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Hirshfeld Surface Analysis of Antimony (III) Chloride Complexes with Thioamides

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Research Article

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ABSTRACT

Hirshfeld surface analysis is a unique method used to investigate intermolecular contacts in crystalline structures. The two-dimensional fingerprint plots are used to give the exact percentage of intermolecular contacts in a molecule. Understanding the intermolecular interactions can be used to design new solids with desired properties. In the present work, the intermolecular contacts of five antimony(III) chloride complexes with heterocyclic thioamides formulated as [SbCl3(HL)2] (HL: 2-mercapto-thiazolidine (MTZD), 2-mercaptopyridine (PYT), 2-mercapto-3,4,5,6-tetrahydro-pyrimidine (tHPMT), 2-mercapto-benzimidazole (MBZIM), 5-ethoxy-2-mercapto-benzimidazole (EtMBZIM)), previously synthesized, and whose chemical structures were elucidated by various spectroscopic techniques and X-ray diffraction, were investigated by using Hirshfeld surface analysis via Crystal Explorer Program Version 17.5. Hirshfeld surface analysis shows that the interactions that contribute most to the crystal packing of the antimony(III) chloride complexes (1-5) are Cl···H/H···Cl, S···H/H···S and H···H.

1. Introduction

Antimony, one of the heavy-pinictogen elements, is a chemical element with atomic number 51, represented by the symbol Sb in the p block of the periodic table [1,2]. Antimonials have been known since ancient times and were often used as medicine and cosmetics [3,4]. Meglumine antimonite (Glucantime) and sodium stibogluconate (Pentostam) are the most important antimony compounds that have been used for many years in the treatment of leishmaniasis, a parasitic infection [5–9]. In recent studies, it has been determined that antimony(III) compounds containing thioamide-derived ligands may have cytotoxic effects against various cancer cells such as human breast adenocarcinoma cells (MCF-7) and human cervix carcinoma cells (HeLa) [10–17]. Therefore, the molecular design of antimony(III) complexes and attempting to determine their non-covalent contacts may be an interesting aspect of metal-based drug research and bioinorganic chemistry. Non-covalent contacts play important roles in biological systems, such as protein stabilization, molecular recognition, and the specificity and efficiency of enzymatic reactions. These contacts, which are often called weak interactions, are also very important in the formation of the supramolecular structure [18,19]. These weak interactions in crystal structures can be analyzed quantitatively with Hirshfeld calculations.

In this work, the intermolecular contacts of five antimony(III) chloride complexes with heterocyclic thioamides (fig. 1) formulated as $[SbCl_3(MTZD)_2]$ (**1**) (MTZD: 2-mercapto-thiazolidine), $[SbCl_3(PYT)_2]$ (**2**) (PYT: 2-mercaptopyridine), $[SbCl_3(tHPMT)_2]$ (**3**) (tHPMT: 2-mercapto-3,4,5,6-tetrahydro-pyrimidine), $[SbCl_3(MBZIM)_2]$ (**4**) (MBZIM: 2-mercapto-benzimidazole) and, $[SbCl_3(EtMBZIM)_2]$ (**5**) (EtMBZIM: 5-ethoxy-2-mercapto-benzimidazole), previously synthesized, and whose chemical structures were elucidated by various spectroscopic techniques and X-ray diffraction [20,21], were investigated by using Hirshfeld surface analysis via Crystal Explorer Program Version 17.5 [22].

2. Materials and Methods

Hirshfeld surface analysis [23] and fingerprint plots [24] for antimony(III) chloride-thioamide complexes 1-5 [20,21] were generated from crystal data and performed with TONTO's combined Crystal Explorer 17.5 program [22]. The first distance functions discovered for mapping on surfaces from the Hirshfeld surface are the distances to the nearest nucleus inside the surface (d_i) and outside the surface (d_e). Molecular HS were obtained using a standard (high) surface resolution with mapped three-dimensional surfaces.

