Corrigendum: g_membed: Efficient insertion of a membrane protein into an equilibrated lipid bilayer with minimal perturbation

Maarten G. Wolf, Martin Hoefling, Camilo Aponte-Santamaría, Helmut Grubmüller, and Gerrit Groenhof

DOI: 10.1002/jcc.24386

[Article in *J. Comput. Chem*. 2010, **31**, 2169–2174, DOI: 10.1002/jcc.21507]

It has come to the authors' attention recently[1] that a similar approach for embedding proteins into equilibrated lipid bilayers described in J. Comp. Chem. **31**, 2169 (2010)[2] had been proposed prior to their work by Dr. Semen Yesylevskyy in J. Chem. Inf. Mod. 47 1986 (2007)[3] and implemented as a ProtSqueeze tool, which the authors have unfortunately overlooked. Although the focus of the above paper was on the implementation of that approach in the Gromacs molecular dynamics program, the authors want to acknowledge Dr. Yesylevskyy's work. Users of the g_membed program should therefore include a citation to his work[3] as well.

The authors regret any inconvenience this may have caused.

References

[1] Semen Yesylevskyy (2016) personal communication.
[2] M. G. Wolf, M. Hoefling, C. Aponte-Santamaria, H. Grubmueller, G. Groenhof. g membed: Efficient insertion of a membrane protein into an equilibrated lipid bilayer with minimal perturbation. *Journal of Computational Chemistry*, *31* (**2010**), 2169.
[3] S.O. Yesylevskyy: ProtSqueeze: simple and effective automated tool for setting up membrane protein simulations, *Journal of Chemical Information and Modeling 47* (**2007**), 1986.

Published online in Wiley Online Library