relatively small trapping force can stall the MT-disassembly-driven movement of the ring.