## **Poster Presentation**

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## Specific energy contributions associated with competing hydrogen bond motifs

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The semi-classical density sums (SCDS-Pixel) method [1] was used to study the intermolecular interaction energies in six polymorphs of phenobarbital, a model system for the barbiturate class of compounds.[2] Barbiturates display a rigid pyrimidinetrione ring whose two N–H and three C=O functions can be employed in H-bonding. The ensuing intermolecular N–H···O=C interactions result in a small set of standard H-bonded chain, layer and framework motifs.[3] Even though the average number of N–H···O=C bonds per molecule is always two, the standard barbiturate H-bond motifs differ in the number of intermolecular two-point and one-point N–H···O=C connections per molecule, i.e. (1; 0), (½; 1), (0; 2). For each polymorph (I, II, III, V, VI, X), cumulated Pixel energies, E(n), were calculated for the first n (n = 1, 2, 3, ...) interactions associated with the highest individual contributions to the lattice energy. The obtained sets of E(n) values were compared to one another to establish the differences associated with the formation of the alternate N–H···O=C motifs. Those polymorphs whose N–H···O bonded structures are dominated by two-point connections have superior E(n) values for small clusters of molecules (low n). However, this advantage diminishes gradually if larger clusters of molecules are considered and is completely compensated at n = 8. This indicates that crystal packing on the basis of one-point connection N–H···O=C motifs is viable only because the latter enable the formation of more advantageous weaker interactions which are dominated by dispersion forces. This case illustrates that an assessment of competing H-bond motifs cannot be restricted to just those molecules that are directly involved in H-bond interactions. Rather, the complete crystal packing has to be taken into account. [Figure: Evolution of the difference between E(n) (form V; one-point connections) and E(n)' (form III; two-point connections) with n].

[1] A. Gavezzotti, Molecular Aggregation: Structure Analysis and Molecular Simulation of Crystals and Liquids, Oxford University Press, 2007, [2] N. Zencirci, T. Gelbrich, D. C. Apperley et al., Cryst. Growth Des., 2010, 10, 302-313, [3] T. Gelbrich, D. Rossi, C. A. Häfele et al., CrystEngComm, 2011, 13, 5502-5509



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