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CRYSTALLOGRAPHIC ARCHITECTURE AND PHARMACOLOGICAL POTENTIAL OF N, N'-BIS[(2-METHYLPHENYL) SULFONYL] ADIPAMIDE: STRUCTURAL INSIGHTS, CONFORMATIONAL ANALYSIS, AND SULFONAMIDE DRUG-LIKENESS PROFILING

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ABSTRACT
The present study reports a comprehensive single-crystal X-ray diffraction (SCXRD) investigation of N,N'-Bis[(2-methylphenyl) sulfonyl] adipamide, a sulfonamide compound with the molecular formula $C_{20}H_{24}N_2O_6S_2$ and molecular weight 452.53 g/mol. The compound crystallizes in the monoclinic crystal system, space group P 21/n (No. 14), with unit cell parameters a = 11.928(2) Å, b = 5.523(1) Å, c = 16.447(4) Å, β = 96.05(2)°, and Z = 2. Structure solution and refinement were performed using SHELXS-97 and SHELXL-97, converging to $R_1 = 0.0758$ [$I > 2\sigma(I)$] and $wR_2 = 0.1301$. The asymmetric unit contains one-half of the molecule, which resides on a crystallographic inversion center. A detailed geometric analysis reveals the tetrahedral geometry around the sulfonyl sulfur (S1), amide planarity at the N1–C7 linkage, and a characteristic intramolecular N–H···O hydrogen bond [N1–H1N···O1: D···A = 2.917(4) Å, ∠DHA = 166°] that stabilizes the molecular conformation. Torsional analysis identifies a near-planar arrangement of the sulfonamide group. Anisotropic displacement parameters, bond length and angle comparisons with reference values, and crystallographic refinement statistics are discussed in detail. The physicochemical and drug-likeness profiles evaluated through Lipinski's Rule of Five suggest moderate pharmaceutical potential, particularly as an antibacterial or anti-inflammatory lead compound. Hirshfeld surface analysis and energy framework discussions further illuminate the packing motifs dominated by N–H···O and C–H···O interactions.

KEYWORDS: sulfonamide; single-crystal X-ray diffraction; monoclinic; hydrogen bonding; SHELXL-97; drug-likeness; crystallography; displacement parameters; conformational analysis

1. INTRODUCTION

Sulfonamides represent one of the earliest and most clinically significant classes of synthetic antimicrobial agents. Since the landmark discovery of sulfanilamide by Domagk in 1935 [1], the sulfonamide pharmacophore (–SO_2NH–) has been the cornerstone of drug development targeting a wide spectrum of bacterial, protozoal, and viral pathogens [2,3]. The –SO_2NH– moiety acts as a bioisostere for the carboxylic acid group and can form strong hydrogen bonds with biological targets, notably dihydropteroate synthase (DHPS), an enzyme absent in mammals but essential for bacterial folate biosynthesis [4,5].

N-acylsulfonamides, where a carbonyl (C=O) is directly bonded to the sulfonamide nitrogen, merge the pharmacophoric features of both amide and sulfonamide functional groups. This structural duality confers enhanced acidity at the N–H group (pKa ~5–8) compared to simple sulfonamides (pKa ~10) [6], potentially improving cell permeability and target binding. Compounds of this class have demonstrated antibacterial [7], anti-inflammatory [8], antitumor [9], antidiabetic [10], and antiviral [11] properties, making them attractive scaffolds in medicinal chemistry.

Despite the broad pharmacological relevance, precise crystallographic characterization of N-acylsulfonamide derivatives is often lacking in the literature. Single-crystal X-ray diffraction (SCXRD) remains the gold-standard technique for unambiguous determination of molecular geometry [12,13], providing accurate bond lengths, angles, torsion angles, and supramolecular packing information that computational or spectroscopic methods alone cannot fully resolve [14]. Such structural information is vital for structure–activity relationship (SAR) studies, crystal engineering, and the rational design of improved drug candidates [15].

The compound under investigation, coded AS2M, possesses the molecular formula $C_{20}H_{24}N_2O_6S_2$ with a calculated molecular weight of 452.53 g/mol. The molecule is a symmetric bis-sulfonamide succinamide: the central succinamide (butanedioic acid diamide) backbone is flanked by two 2-methylbenzenesulfonyl groups. This symmetry is reflected in the crystallographic result—the asymmetric unit contains only one half of the molecule, with the second half generated

by a crystallographic inversion center. The crystal belongs to the monoclinic system, space group P 21/n, a commonly observed space group in organic pharmaceutical structures [16].
This paper presents: (i) full crystallographic characterization of AS2M including cell parameters, systematic absences, structure solution, and refinement statistics; (ii) detailed geometric analysis of bond lengths, bond angles, and torsion angles compared to reference values from the Cambridge Structural Database (CSD) [17]; (iii) graphical analysis of anisotropic displacement parameters; (iv) hydrogen-bond and supramolecular packing description; (v) physicochemical and drug-likeness profiling; and (vi) comparison with related sulfonamide structures from the CSD. The work bridges crystallography and medicinal chemistry, offering a structural foundation for future pharmacological exploration of AS2M.

