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# Correlation of H-bonding Distances and Strengths in API Solvates Case Study on Nitrofurantoin and Pyridoxine

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Hydrogen bond solvation affects molecular properties and functions both in solution and solid-state formation of solvates. Many of Active Pharmaceutical Ingredients (APIs) exist as solvates with different solvents that, depend on the nature and polarity, co-crystallize with their appropriate molecular structures in wide range of polarity, either non-ionizable or deprotonated acids and bases and their protonated forms, respectively. Despite H-bonding networking that occurs in a highly competitive solvent in biological systems, synthetic chemists have been facing difficulties to control and predict the H-bonding motifs from de novo in competitive solvents media. The concept of crystal engineering, based on molecular noncovalent recognitions and formation of self-assembled supramolecular clusters opens the opportunities for designing the solvate type of crystals with desirable properties.[1]

The crystallographic parameters of the determined crystal structure of two types of API solvates are presented. The N,N dimethylformamide solvate of the chemotherapeutic class of API for treatment of urinary infection, nitrofurantoin, and hydrated form of molecular salt that pyridoxine (vit B6) form with ferulic acid (derivate of hydroxybenzoic acid) .[2,3] The correlation of the H-bond distances with the bond strength are depicted on Hirshfeld surface's 2D fingerprint plots.

Though many of solvents are not with pharmaceutical relevance in terms of their high risk for toxicity, their co-crystallization with API molecules in crystalline systems offer opportunities to analyze the H-bond patterns and study the propensity of occurring the motifs i.e., synthons among solvated crystals that are deposited in Cambridge Crystal Crystallography Database (CCCD).

**Keywords**: Crystal engineering, solvates, Hydrogen bonding, molecular recognition

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