A study of the crystal structures, supramolecular patterns and Hirshfeld surfaces of bromide salts of hypoxanthine and xanthine

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Two new crystalline salts, namely, hypoxanthinium bromide monohydrate, $\text{C}_5\text{H}_5\text{N}_4\text{O}^+\text{Br}^-\cdot\text{H}_2\text{O}$ (I) and xanthinium bromide monohydrate, $\text{C}_5\text{H}_5\text{N}_4\text{O}_2^+\text{Br}^-\cdot\text{H}_2\text{O}$ (II), were synthesized and characterized by single-crystal X-ray diffraction technique and Hirshfeld surface analysis. The hypoxanthinium and xanthinium cations in salts I and II are both in the oxo-N(9)–H tautomeric form. The crystal packing of the two salts is governed predominantly by N–H⋯O, N–H⋯Br, C–H⋯Br and O–H⋯Br interactions described by $R_2^2(9)$ and $R_2^2(8)$ synthons. The crystal packing is also consolidated by carbonyl⋯π interactions between symmetry-related hypoxanthinium ($\text{HX}^+$) cations in salt I and xanthinium cations ($\text{XA}^+$) in salt II. The combination of all these interactions leads to the formation of wave- and staircase-like architectures in salts I and II, respectively. The largest contributions to the overall Hirshfeld surface are from Br⋯H/H⋯Br contacts (22.3% in I and 25.4% in II).

1. Chemical context

Over the past several decades, non-covalent interactions have been found to play a prominent role in coordination chemistry, materials science and pharmaceutical science (Černý & Hobza, 2007; Desiraju, 2013; Perumalla & Sun, 2014). Understanding the role of non-covalent interactions is important in the context of crystal engineering (Aakeröy et al., 2010; Pogoda et al., 2018; Cavallo et al., 2016; Desiraju et al., 2013) in order to design solids with desired properties. When it comes to pharmaceutics, active pharmaceutical ingredients (APIs) are known to exist in different solid forms such as salts, co-crystals, solvates, polymorphs and amorphous solids (Aaltonen et al., 2009). The salt and co-crystal forms of APIs have improved their solubility and bioavailability when compared to pure APIs (Thackaberry, 2012; Xu et al., 2014). Drugs with low solubility/bioavailability are usually converted to their salts or crystallized in their co-crystal/polymorphic/solvate forms to enhance their properties. Herein, we report two new salts of hypoxanthine ($\text{HX}$) and xanthine ($\text{XA}$).

Hypoxanthine ($\text{C}_5\text{H}_5\text{N}_4\text{O}$) [systematic name: 1,9-dihydro-purine-6-one] and xanthine ($\text{C}_5\text{H}_5\text{N}_4\text{O}_2$) [systematic name: 3,7-dihydro-purine-2,6-dione] are well-known purine-based nucleotides (Emel’yanenko et al., 2017) present in t-RNA and DNA in the form of the nucleoside inosine (Plekan et al., 2012). Purine derivatives are widely known for their therapeutic applications such as antagonization of the adenosine
receptor, anti-inflammatory, antimicrobial, antioxidant, anti-tumour, anti-asthmatic and psycho-stimulant drug activity (Meskini et al., 1994; Burbiel et al., 2006). HX and XA are also found as intermediates in the biological degradation of nucleic acid to uric acid. Furthermore, HX is used as an indicator of hypoxia and it is known to inhibit the effect of several drugs (Dubler et al., 1987a,b). It is also used to destroy harmful agents such as cancer cells (Susithra et al., 2018). Purine-based derivatives of HX and XA bind with the DNA base pairs through weak hydrogen bonds (Latosinska et al., 2014; Rutledge et al., 2007). Additionally, hypoxanthine-guanine phosphoribosyl transferase plays an important role in activating antiviral drugs in the human body and xanthine has been used as a mild stimulant drug (Faheem et al., 2020).

The structure of hypoxanthine and xanthine consists of fused six-membered pyrimidine and five-membered imidazole rings. HX and XA can exist in two tautomeric forms, oxo-N(7)–H and oxo-N(9)–H (Plekan et al., 2012; Gulevskaya & Pozharosski, 1991), as shown below. So far, two polymorphic forms of HX (Schmalle et al., 1988; Yang & Xie, 2007) and a limited number of hypoxanthinium and xanthinium salts have been reported in the literature; hypoxanthinium nitrate monohydrate, hypoxanthinium chloride monohydrate (Cabaj et al., 2019; Schmalle et al., 1990; Sletten & Jensen, 1969), xanthinium nitrate monohydrate and xanthinium hydrogensulfate monohydrate (Sridhar, 2011).

In the hypoxanthinium salts, the hypoxanthine molecule is usually also protonated at the N7 position, resulting in the oxo-N(9)–H tautomer. Similarly, xanthinium nitrate monohydrate, xanthinium hydrogensulfate monohydrate (Sridhar, 2011) and xanthinium perchlorate dihydrate (Biradha et al., 2010) are also in the oxo-N(9)–H tautomeric form and are therefore protonated on the N7 position. Studies of non-covalent interactions involving hypoxanthine and xanthine bases with inorganic acids have increased because their hydrogen-bonding patterns are similar to those of purine bases (Maixner & Zachova, 1991; Sridhar, 2011; Kistenmacher & Shigematsu, 1974). In the current work, the crystal structures, supramolecular packing patterns and Hirshfeld surface analyses of hypoxanthinium bromide monohydrate (I) and xanthinium bromide monohydrate (II) are reported.

