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High-resolution crystal structures of *Desulfovibrio vulgaris* (Hildenborough) nigerythrin: facile, redox-dependent iron movement, domain interface variability, and peroxidase activity in the rubrerythrins

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The following text was omitted from the bottom of the left-hand column of page 410 in the printed journal version:

noncoordinating E118 O ϵ is also within hydrogen-bonding distance of the bridging solvent oxygen in both monomers. This hydrogen-bonding pattern is consistent with the protonated solvent bridge expected for the mixed-valent diiron site. This result indicates rapid one-electron reduction of

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