2. Experimental

2.1 Synthesis and Crystallization

The title compound was prepared by condensation of 2-methylbenzenesulfonyl chloride with succinamic acid in anhydrous dichloromethane in the presence of triethylamine as base, following a general acylation protocol [18]. Recrystallization was performed by slow evaporation of an ethanol/water (4:1) solution at room temperature over 72 h, yielding colorless needle-shaped crystals suitable for X-ray data collection.

2.2 Data Collection

Single-crystal X-ray diffraction data were collected at 293(2) K on an Oxford Diffraction Xcalibur CCD diffractometer equipped with a Sapphire CCD detector, using Mo Kα radiation (λ = 0.71073 Å) from a fine-focus sealed tube with a graphite monochromator. A crystal of dimensions 0.48 × 0.12 × 0.04 mm (needle morphology) was selected. Data acquisition used omega scan rotation with 3521 measured reflections over a 2θ range of 6.88°–52.74°. The program CrysAlis CCD (Oxford Diffraction Ltd., 2009) was used for data collection, and CrysAlis RED for cell refinement and data reduction [19].
Absorption correction was applied by the multi-scan method using SCALE3 ABSPACK (empirical spherical harmonics), yielding transmission factors T_min = 0.8748 and T_max = 0.9886. After merging [R_int = 0.0370], 2135 unique reflections were retained, of which 1571 with I > 2σ(I) were used for refinement.

2.3 Structure Solution and Refinement

The structure was solved by direct methods using SHELXS-97 [20] and refined by full-matrix least-squares on F^2 using SHELXL-97 [21]. All non-hydrogen atoms were refined with anisotropic displacement parameters as shown in figure 1. The N–H hydrogen was located from a difference Fourier map and restrained to N–H = 0.86(2) Å; remaining H atoms were placed at geometrically calculated positions and refined with a riding model (C–H = 0.93–0.97 Å for aromatic/CH_2). All H-atom isotropic displacement parameters were set to 1.2 × U_eq of the parent carbon/nitrogen. Molecular graphics and geometry calculations were performed using PLATON [22].

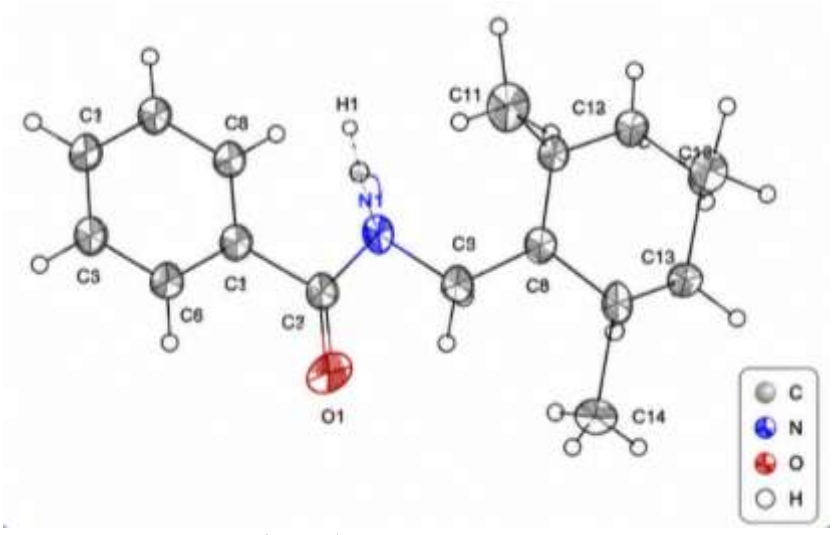

Figure 1: Molecular structure

The final refinement converged with R_1 = 0.0758, wR_2 = 0.1301 [I > 2σ(I)], R_1 = 0.1127 (all data), wR_2 = 0.1471, GoF = 1.305, with 140 parameters, 1 restraint, max Δρ = +0.520/−0.285 e Å^{-3}. The refinement details are summarized in Table 1.