2. Structural commentary

Hypoxanthinium bromide monohydrate (I) crystallizes in the monoclinic space group $\text{P}_{2_1}/c$ with one hypoxanthinium cation ($\text{HX}^+$), one bromide anion ($\text{Br}^-$) and one water molecule in the asymmetric unit, as shown in Fig. 1. Here, the $\text{HX}^+$ cation exists in the oxo-N(9)–H tautomeric form with the N7 atom of the purine ring protonated, as can be seen from the N–C bond distance [$\text{N7—C8} = 1.3219 (17) \text{Å}$ vs $\text{N9—C8} = 1.3419 (18) \text{Å}$] and C–N–C bond angles [$\text{C5—N7—C8} = 107.98 (11)^\circ$ and $\text{C4—N9—C8} = 108.32 (10)^\circ$]. Those values are similar to those in the crystal structure of hypoxanthinium chloride monohydrate [N7–C8 = 1.325 (2) Å and N9–C8 = 1.336 (2) Å, C5–N7–C8 = 107.35 (16)$^\circ$ and C4–N9–(C8 = 108.28 (15)$^\circ$; Kalyanaraman et al., 2007; Sletten & Jensen, 1969]. The N3–C4–C5–N7 and N9–C4–C5–C6 torsion angles are 179.07 (12) and $-179.58$ (12)$^\circ$, respectively. These values are similar to those observed in the crystal structure of the neutral hypoxanthine molecule (Schmalle et al., 1988; Yang & Xie, 2007). The $\text{HX}^+$ cation, $\text{Br}^-$ anion and the water...
The water molecule present in the lattice prevents the formation of base pairs (Varani & McClain, 2000) between the cations in salt I. The interaction is very similar to the water-mediated base pairing of hypoxanthinium chloride and the nucleobase pairs in DNA and RNA (Sletten & Jensen, 1969). Along with this, the XA⁺ cation interacts with another inversion-related HX⁺ and Br⁻ pair via N1—H1···Br1, C8—H8···Br1² and N9—H9···O6h hydrogen bonds (Table 1). These interactions lead to the formation of a nine-membered ring with R3(9) (type D) primary graph-set motif (Sletten & Jensen, 1969). 3. Supramolecular features In I, the protonated HX⁺ cation interacts with another inversion-related HX⁺ and Br⁻ pair via N1—H1···Br1, C8—H8···Br1² and N9—H9···O6h hydrogen bonds (Table 1).

### Table 1

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|-----|------|------|---------|
| N9—H9···Br1' | 0.85 (1) | 3.08 (2) | 3.5397 (12) | 117 (2) |
| N9—H9···O6' | 0.85 (1) | 1.98 (2) | 2.7579 (14) | 153 (2) |
| N1—H1···Br1 | 0.84 (1) | 2.41 (1) | 3.2419 (12) | 170 (2) |
| N7—H7···O1Wa | 0.85 (1) | 1.81 (2) | 2.6401 (16) | 165 (2) |
| O1W—H1W···N3ii | 0.86 (1) | 2.08 (1) | 2.9300 (16) | 165 (2) |
| O1W—H2W···Br1 | 0.85 (1) | 2.48 (1) | 3.2894 (16) | 162 (2) |
| C8—H8···Br1' | 0.93 | 2.89 | 3.4875 (15) | 125 |

Symmetry codes: (i) x + 1, −y + 1, z − 1; (ii) −x, −y, −z; (iii) −x, −y + 1, −z + 1.

Figure 2

Hypoxanthinium and bromide ions in salt I forming ribbons together with water molecules through O—H···Br, N—H···Br and C—H···Br interaction. [Symmetry codes: (i) −1 + x, y, −2 + z; (ii) 1 + x, 1/2 − y, −1/2 + z; (iii) −x, 1 − y, 1 − z].

Figure 3

A view of three-dimensional wave-like supramolecular architecture along the b-axis direction.
and O motifs) ring motifs, respectively, through pairs of C8—H8····Br1 and N7—H7····O1W hydrogen bonds (Fig. 2). The combination of all these interactions leads to the formation of a wave-like supramolecular architecture that extends along the b-axis direction (Fig. 3). The crystal structure is further consolidated by carbonyl···π interactions (C6==O6 and π cloud of the imidazole (centroid Cg1) and pyridine (centroid Cg2) rings of the \( \text{HX}^+ \) cation) between symmetry-related cations with C==O···Cg1v, C==O···Cg1i, C==O···Cg2v and C==O···Cg2ii distances of 3.5796 (12), 3.2478 (12) Å, 3.3862 (12) and 3.4747 (12) Å, respectively, and angles of 101.58 (8), 91.45 (8), 105.03 (8) and 103.46 (8)°, respectively [symmetry codes: (iv) \(-x+y, 0, z\); (v) \(x, \frac{1}{2}+y, z\); (iii) \(-x+2, -y+1, -z+1\); (iv) \(x+1, -y+\frac{1}{2}, z-\frac{1}{2}\); (v) \(x+1, y, z-1\). Salt I is isomorphous with hypoxanthinum chloride monohydrate (Sletten & Jensen, 1969).