3. Results and Discussion

Hirshfeld surface analysis is a quantitative tool used to study the intermolecular interactions and short or long contacts of molecules in a crystal structure. Hirshfeld surface analysis enables these interactions and contacts to be visualized by presenting them with different colors and color intensities, and to create 2D fingerprint graphs. All the Hirshfeld surfaces were generated for all the structure of the antimony(III) chloride complexes 1-5. The maps of interior distance (d_i), exterior

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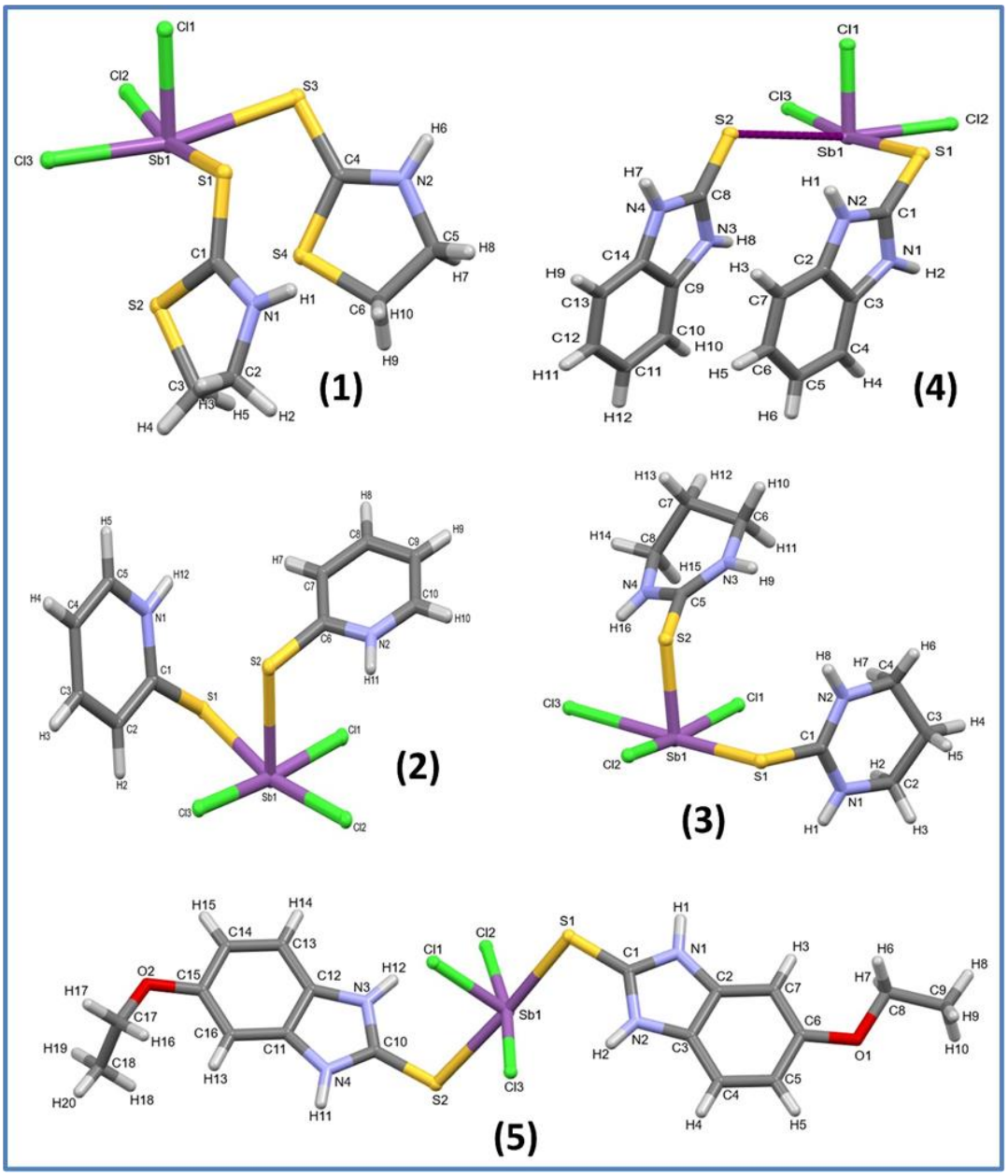

Fig. 1 Molecular structure of the antimony(III) chloride complexes 1-5.

distance (d_e), normalized contact distance (d_{norm}), shape index, curvedness, and fragment patch on molecular hirshfeld surfaces are shown in Figs. 2 and 3.

