

## Microsymposium

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*First-year experience with fully automated crystal structure prediction*

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With improving hardware and software performance, usability has become one of the main obstacles to a more widespread use of Crystal Structure Prediction (CSP) with the GRACE program. In terms of method development, important milestones had already been passed by the time of the 5th blind test [1] in 2010, including the parameterization of dispersion-corrected Density Functional Theory (DFT-D) [2], the generation of tailor-made force fields from ab-initio reference data [3], a Monte-Carlo parallel tempering crystal structure generation engine and a DFT-d reranking procedure exploiting statistical correlations. These components have now been incorporated in automated data flow processes that remove the burden of scores of expert decisions from the user. Summarizing the results of CSP studies performed with the new Force Field Factory and CSP Factory modules throughout a year, the current performance of CSP is critically assessed and further method development needs are pinpointed. Studied compounds include 20 small molecules with competing hydrogen bonds motifs, 4 mono-hydrates of non-ionic molecules and the hydrates and chloride salts of several amino acids. The ability to handle flexible pharmaceutical molecules is demonstrated by a validation study on aripiprazole with one and two molecules per asymmetric unit. Salient features of the energy landscapes of other pharmaceutical molecules are discussed. Statistics are presented for the accuracy of tailor-made force fields, and the energy ranking performance of several DFT-d flavors is compared.

[1] D. A. Bardwell, C. S. Adjiman, Y. A. Arnautova, *et al.*, *Acta Cryst. B*, 2011, 67, 535-551, [2] M. A. Neumann, M.-A. Perrin, *J. Phys. Chem. B*, 2005, 109, 15531-15541, [3] M. A. Neumann, *J. Phys. Chem. B*, 2008, 112, 9810-9829

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