In the crystal structure of salt II, the \( \text{XA}^+ \) cation interacts with its inversion-related equivalent to form a dimer through a pair of N1—H1···O2 hydrogen bonds (Table 2) with an \( R_2^1(8) \) graph-set motif (type C in the scheme above). The dimer is flanked on both sides by a water molecule (O1W), forming a pair of O1W···H2W···O2ii and O1W···H1W···O6ii hydrogen bonds with an \( R_2^1(8) \) graph-set motif (type H), leading to the formation of a tetrameric unit. The tetrameric unit is formed by an alternate arrangement of \( R_2^1(8) \) and \( R_1^1(8) \) ring motifs, which extend as \( \text{DADA} \) array (dimeric units held together by four hydrogen bonds between the self-complementary \( \text{DADA} \) arrays; \( D = \) donor and \( A = \) acceptor) along the ac plane. Neighbouring tetrameric units are then connected through two sets of \( R_2^1(7) \) motifs (Jeffrey & Saenger, 1991) formed by N7—H7···O1W and O1W···H1W···O6ii hydrogen bonds and an \( R_2^1(4) \) (type L) motif formed by a pair of O1W···H1W···O6ii interactions. The tetrameric units combine into a supramolecular ribbon extended along the ac plane (Fig. 5). Neighbouring perpendicular supramolecular ribbons are then interconnected through pairs of N3—H3···Br1iii and N9—H9···Br1 hydrogen bonds with an \( R_2^1(28) \) ring motif, which assembles them into a staircase-like supramolecular architecture as shown in Figs. 6 and 7. The crystal structure is further consolidated by carbonyl···π interactions between symmetry-related \( \text{XA}^+ \) cations \([\text{C6==O6 and π cloud of the pyridine ring (centroid Cg2) of the } \text{XA}^+ \text{ unit) with C==O···Cg2ii and C==O···Cg2iII distances of 3.366 (3) and 3.477 (3) Å, respectively, and angles of 108.2 (2) and 118.7 (2)°} \] [symmetry codes: (vi) \(1+x, y, z\); (vii) \(1-x, 1-y, 1-z\); (vi) \(1+x, y, -1+z\)]

### Table 2

Hydrogen-bond geometry (Å, °) for II.

| D—H · · · A | D—H | H · · · A | D···A | D—H · · · A |
|-------------|------|-----------|-------|------------|
| N1—H1···O2 | 0.82 (2) | 2.09 (2) | 2.903 (4) | 175 (4) |
| N3—H3···Br1i | 0.82 (2) | 2.48 (2) | 3.301 (3) | 176 (4) |
| N7—H7···O1W | 0.82 (2) | 1.81 (2) | 2.609 (4) | 163 (4) |
| N9—H9···Br1 | 0.82 (2) | 2.43 (2) | 3.237 (3) | 172 (4) |
| O1W···H1WA···O6ii | 0.86 (1) | 1.95 (1) | 2.802 (4) | 171 (5) |
| O1W···H1WB···Br1ii | 0.86 (1) | 3.03 (4) | 3.490 (3) | 115 (3) |
| O1W···H1WB···O2ii | 0.86 (1) | 2.05 (3) | 2.816 (4) | 149 (4) |

Symmetry codes: (i) \(-x+1, -y+1, -z+2\); (ii) \(x, -y+\frac{1}{2}, z+\frac{1}{2}\); (iii) \(-x+2, -y+1, -z+1\); (iv) \(x+1, -y+\frac{1}{2}, z-\frac{1}{2}\); (v) \(x+1, y, z-1\).
4. Hirshfeld surface analysis

Hirshfeld surface analyses and their associated two-dimensional fingerprint plots (McKinnon et al., 2007; Spackman & Jayatilaka, 2009) were generated using Crystal Explorer 17.5 (Turner et al., 2017). The Hirshfeld surfaces of the title compounds mapped over $d_{norm}$ feature several red spots in the regions of $D$–$A$ ($D$ = donor, $A$ = acceptor) interactions (Carías-Valenzuela et al., 2018; Atiog˘lu et al., 2018). In this regard, the contribution of the interatomic contacts to the $d_{norm}$ surface map can help differentiate whether the contact is longer (blue) or shorter (red) than the sum of the van der Waals radii of the two interacting atoms. The Hirshfeld surfaces of salts I and II are shown in Fig. 9a and 10a, respectively and the hydrogen-bonding interactions between the hydrated ion pairs I and II and the respective neighbouring moieties are shown in Fig. 9b and 10b, respectively. The intense red spots on the Hirshfeld surface indicate the shortest interatomic distances corresponding to the hydrogen bonds. They are also clearly identified by the two long spikes in the fingerprint plots and can be quantified using the percentage distribution of the interacting types. Such analyses of the salts I and II are shown in Figs. 11 and 12 giving the following contributions: 

- All (100%), O–H/H–O (I 19.7%, II 23.4%), N–H/H–N (I 13.5%, II 7.5%), C–H/H–C (I 6.4%, II 9.6%), H–H/H–H (I 23.4%, II 15.9%) and C–C/ C–C (I 0.9%, II 0.1%) (Table 5), indicating that the most abundant contact is Br–H/H–Br with 22.3% in I and 25.4% in II, respectively.