The 3D Hirshfeld surfaces were mapped based on d_{norm} having range -0.2629 Å to 1.0360 Å for **1**, -0.4885 Å to 1.0534 Å for **2**, -0.4608 Å to 1.9121 Å for **3**, -0.4338 Å to 1.2897 Å for **4**, and -0.2983 Å to 1.3989 Å for **5**; shape index having range -1.0 Å to 1.0 Å; and curvedness having range -4.0 Å to 0.4 Å.

As shown in Fig. 2, d_{norm} maps of the Hirshfeld surfaces of the antimony(III) complexes **1-5** revealed several red dots of varying size and density. These red dots indicate significant intermolecular interactions and prove that the intramolecular distance is significantly shorter than the sum of the van der Waals radii. The intense red spots on the d_{norm} surface of complex **1** indicate H···Cl/Cl···H and S···S type intermolecular interactions. The H···Cl/Cl···H interactions arise from N–H···Cl type intermolecular hydrogen bondings. The paler red spots on the Hirshfeld surface show H···Cl/Cl···H type intermolecular hydrogen bonds. The intense red spots on the d_{norm} surface of complex **2** indicate H···Cl/Cl···H and Sb···S type intermolecular interactions. The H···Cl/Cl···H interactions arise from N–H···Cl type intermolecular hydrogen bondings. The paler red spots on the Hirshfeld surface show H···Cl/Cl···H type intermolecular interactions derived from C–H···Cl type intermolecular hydrogen bonds. The intense red spots on the d_{norm} surface of complex **3** indicate H···Cl/Cl···H type intermolecular contacts. The H···Cl/Cl···H contacts arise from N–H···Cl type intermolecular hydrogen bondings. The intense red spots on the d_{norm} surface of complex **4** indicate Sb···Cl type intermolecular interactions. The paler red spots on the Hirshfeld surface indicate H···Cl/Cl···H type intermole cular interactions which arise from N-H···Cl type and C–H···Cl type intermolecular hydrogen bonds. The intense red spots on the d_{norm} surface of complex 5 indicate H···S/S···H type intermole-

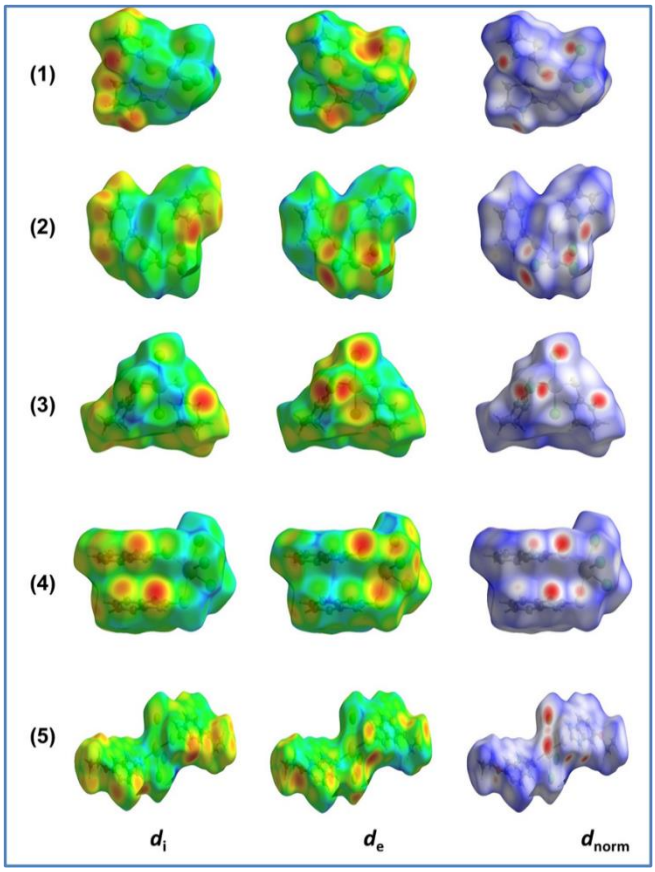

Fig. 2 Hirshfeld surface mapped of interior distance (di), exterior distance (de), normalized contact distance (dnorm) in complexes 1-5.

