



# Correction to Multiscale Reactive Molecular Dynamics for Absolute $pK_a$ Predictions and Amino Acid Deprotonation

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With this erratum, we present a correction to the equation for the calculation of a  $pK_a$  from a PMF (eq 9 in the original publication)<sup>1</sup>

$$pK_a = -\log \left[ C^0 \int_0^\ddagger 4\pi r^2 \exp[-\beta w(r)] dr \right]^{-1}$$

where  $w(r)$  is the free energy from the PMF, and  $\beta$  is the product of the simulation temperature and the Boltzmann constant. The integral is calculated from zero to the transition state, as denoted by  $\ddagger$ .  $C^0$  is the standard state concentration whose value is 1 molecule/1660 Å<sup>3</sup> and results from the entropic freedom that is gained by the proton when it dissociates from the acid.<sup>2,3</sup> The  $pK_a$  was calculated correctly in the original publication; this correction does not influence the results presented therein.<sup>1</sup>

## REFERENCES

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- (3) Gilson, M. K.; Given, J. A.; Bush, B. L.; McCammon, J. A. The Statistical-Thermodynamic Basis for Computation of Binding Affinities: A Critical Review. *Biophys. J.* 1997, 72, 1047–1069.

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