Enzyme-catalyzed charge transfer involves dynamics that span timescales that range from slow fluctuations in the protein to fast quantum mechanical reaction dynamics at the active site. We use quantized molecular dynamics simulations to model hydride transfer in dihydrofolate reductase. By sampling the full ensemble of reactive trajectories, we are able to quantify and distinguish between statistical and dynamical correlations in enzyme motion. We demonstrate the existence of nonequilibrium dynamical coupling between protein residues and the hydride tunneling reaction, and we characterize the spatial and temporal extent of these dynamical effects. Unlike statistical correlations, which give rise to nanometer-scale coupling between distal protein residues and the intrinsic reaction, dynamical correlations vanish at distances beyond 4–6 Å from the transferring hydride [Boekelheide et al. (2011) PNAS 108:16159-16163]. Additionally, we apply analysis of statistical coupling to identify residues that strongly couple to environmental reorganization in a 2-state model of electron transfer in azurin. We confirm the contribution of these residues to the kinetics and energetics of the electron transfer reaction in mutant systems.