Poster Presentation

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Crystal structure prediction of indomethacin

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Indomethacin is a non-steroidal anti-inflammatory and antipyretic agent. Because different packing arrangements of the same drug can greatly affect drug properties such as colours, solubility, stability, melting point, dissolution rate and so forth, it is important to predict its polymorphs. The computational prediction of the stable form will reduce undesirable risks in both clinical trials and manufacturing. Reported polymorphs of indomethacin include α, β, γ, δ, ε, η and ζ [1], of which only the thermodynamically stable form γ and the metastable form α are determined. Density functional theory with dispersion-correction (DFT-D) has been used extensively to study molecular crystal structures[2]. It gives better results with a compromise between the computational cost and accuracy towards the reproduction of molecular crystal structures. In the fourth blind test of crystal structure prediction in 2007, the DFT-D method gave a very successful result that predicted all four structures correctly. Rather than using transferable force fields, a dedicated tailor-made force field (TMFF) parameterised by DFT-D calculations[3] is used for every chemical compound. The force field is used to generate a set of crystal structures and delimit a candidate window for energy ranking. The powder diffraction patterns of predicted polymorphs are calculated to compare with experimental data.

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