Correction:

Dagmar Flöck and Volkhard Helms. 2004. A Brownian dynamics study: the effect of a membrane environment on an electron transfer system. *Biophys. J.* 87:65–74.

Upon rerunning the Brownian dynamics simulations of this study in our group, we noted that, in the original publication above, each lipid molecule in the membrane was assigned an incorrect positive net charge of +0.3 e. As a result, the right panel in Fig. 2 in this article was incorrect. The correct figure is shown below. The figure legends below apply to the corrected images. This mistake explains why the partial charges of the membrane had a huge impact on the calculated association rates in this work. After the correction, we find only relatively small effects of the membrane on the computed association rates, no matter whether the partial charges of the membrane are switched on or off, see the corrected Fig. 9 below.

We thank Dr. Alexander Spaar for sharing data from his Brownian Dynamics simulations of this system.

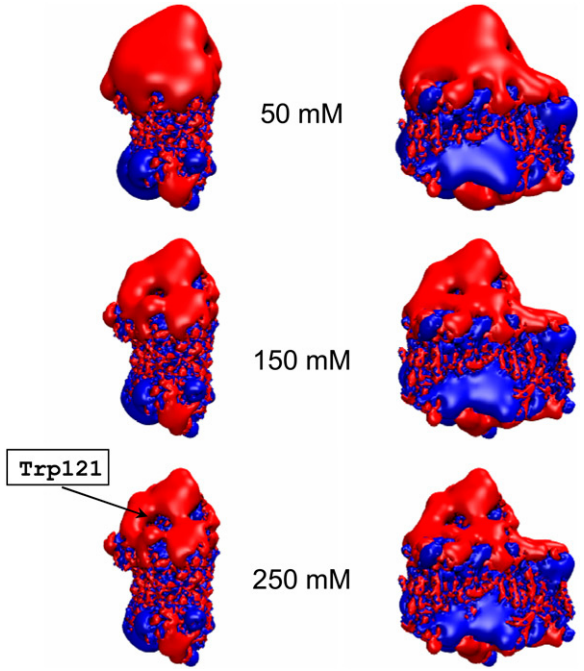

FIGURE 2 Potential isocontours shown at +1 kT/e (*blue*) and −1 kT/e (*red*) of COX alone (*left*) and of the central unit of COX surrounded by lipid bilayer (*right*). The electron entry site Trp121 is less exposed when COX is membrane-embedded.

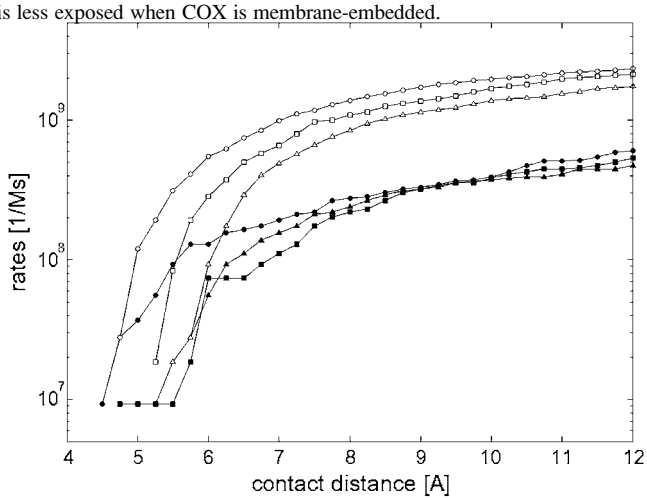

FIGURE 9 The effects of the membrane on the association rates for reduced cyt c_{552} (*solid symbols*) and reduced cyt c_h (*open symbols*) with three times reduced COX at 200 mM. The rates are displayed with respect to the distance between three inter-residue pairs for three different scenarios: association of

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