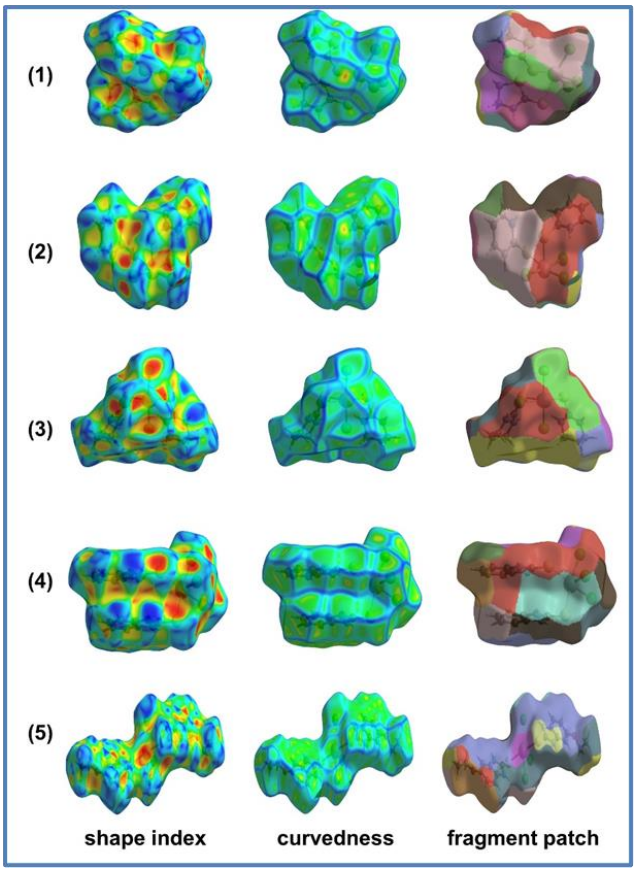

Fig. 3 Hirshfeld surface mapped of shape index, curvedness, and fragment patch in antimony(III) chloride complexes 1-5.

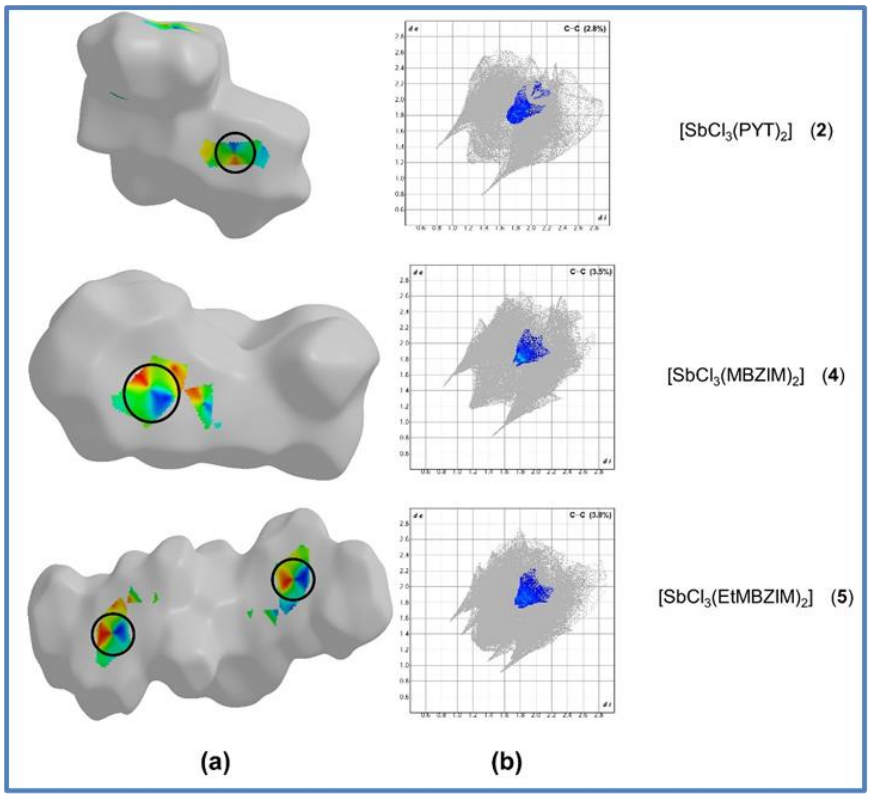

Fig. 4 (a) π–π interactions shown by adjacent red and blue triangles in the shape index map in complexes 2, 4, and 5. **(b)** Two-dimensional fingerprint plots for complexes 2, 4, and 5 showing contributions from C···C contacts.

cular interactions. The H···S/S···H interactions arise from N–H···S type intermolecular hydrogen bondings. The paler red spots on the Hirshfeld surface indicate H···Cl/Cl···H type intermolecular contacts which arise from N-H···Cl type and C–H···Cl type intermolecular hydrogen bonds.

