Proposed crystal structure of protriptyline hydrochloride Form A, $C_{19}H_{22}NCl$

James Kaduk[1,2], Anja Dosen[3] and Tom Blanton[3]
[1]*Illinois Institute of Technology, Department of Chemistry, 3101 South Dearborn Street, Chicago, IL 60616, USA*
[2]*North Central College, Department of Physics, 131 South Loomis Street, Naperville, IL 60540 USA*
[3]*International Centre for Diffraction Data (ICDD), 12 Campus Boulevard, Newtown Square, PA 19073-3273, USA*

(Received 24 July 2025; revised 07 October 2025; accepted 14 October 2025)

Abstract: The crystal structure of protriptyline hydrochloride has been solved and refined using synchrotron X-ray powder diffraction data and optimized using density functional theory techniques. Protriptyline hydrochloride crystallizes in space group $P2_1/n$ (#14) with a = 10.10772(19), b = 32.0908(6), c = 10.45302(21) Å, β = 92.8748(10)°, V = 3,386.33(15) Å^3, and Z = 8 at 298 K. The crystal structure contains the expected N–H···Cl hydrogen bonds, which link the cations and anions into crankshaft-shaped chains along the c-axis. The cations and the anions form layers parallel to the ac-plane, with van der Waals interactions between the layers. The powder pattern has been submitted to the International Centre for Diffraction Data (ICDD®) for inclusion in the Powder Diffraction File™ (PDF®).
© The Author(s), 2025. Published by Cambridge University Press on behalf of International Centre for Diffraction Data. This is an Open Access article, distributed under the terms of the Creative Commons Attribution licence (http://creativecommons.org/licenses/by/4.0), which permits unrestricted re-use, distribution and reproduction, provided the original article is properly cited.
[doi:10.1017/S0885715625101024]

Key words: protriptyline, Concordin, crystal structure, Rietveld refinement, density functional theory

I. INTRODUCTION

Protriptyline hydrochloride (sold under the brand names Concordin and Maximen, among others) is used to treat depression and attention-deficit hyperactivity disorder. It is a tricyclic secondary amine hydrochloride salt of Protriptyline (Vivactil) and results in energizing rather than sedating a user. The systematic name (CAS Registry No. 1225-55-4) is *N*-methyl-3-(2-tricyclo[9.4.0.03,8]pentadeca-1(15),3,5,7,9,11,13-heptaenyl)propan-1-ammonium chloride. A two-dimensional molecular diagram of protriptyline hydrochloride is shown in Figure 1.

Crystalline Forms A and B of protriptyline hydrochloride are claimed in U.S. Patent Application 2007/0112073 A1 (Ventimiglia et al., 2007; Diparma S.p.A.), and powder diffraction data are provided.

This work was carried out as part of a project (Kaduk et al., 2014) to determine the crystal structures of large-volume commercial pharmaceuticals and include high-quality powder diffraction data for them in the Powder Diffraction File (Kabekkodu et al., 2024).

II. EXPERIMENTAL

The commercial reagent protriptyline hydrochloride from TargetMol (Batch #146002, 99.98% purity) was used as received. The white powder was packed into a 0.5-mm-diameter Kapton capillary and rotated during the measurement at ~2 Hz. The powder pattern was measured at 298(1) K at the Wiggler Low Energy Beamline (Leontowich et al., 2021) of the Brockhouse X-ray Diffraction and Scattering Sector of the Canadian Light Source using a wavelength of 0.819826(2) Å (15.1 keV) from 1.6 to 75.0° 2θ with a step size of 0.0025° and a collection time of 3 minutes. The high-resolution powder diffraction data were collected using eight Dectris Mythen2 X series 1K linear strip detectors. NIST SRM 660b LaB_6 was used to calibrate the instrument and refine the monochromatic wavelength used in the experiment.

Initial attempts to index the pattern using multiple programs yielded a primitive monoclinic unit cell with a = 10.43, b = 32.05, c = 20.19 Å, β = 92.87°, and V = 6,744.17 Å^3, but no chemically reasonable crystal structures. Indexing with DICVOL06 (Louër and Boultif, 2007) as incorporated into FOX (Favre-Nicolin and Černý, 2002) yielded a primitive monoclinic cell with a = 10.112, b = 32.099, c = 10.459 Å, β = 92.85°, V = 3,309.4 Å^3, and Z = 8. The suggested space group was $P2_1/n$, which was confirmed by the successful solution and refinement of the crystal structure. A reduced cell search in the Cambridge Structural Database (Groom et al., 2016) yielded 12 hits, but no structures of protriptyline or its derivatives. This cell does not index all peaks observed in this study's synchrotron diffraction pattern (including peaks at 2.31, 5.16, and 8.24° 2θ), suggesting the presence of at least one unidentified crystalline impurity.

