Abstract Submitted
for the MAR10 Meeting of
The American Physical Society

Protein-Protein Interactions from Linear-Scaling First Principles Quantum Mechanical Calculations DANIEL COLE, University of Cambridge, CHRIS-KRITON SKYLARIS, University of Southampton, EESON RAJENDRA, ASHOK VENKITARAMAN, Hutchison/MRC Research Centre, Cambridge, MIKE PAYNE, University of Cambridge — A modification of the MM-PBSA technique for calculating binding affinities of biomolecular complexes is presented. Classical molecular dynamics is used to explore the motion of the extended interface between two peptides derived from the BRC4 repeat of BRCA2 and the eukaryotic recombinase RAD51. The resulting trajectory is sampled using the linear-scaling density functional theory code, ONETEP, to determine from first principles, and with high computational efficiency, the relative free energies of binding of the ∼2800 atom receptor-ligand complexes. This new method provides the basis for computational interrogation of protein-protein and protein-ligand interactions, within fields ranging from chemical biological studies to small molecule binding behaviour, with both unprecedented chemical accuracy and affordable computational expense.

Daniel Cole
University of Cambridge

Date submitted: 20 Nov 2009 Electronic form version 1.4