Shape index and curvature can be used to identify stacking interactions. For the complexes **2**, **4** and **5**, red and blue triangles (bow tie pattern) were observed in the shape indexes (Fig. 4), and there are flat surface patches in the curvatures (Fig. 3), which indicate that there are π-π stacking interactions. However, for the complexes **1** and **3**, there is no case similar to the complexes **2**, **4** and **5** in shape indexes and curvatures.

2D fingerprint plots of all studied antimony(III) chloride complexes **1**-**5** are shown in Fig. 5. The most significant interaction in complex **1** is attributed to H···Cl/Cl···H interactions with 44.6%, which appear as distinct spikes. H···S/S···H interactions are the second most frequent

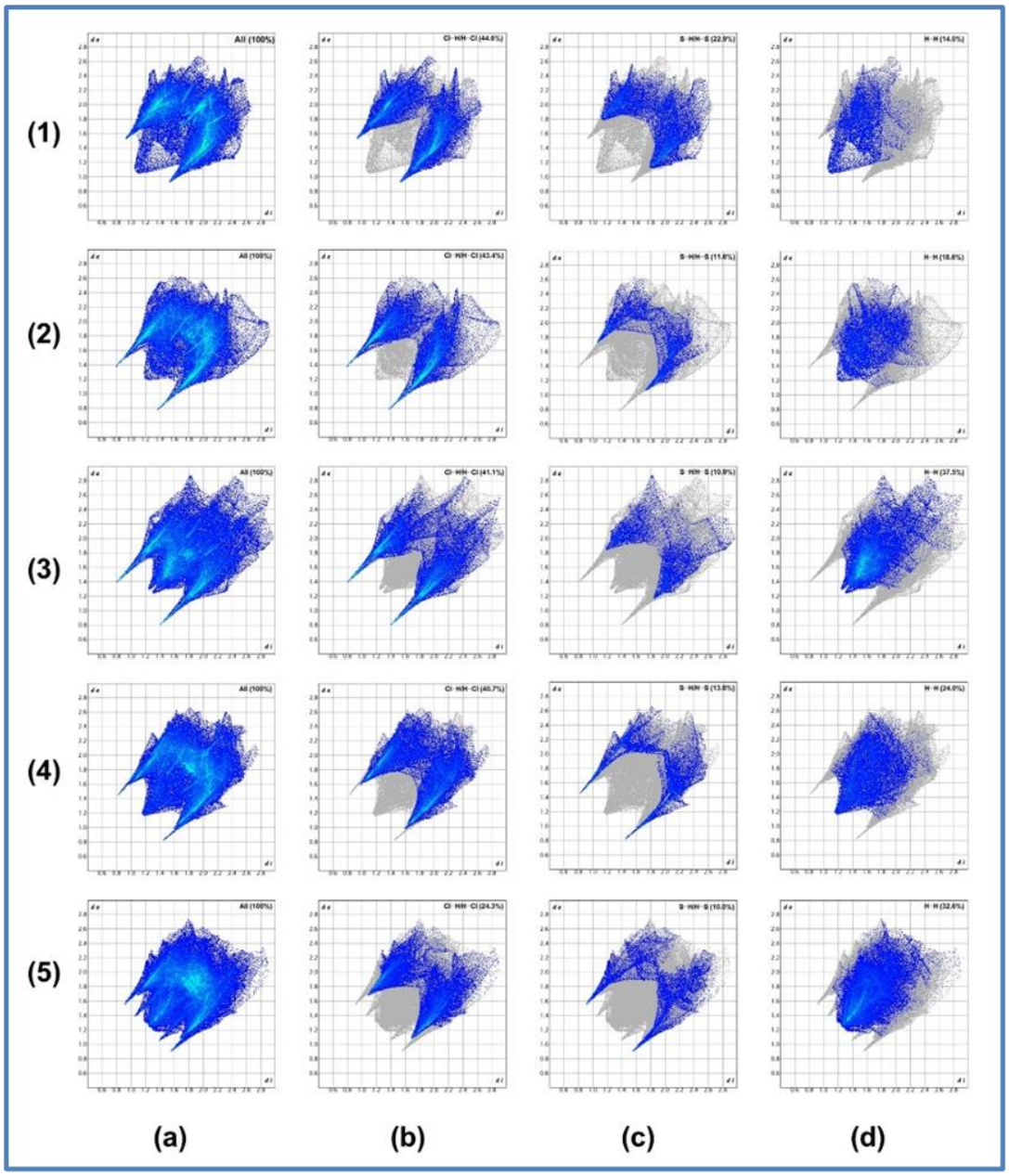

Fig. 5 Two-dimensional fingerprint plots and relative contributions of various interactions to the Hirshfeld surface of the antimony(III) chloride complexes **1**-**5**, corresponding to (a) All interactions, (b) Cl···H/H···Cl, (c) S···H/H···S, (d) H···H.

interaction in complex **1** at 22.9% and are expressed as wings on the 2D fingerprint. The H···H interactions occur in the middle of the 2D fingerprint, accounting for 14.0% of the complex **1**. The highest interactions in the complex **2** are the Cl···H/H···Cl contacts, which appear as distinct spikes. The Cl···H/H···Cl contacts make contributions of 42.5% to the Hirshfeld surface. The H···H interactions are the second most frequent interaction in complex **2** at 18.6% and they occur in the middle of the 2D fingerprint. H···S/S···H interactions, expressed as wings on a 2D fingerprint, contribute 11.6% to the Hirshfeld surface of complex **2**. In complex **3**, the most significant interaction is attributed to H···Cl/Cl···H interactions

with 41.1%, which appear as distinct spikes. The second most common interaction in complex **3** is H···H interactions with 37.5%. These interactions take place in the middle of the 2D fingerprint. The third most common interaction in complex **3** is H···S/S···H interactions with 10.9% and these interactions are expressed as wings on the 2D fingerprint. H···Cl/Cl···H interactions are the highest interactions