Unveiling crystal packing of *N*-(6-aminopyridin-2-yl)formamide through intermolecular interaction energies

M.G. Bogdanović[1], M.N. Wyshusek[2], G.J. Reiss[2] M.V. Rodić[1]

[1]University of Novi Sad, Faculty of Sciences, Novi Sad, Serbia, [2]Institut fur Bioanorganische Chemie, Heinrich-Heine-Universitat Dusseldorf, Dusseldorf, Germany
milica.bogdanovic@dh.uns.ac.rs

1,2,4-Triazole and its derivatives are particularly intriguing as bridging ligands. Following the synthetic procedure [1] we successfully isolated the new compound, *N*-(6-aminopyridin-2-yl)formamide after recrystallization from ethanol. Typically, crystal packing obtained from X-ray diffraction studies is described using a geometric approach, primarily focused on identifying intermolecular hydrogen bonds or stacking interactions within the crystal [2]. However, it is important to note that this geometric approach does not always provide a clear understanding of the main motifs of crystal structure. Analyzing the crystal architecture based on intermolecular interaction energies offers a clearer and more definitive understanding of their true significance and provides deeper insights into crystal packing.

This compound crystallizes in the orthorhombic $P2_12_12_1$ space group, with two chemically identical but crystallographically independent molecules in the asymmetric unit, designated as molecule A and molecule B. From a geometric standpoint, the crystal structure reveals hydrogen bonds between molecules A and B, forming dimers that serve as structural motifs. Additionally, the presence of an amino group in the molecule facilitates further intermolecular hydrogen bonding: molecule B from one dimer unit connects with molecules A and B from another dimer unit, while molecule A from one dimer unit is bonded only with molecule B from another dimer unit. This manner of extending hydrogen bonds leads to the formation of a herringbone packing motif. However, understanding the preferred pattern of crystal packing for such molecules based solely on geometrical considerations remains quite challenging.

In this study, intermolecular interaction energies surrounding molecules A and B were calculated using the CE–B3LYP/6–31G(d,p) energy model implemented in *CrystalExplorer*. Analysis of the crystal structure revealed 10 interactions with energies exceeding 10 kJ mol^{-1}. The strongest interaction in the crystal structure is between molecules A and B, mediated through four hydrogen bonds with a total energy of -96 kJ mol^{-1} primarily influenced by electrostatic component contributions, establishing this dimer as the basic structural unit. Additional weaker interactions (-29 kJ mol^{-1} and -20 kJ mol^{-1}), also mediated through hydrogen bonds, contribute to the formation of a layered motif (Fig 1a) within the crystal structure. These layers are interconnected by interactions with energies below 20 kJ mol^{-1}, resulting in formation of a framework type structure (Fig 1b). Overall, while geometric considerations provide superficial insights into crystal packing, only analysis through energetic perspective reveals true significant of interactions.

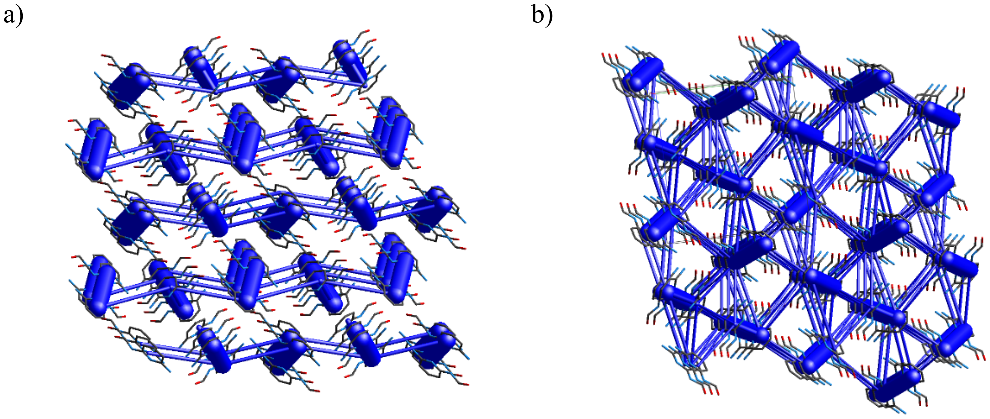

Figure 1 a). Schematic representation of the layer as the basic structural motif in the crystal structure and **b)** framework type structure formed by interlayer interactions.

[1] Yuan S., & Ying W. (2011). 2001). Acta Cryst. E ***67****, 1631.*
[2] Brock C. P. & Dunitz J.D. (1994). Chem. Mater ***6****, 1118.*

Acknowledgement: This research was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Grants No. 451-03-66/2024-03/ 200125 & 451-03-65/2024-03/200125) and German–Serbian joint scientific co-operation project: Application of quantum-crystallographic methods in extended routine X-ray structural analysis of small molecules (Grant No. 337-00-253/2023-05/12).