

Erratum: Monte Carlo studies on the hydrophobic hydration in dilute aqueous solutions of nonpolar molecules [J. Chem. Phys. 7 1, 2421 (1979)]

Susumu Okazaki, Koichiro Nakanishi, Hidekazu Touhara, and Yoshinori Adachi

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trusive, convenient, and accurate method for determining D_m . This is even true for unliganded Hb, which must be considered a worst case because of its large molar absorbance. In contrast to this, the classical diaphragm method, while deceptively simple to analyze, is beset with difficulties when applied to proteins.

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Susumu Okazaki, Koichiro Nakanishi, and Hidekazu Touhara

Department of Industrial Chemistry, Kyoto University, Kyoto 606, Japan

Yoshinori Adachi

Nagoya Institute of Technology, Nagoya 466, Japan

Some of internal energy values given in Table III are incorrectly calculated. Tables III and IV should be corrected to read as shown below.

TABLE III.

| | Pure water | Aqueous methane solution | Aqueous isobutane solution |
|-------------------|---------------|---------------------------------|----------------------------|
| U_N | -35.1 ± 0.2 | -36.1 ± 0.2 | -35.0 ± 0.7 |
| U_{vw} | | -36.4 ± 0.6 | -35.0 ± 0.5 |
| U_{dw} | | -36.8 ± 0.4 | -35.7 ± 0.8 |
| $U_{\mathbf{s}}$ | | -0.5 ± 0.2 | -6.1 ± 1.2 |
| $U_{vw} - U_{dw}$ | | $\textbf{0.3} \pm \textbf{0.9}$ | 0.8 ± 0.5 |
| z | - 0. 10 | 0.95 | 1.28 |

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TABLE IV. Thermodynamic functions of dissolution of methane into water at 295.15 K in kJ mol⁻¹.

| $A - A_0$ | $U - U_0$ | $T(S-S_0)$ |
|-----------|-----------|------------|
| 0.8 | -1.0 | -1.8 |

Some numerical values cited in the text should also be corrected according to the above figures. Revised discussion will appear in the forthcoming article.