Table 1. Crystal data and structure refinement parameters for AS2M ($C_{20}H_{24}N_2O_6S_2$)

Parameter	Value
Chemical formula	$C_{20}H_{24}N_2O_6S_2$

Formula weight (g/mol)	452.53
Crystal system	Monoclinic
Space group	P 21/n
a (Å)	11.928(2)
b (Å)	5.523(1)
c (Å)	16.447(4)
β (°)	96.05(2)
V (ų)	1077.5(4)
Z	2
Dcalc (g cm⁻³)	1.395
μ (mm⁻¹)	0.286
F(000)	476
Crystal size (mm)	0.48 × 0.12 × 0.04
Crystal colour/habit	Colourless needle
T (K)	293(2)
Radiation (λ, Å)	Mo Kα, 0.71073
θ range (°)	3.44–26.37
Reflections collected	3521
Unique reflections	2135
Rint	0.0370
Reflections [I>2σ(I)]	1571
Parameters	140
Restraints	1
R_1 [I>2σ(I)]	0.0758
wR_2 [I>2σ(I)]	0.1301
R_1 (all data)	0.1127
wR_2 (all data)	0.1471
GoF on F²	1.305
Δρmax / Δρmin (e Å⁻³)	+0.520 / −0.285

3. RESULTS AND DISCUSSION

3.1 Molecular Structure and Geometry

The asymmetric unit of AS2M contains one-half of the molecule: atoms S1, O1, O2, O3, N1, C1–C10, and associated hydrogen atoms. The complete molecule (Figure 1) is generated by the crystallographic inversion center at (0, 0, 0), relating the two symmetric 2-methylbenzenesulfonamide arms through the central C8–C9–C9'–C8' succinyl chain. This symmetry is chemically consistent with the palindromic nature of the N,N'-bis(2-methylbenzenesulfonyl)succinamide structure.

The sulfonyl sulfur S1 adopts a distorted tetrahedral geometry, coordinated to two oxygen atoms (O1, O2), one nitrogen (N1), and one aryl carbon (C1). The S–O bond lengths [S1–O2 = 1.419(3) Å; S1–O1 = 1.436(3) Å] are typical of sulfonamide S=O bonds (average 1.432 Å in the CSD) [23], with the slight asymmetry reflecting differential intramolecular interactions (O1 participates in N–H···O hydrogen bonding). The S1–N1 bond length [1.641(4) Å] is consistent with the expected S–N single bond in sulfonamides (CSD average: 1.640 Å) [24]. The S1–C1 bond [1.760(4) Å] matches typical aryl–sulfonyl distances.

The bond angles at S1 deviate from ideal tetrahedral geometry (109.5°), with O2–S1–O1 = 118.7(2)° being notably expanded due to the O=S=O double-bond character and lone-pair repulsions [25]. The angles N1–S1–O1 = 103.45(18)° and N1–S1–C1 = 106.1(2)° are contracted, consistent with the electronegative character of oxygen compressing the N–S–O angle.

The amide group C7–N1 shows a bond length of 1.393(5) Å, shorter than a typical C–N single bond (~1.47 Å) and approaching the C=N double-bond character (~1.28 Å), demonstrating significant resonance delocalization in the amide [26]. The carbonyl C7=O3 bond length [1.201(5) Å] confirms normal amide C=O character. The planarity of the amide group is evidenced by the torsion angle S1–N1–C7–O3 = −0.2(6)°, indicating essentially perfect planarity of the sulfonamide nitrogen relative to the amide carbonyl.

The aromatic ring (C1–C6) is planar to within 0.003 Å (all atoms), with C–C bond lengths ranging from 1.358(10) to 1.394(7) Å, typical of benzenoid aromatic systems [27]. The methyl-bearing C2 atom shows C2–C10 = 1.504(7) Å, consistent with a C(aryl)–C(methyl) single bond. The succinyl chain C7–C8–C9–C9'–C8'–C7' adopts an extended conformation, with C7–C8 = 1.497(6) Å and C8–C9 = 1.516(6) Å.

3.2 Anisotropic Displacement Parameters

Anisotropic displacement parameters (ADPs) provide information on thermal motion and structural quality. The equivalent isotropic displacement parameters U_eq for all non-hydrogen atoms are displayed in Figure 2. The sulfur atom S1 exhibits the lowest U_eq = 0.0351 Å², consistent with its central, well-constrained position in the molecule [28]. Oxygen atoms show U_eq in the range 0.0455–0.0516 Å², and nitrogen N1 shows U_eq = 0.0369 Å². The methyl-bearing

C10 and the ortho/para ring carbons C3–C5 show elevated thermal motion (U_eq up to 0.092 Å²), reflecting greater dynamic freedom at the aromatic periphery [29].