A protriptyline molecule was downloaded from PubChem (Kim et al., 2023) as Conformer3D_COMPOUND_CID_4976.sdf. It was converted to a *.mol2 file using Mercury (Macrae

Corresponding author: James Kaduk; Email: kaduk@polycrystallography.com

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

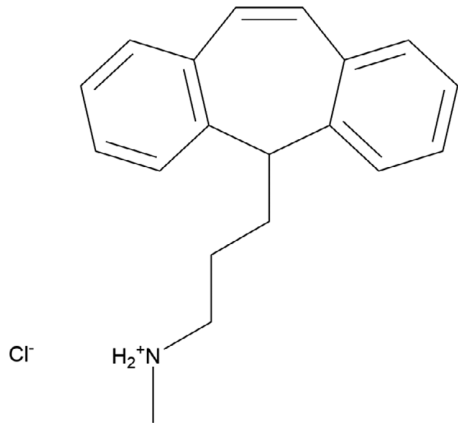


Figure 1. The two-dimensional structure of protriptyline hydrochloride.

et al., 2020) and then converted to a cation using Materials Studio (Dassault Systèmes, 2023). The structure was solved by Monte Carlo-simulated annealing techniques as implemented in EXPO2014 (Altomare et al., 2013), using two cations and two Cl atoms as fragments, incorporating a bump penalty for the non-H atoms and [010] preferred orientation (suggested by the anisotropy of the lattice parameters). Two of the 10 solutions had figures of merit significantly better than the others.

Rietveld refinement was carried out using GSAS-II (Toby and Von Dreele, 2013). Only the 2.0–40.0° portion of the pattern was included in the refinements (d_{min} = 1.198 Å). All non-H-bond distances and angles were subjected to restraints, based on a Mercury/Mogul Geometry Check (Bruno et al., 2004; Sykes et al., 2011). The Mogul average and standard deviation for each quantity were used as the restraint parameters. The benzene rings were restrained to be planar. The restraints contributed 12.5% to the overall χ^2. Using lower restraint weights resulted in some unreasonably long C–C bond distances in the side chains. The hydrogen atoms were included in calculated positions, which were recalculated during the refinement using Materials Studio (Dassault Systèmes, 2023). Separate U_{iso} were refined for the ring and side chain atoms in the independent molecules. The displacement coefficient of the side chain atoms in molecule 1 was refined to a slightly negative value, so it was fixed at a reasonable value of 0.05 Å^2. The U_{iso} for the H atoms were fixed at 1.3× the U_{iso} of the heavy atoms to which they are attached. The peak profiles were described using the generalized (Stephens, 1999) microstrain model. The background was modeled using a six-term shifted Chebyshev polynomial, with peaks at 3.02 and 10.89° to model the narrow and broad scattering from the Kapton capillary and any amorphous component.

The final refinement (begun from the density functional theory (DFT-optimized structure)) of 166 variables using 15,201 observations and 106 restraints yielded the residual R_{wp} = 0.05252. The largest peak (1.68 Å from C19) and hole (1.38 Å from H24) in the difference Fourier map were 0.43 (10) and −0.46(10) eÅ^{-3}, respectively. The final Rietveld plot is shown in Figure 2. The largest features in the normalized error plot are in the shapes of some of the strong low-angle peaks and at the peaks of the impurity phase(s).

The crystal structure of protriptyline hydrochloride was optimized (fixed experimental unit cell) with density functional techniques using VASP (Kresse and Furthmüller, 1996) through the MedeA graphical interface (MDI, 2024). The calculation was carried out on 32 cores of a 144-core (768 GB memory) HPE Superdome Flex 280 Linux server at North Central College. The calculation used the GGA-PBE functional, a plane wave cutoff energy of 400.0 eV, and a k-point spacing of 0.5 Å^{-1}, leading to a 2 × 1 × 2 mesh, and took ~129.7 hours. Single-point density functional theory calculations (fixed experimental cell) and population analysis were carried out using CRYSTAL23 (Erba et al., 2023). The basis sets for the H, C, and O atoms in the calculation were those of Gatti et al. (1994), and that for Cl was that of Peintinger et al.