in complex **4** and the ratio of this interaction among all interactions is 40.7%; and these interactions are located in the region expressed as wings on the 2D fingerprint, unlike the other first three complexes (**1-3**). The H···H interactions are the second most frequent interaction in complex **4** at 24.0% and they occur in the middle of the 2D fingerprint. The third most common interaction in complex **3** is H···S/S···H interactions with 13.8%. These interactions in complex **4** appear as distinct spikes in the 2D fingerprint, unlike the other three complexes (**1-3**). Unlike the other four complexes, the highest interaction in complex **5** is 32.6% H···H interactions and occurs in the middle of the 2D fingerprint. The second most common interaction in complex **5** is H···Cl/Cl···H interactions with 24.3%, and these interactions take place in the region expressed as wings on the 2D fingerprint, as in complex **4**. The third most common interaction in complex **5** is H···S/S···H interactions with 10.0%, and these interactions appear as distinct spikes in the 2D fingerprint, as in complex **4**.

The relative contributions to the Hirshfeld surface area due to main contacts for the antimony(III) complexes 1–5 are shown as a histogram in Fig. 6. Other weak contact contributions observed for complexes 1–5 are summarized in Table 1.

Table 1. Intermolecular interactions of the antimony(III) chloride complex **1-5**.

Interactions	Complex 1	Complex 2	Complex 3	Complex 4	Complex 5
Cl···H/H···Cl	44.6	43.4	41.1	40.7	24.3
S···H/H···S	22.9	11.6	10.9	13.8	10.0
H···H	14.0	18.6	37.5	24.0	32.6
Cl···Cl	1.9	0.4	-	0.8	0.4
S···S	4.4	1.4	0.4	1.1	0.3
C···C	-	2.8	-	3.5	3.8
N···N	-	0.1	-	-	0.1
Sb···Sb	-	-	-	-	0.2
Cl···N/N···Cl	0.5	0.7	0.7	0.4	-
Cl···S/S···Cl	3.2	0.4	0.2	1.3	1.1
Cl···C/C···Cl	-	1.9	0.9	0.3	-
S···C/C···S	2.0	0.6	1.3	1.1	1.8
S···N/N···S	1.5	0.1	1.5	0.5	0.2
S···O/O···S	-	-	-	-	1.0
C···H/H···C	2.5	11.5	0.3	6.7	10.4
N···H/H···N	0.5	0.8	0.9	1.4	2.2
O···H/H···O	-	-	-	-	5.1
N···C/C···N	-	1.2	-	2.1	3.0
O···C/C···O	-	-	-	-	0.8
Sb···Cl/Cl···Sb	1.7	-	0.2	2.3	1.7
Sb···H/H···Sb	0.3	2.0	1.8	-	-
Sb···S/S···Sb	-	2.6	2.4	-	0.8
TOTAL	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**