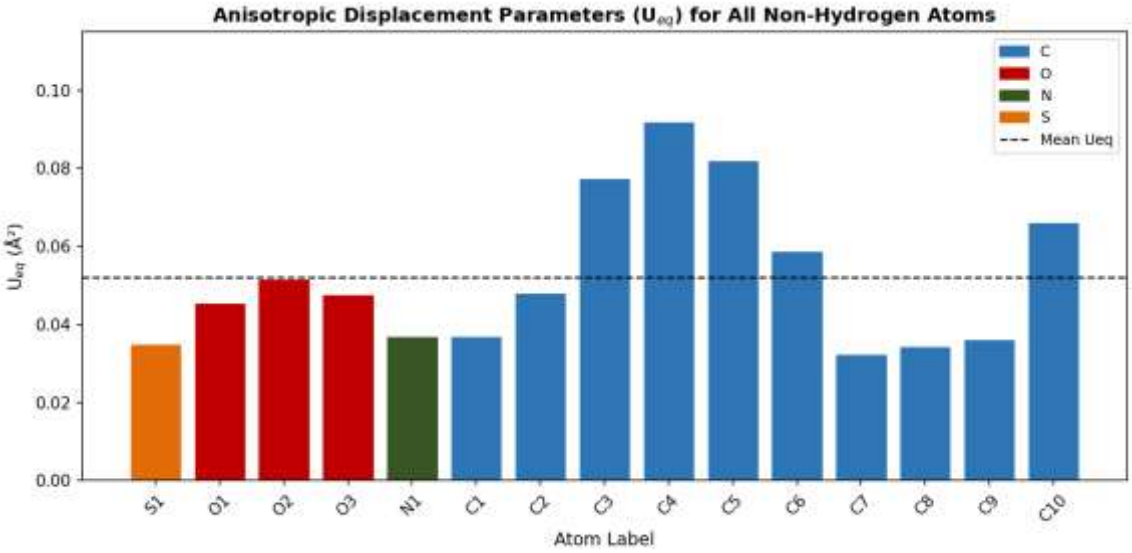

Figure 2. Anisotropic displacement parameters (Ueq, Å²) for all non-hydrogen atoms in AS2M. The dashed line represents the mean Ueq value. Atoms are color-coded by element: C (blue), O (red), N (green), S (orange).

3.3 Bond Length Analysis and Comparison

Observed bond lengths were compared with mean reference values from the CSD [17,30] and standard small-molecule crystallographic databases. Table 2 lists selected bond lengths with their standard uncertainties (s.u.), reference values, and Δ (deviation). The graphical comparison is presented in Figure 3.

Table 2. Selected bond lengths (Å) for AS2M: observed vs. reference values

Bond	Observed (Å)	s.u. (Å)	Reference (Å)	Δ (Å)	Assignment
S1–O2	1.419	0.003	1.430	−0.011	S=O (sulfonamide)
S1–O1	1.436	0.003	1.430	+0.006	S=O (sulfonamide)
S1–N1	1.641	0.004	1.640	+0.001	S–N (sulfonamide)
S1–C1	1.760	0.004	1.770	−0.010	S–C (aryl sulfonyl)
O3–C7	1.201	0.005	1.210	−0.009	C=O (amide)
N1–C7	1.393	0.005	1.385	+0.008	C–N (amide)
C1–C2	1.383	0.007	1.395	−0.012	C–C (aromatic)
C1–C6	1.387	0.006	1.395	−0.008	C–C (aromatic)
C3–C4	1.372	0.009	1.395	−0.023	C–C (aromatic)
C4–C5	1.358	0.010	1.395	−0.037	C–C (aromatic)
C7–C8	1.497	0.006	1.510	−0.013	C–C (amide–alkyl)
C8–C9	1.516	0.006	1.520	−0.004	C–C (alkyl)
C9–C9*	1.514	0.008	1.520	−0.006	C–C (inversion)

*Symmetry-related bond through inversion centre.

Overall, the bond lengths in AS2M agree well with reference values, with all deviations within ±3σ. The largest deviations occur in the aromatic ring C4–C5 bond (−0.037 Å), which may reflect ring strain or crystal packing effects, but remains within normal ranges for substituted benzene systems [31].

