Corrections

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2011. The role of bulk protein in local models of ion-binding to proteins: Comparative study of KcsA, its semisynthetic analog with a locked-in binding site, and valinomycin. *Biophys. J.* 100:1542–1549.

In Tables 1 and 3, we incorrectly noted three energy values. We rectify those errors here. The changes are small and do not affect the conclusions in the article.

In Table 1 for wild-type KcsA in column A_3, $\Delta\langle\varepsilon_{local}\rangle$ is -21.0 not -19.6.

In Table 3 for wild-type KcsA, the ion site interactions, $\Delta\langle\varepsilon_{local}\rangle$ is -21.0 not -19.6.

In Table 3 for wild-type KcsA, the ion-medium interactions, $\Delta\langle\varepsilon_{m}\rangle$ is 2.2 not 0.8.

In Table 3 for wild-type KcsA, the local entropy change, $T\Delta s^{ex}_{local}$ is 2.1 not 3.5.

We reproduce Tables 1 and 3 here for completeness. The updated values are noted in bold.

TABLE 1 Free energy and binding energy for KcsA, KcsA-G77A$_D$, and valinomycin according to three different methods of assessing ion-protein interactions (see Methods)

	A_1	A_2	A_3
KcsA			
$\Delta\mu^{ex}(S)/\Delta W_{local}$	−14.7	−15.7	−15.8
$\Delta\langle\varepsilon_{local}\rangle$	−20.9	−18.8	**−21.0**
KcsA-G77A$_D$			
$\Delta\mu^{ex}(S)/\Delta W_{local}$	−9.0	−10.0	−9.9
$\Delta\langle\varepsilon_{local}\rangle$	−28.3	−19.3	0.8
Valinomycin			
$\Delta\mu^{ex}(S)/\Delta W_{local}$	−11.3		−11.0
$\Delta\langle\varepsilon_{local}\rangle$	−17.7		−9.4

ΔW_{local} is insensitive to these choices and is sufficiently close to the actual free energy change, $\Delta\mu^{ex}(S)$. The local model adequately captures binding energetics in KcsA but not in KcsA-G77A$_D$ and valinomycin. For the latter two systems, Na^+ is stabilized by interactions with medium outside the binding site. Statistical uncertainties in energy values are ~0.8 kcal/mol.

TABLE 3 Energetic decomposition for KcsA and KcsA-G77A$_D$

		KcsA	KcsA-G77A$_D$
	$\Delta\mu^{ex}(S)$	−15.7	−10.0
	ΔW_{local}	−15.8	−9.9
	$T\Delta s^{ex}$	1.3	−1.1
	$T\Delta s^{ex}_{local}$	**2.1**	4.7
Ion-site	$\Delta\langle\varepsilon_{local}\rangle$	**−21.0**	0.8
Ion-medium	$\Delta\langle\varepsilon_{m}\rangle$	**2.2**	−20.1
Site-site	$\Delta\langle U_S\rangle$	7.3	−6.0
Site-medium	$\Delta\langle U_{S-M}\rangle$	−2.9	14.5
Medium-medium	$\Delta\langle U_M\rangle$	0.0	−0.3

Eight carbonyl ligands comprise the local site. We consider the water molecules in the S_1 and S_3 sites adjoining the S_2 site as the medium. Similar to valinomycin, the change in ion-medium interactions is inversely related to the change in site-medium interactions. All values are in kcal/mol.

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2011. Impact of heparan sulfate chains and sulfur-mediated bonds on the mechanical properties of bovine lens capsule. *Biophys. J.* 100:2077–2083.

Author L. B. Dyksterhuis' middle initial is incorrect in the published article and is corrected here.

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