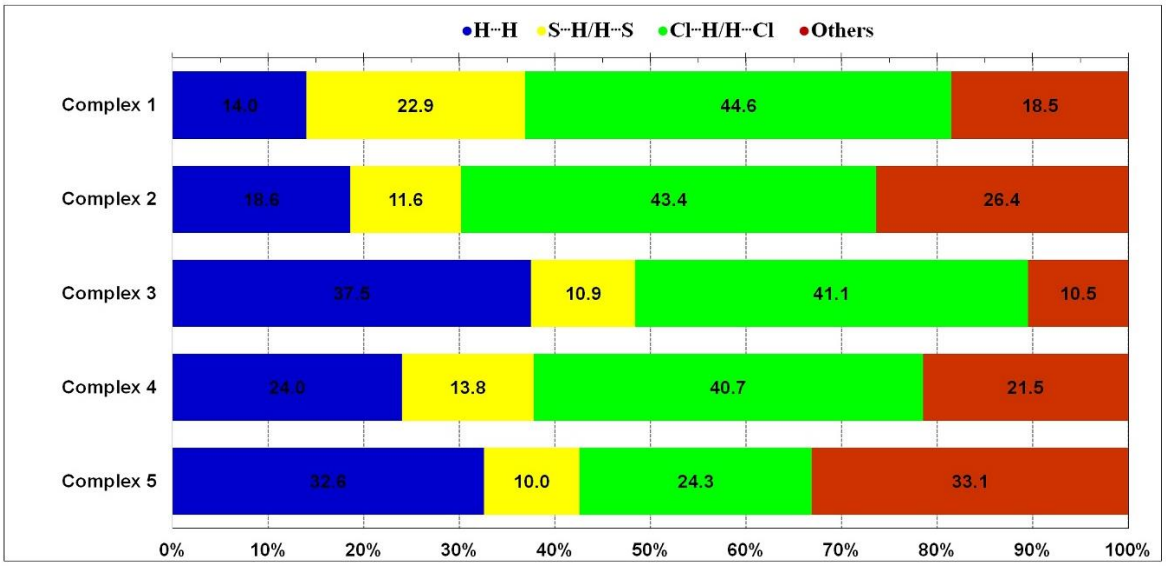

Fig. 6 Relative contributions of intermolecular contacts to the Hirshfeld surface area for antimony(III) chloride complexes 1-5.

4. Conclusion

In this study, Hirshfeld surfaces of five antimony(III) chloride-thioamide complexes with three different isomeric forms of square pyramid geometry were investigated. The chemical structures of these complexes have been characterized by various spectroscopic methods and X-ray analysis in previous studies. The crystal packing of all compounds is dominated by Cl···H/H···Cl, S···H/H···S, and H···H interactions, which is evidenced by the Hirshfeld surface analysis. The most dominant interaction in the crystal packaging of complexes **1** and **4**, which have *cis*-S and *cis*-Cl arrangement at the base and a square pyramid geometry with Cl atoms in its apical position, is Cl···H/H···Cl interactions. Likewise, the most dominant interaction in the crystal packaging of complexes **2** and **3**, which have a square pyramid geometry with one sulfur and three chlorine atoms at the base and one S atom at the apical position, is Cl···H/H···Cl interactions. Unlike the other four complexes, the most dominant interaction in the crystal packaging of complex **5**, which has a square pyramid geometry with a *trans*-S and *trans*-Cl arrangement at the base and a Cl atom in its apical position, is H···H interactions. Complex **1** has the highest H···S/S···H interaction. This may be due to the greater number of sulfur atoms in the 2-mercapto-thiazolidine ligand.

Declaration

Author Contribution: Conceive-I.I.O; Design- I.I.O; Supervision- I.I.O, Experimental Performance, Data Collection and/or Processing- I.I.O; Analysis and/or Interpretation- I.I.O; Literature Review- I.I.O; Writer- I.I.O; Critical Reviews– I.I.O.

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