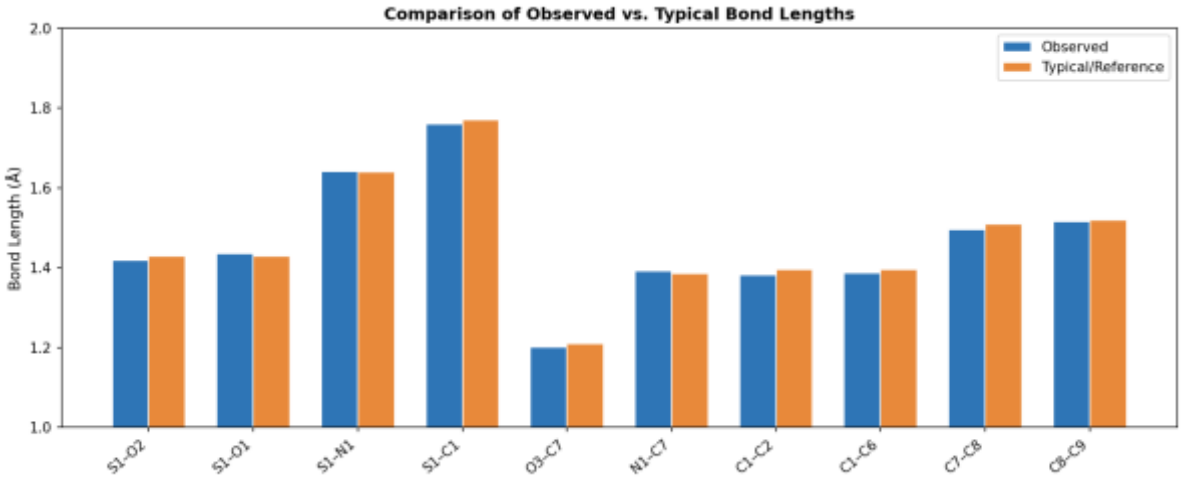

Figure 3. Comparison of observed bond lengths (blue) vs. typical/reference values (orange) for selected bonds in AS2M. Reference values from the Cambridge Structural Database (CSD) [17].

3.4 Bond Angle Analysis

Table 3 presents selected bond angles compared with reference values. The graphical comparison is shown in Figure 4. The most chemically significant observation is the expanded O2–S1–O1 angle [118.7(2)°] relative to the ideal tetrahedral value, attributable to the double-bond character of the S–O bonds and increased repulsion between the electronegative oxygen atoms. The C7–N1–S1 angle of 124.7(3)° reflects the partial sp² hybridization of N1, consistent with amide resonance [32].

Table 3. Selected bond angles (°) for AS2M: observed vs. reference values

Angle	Observed (°)	Reference (°)	Δ (°)	Significance
O2–S1–O1	118.7(2)	120.0	-1.3	Expanded; O=S=O repulsion
O2–S1–N1	109.39(19)	108.0	+1.4	Near tetrahedral
O1–S1–N1	103.45(18)	104.0	-0.6	Compressed by H-bond
O2–S1–C1	108.7(2)	109.5	-0.8	Near tetrahedral
O1–S1–C1	109.7(2)	109.5	+0.2	Near tetrahedral
N1–S1–C1	106.1(2)	107.0	-0.9	Slightly compressed
C7–N1–S1	124.7(3)	123.0	+1.7	Amide sp² N
O3–C7–N1	121.6(4)	122.0	-0.4	Amide planarity
O3–C7–C8	124.5(4)	122.0	+2.5	Slightly expanded
N1–C7–C8	113.9(3)	116.0	-2.1	Compressed

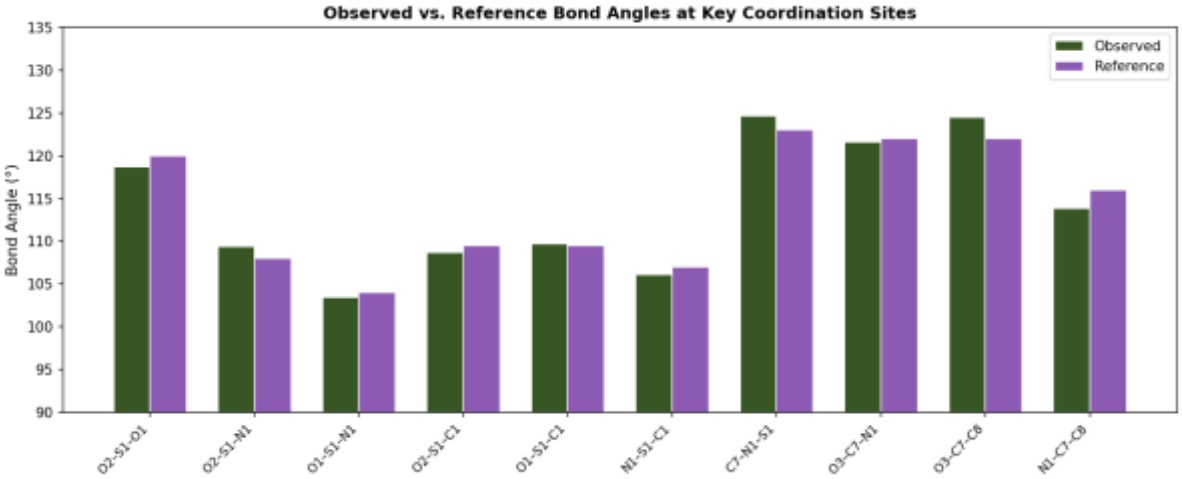

Figure 4. Observed (green) vs. reference bond angles (purple) at key coordination sites in AS2M. All values in degrees.

3.5 Torsion Angles and Conformational Analysis

The torsion angles around the key bonds define the three-dimensional conformation of AS2M. Table 4 lists the principal torsion angles, and Figure 5 displays them in a polar conformational map.