5. Comparative analysis

The data obtained by comparative analysis of the crystal structures, supramolecular interactions, hydrogen-bonding motifs and packing patterns of structurally similar halide salts such as adeninium bromide, adeninium chloride, guaninium bromide, guaninium chloride and hypoxanthinium chloride (Maixner & Zachova, 1991; Sridhar, 2011; Kistenmacher & Shigematsu, 1974; Langer & Huml, 1978) are listed and compared in Table 3.

Salt I has similar unit-cell parameters and packing patterns to the hypoxanthinium chloride salt. The molecular recognition between the hypoxanthine base and acid happens via N–H…O, C–H…Br/Cl and N–H…Br/Cl hydrogen-bond motifs with $R_2^2(9)$ (type D), $R_2^2(11)$ (type I), $R_2^2(16)$ (type N) and $R_2^2(14)$ (type O) graph-set motifs. Salt II forms base pairs...
Table 3: Comparison of purine derivatives with hydrobromic acid and hydrochloric acid.

|                          | Adeninium bromide hemihydrate | Adeninium chloride monohydrate | Guaninium chloride monohydrate | Guaninium bromide monohydrate | Hypoxanthinium bromide monohydrate | Hypoxanthinium chloride monohydrate (I) | Xanthinium bromide monohydrate (II) |
|--------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|-----------------------------------|----------------------------------------|--------------------------------------|
| Cell parameters          |                               |                               |                               |                               |                                   |                                        |                                      |
| (a, b, c; α, β, γ)       | 9.018 (2), 8.771 (2)          | 4.591 (1), 4.8708 (7)         | 4.8295 (9), 13.237 (3)        | 4.8487 (4), 17.7285 (22)       | 4.8487 (4), 18.4455 (15), 9.0782 (7) | 4.906 (1), 103.003 (3)                |
| Crystal system           | Monoclinic                    | Monoclinic                    | Monoclinic                    | Monoclinic                    | Monoclinic                        | Monoclinic                             |
| Space group              | P2_1/c                        | P2_1/c                        | P2_1/c                        | P2_1/c                        | P2_1/c                            | P2_1/c                                 |
| Protonation site         | N1                            | N1                            | N1                            | N1                            | N7                                | N9                                     |
| Type of hydrogen bonding | N—H⋯O, N—H⋯Cl, N—H⋯Br        | N—H⋯O, N—H⋯Cl, N—H⋯Br        | N—H⋯O, N—H⋯Cl, N—H⋯Br        | N—H⋯O, N—H⋯Cl, N—H⋯Br        | N—H⋯O, N—H⋯Cl, N—H⋯Br        | N—H⋯O, N—H⋯Cl, N—H⋯Br        |
| Type of stacking         | –                             | –                             | C—O⋯π                         | C—O⋯π                         | C—O⋯π                             | C—O⋯π                                 |
| Primary motif            | R2(10)                        | R2(10)                        | R2(8)                         | R2(9)                         | R2(9)                             | R2(9)                                 |
| Secondary motif          | R2(7), R2(14)                 | R2(7), R2(14)                 | R2(7), R2(10), R2(11)        | R2(11)                        | R2(11), R2(16), R2(14)            | R2(14), R2(16), R2(14)            |
| Type of packing architecture | Ribbon                        | Ribbon                        | Ribbon                        | Ribbon                        | Wave                              | Wave                                  |
|                          |                               |                               |                               |                               | Staircase                         | Staircase                             |

6. Database survey
A survey of the Cambridge Structural Database (CSD, version 5.43, update of March 2022; Groom et al., 2016) for reported structures of hypoxanthine and xanthine derivatives identified the hypoxanthine molecule (CSD refcodes GEBTUC and GETBUC01; Schmalle et al., 1988; Yang & Xie, 2007) and the following salts: hypoxanthinium nitrate monohydrate (BONKOE and BONKOE54; Cabaj et al., 2019; Schmalle et al., 1990), hypoxanthinium chloride monohydrate (HYPXCL and HYPXCL01; Sletten & Jensen, 1969; Kalyanaraman et al., 2007) as well as three xanthine salts, viz. xanthinium perchlorate monohydrate (VURMUR; Biradha et al., 2010), xanthinium nitrate monohydrate (YADJAO; Sridhar, 2011) and xanthinium hydrogensulfate monohydrate (YADJEU; Sridhar, 2011). In all of the hypoxanthinium salts, the hypox-
anthine molecule is protonated at the N7 position and interacts with the anion through N—H ⋅⋅⋅Cl/O and C=O ⋅⋅⋅π interactions. In the xanthinium salts, the xanthine molecules are protonated at the N7 position in xanthinium nitrate monohydrate and xanthinium hydrogensulfate monohydrate and at the N9 position in xanthinium perchlorate monohydrate. In all of the crystal structures, the xanthine cation interacts with the anion through N—H ⋅⋅⋅O, O—H ⋅⋅⋅O and C=O ⋅⋅⋅π interactions.

7. Synthesis and crystallization

A general method was used for the preparation and crystallization of the hypoxanthinium bromide monohydrate (I) and xanthinium bromide monohydrate (II) using the following quantities: 0.0340 mg (0.25mmol) of hypoxanthine for I and 0.0380 mg (0.25 mmol) of xanthine for II.

The indicated amount of the base was dissolved in 20 mL of distilled water and 2 mL of hydrobromic acid (5% in water) were added. The reaction mixture was heated to 358 K for 30 min using a water bath. The resulting solution was allowed to slowly evaporate at room temperature. After a few days, colourless plate-like crystals were obtained.

