**Erratum: Mobility Measurements Probe Conformational
Changes in Membrane Proteins due to Tension
[Phys. Rev. Lett. **115**, 198101 (2015)]**

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(Received 11 April 2016; published 8 June 2016)

DOI: [10.1103/PhysRevLett.116.239901](https://doi.org/10.1103/PhysRevLett.116.239901)

Our analysis neglected the role of the Gaussian curvature K in the membrane Hamiltonian, implicitly setting the saddle-splay modulus $\bar{\kappa} = 0$. For the general case $\bar{\kappa} \neq 0$, Eq. (1) should contain an extra term $\bar{\kappa}K$ under the integral sign. (Note that since the shape of the protein may change, so can the geodesic curvature c_g of the boundary between the protein and the membrane, and, as a result, the Gauss-Bonnet theorem $\int_S K dA = 2\pi - \int_{\partial S} c_g dl$ cannot be used to equate the additional term to a constant, as would normally be the case.) Incorporating such a saddle-splay term does not affect either the shape of the membrane [Eq. (2)] or the hydrodynamic calculations, but it does modify the expression for the torque exerted at the boundary [given by Eq. (9)] which then reads $\tau = 2\pi\alpha[a\sigma h(a) - \bar{\kappa}]$. Reflecting the data summarized in Ref. [1], we set $\bar{\kappa} \approx -0.9\kappa$, which, with the remaining calculation and fitting procedure unchanged, leads to a modified prediction for the torsional rigidity of $86.3k_B T$, rather stiffer than originally reported. None of the discussion or our overall conclusions are otherwise affected.

[1] M. Hu, J. J. Briguglio, and M. Deserno, *Biophys. J.* **102**, 1403 (2012).