Enzyme catalysis from linear-scaling DFT: Application to Chorismate Mutase

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Combined quantum mechanics/molecular mechanics (QM/MM) methods, where only the substrate and a few residues are treated quantum mechanically, have become an important tool in computational enzymology. A recent QM/MM study [*Org. Biomol. Chem.*, **9**, 157, (2011)] has identied reaction pathways for the chorismate to prephenate rearrangement in solution and catalysed by Chorismate Mutase (CM). However, QM/MM approaches can be limited in accuracy by the empirical nature of classical force fields and from the interface between the QM and MM regions. The density functional theory code, ONETEP, uniquely combines near-complete basis set accuracy with computational costs that scale linearly with number of atoms, allowing accurate QM descriptions of the enzyme. We present linear-scaling DFT calculations on structures taken from the CM pathways described above, to examine the convergence of activation and reaction energies as the size of the QM region increases to thousands of atoms.