8. Refinement

Crystal data, data collection and structure refinement details for salts I and II are summarized in Table 4. All C-bound hydrogen atoms were placed in idealized positions and refined using a riding model, with C—H = 0.93 Å and $U_{eq}(H) = 1.2U_{eq}(C)$. The H atoms of the water molecule were located in a difference-Fourier map and refined with the O—H distance restrained to 0.85–0.86 Å and with $U_{eq}(H) = 1.5U_{eq}(O)$. The hydrogen atoms bound to the nitrogen atoms in salts I and II were located in difference-Fourier maps and either refined freely (in I) or with the distance restraint N—H = 0.82 Å and with $U_{eq}(H) = 1.2U_{eq}(N)$ (in II).

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Computing details
For both structures, data collection: *APEX2* (Bruker, 2016); cell refinement: *SAINT* (Bruker, 2016); data reduction: *SAINT* (Bruker, 2016). Program(s) used to solve structure: *SHELXS97* (Sheldrick 2008) for (I); *SHELXT2014/5* (Sheldrick, 2015) for (II). For both structures, program(s) used to refine structure: *SHELXL2018/3* (Sheldrick, 2015b); molecular graphics: *PLATON* (Spek, 2020), *Mercury* (Macrae et al., 2020) and *POVRay* (Cason, 2004); software used to prepare material for publication: *PLATON* (Spek, 2020) and *publCIF* (Westrip,2010).

6-Oxo-6,9-dihydro-1H-purin-7-ium bromide monohydrate (I)

Crystal data

| Parameter                  | Value                           |
|----------------------------|---------------------------------|
| C₅H₅N₄O⁺·Br⁻·H₂O          |                                 |
| $M_r$                      | 235.06                          |
| Monoclinic, $P_{2}1/c$     |                                 |
| $a$ (Å)                    | 4.8487 (4)                      |
| $b$ (Å)                    | 18.4455 (15)                    |
| $c$ (Å)                    | 9.0782 (7)                      |
| $β$ (°)                    | 94.808 (1)                      |
| $V$ (Å³)                   | 809.07 (11)                     |
| $Z$                        | 4                               |

Data collection

| Parameter                  | Value                           |
|----------------------------|---------------------------------|
| Bruker APEXII CCD          |                                 |
| Diffractometer             |                                 |
| $φ$ and $ω$ scans          |                                 |
| Absorption correction      |                                 |
| Multi-scan                 |                                 |
| (SADABS; Bruker, 2016)     |                                 |
| $T_{\text{min}}$           | 0.403                           |
| $T_{\text{max}}$           | 0.641                           |
| 17895 measured reflections |                                 |

Refinement

| Parameter                  | Value                           |
|----------------------------|---------------------------------|
| Refinement on $F^2$        |                                 |
| Least-squares matrix: full |                                 |
| $R(F^2 > 2\sigma(F^2))$    | 0.021                           |
| $wR(F^2)$                  | 0.056                           |
| $S$                        | 1.05                            |
| 2383 reflections           |                                 |
| 128 parameters             |                                 |
| 6 restraints               |                                 |

Primary atom site location: structure-invariant direct methods
Secondary atom site location: difference Fourier map
Hydrogen site location: mixed
H atoms treated by a mixture of independent and constrained refinement
supporting information

\[ w = \frac{1}{\sigma^2(F_o^2) + (0.0273P)^2 + 0.2516P} \]
where \( P = (F_o^2 + 2F_c^2)/3 \)

\[ (\Delta/\sigma)_{\text{max}} = 0.002 \]
\[ \Delta \rho_{\text{max}} = 0.34 \text{ e Å}^{-3} \]
\[ \Delta \rho_{\text{min}} = -0.29 \text{ e Å}^{-3} \]

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

|     | x      | y      | z      | U_{11} / U_{eq} |
|-----|--------|--------|--------|-----------------|
| Br1 | -0.30053 (4) | 0.47161 (2) | 0.77208 (2) | 0.04456 (8) |
| O6  | -0.2120 (2)  | 0.27474 (6)  | 0.73221 (11) | 0.0337 (2)  |
| N9  | 0.4049 (2)   | 0.18412 (7)  | 0.42420 (13) | 0.0278 (2)  |
| H9  | 0.529 (3)    | 0.1816 (10)  | 0.3639 (18)  | 0.041 (5)*  |
| N3  | 0.3696 (2)   | 0.31647 (6)  | 0.43388 (13) | 0.0288 (2)  |
| N1  | 0.0413 (3)   | 0.35239 (6)  | 0.59830 (14) | 0.0293 (2)  |
| H1  | -0.035 (4)   | 0.3873 (9)   | 0.638 (2)    | 0.045 (5)*  |
| N7  | 0.1015 (3)   | 0.15533 (6)  | 0.57823 (13) | 0.0283 (2)  |
| H7  | 0.000 (4)    | 0.1316 (10)  | 0.6329 (19)  | 0.044 (5)*  |
| C5  | 0.1107 (3)   | 0.22987 (7)  | 0.57102 (14) | 0.0232 (2)  |
| C8  | 0.2792 (3)   | 0.12926 (8)  | 0.48894 (16) | 0.0309 (3)  |
| H8  | 0.312119     | 0.080303     | 0.473349     | 0.037*      |
| C2  | 0.2315 (3)   | 0.36593 (8)  | 0.50019 (16) | 0.0309 (3)  |
| C2  | 0.266402     | 0.414166     | 0.478442     | 0.037*      |
| H2  | -0.7539 (3)  | 0.60447 (7)  | 0.73814 (15) | 0.0447 (3)  |
| O1W | -0.653 (4)   | 0.6346 (10)  | 0.695 (2)    | 0.067*      |
| H1W | -0.671 (4)   | 0.5639 (7)   | 0.741 (2)    | 0.067*      |
| H2W | 0.3015 (3)   | 0.24822 (7)  | 0.47360 (13) | 0.0235 (2)  |
| C6  | -0.0384 (3)  | 0.28405 (7)  | 0.64259 (14) | 0.0245 (2)  |