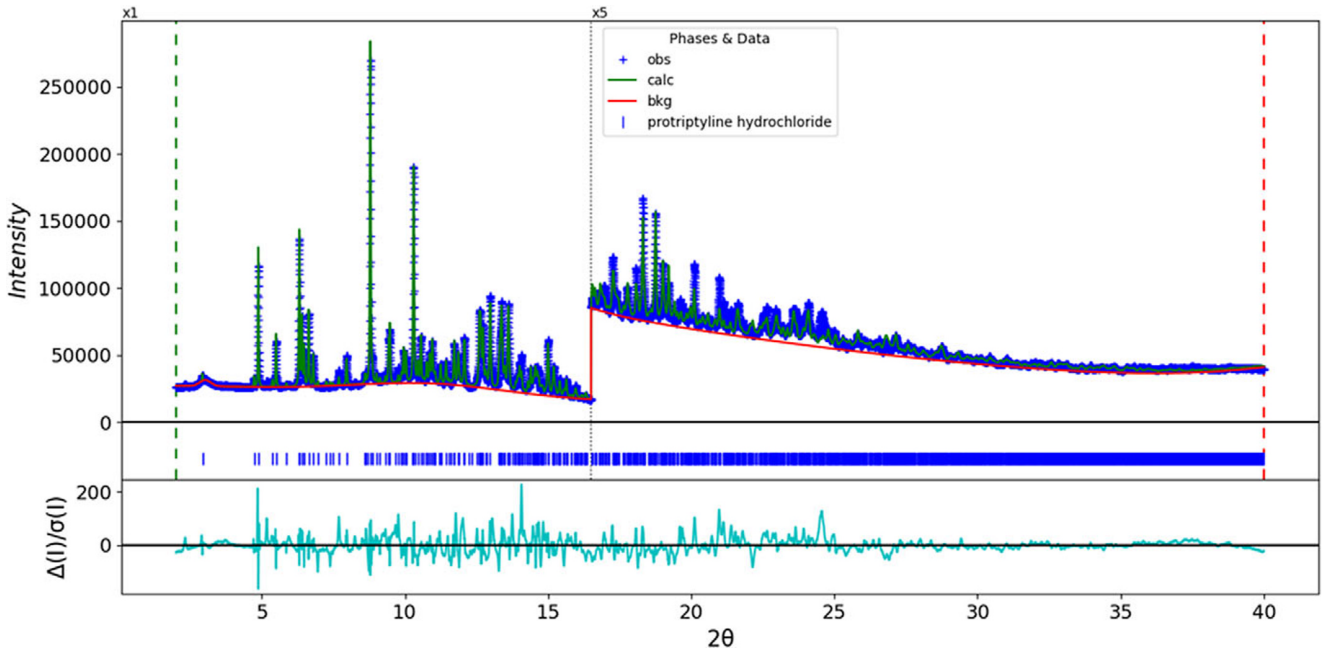


Figure 2. The Rietveld plot for protriptyline hydrochloride. The blue crosses represent the observed data points, and the green line represents the calculated pattern. The cyan curve is the normalized error plot, and the red line is the background curve. The blue tick marks indicate the protriptyline hydrochloride peak positions. The vertical scale has been multiplied by a factor of 5× for 2θ > 16.5°.

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

(2013). The calculations were run on a 3.5 GHz PC using eight *k*-points and the B3LYP functional, and took ∼6.3 hours.

III. RESULTS AND DISCUSSION

This synchrotron powder pattern of protriptyline hydrochloride matches the one reported by Ventimiglia et al. (2007) (Figure 3) well enough to conclude that they represent the same material, and that the protriptyline hydrochloride characterized here is Form A. The unidentified crystalline impurity does not correspond to Form B.

The root-mean-square difference of the non-H atoms in the Rietveld-refined and VASP-optimized structures, calculated using the Mercury CSD-Materials/Search/Crystal Packing Similarity tool, is 0.405 Å (Figure 4). The root-mean-square Cartesian displacements of the non-H atoms in the Rietveld-refined and VASP-optimized structures of the cations, calculated using the Mercury Calculate/Molecule Overlay tool, are 0.467 and 0.279 Å (Figures 5 and 6). The largest differences are in the conformation of the side chain in cation 1. The agreements are at or outside the normal range for correct structures (van de Streek and Neumann, 2014). The asymmetric unit is illustrated in Figure 7. The U_{iso} values for most of the atoms are relatively high, and those for one part of one cation are refined to a very low value, suggesting that this structure might be approximate. Hence, the structure is described as "proposed.". The remaining discussion will emphasize the VASP-optimized structure.

Almost all the bond distances, bond angles, and torsion angles fall within the normal ranges indicated by a Mercury Mogul Geometry check (Macrae et al., 2020). The C4–C3–C5 angle of 111.6° (average = 115.0(10)°, *Z*-score = 3.5) is flagged as unusual. The standard uncertainty of the average is smaller than usual (inflating the *Z*-score). The C7–C10–N2–C4 torsion angle lies on the tail of a minor *gauche* population in a mainly *trans* distribution of similar torsion angles. The C4–C7–C10–N2 torsion angle lies on the tail of a mainly *trans* distribution. Torsion angles involving rotation about the C3–C4 bond are truly unusual; these represent the orientation of the side chain with respect to the ring system. The conformation of molecule 1 in the refined structure is actually slightly less unusual than in the DFT-optimized structure. Molecule 1 has an unusual conformation, whereas molecule 2 is normal.

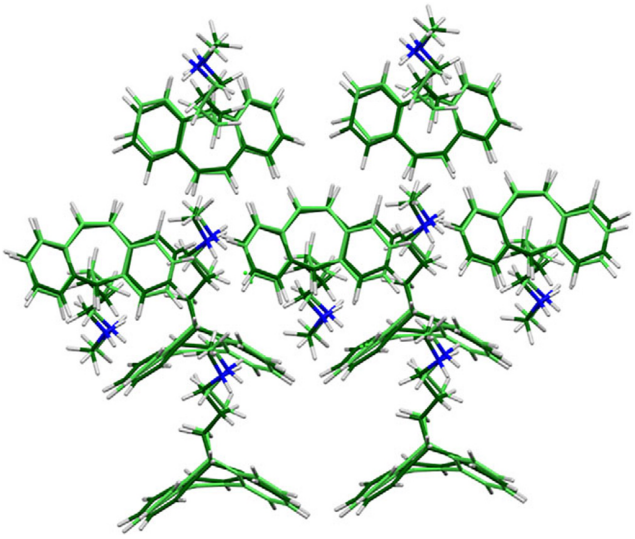


Figure 4. Comparison of the Rietveld-refined (colored by atom type) and VASP-optimized (green) structures of protriptyline hydrochloride using the Mercury CSD-Materials/Search/Crystal Packing Similarity tool. The root-mean-square Cartesian displacement is 0.405 Å. Image generated using Mercury (Macrae et al., 2020).

The difference in the two conformations is illustrated in Figure 8. Quantum chemical geometry optimization of the isolated protriptyline cations (DFT/B3LYP/6-31G*/water) using Spartan '24 (Wavefunction, 2023) indicated that

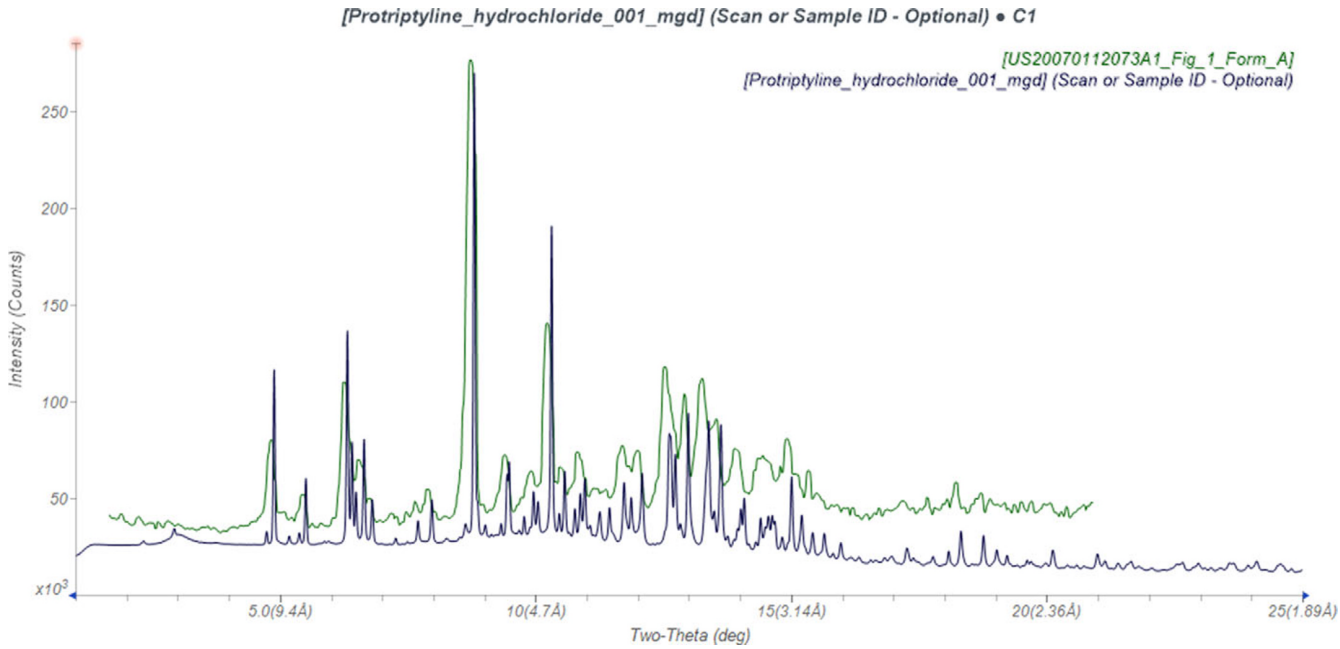


Figure 3. Comparison of the synchrotron pattern of protriptyline hydrochloride (black) to that of Form A reported by Ventimiglia et al. (2007) (green). The literature pattern (measured using Cu K_α radiation) was digitized using UN-SCAN-IT (Silk Scientific, 2013) and converted to the synchrotron wavelength of 0.819826(2) Å using JADE Pro (MDI, 2024). Image generated using JADE Pro (MDI, 2024).

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

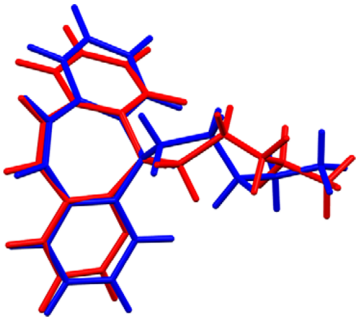


Figure 5. Comparison of the Rietveld-refined (red) and VASP-optimized (blue) structures of cation 1 in protriptyline hydrochloride. The root-mean-square Cartesian displacement is 0.467 Å. Image generated using Mercury (Macrae et al., 2020).

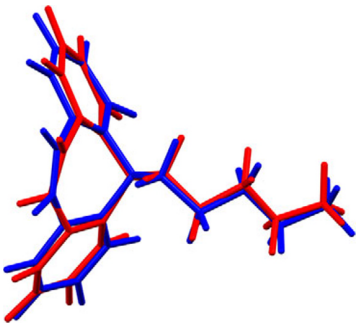


Figure 6. Comparison of the Rietveld-refined (red) and VASP-optimized (blue) structures of cation 2 in protriptyline hydrochloride. The root-mean-square Cartesian displacement is 0.279 Å. Image generated using Mercury (Macrae et al., 2020).

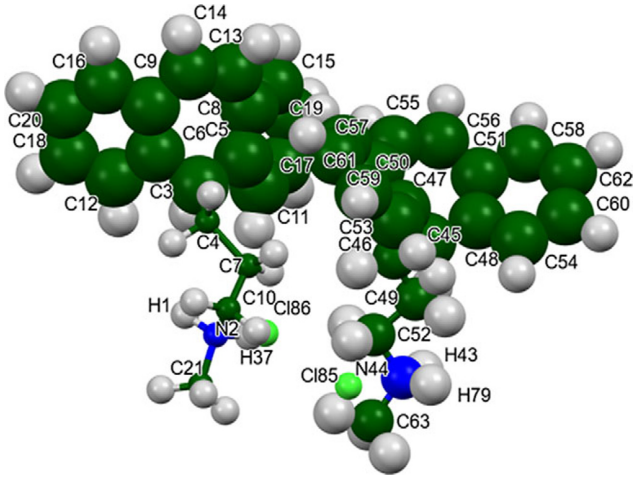


Figure 7. The asymmetric unit of protriptyline hydrochloride, with the atom numbering. The atoms are represented by 50% probability spheroids. Image generated using Mercury (Macrae et al., 2020).

cation 2 is 1.0 kcal/mol lower in energy than cation 1. In the global minimum-energy conformation, the side chain is folded to lie parallel to the ring system, showing that intermolecular interactions are important in determining the solid-state conformations.

The crystal structure (Figure 9) contains the expected N–H···Cl hydrogen bonds, which link the cations and the anions into chains along the *c*-axis. The cations and the anions

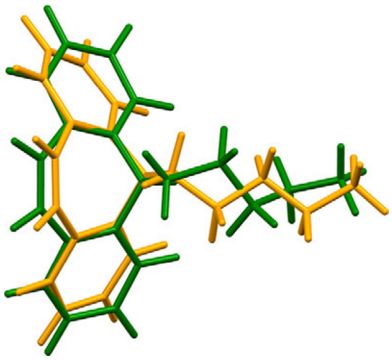


Figure 8. Comparison of cation 1 (green) and cation 2 (orange) in protriptyline hydrochloride. The root-mean-square Cartesian displacement is 0.591 Å. Cation 2 is 1.0 kcal/mol lower in energy than cation 1. Image generated using Mercury (Macrae et al., 2020).

form layers parallel to the *ac*-plane, with van der Waals interactions between the layers. The mean planes of the ring systems of cation 1 and cation 2 are approximately (−2, −1, 0) and (−1, 3, 0). The Mercury Aromatics Analyser indicates one moderate interaction between the phenyl rings of cations 1 and 2, with a distance of 5.01 Å, as well as several weak interactions with distances >7.0 Å.

Analysis of the contributions to the total crystal energy of the structure using the Forcite module of Materials Studio (Dassault Systèmes, 2023) indicates that bond, angle, and torsion distortion terms contribute about equally to the intramolecular energy. The intermolecular energy is dominated by van der Waals attractions and electrostatic repulsions, which in this force field-based analysis also include hydrogen bonds. The hydrogen bonds are better discussed using the results of the DFT calculation.

As expected, there are four strong N–H···Cl hydrogen bonds between the cations and anions (Table I). The N–H···Cl hydrogen bonds link the cations and the anions into crankshaft-shaped chains (Figure 10) along the *c*-axis. The chains have the graph set *D2,2(5)* (Etter, 1990; Bernstein et al., 1995; Motherwell et al., 2000. Several C–H···Cl hydrogen bonds also contribute to the lattice energy.

The volume enclosed by the Hirshfeld surface of protriptyline hydrochloride (Figure 11; Hirshfeld, 1977; Spackman et al., 2021) is 836.88 Å^3, 98.88% of one-fourth of the unit cell volume. The packing density is thus typical. The only significant close contacts (red in Figure 11) involve the hydrogen bonds. The volume/non-hydrogen atom is larger than usual, at 20.1 Å^3, reflecting the presence of the chloride anions.

The Bravais–Friedel–Donnay–Harker (Bravais, 1866; Friedel, 1907; Donnay and Harker, 1937) algorithm suggests that we might expect platy morphology for protriptyline hydrochloride, with {010} as the major faces, as expected from both the anisotropy of the lattice parameters and the layered structure. A fourth-order spherical harmonic texture model was included in the refinement. The texture index was 1.020(1), indicating that preferred orientation was (perhaps surprisingly) slight in this rotated capillary specimen.

DEPOSITED DATA

The powder pattern of protriptyline hydrochloride from this synchrotron dataset has been submitted to the ICDD for

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

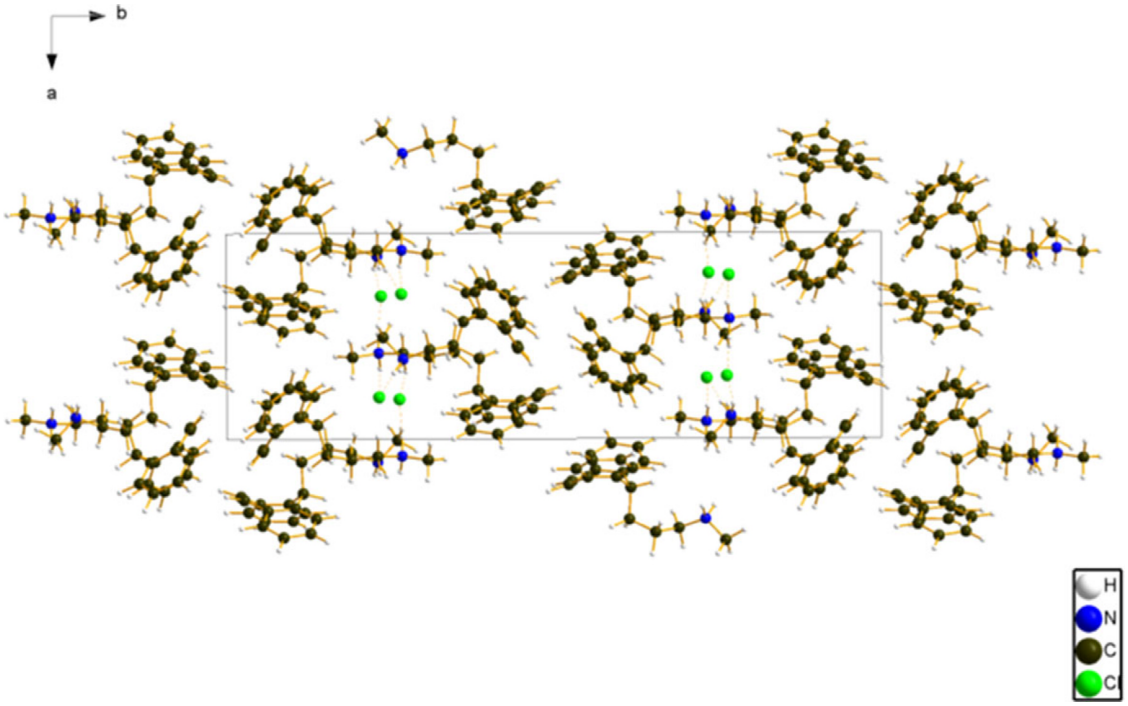


Figure 9. The crystal structure of protriptyline hydrochloride, viewed down the *c*-axis. Image generated using Diamond (Crystal Impact, 2023).

TABLE I. Hydrogen bonds (CRYSTAL23) in protriptyline hydrochloride.

H bond	D–H, Å	H···A, Å	D···A, Å	D–H···A, °	Mulliken overlap, *e*
N2–H1···Cl85	1.068	1.948	3.015	177.1	0.114
N2–H37···Cl86	1.057	2.109	3.134	162.6	0.091
N44–H43···Cl85	1.060	2.041	3.097	173.5	0.104
N44–H79···Cl86	1.066	2.005	3.064	172.1	0.110
C1–H29···Cl86	1.094	2.727	3.802	167.0	0.032
C12–H30···Cl85	1.094	3.267	4.306	158.8	0.014
C21–H40···Cl85	1.097	2.397	3.487	172.1	0.047
C21–H42···Cl86	1.099	2.833	3.910	166.3	0.025
C52–H69···Cl86	1.100	2.540	3.613	164.7	0.038
C52–H70···Cl85	1.101	2.654	3.740	168.4	0.029
C53–H71···Cl85	1.092	2.819	3.627	130.6	0.020
C54–H72···Cl86	1.093	3.304	4.190	138.9	0.011

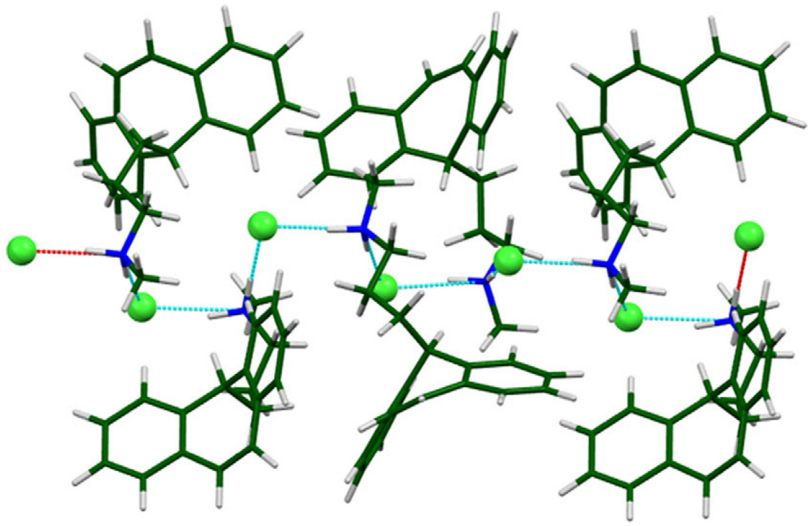


Figure 10. The crankshaft-shaped hydrogen bond chains in the structure of protriptyline hydrochloride. The Cl anions are represented by green spheres. The cyan and red dashed lines indicate the hydrogen bonds. Image generated using Mercury (Macrae et al., 2020).

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

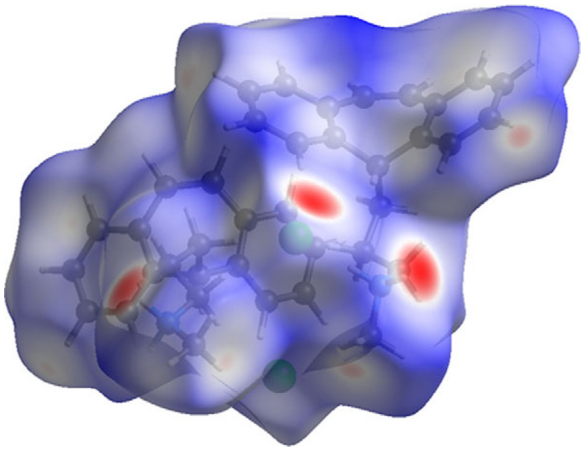


Figure 11. The Hirshfeld surface of protriptyline hydrochloride. Intermolecular contacts longer than the sum of the van der Waals radii are colored blue, while contacts shorter than the sum of the radii are colored red. Contacts equal to the sum of radii are white. Image generated using CrystalExplorer (Spackman et al., 2021).

inclusion in the Powder Diffraction File. The Crystallographic Information Framework (CIF) files containing the results of the Rietveld refinement (including the raw data) and the DFT geometry optimization were deposited with the ICDD. The data can be requested at pdj@icdd.com.

ACKNOWLEDGEMENTS

We thank Adam Leontowich for his assistance in the data collection. We also thank the ICDD team – Megan Rost, Steve Trimble, and Dave Bohnenberger – for their contribution to research, sample preparation, and in-house XRD data collection and verification.

FUNDING STATEMENT

Part of the research described in this paper was performed at the Canadian Light Source, a national research facility of the University of Saskatchewan, which is supported by the Canada Foundation for Innovation (CFI), the Natural Sciences and Engineering Research Council (NSERC), the Canadian Institute of Health Research (CIHR), the Government of Saskatchewan, and the University of Saskatchewan. This work was partially supported by the International Centre for Diffraction Data.

COMPETING INTEREST

The authors have no competing interests to declare.

REFERENCES

Altomare, A., C. Cuocci, C. Giacovazzo, A. Moliterni, R. Rizzi, N. Corriero, and A. Falcicchio. 2013. "EXPO2013: A Kit of Tools for Phasing Crystal Structures from Powder Data." *Journal of Applied Crystallography* 46: 1231–35.

Bernstein, J., R. E. Davis, L. Shimoni, and N. L. Chang. 1995. "Patterns in Hydrogen Bonding: Functionality and Graph Set Analysis in Crystals." *Angewandte Chemie International Edition in English* 34: 1555–73.

Bravais, A. 1866. *Etudes Cristallographiques*. Paris: Gauthier Villars.

Bruno, I. J., J. C. Cole, M. Kessler, J. Luo, W. D. S. Motherwell, L. H. Purkis, B. R. Smith, et al. 2004. "Retrieval of Crystallographically Derived Molecular Geometry Information." *Journal of Chemical Information and Computer Sciences* 44: 2133–44.

Crystal Impact. 2023. *Diamond V. 5.0.0*. Bonn: Crystal Impact – Dr. H. Putz & Dr. K. Brandenburg.

Dassault Systèmes. 2023. *BIOVIA Materials Studio 2024*. San Diego, CA: BIOVIA.

Donnay, J. D. H., and D. Harker. 1937. "A New Law of Crystal Morphology Extending the Law of Bravais." *American Mineralogist* 22: 446–67.

Erba, A., J. K. Desmarais, S. Casassa, B. Civalleri, L. Donà, I. J. Bush, B. Searle, et al. 2023. "CRYSTAL23: A Program for Computational Solid State Physics and Chemistry." *Journal of Chemical Theory and Computation* 19: 6891–932. https://doi.org/10.1021/acs.jctc.2c00958.

Etter, M. C. 1990. "Encoding and Decoding Hydrogen-Bond Patterns of Organic Compounds." *Accounts of Chemical Research* 23: 120–26.

Favre-Nicolin, V., and R. Černý. 2002. "FOX, 'Free Objects for Crystallography': A Modular Approach to Ab Initio Structure Determination from Powder Diffraction." *Journal of Applied Crystallography* 35: 734–43.

Friedel, G. 1907. "Etudes sur la loi de Bravais." *Bulletin de la Société Française de Minéralogie* 30: 326–455.

Gatti, C., V. R. Saunders, and C. Roetti. 1994. "Crystal-Field Effects on the Topological Properties of the Electron-Density in Molecular Crystals – the Case of Urea." *Journal of Chemical Physics* 101: 10686–96.

Groom, C. R., I. J. Bruno, M. P. Lightfoot, and S. C. Ward. 2016. "The Cambridge Structural Database." *Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials* 72: 171–79.

Hirshfeld, F. L. 1977. "Bonded-Atom Fragments for Describing Molecular Charge Densities." *Theoretica Chemica Acta* 44: 129–38.

Kabekkodu, S., A. Dosen, and T. N. Blanton. 2024. "PDF-5+: A Comprehensive Powder Diffraction File™ for Materials Characterization." *Powder Diffraction* 39: 47–59.

Kaduk, J. A., C. E. Crowder, K. Zhong, T. G. Fawcett, and M. R. Suchomel. 2014. "Crystal Structure of Atomoxetine Hydrochloride (Strattera), $C_{17}H_{22}NOCl$." *Powder Diffraction* 29: 269–73.

Kim S., J. Chen, T. Cheng, A. Gindulyte, J. He, S. He, Q. Li, et al. 2023. "PubChem 2023 Update." *Nucleic Acids Research* 51(D1): D1373–80. https://doi.org/10.1093/nar/gkac956.

Kresse, G., and J. Furthmüller. 1996. "Efficiency of Ab-Initio Total Energy Calculations for Metals and Semiconductors Using a Plane-Wave Basis Set." *Computational Materials Science* 6: 15–50.

Leontowich, A. F. G., A. Gomez, B. Diaz Moreno, D. Muir, D. Spasyuk, G. King, J. W. Reid, C.-Y. Kim, and S. Kycia. 2021. "The Lower Energy Diffraction and Scattering Side-Bounce Beamline for Materials Science at the Canadian Light Source." *Journal of Synchrotron Radiation* 28: 1–9. https://doi.org/10.1107/S1600577521002496.

Louër, D., and A. Boultif. 2007. "Powder Pattern Indexing and the Dichotomy Algorithm." *Zeitschrift für Kristallographie Supplement* 26: 191–96.

Macrae, C. F., I. Sovago, S. J. Cottrell, P. T. A. Galek, P. McCabe, E. Pidcock, M. Platings, et al. 2020. "*Mercury 4.0*: From Visualization to Design and Prediction." *Journal of Applied Crystallography* 53: 226–35.

MDI. 2024. *JADE Pro Version 9.0*. Livermore, CA: Materials Data.

Motherwell, W. D. S., G. P. Shields, and F. H. Allen. 2000. "Graph-Set and Packing Analysis of Hydrogen-Bonded Networks in Polyamide Structures in the Cambridge Structural Database." *Acta Crystallographica B* 56: 857–71.

Peintinger, M. F., D. Vilela Oliveira, and T. Bredow. 2013. "Consistent Gaussian Basis Sets of Triple-Zeta Valence with Polarization Quality for Solid-State Calculations." *Journal of Computational Chemistry* 34: 451–59.

Silk Scientific. 2013. *UN-SCAN-IT 7.0*. Orem, UT: Silk Scientific Corporation.

Spackman, P. R., M. J. Turner, J. J. McKinnon, S. K. Wolff, D. J. Grimwood, D. Jayatilaka, and M. A. Spackman. 2021. "CrystalExplorer: A Program for Hirshfeld Surface Analysis, Visualization and Quantitative Analysis of Molecular Crystals." *Journal of Applied Crystallography* 54: 1006–11. https://doi.org/10.1107/S1600576721002910; https://crystalexplorer.net.

Stephens, P. W. 1999. "Phenomenological Model of Anisotropic Peak Broadening in Powder Diffraction." *Journal of Applied Crystallography* 32: 281–89.

Sykes, R. A., P. McCabe, F. H. Allen, G. M. Battle, I. J. Bruno, and P. A. Wood. 2011. "New Software for Statistical Analysis of Cambridge Structural Database Data." *Journal of Applied Crystallography* 44: 882–86.

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press

Toby, B. H., and R. B. Von Dreele. 2013. "GSAS II: The Genesis of a Modern Open Source All Purpose Crystallography Software Package." *Journal of Applied Crystallography* 46: 544–49.
van de Streek, J., and M. A. Neumann. 2014. "Validation of Molecular Crystal Structures from Powder Diffraction Data with Dispersion-Corrected Density Functional Theory (DFT-D)." *Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials* 70: 1020–32.
Ventimiglia, G., D. Magrone, P. Allegrini, and G. Razzetti. 2007. "Protriptyline Hydrochloride Crystalline Form." U.S. Patent Application 2007/0112073 A1.
Wavefunction, Inc. 2023. *Spartan '24.* V. 1.0.0. Irvine, CA: Wavefunction, Inc.

https://doi.org/10.1017/S0885715625101024 Published online by Cambridge University Press