PROTEIN CHARGE TRANSFER REACTIONS AS BENCHMARKS FOR FREE ENERGY CALCULATIONS BASED ON MOLECULAR DYNAMICS SIMULATIONS

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Biological charge transfer is a phenomenon underlying many fundamental processes of life, such as photosynthesis, respiration and DNA damage or repair. It plays an important role in bio-nano devices and sensor applications. Charge transfer is usually described within the seminal theory of Marcus, which is based on three characteristic energies, *viz.* the thermodynamic driving force or free energy difference, ΔG, the reorganization energy, λ, and the donor-acceptor tunnel splitting, t. The driving forces are related to the experimentally observable midpoint potentials, thus providing benchmarks for theory and simulation.

We present a variant of the thermodynamic integration method adapted to charge transfer reactions [1]. With the help of this molecular dynamics based approach we have identified unusual charge transfer pathways in cryptochromes [2], studied the versatility of heme cofactors in nitrite reductase [3] and identified active sites in peroxidases. A thermodynamic network analysis is formulated and found to greatly enhance the statistical accuracy of free energy calculations.

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