Quantum Mechanical Prediction of ¹H and ¹³C NMR

Chemical Shifts in Large Protein Systems

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Abstract

We have implemented a methodology for qualitative description Nuclear Magnetic Resonance (NMR) chemical shift tensors at the semi-empirical AM1 level and have generated the associated ¹H and ¹³C protein NMR-specific AM1 parameters. Using our linear-scaling divide-and-conquer algorithm to perform the quantum mechanical calculations, we carried out this parameterization using a series of globular protein systems with a variety of secondary structure as the training set. Our approach can be employed using semi-empirical (AM1/PM3) geometries and can be executed at a fraction of the cost of *ab initio* methods, thus providing an attractive option for the quantum mechanical studies of NMR on large protein systems.