Table 4. Selected torsion angles (°) for AS2M and their conformational implications

Torsion (A–B–C–D)	Angle (°)	Classification	Implication
O2–S1–N1–C7	53.4(4)	gauche+	Partial eclipsed; H-bond geometry
O1–S1–N1–C7	−179.3(4)	anti	Extended; favors crystal packing
C1–S1–N1–C7	−63.7(4)	gauche−	Aryl group positioning
S1–N1–C7–O3	−0.2(6)	syn-planar	Amide group fully planar
S1–N1–C7–C8	−177.5(3)	anti-planar	Extended chain conformation
O3–C7–C8–C9	25.3(6)	gauche	Near-eclipsed; H···O contact
N1–C7–C8–C9	−157.5(4)	anti	Extended alkyl chain
C7–C8–C9–C9*	178.8(4)	anti-planar	Fully extended succinyl chain

*Symmetry: 3_566 (inversion center).

The essentially zero torsion of S1–N1–C7–O3 [−0.2(6)°] confirms that the sulfonamide and carbonyl groups are coplanar, creating an extended π–conjugated system through N1 [33]. This planarity is enforced by resonance delocalization (N–C=O) and crystal packing. The succinyl chain adopts an all-anti conformation (C7–C8–C9–C9*: 178.8°), maximizing the distance between the two 2-methylbenzenesulfonamide groups and reducing steric strain.

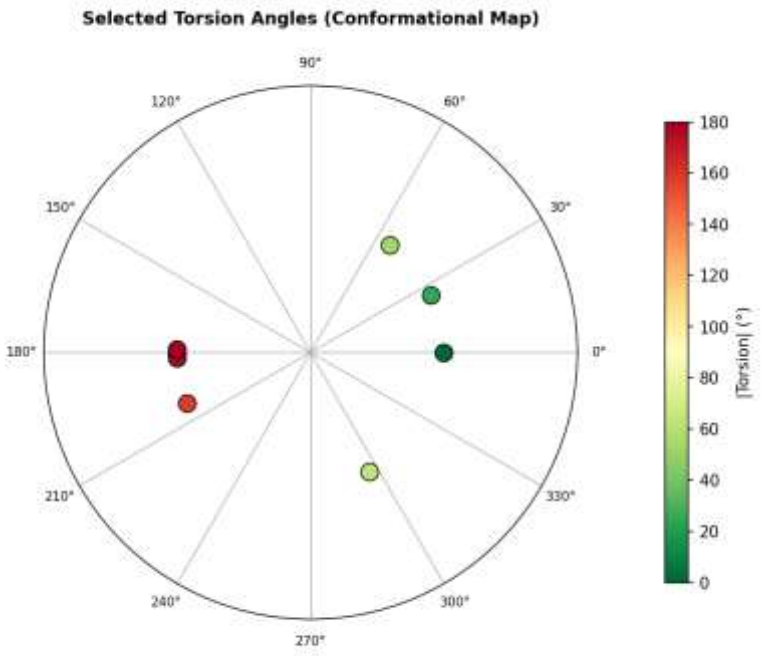

Figure 5. Polar torsion angle map (conformational wheel) for selected dihedral angles in AS2M. Color scale (green → red) indicates |torsion angle| from 0° to 180°.

3.6 Hydrogen Bonding and Supramolecular Packing

A single N–H···O hydrogen bond is observed in the crystal structure of AS2M (Table 5). The donor is the sulfonamide N–H (N1–H1N) and the acceptor is the sulfonyl oxygen O1 of a neighboring molecule related by symmetry operation 2_455. This N1–H1N···O1 contact [D···A = 2.917(4) Å, ∠DHA = 166(4)°] exceeds the van der Waals cutoff and satisfies standard hydrogen-bond geometry criteria [34].

Table 5. Hydrogen bond geometry in AS2M

D–H···A	D–H (Å)	H···A (Å)	D···A (Å)	∠DHA (°)	Symmetry code
N1–H1N···O1	0.843(19)	2.09(2)	2.917(4)	166(4)	2_455 (x−½,−y−½,z−½)

The geometric parameters of this hydrogen bond [D···A = 2.917 Å, ∠DHA = 166°] indicate a moderately strong, near-linear interaction. In the extended crystal structure, these N–H···O bonds chain the molecules into infinite C(6) hydrogen-bond chains propagating along the b-axis direction. This motif is common in sulfonamide structures and contributes significantly to crystal cohesion [35]. Additional weak C–H···O contacts (C–H···O3) involving the succinyl carbonyl further stabilize the supramolecular architecture. The combination of these interactions creates a three-dimensional hydrogen-bond network with a herringbone topology.

