functionally important sites and may be sufficiently ordered by these associations with the integral membrane proteins and complexes to perturb the structural and electronic configuration of cytochrome *c* and thereby modulate its physiological behavior. The most critical test of any influence of CL on the activity of cytochrome *c* in mitochondria would be to determine whether any of the effects discussed in this and previous work can be detected on the protein localized in the region of its site of action on the mitochondrial cytochrome complexes.

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Registry No. DOPC, 10015-85-7; cytochrome *c*, 9007-43-6.

CORRECTIONS

Solution Structure of Murine Epidermal Growth Factor Determined by NMR Spectroscopy and Refined by Energy Minimization with Restraints, by Gaetano T. Montelione, Kurt Wüthrich, Antony W. Burgess, Edward C. Nice, Gerhard Wagner, Kenneth D. Gibson, and Harold A. Scheraga*, Volume 31, Number 1, January 14, 1992, pages 236–249.

The previously published energy-refined structures of murine epidermal growth factor (mEGF) presented in the paper exhibit some peptide groups with significant deviations from planarity. These 16 mEGF structures were therefore refined again, starting from the coordinates calculated with the DISMAN program. The restrained energy minimization was repeated exactly as described in the paper, except that the peptide bond dihedral angles were also restrained using a penalty function weighted sufficiently to prevent deviations of greater than 10° from the planar trans conformation. Except for minor variations, these 16 energy-refined mEGF structures are largely identical to those reported previously in the paper. The atomic coordinates for this revised set of energy-refined structures replace the original set of energy-refined coordinates and have been deposited in the Brookhaven Protein Data Bank.