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Addition/Correction

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Correction to Protein Nanopore-Based, Single-Molecule Exploration of Copper Binding to an Antimicrobial-Derived, Histidine-Containing Chimera Peptide

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Langmuir **2012**, *28* (49), 17079−17091. DOI: 10.1021/la303782d.

Due to the existence of some typing errors that escaped our notice, the caption of Figure 3 should read as follows:

Figure 3. Voltage dependence of the association (τ_{ON}) and dissociation (τ_{OFF}) average time intervals which describe the interaction of a single CAMA peptide with the α-HL protein pore in the absence of Cu^{2+} (panels a and b) and presence of 100 μM Cu^{2+} added on the trans side of the membrane. By invoking Eyring's transition state theory (see also text), and considering that within a qualitative kinetic model for the peptide−protein pore interaction, the effects of the transmembrane potential can be reckoned as alterations of the association and dissociation activation free energies, the rate constants can be fitted with single decaying exponentials (dashed lines; $y_{(\tau_{OFF},\tau_{ON})} = Ae^{-((x_{(\Delta V)})/(\Delta V_0))}$ for data presented in panels a, b, and c), and a raising exponential (dashed line; $y_{(\tau_{OFF})} = Ae^{((x_{(\Delta V)})/(\Delta V_0))}$ for data presented in the panel d, see also text). The nonlinear fit of data displayed in panels a and b, in the Cu^{2+} free buffer, gave $\Delta V_{0,a} = 63.4 \pm 4.7$ mV ($R^2 = 0.97$) and respectively $\Delta V_{0,b} = 67 \pm 6.2$ mV ($R^2 = 0.96$), whereas data in panels c and d (100 μM Cu^{2+}) fitted with single exponentials resulted in $\Delta V_{0,c} = 43.3 \pm 9.2$ mV ($R^2 = 0.86$) and respectively $\Delta V_{0,d} = 36.4 \pm 4.3$ mV ($R^2 = 0.95$).

We would like to mention that this erratum does not affect in any way the presented experimental results, discussion, or conclusions drawn, and authors apologize for this unintended mistake.

Published: May 22, 2013