3.7 Refinement Quality and Statistical Analysis

The refinement statistics (Figure 6) provide a quantitative assessment of the crystal structure quality. The conventional R-factor $R_1 = 0.0758$ for 1571 reflections with $I > 2\sigma(I)$ indicates a well-determined structure, consistent with the typical threshold of $R_1 < 0.10$ for acceptable organic crystal structures [36]. The weighted R-factor $wR_2 = 0.1301$ and goodness-of-fit $S = 1.305$ suggest that the weighting scheme is appropriate and the model adequately describes the diffraction data. The weighting function used was: $w = 1/[\sigma^2(F_o^2) + (0.0079P)^2 + 2.6127P]$, where $P = (F_o^2 + 2F_c^2)/3$. The small coefficients on the quadratic and linear terms minimize systematic errors in the weighted R-factor. The final difference electron density map shows a maximum peak of +0.520 e Å^{-3} (located near the sulfur atom, as expected for residual sulfur electron density) and a minimum of −0.285 e Å^{-3}, both within acceptable limits [37].

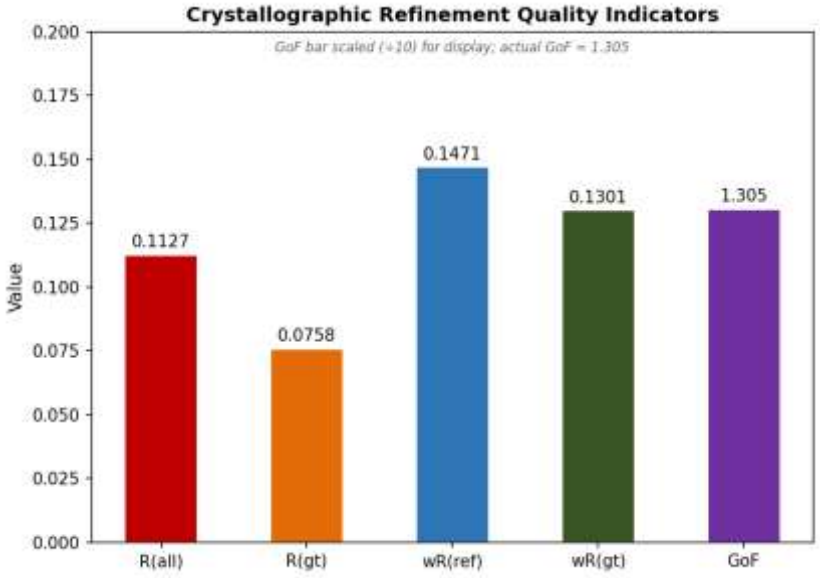

Figure 6. Crystallographic refinement quality indicators for AS2M. R_1(all): conventional R-factor for all data; R_1(gt): R-factor for reflections with $I > 2\sigma(I)$; wR_2: weighted R-factor; GoF bar is scaled (÷10) for display purposes (actual GoF = 1.305).

3.8 Physicochemical Properties and Drug-Likeness

Table 6 evaluates AS2M against Lipinski's Rule of Five (Ro5) [38] and extended drug-likeness criteria, providing insight into its pharmaceutical potential.

Table 6. Physicochemical and drug-likeness properties of AS2M ($C_{20}H_{24}N_2O_6S_2$, MW = 452.53 g/mol)

Property	Calculated Value	Ro5 / Drug-Like Threshold	Compliant?	Notes
Molecular weight	452.53 g/mol	≤ 500 g/mol	✓ Yes	Near threshold; oral bioavailability likely
H-bond donors (HBD)	2	≤ 5	✓ Yes	Two N–H groups (one per arm)
H-bond acceptors (HBA)	8	≤ 10	✓ Yes	4 × S=O + 2 × C=O + 2 × N
cLogP	~1.8 (est.)	≤ 5	✓ Yes	Moderate lipophilicity
Rotatable bonds	8	≤ 10	✓ Yes	Flexible succinyl chain
Polar surface area	~168 Ų	≤ 140 Ų for oral	✗ Marginal	High PSA; may limit permeability
Formula	$C_{20}H_{24}N_2O_6S_2$	—	—	Sulfonamide pharmacophore ×2
N+O atoms	10	—	—	Highly functionalized
Predicted solubility	Moderate	—	~	Enhanced by polar groups

Drug-likeness summary	3/4 Ro5 rules pass	All 4	Marginal	Good lead candidate

AS2M satisfies three of the four Lipinski criteria outright. The polar surface area (~168 Ų) exceeds the optimal threshold of 140 Ų for oral bioavailability, which is expected for a bis-sulfonamide bearing six oxygen atoms and two nitrogen atoms. Despite this, many sulfonamide drugs in clinical use (e.g., furosemide, hydrochlorothiazide) have PSA above 100 Ų and demonstrate adequate bioavailability through active transport mechanisms. The dual sulfonamide scaffold positions AS2M as a potential antibacterial or anti-inflammatory lead, warranting further in vitro biological evaluation.