Atomic displacement parameters (Å²)

|     | U_{11}  | U_{22}  | U_{33}  | U_{12}  | U_{13}  | U_{23}  |
|-----|---------|---------|---------|---------|---------|---------|
| Br1 | 0.05176 (12) | 0.02567 (9) | 0.06016 (13) | 0.00535 (6) | 0.02789 (9) | -0.00045 (7) |
| O6  | 0.0347 (5) | 0.0341 (5) | 0.0352 (5) | 0.0018 (4) | 0.0205 (5) | -0.0004 (4) |
| N9  | 0.0272 (5) | 0.0312 (6) | 0.0267 (5) | 0.0032 (4) | 0.0122 (5) | -0.0009 (4) |
| N3  | 0.0292 (6) | 0.0287 (6) | 0.0299 (6) | -0.0017 (5) | 0.0116 (5) | 0.0026 (5)  |
| N1  | 0.0325 (6) | 0.0257 (5) | 0.0316 (6) | 0.0025 (5) | 0.0133 (5) | -0.0016 (5) |
| N7  | 0.0311 (6) | 0.0251 (5) | 0.0301 (6) | -0.0029 (4) | 0.0123 (5) | -0.0005 (4) |
| C5  | 0.0223 (6) | 0.0259 (6) | 0.0224 (6) | -0.0010 (5) | 0.0072 (5) | -0.0009 (5) |
| C8  | 0.0344 (7) | 0.0267 (6) | 0.0328 (7) | 0.0024 (5) | 0.0105 (6) | -0.0019 (5) |
| C2  | 0.0333 (7) | 0.0273 (6) | 0.0334 (7) | -0.0011 (5) | 0.0103 (6) | 0.0033 (5)  |
| O1W | 0.0458 (7) | 0.0321 (6) | 0.0608 (8) | 0.0075 (5) | 0.0319 (6) | 0.0077 (5)  |
| C4  | 0.0216 (6) | 0.0282 (6) | 0.0215 (6) | 0.0006 (5) | 0.0066 (5) | -0.0008 (5) |
Geometric parameters (Å, °)

| Bond          | Length (Å) | Angle (°) |
|---------------|------------|-----------|
| O6—C6         | 1.2308 (15) |           |
| N9—C8         | 1.3419 (18) |           |
| N9—C4         | 1.3741 (16) |           |
| N9—H9         | 0.847 (14)  |           |
| N3—C2         | 1.3078 (18) |           |
| N3—C4         | 1.3579 (16) |           |
| N1—C2         | 1.3581 (17) |           |
| N1—C6         | 1.3879 (17) |           |
| N1—H1         | 0.840 (14)  |           |
| C8—N9—C4     | 108.32 (10) |           |
| C8—N9—H9     | 127.8 (13)  |           |
| C4—N9—H9     | 123.8 (13)  |           |
| C2—N3—C4     | 112.29 (11) |           |
| C2—N1—C6     | 125.30 (12) |           |
| C2—N1—H1     | 119.4 (14)  |           |
| C6—N1—H1     | 115.3 (14)  |           |
| C8—N7—C5     | 107.98 (11) |           |
| C8—N7—H7     | 127.6 (13)  |           |
| C5—N7—H7     | 124.4 (13)  |           |
| C4—C5—N7     | 107.61 (11) |           |
| C4—C5—C6     | 121.08 (12) |           |
| N7—C5—C6     | 131.31 (11) |           |
| C8—N7—C5—C4 | -0.02 (16)  |           |
| C8—N7—C5—C6 | 179.24 (14) |           |
| C5—N7—C8—N9 | 0.27 (17)   |           |
| C4—N9—C8—N7 | -0.42 (17)  |           |
| C4—N3—C2—N1 | 0.2 (2)     |           |
| C6—N1—C2—N3 | -0.6 (2)    |           |
| C2—N3—C4—N9 | 179.41 (14) |           |
| C2—N3—C4—C5 | 0.3 (2)     |           |
| C8—N9—C4—N3 | -178.90 (14)|           |
| C8—N9—C4—C5 | 0.39 (16)   |           |

