

Corrigendum

DNA binds to a specific site of the adhesive blood-protein von Willebrand factor guided by electrostatic interactions

Angélica Sandoval-Pérez¹, Ricarda M. L. Berger², Adiran Garaizar³, Stephen E. Farr³, Maria A. Brehm⁴, Gesa König⁴, Stefan W. Schneider⁵, Rosana Colleparado-Guevara^{3,6,7}, Volker Huck⁵, Joachim O. Rädler² and Camilo Aponte-Santamaría^{1,8,*}

¹Max Planck Tandem Group in Computational Biophysics, University of Los Andes, Cra. 1, 18A-12, 111711, Bogotá, Colombia, ²Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 Munich, Germany, ³Maxwell Centre, Cavendish Laboratory, Department of Physics, University of Cambridge, J J Thomson Avenue, Cambridge CB3 0HE, UK, ⁴Department of Pediatric Hematology and Oncology, University Medical Center Hamburg-Eppendorf, Martinistr. 52, 20246 Hamburg, Germany, ⁵Department of Dermatology, Center for Internal Medicine, University Medical Center Hamburg-Eppendorf, Martinistr. 52, 20246 Hamburg, Germany, ⁶Department of Genetics, University of Cambridge, Cambridge CB2 3EH, UK, ⁷Department of Chemistry, University of Cambridge, Cambridge CB2 1EW, UK and ⁸Interdisciplinary Center for Scientific Computing, Heidelberg University, Im Neuenheimer Feld 205, 69120 Heidelberg, Germany

Nucleic Acids Research, 2020, 48(13): 7333–7344, <https://doi.org/10.1093/nar/gkaa466>

The authors would like to apologize for mistakes in the *P*-value calculations of the DNA bending angle distributions. The following corrections have been made to the published article.

SUPPLEMENTARY TEXT

S1 SUPPORTING MATERIALS AND METHODS

Atomistic Molecular Dynamics (MD) simulations

Analysis of atomistic MD simulations

The distributions of the bending angle before and after association were compared using the two-sample Kolmogorov-Smirnov test (22).

has been corrected to

The distributions of the bending angle before and after association were compared using the two-sample Kolmogorov-Smirnov test (22). The test was carried out for a subset of N_{bound} and N_{unbound} uncorrelated angle values which were randomly-chosen from the angle time traces, in the bound and unbound states, respectively. To avoid correlation between chosen data points, the values were separated by a time window of at least 10 to 100 ns (time in which the autocorrelation function of the angle traces diminished from 1 to 0.1), thus yielding sample sizes between 23 and 152. The test was repeated

*To whom correspondence should be addressed. Tel: +57 1 3394949 (Ext. 1863); Email: ca.aponte@uniandes.edu.co

200 times considering different N_{bound} and N_{unbound} values and the number of cases the P -value was larger than 0.05 was quantified.

Figure 2A

Both states, bound/unbound exhibited similar distribution as evaluated by the Kolmogorov-Smirnov test ($D = 0.13$ and $P\text{-value} = 0.34$).

has been corrected to

Both states, bound/unbound exhibited similar distribution as evaluated by the Kolmogorov-Smirnov test ($P\text{-value} \geq 0.05$ in 65% of 200 resample rounds, with $N_{\text{bound}}=60$ and $N_{\text{unbound}}=23$ randomly-chosen values for each round).

Figure 4B

The bending angle distribution in bound/unbound states exhibited similar distributions (Kolmogorov-Smirnov test: $D = 0.18$ and $P = 0.08$).

Has been corrected to

The bending angle distribution in bound/unbound states exhibited similar distributions ($P\text{-value} \geq 0.05$ in 55% of 200 re-sample rounds, with $N_{\text{bound}} = 118$ and $N_{\text{unbound}}=53$ randomly-chosen values for each round).

RESULTS

Specific binding site in vWF A1 interacts with multiple unspecific sites in DNA:

Furthermore, the bending-angle distribution for ds DNA in the bound and unbound states is statistically equivalent (Kolmogorov-Smirnov test: $D = 0.18$, $P = 0.08$).

Has been corrected to

Furthermore, the bending-angle distribution for ds DNA in the bound and unbound states is statistically equivalent ($P\text{-value} \geq 0.05$ in 55% of 200 resample rounds, with $N_{\text{bound}} = 118$ and $N_{\text{unbound}}=53$ randomly-chosen values for each round).

Figure S9

Both states, bound and unbound, exhibited similar distribution as evaluated by the Kolmorov-Smirnov test ($D=0.11$ and $P\text{-value}=0.58$).

Has been corrected to

Both states, bound and unbound, exhibited similar distribution as evaluated by the Kolmorov-Smirnov test ($P\text{-value} \geq 0.05$ in 96% of 200 resample rounds, with $N_{\text{bound}}=89$ and $N_{\text{unbound}}=152$ randomly-chosen values for each round)

None of these corrections affect the conclusion ‘the bending angle, before and after dsDNA encountered the vWF A1 domain, did not display statistically-significant differences’ or any other conclusion of the article.