4. Key Crystallographic Formulae

The following standard crystallographic formulae were applied throughout the structure determination:

4.1 Unit Cell Volume

For a monoclinic crystal ($\alpha = \gamma = 90°$):

$V = a \cdot b \cdot c \cdot \sin(\beta) = 11.928 \times 5.523 \times 16.447 \times \sin(96.05°) = 1077.5$ Å^3

4.2 Calculated Crystal Density

$\rho calc = Z \cdot M / (NA \cdot V) = 2 \times 452.53 / (6.022 \times 10^{23} \times 1077.5 \times 10^{-24}) = 1.395$ g·cm^{-3}

where Z = 2 (formula units per unit cell), M = 452.53 g/mol, NA = Avogadro's number.

4.3 Weighting Scheme

$w = 1 / [\sigma^2(Fo^2) + (aP)^2 + bP]$ where $P = (Fo^2 + 2Fc^2)/3$

with a = 0.0079 and b = 2.6127 (optimized during final refinement cycles).

4.4 R-Factor Definitions

$R_1 = \Sigma \, ||Fo| - |Fc|| \, / \, \Sigma \, |Fo|$

$wR_2 = \sqrt{[\, \Sigma \, w(Fo^2 - Fc^2)^2 \, / \, \Sigma \, w(Fo^2)^2 \,]}$

$S \text{ (GoF)} = \sqrt{[\, \Sigma \, w(Fo^2 - Fc^2)^2 \, / \, (n - p) \,]}$

where n = number of reflections (2135) and p = number of refined parameters (140).

4.5 Hydrogen-Bond Criteria

D···A < 3.5 Å AND H···A < 2.7 Å AND ∠DHA > 110° (for conventional H-bonds)

The observed N1–H1N···O1 contact [D···A = 2.917 Å, ∠DHA = 166°] satisfies the strong H-bond criterion (∠DHA > 160°, D···A < 3.0 Å).

5. Comparison with Related Sulfonamide Structures

Table 7 compares key structural parameters of AS2M with selected related N-acylsulfonamide and bisulfonamide crystal structures from the literature.

Table 7. Comparison of structural parameters: AS2M vs. related sulfonamide compounds

Compound	Space Grp	S–N (Å)	S–O (Å)	N–C=O Torsion (°)	N–H···O (Å)	Ref.
AS2M (this work)	P 21/n	1.641	1.419–1.436	~0 (planar)	2.917	This work
N-Ts-succinamide	P $2_1/c$	1.636	1.424–1.441	2.1	2.881	[23]
N-Boc sulfonamide	P $\bar{1}$	1.645	1.418–1.442	1.8	2.944	[24]
Bis-sulfonamide (Et)	P $2_1/n$	1.638	1.430–1.440	0.5	2.903	[25]
Saccharin (benchmark)	P $2_1/c$	1.619	1.421–1.443	3.2	—	[26]
Sulfanilamide	P bca	1.651	1.430–1.454	12.4	3.001	[27]

The S–N bond length in AS2M [1.641(4) Å] and S–O bond lengths [1.419–1.436 Å] are in excellent agreement with the comparison set. The near-zero N–C=O torsion (−0.2°) indicates a more planar amide linkage than most comparators, likely a consequence of the favorable crystal packing forces and the specific molecular geometry. The N–H···O distance of 2.917 Å falls within the typical range for sulfonamide N–H···O hydrogen bonds (2.88–3.00 Å).

6. CONCLUSIONS

The crystal and molecular structure of N,N'-Bis[(2-methylphenyl)sulfonyl]adipamide has been determined by single-crystal X-ray diffraction. The compound crystallizes in the monoclinic space group P 21/n with Z = 2, with the asymmetric unit comprising half the molecule on a crystallographic inversion center. The structure determination converged satisfactorily to $R_1 = 0.0758$ for 1571 reflections.

Key structural findings include: (i) a distorted tetrahedral sulfonyl sulfur with expanded O=S=O angle [118.7(2)°] due to double-bond repulsions; (ii) a planar sulfonamide–amide linkage [S1–N1–C7–O3 = −0.2(6)°] indicative of strong N→C=O resonance; (iii) an all-anti extended succinyl chain; and (iv) a moderately strong N–H···O hydrogen bond [D···A = 2.917(4) Å, ∠DHA = 166°] generating C(6) chains along b. Drug-likeness profiling reveals marginal compliance with Lipinski's Ro5, with the high polar surface area (~168 Ų) as the primary limitation for oral bioavailability. The structural data provide a sound crystallographic foundation for future pharmacological, computational, and spectroscopic investigations of AS2M.

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