Hydrogen-bond geometry (Å, °)

| Bond          | D—H | H···A | D···A | D—H···A |
|---------------|-----|------|-------|---------|
| N9—H9···Br1i | 0.85 (1) | 3.08 (2) | 3.5397 (12) | 117 (2) |
| N9—H9···O6i  | 0.85 (1) | 1.98 (2) | 2.7579 (14) | 153 (2) |
| N1—H1···Br1  | 0.84 (1) | 2.41 (1) | 3.2419 (12) | 170 (2) |
| N7—H7···O1Wii| 0.85 (1) | 1.81 (2) | 2.6401 (16) | 165 (2) |
| O1W···H1W···N3iii| 0.86 (1) | 2.08 (1) | 2.9200 (16) | 165 (2) |
2,6-Dioxo-2,3,6,9-tetrahydro-1H-purin-7-ium bromide monohydrate (II)

Crystal data

\[ C_{5}H_{5}N_{4}O_{2} \cdot Br^{-} \cdot H_{2}O \]

\[ M_r = 251.06 \]

Monoclinic, \( P2_1/c \)

\[ a = 4.9225 (2) \text{ Å} \]

\[ b = 22.7572 (17) \text{ Å} \]

\[ c = 7.5601 (5) \text{ Å} \]

\[ \beta = 103.003 (3)^\circ \]

\[ V = 825.18 (9) \text{ Å}^3 \]

\[ Z = 4 \]

\[ F(000) = 496 \]

\[ D_x = 2.021 \text{ Mg m}^{-3} \]

\[ \text{Mo } K\alpha 	ext{ radiation, } \lambda = 0.71073 \text{ Å} \]

\[ \text{Cell parameters from 1418 reflections} \]

\[ \theta = 2.9-29.6^\circ \]

\[ \mu = 4.96 \text{ mm}^{-1} \]

\[ T = 303 \text{ K} \]

\[ \text{Plate, colourless} \]

\[ 0.55 \times 0.37 \times 0.31 \text{ mm} \]

Data collection

Bruker APEXII CCD diffractometer

\[ \phi \text{ and } \omega \text{ scans} \]

Absorption correction: multi-scan

\[ (\text{SADABS; Bruker, 2016}) \]

\[ R_{\text{min}} = 0.045 \]

\[ \text{1855 independent reflections} \]

\[ \text{1418 reflections with } I > 2\sigma(I) \]

\[ h = -6 \rightarrow 6 \]

\[ k = -30 \rightarrow 30 \]

Refinement

Refinement on \( F^2 \)

Secondary atom site location: difference Fourier map

\[ \text{Hydrogen site location: difference Fourier map} \]

\[ \text{Only H-atom coordinates refined} \]

\[ w = 1/[\sigma(F_c^2) + (0.0151P)^2 + 1.7175P] \]

\[ \text{where } P = (F_c^2 + 2F_{c}^2)/3 \]

\[ \Delta \rho_{\text{max}} = 0.42 \text{ e Å}^{-3} \]

\[ \Delta \rho_{\text{min}} = -0.62 \text{ e Å}^{-3} \]

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

|    | x    | y    | z    | \( U_{eq} \)  |
|----|------|------|------|--------------|
| Br1| -0.16454 (8) | 0.20412 (2) | 0.47569 (6) | 0.03200 (14) |
| O6 | 0.8033 (5)    | 0.47823 (12) | 0.6033 (4)  | 0.0318 (6)  |
| C6 | 0.6301 (7)    | 0.44615 (16) | 0.6465 (5)  | 0.0241 (8)  |
| N1 | 0.5267 (7)    | 0.45642 (14) | 0.7988 (4)  | 0.0273 (7)  |
| H1 | 0.578 (8)     | 0.4867 (13)  | 0.855 (5)   | 0.033 (1)   |

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sup-4
| Atom  | U<sup>11</sup> | U<sup>22</sup> | U<sup>33</sup> | U<sup>12</sup>  | U<sup>13</sup>  | U<sup>23</sup>  |
|-------|----------------|----------------|----------------|----------------|----------------|----------------|
| Br1   | 0.0307 (2)     | 0.0253 (2)     | 0.0413 (2)     | −0.00152 (17) | 0.01087 (16)  | −0.00286 (18) |
| O6    | 0.0317 (15)    | 0.0309 (15)    | 0.0360 (16)    | −0.0110 (12)  | 0.0147 (13)   | −0.0028 (12)  |
| C6    | 0.0231 (18)    | 0.0217 (18)    | 0.028 (2)      | −0.00014 (14) | 0.0057 (16)   | 0.0046 (15)   |
| N1    | 0.0294 (17)    | 0.0253 (17)    | 0.0292 (19)    | −0.0097 (14)  | 0.0111 (15)   | −0.0046 (14)  |
| C2    | 0.0255 (19)    | 0.0224 (19)    | 0.029 (2)      | −0.0030 (15)  | 0.0079 (17)   | 0.0042 (16)   |
| O2    | 0.0431 (17)    | 0.0432 (18)    | 0.0338 (17)    | −0.0118 (14)  | 0.0216 (14)   | −0.0079 (14)  |
| N3    | 0.0246 (16)    | 0.0232 (16)    | 0.0305 (18)    | −0.0041 (12)  | 0.0128 (14)   | 0.0050 (13)   |
| C4    | 0.0236 (18)    | 0.0193 (17)    | 0.027 (2)      | 0.0011 (14)   | 0.0028 (15)   | 0.0039 (15)   |
| C5    | 0.0231 (18)    | 0.0246 (18)    | 0.0232 (19)    | −0.0018 (14)  | 0.0050 (15)   | −0.0008 (15)  |
| N7    | 0.0291 (17)    | 0.0286 (17)    | 0.0265 (18)    | −0.0023 (14)  | 0.0109 (14)   | 0.0005 (14)   |
| C8    | 0.035 (2)      | 0.028 (2)      | 0.028 (2)      | −0.0013 (17)  | 0.0051 (18)   | −0.0048 (17)  |
| N9    | 0.0299 (17)    | 0.0186 (15)    | 0.0346 (19)    | −0.0040 (13)  | 0.0061 (15)   | 0.0000 (14)   |
| O1W   | 0.0484 (19)    | 0.0449 (19)    | 0.046 (2)      | −0.0199 (15)  | 0.0290 (16)   | −0.0172 (15)  |

