

CORRECTION

Open Access



Correction to: Long range Debye-Hückel correction for computation of grid-based electrostatic forces between biomacromolecules

Paolo Mereghetti^{1,2}, Michael Martinez¹ and Rebecca C. Wade^{1,3*}

Correction to: *BMC Biophys* 7, 4 (2014)
[doi:10.1186/2046-1682-7-4](https://doi.org/10.1186/2046-1682-7-4)

The original publication of this article [1] contained an error. This error is due to the misassignment of one value (the molecular weight of hen egg white lysozyme (HEWL)).

In the section “**BD simulations of protein solutions**”, the concentrations of HEWL given for the simulations are incorrect.

The incorrect and correct text is as followed.

1. Incorrect

- a. Simulations of HEWL were performed at 14, 28, 57 and 85 g/L for comparison with experimental long-time translational self-diffusion coefficients [35]

2. Correct

- a. Simulations of HEWL were performed at 3.1, 6.1, 12.3 and 18.4 g/L for comparison with experimental long-time translational self-diffusion coefficients [35]

Consequently, in Figure 4, the computed normalized HEWL translational diffusion coefficients (green and red squares) are shown at the wrong HEWL concentrations. They should be shown at HEWL concentrations of 3.1, 6.1, 12.3, and 18.4 g/L instead of 14.3, 28.6, 57.2 and 85.8 g/L, respectively.

The methodology introduced in this paper and the overall conclusions are not affected by this correction.

Author details

¹Molecular and Cellular Modeling Group, Heidelberg Institute for Theoretical Studies (HITS), Schloß-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany.

²Center for Nanotechnology Innovation@NEST, Italian Institute of Technology, Piazza San Silvestro 12, Pisa, Italy. ³Center for Molecular Biology (ZMBH), University of Heidelberg, Im Neuenheimer Feld 282, 69120 Heidelberg, Germany.

Published: 11 February 2020

Reference

1. Mereghetti P, Martinez M, Wade RC. Long range Debye-Hückel correction for computation of grid-based electrostatic forces between biomacromolecules. *BMC Biophys*. 2014;7:4. <https://doi.org/10.1186/2046-1682-7-4>.

The original article can be found online at <https://doi.org/10.1186/2046-1682-7-4>

* Correspondence: rebecca.wade@h-its.org

¹Molecular and Cellular Modeling Group, Heidelberg Institute for Theoretical Studies (HITS), Schloß-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany

³Center for Molecular Biology (ZMBH), University of Heidelberg, Im Neuenheimer Feld 282, 69120 Heidelberg, Germany

Full list of author information is available at the end of the article



© The Author(s). 2020 **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated.