

Powder X-ray diffraction of daclatasvir dihydrochloride Form N-2 (Daklinza®), C₄₀H₅₂N₈O₆Cl₂

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The crystal structure of daclatasvir dihydrochloride Form N-2 (Daklinza®) has been refined using synchrotron X-ray powder diffraction data and optimized using density functional theory techniques. Daclatasvir dihydrochloride, Form N-2, crystallizes in space group *P1* (#1) with $a = 7.54808$ (15), $b = 9.5566$ (5), $c = 16.2641$ (11) Å, $\alpha = 74.0642$ (24), $\beta = 84.0026$ (13), $\gamma = 70.6322$ (5)°, $V = 1064.150$ (11) Å³, and $Z = 1$. The hydrogen bonds were identified and quantified. Strong N–H⋯Cl hydrogen bonds link the cations and anions in chains along the *a*-axis. The powder pattern has been submitted to ICDD® for inclusion in the Powder Diffraction File™ (PDF®). © The Author(s), 2021. Published by Cambridge University Press on behalf of International Centre for Diffraction Data. [doi:10.1017/S0885715621000397]

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I.

Daclatasvir, under the trade name Daklinza, is used in combination with other drugs to treat hepatitis C. No daclatasvir crystal structures are reported in the Cambridge Structural Database (Groom *et al.*, 2016) as of the completion of the current study. A search of the primary literature yielded International Patent Application WO 2009/020828 A1 (Kim *et al.*, 2009; Bristol-Myers Squibb), which reports the crystal structure of daclatasvir dihydrochloride Form N-2, determined using single-crystal X-ray measurements. A powder diffraction pattern for daclatasvir dihydrochloride Form N-2 is provided in WO 2009/020828 A1 (Figure 1); however, the *d*-spacings of only 11 diffraction peaks without intensity data are reported supporting the need for a complete powder diffraction data set that can be used as a reference for phase identification. Two additional daclatasvir dihydrochloride forms, Forms L1 and Form L2, are reported in International Patent Application WO 2018/007984 A1 (Sanpuhi *et al.*, 2018; Lupin). The reported Forms L1 and L2 powder X-ray diffraction peak data do not match the data for Form N-2.

In this work, the sample was ordered from TargetMol (Batch #115989) and analyzed as-received. The diffraction data for this study were collected on beamline 11-BM at the Advanced Photon Source, Argonne National Laboratory. The room temperature (295 K) crystal structure was refined (Figure 2) using synchrotron powder diffraction data ($\lambda = 0.458119$ (2) Å) and optimized using density functional

theory techniques. The structure was refined using GSAS-II (Toby and Von Dreele, 2013) with $d_{\min} = 1.058$ Å. Commercial daclatasvir dihydrochloride (CAS #1009119-65-6) crystallizes in space group *P1* (#1) with $a = 7.54808$ (15), $b = 9.5566$ (5), $c = 16.2641$ (11) Å, $\alpha = 74.0642$ (24), $\beta = 84.0026$ (13), $\gamma = 70.6322$ (5)°, $V = 1064.150$ (11) Å³, and $Z = 1$. All bond distances and angles were restrained using the results of a Mercury Mogul Geometry Check (Bruno *et al.*, 2004; Sykes *et al.*, 2011; Figure 3). The DFT optimization was carried out, along with a Mulliken population analysis, using CRYSTAL14 (Dovesi *et al.*, 2014); the B3LYP functional and 8 *k*-points were used. The basis sets for the H, C, N, and O atoms were those of Gatti *et al.* (1994), and the basis set for Cl was that of Peintinger *et al.* (2013).

As expected, all four protonated nitrogen atoms of the imidazole rings form strong hydrogen bonds to the chloride anions (Table I). These N–H⋯Cl hydrogen bonds link the molecules along the *a*-axis. Several C–H groups act as donors in C–H⋯Cl bonds to the chloride anions. Both inter- and intramolecular N–H⋯O hydrogen bonds are present. The energies of the N–H⋯O hydrogen bonds were calculated using the correlation of Wheatley and Kaduk (2019). Several inter- and intramolecular C–H⋯O hydrogen bonds also contribute to the lattice energy.

The X-ray powder diffraction pattern and structure data from this study have been submitted to ICDD for inclusion in the Powder Diffraction File (Gates-Rector and Blanton, 2019).

II. DEPOSITED DATA

CIF files were deposited with ICDD. You may request this data from info@icdd.com.

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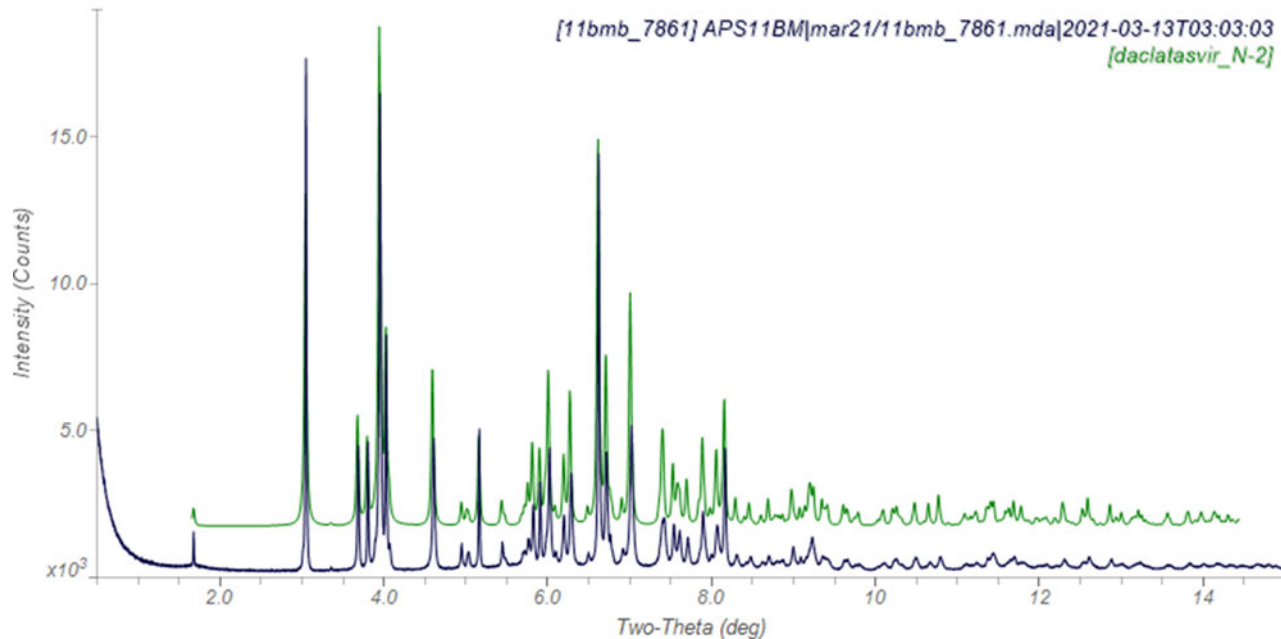


Figure 1. Comparison of the synchrotron powder diffraction pattern from this study of daclatasvir dihydrochloride Form N-2 (black) to the powder diffraction pattern of Form N-2 (green) calculated from the structure of Kim *et al.* (2009).

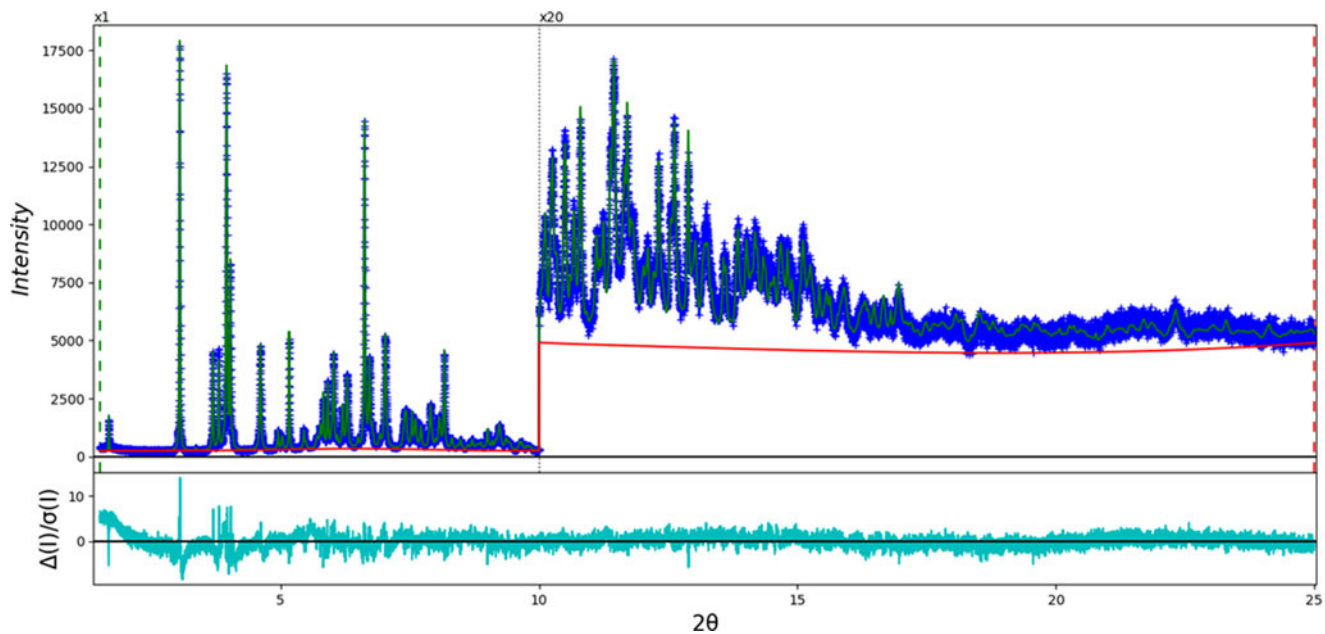


Figure 2. The Rietveld plot for daclatasvir dihydrochloride Form N-2. The blue crosses represent the observed data points, and the green line is the calculated pattern. The cyan curve is the normalized error plot. The vertical scale has been multiplied by a factor of 20× for $2\theta > 10.0^\circ$.

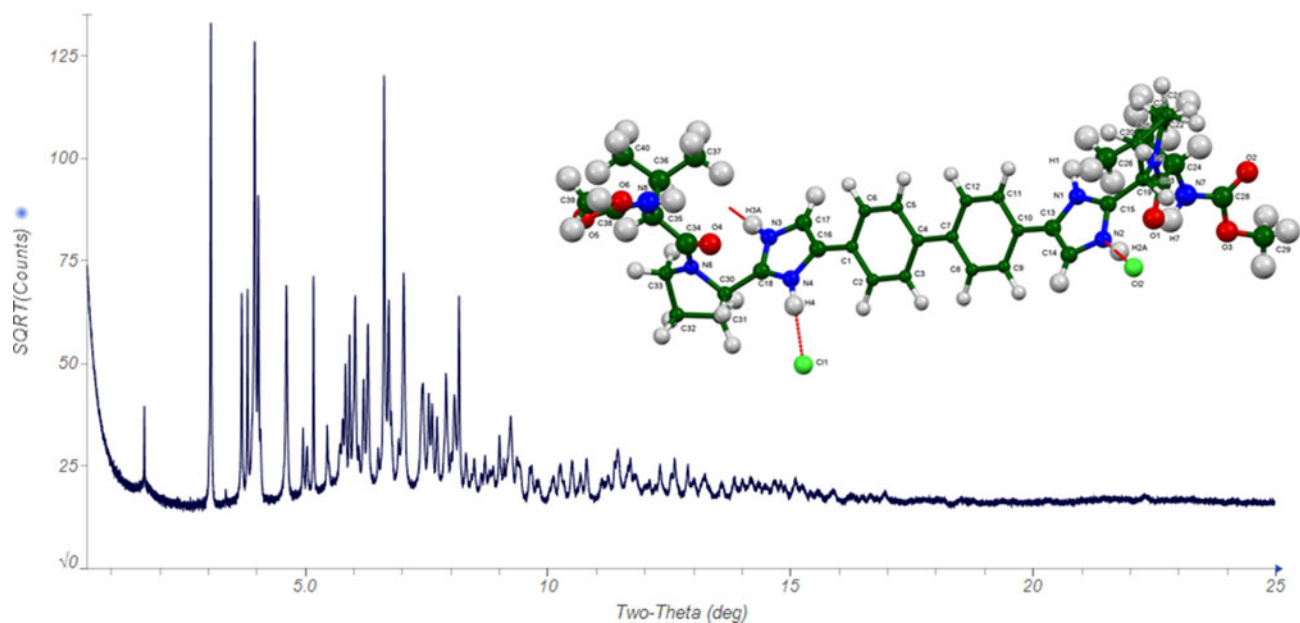


Figure 3. The powder diffraction pattern of daclatasvir dihydrochloride Form N-2 from this study (note that the vertical scale is the square root of the observed intensity) and the refined molecular structure (inset). The atoms are represented by 50% probability spheroids.

TABLE I. Hydrogen bonds (CRYSTAL14) in daclatasvir dihydrochloride, Form N-2

| H-bond | D–A (Å) | H...A (Å) | D...A (Å) | D–H...A (°) | Overlap (e) | <i>E</i> (kcal mol ⁻¹) |
|----------------|---------|--------------------|-----------|-------------|-------------|------------------------------------|
| N3–H3A...C11 | 1.048 | 2.025 | 3.053 | 166.2 | 0.113 | |
| N2–H2A...C12 | 1.044 | 2.036 | 3.030 | 158.3 | 0.102 | |
| N1–H1...C12 | 1.042 | 2.067 | 3.075 | 162.1 | 0.096 | |
| N4–H4...C11 | 1.042 | 2.069 | 3.057 | 157.3 | 0.093 | |
| C11–H11...C12 | 1.087 | 2.695 | 3.715 | 156.2 | 0.034 | |
| C2–H2...C11 | 1.087 | 2.845 | 3.817 | 148.9 | 0.028 | |
| C8–H8...C12 | 1.083 | 2.644 | 3.591 | 145.7 | 0.027 | |
| C5–H5...C11 | 1.084 | 2.688 | 3.651 | 147.7 | 0.027 | |
| C3–H3...C12 | 1.085 | 2.812 | 3.838 | 157.7 | 0.026 | |
| C33–H33A...C11 | 1.095 | 2.723 | 3.663 | 143.6 | 0.025 | |
| C12–H12...C11 | 1.085 | 3.089 | 4.064 | 149.9 | 0.016 | |
| C20–H20A...C12 | 1.094 | 3.082 | 3.890 | 131.1 | 0.012 | |
| C36–H36...C11 | 1.096 | 3.160 | 4.073 | 141.2 | 0.010 | |
| N8–H8A...O4 | 1.017 | 2.213 ^a | 2.627 | 102.4 | 0.025 | 3.6 |
| N7–H7...O1 | 1.015 | 2.263 ^a | 2.627 | 99.3 | 0.024 | 3.6 |
| N8–H8A...O3 | 1.017 | 2.321 | 3.298 | 160.6 | 0.022 | 3.4 |
| N7–H7...O6 | 1.015 | 2.281 | 3.209 | 151.4 | 0.022 | 3.4 |
| C21–H21B...O5 | 1.093 | 2.514 | 3.409 | 138.3 | 0.016 | |
| C24–H24...O2 | 1.094 | 2.408 ^a | 2.870 | 103.6 | 0.015 | |
| C35–H35...O5 | 1.093 | 2.423 ^a | 2.879 | 103.3 | 0.015 | |
| C27–H27C...O1 | 1.094 | 2.600 | 3.665 | 164.2 | 0.014 | |
| C32–H32B...O2 | 1.093 | 2.594 | 3.468 | 136.4 | 0.013 | |
| C19–H19...O5 | 1.096 | 2.511 | 3.351 | 132.6 | 0.012 | |
| C39–H39B...O1 | 1.088 | 2.538 | 3.387 | 134.1 | 0.012 | |
| C30–H30...O2 | 1.094 | 2.581 | 3.377 | 128.9 | 0.011 | |
| C29–H29B...O4 | 1.087 | 2.428 | 3.200 | 126.8 | 0.011 | |

^aIntramolecular.

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CONFLICTS OF INTEREST

The authors have no conflicts of interest to declare.

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