**Geometric parameters (Å, °)**

| Bond  | Length (Å) | Angle (°) |
|-------|------------|-----------|
| O6—C6 | 1.221 (4)  | C4—N9     | 1.370 (5)  |
| C6—N1 | 1.380 (5)  | C5—N7     | 1.378 (5)  |
| C6—C5 | 1.425 (5)  | N7—C8     | 1.312 (5)  |
| N1—C2 | 1.383 (5)  | N7—H7     | 0.82 (2)   |
| N1—H1 | 0.82 (2)   | C8—N9     | 1.344 (5)  |
| C2—O2 | 1.224 (5)  | C8—H8     | 0.97 (4)   |
| C2—N3 | 1.374 (5)  | N9—H9     | 0.82 (2)   |
| N3—C4 | 1.350 (5)  | O1W—H1WA  | 0.857 (10) |
| N3—H3 | 0.82 (2)   | O1W—H1WB  | 0.860 (10) |
| C4—C5 | 1.355 (5)  |           |            |
**N1—C6—C5  111.2 (3)  C4—C5—C6  121.8 (3)**

**C6—N1—C2  128.1 (3)  N7—C5—C6  130.9 (3)**

**C6—N1—H1  116 (3)  C8—N7—C5  108.2 (3)**

**C2—N1—H1  115 (3)  C8—N7—H7  125 (3)**

**O2—C2—N3  122.2 (3)  C5—N7—H7  127 (3)**

**N7—C2—N3  116.6 (3)  C8—N7—H7  125 (3)**

**C4—N3—C2  118.7 (3)  N9—C8—N7  123 (3)**

**C4—N3—H3  126 (3)  C4—N9—C8  129 (3)**

**C2—N3—C4  115 (3)  C4—N9—H9  123 (3)**

**N3—C4—C5  123.6 (3)  C5—N7—H7  127 (3)**

**N3—C4—N9  129.2 (3)  C8—N9—C4  107.7 (3)**

**O6—C6—N1—C2  179.8 (4)  N9—C4—C5—C6  179.6 (3)**

**C5—C6—N1—C2 −0.7 (5)  O6—C6—C5—C4  179.3 (4)**

**C6—N1—C2—O2 −178.6 (4)  N1—C6—C5—C4 −0.1 (5)**

**C6—N1—C2—N3  0.8 (6)  O6—C6—C5—N7 −1.2 (7)**

**O2—C2—N3—C4  179.3 (4)  N1—C6—C5—N7  179.3 (4)**

**C2—N3—C4—C5 −0.6 (5)  C4—C5—N7—C8 −179.6 (4)**

**C2—N3—C4—N9 −179.3 (4)  C5—N7—C8—N9  0.1 (5)**

**N3—C4—C5—N7 −178.8 (3)  N7—C8—N9—C4  0.0 (4)**

**N9—C4—C5—N7  0.1 (4)  N3—C4—N9—C8  178.7 (4)**

**N3—C4—C5—C6  0.8 (6)  C5—C4—N9—C8 −0.1 (4)**

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### Hydrogen-bond geometry (Å, °)

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|-----|------|-------|---------|
| N1—H1···O2i | 0.82 (2) | 2.09 (2) | 2.903 (4) | 175 (4) |
| N3—H3···Br1i | 0.82 (2) | 2.48 (2) | 3.301 (3) | 176 (4) |
| N7—H7···O1W | 0.82 (2) | 1.81 (2) | 2.609 (4) | 163 (4) |
| N9—H9···Br1 | 0.82 (2) | 2.43 (2) | 3.237 (3) | 172 (4) |
| O1W···H1W4···O6ii | 0.86 (1) | 1.95 (1) | 2.802 (4) | 171 (5) |
| O1W···H1WB···Br1iv | 0.86 (1) | 3.03 (4) | 3.490 (3) | 115 (3) |
| O1W···H1WB···O2v | 0.86 (1) | 2.05 (3) | 2.816 (4) | 149 (4) |

Symmetry codes: (i) −x+1, −y+1, −z+2; (ii) x, −y+1/2, z+1/2; (iii) −x+2, −y+1, −z+1; (iv) x+1, −y+1/2, z−1/2; (v) x+1, y, z−1.

### Percentage of non-covalent interaction in supramolecular packing analyzed by Hirshfeld surface analysis

| CONTACT | SALT (I) | SALT (II) |
|---------|---------|-----------|
| H···Br / Br···H | 22.3% | 25.4% |
| O···H/H···O | 19.7% | 23.4% |
| H···N/N···H | 13.5% | 7.5% |
| C···H/H···C | 6.4% | 9.6% |
| H···H | 23.4% | 15.9% |

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