N-Cycloamino substituent effects on the packing architecture of ortho-sulfanilamide molecular crystals and their in silico carbonic anhydrase II and IX inhibitory activities

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In the search for new ‘sulfa drugs’ with therapeutic properties, o-nitrosulfonamides and N-cycloamino-o-sulfanilamides were synthesized and characterized using techniques including 1H NMR, 13C NMR and FT–IR spectroscopy, and single-crystal X-ray diffraction (SC-XRD). The calculated density functional theory (DFT)-optimized geometry of the molecules showed similar conformations to those obtained by SC-XRD. Molecular docking of N-piperidinyl-o-sulfanilamide and N-indolinyl-o-sulfanilamide supports the notion that o-sulfanilamides are able to bind to human carbonic anhydrase II and IX inhibitors (hCA II and IX; PDB entries 4iwz and 5fl4). Hirshfeld surface analyses and DFT studies of three o-nitrosulfonamides [1-[(2-nitrophenyl)sulfonyl]pyrrolidine, C10H12N2O4S, 1, 1-[(2-nitrophenyl)sulfonyl]piperidine, C11H14N2O4S, 2, and 1-[(2-nitrophenyl)sulfonyl]-2,3-dihydro-1H-indole, C14H12N2O4S, 3] and three N-cycloamino-o-sulfanilamides [2-(pyrrolidine-1-sulfonyl)aniline, C10H14N2O2S, 4, 2-(piperidine-1-sulfonyl)aniline, C11H16N2O2S, 5, and 2-(2,3-dihydro-1H-indole-1-sulfonyl)aniline, C14H14N2O2S, 6] suggested that forces such as hydrogen bonding and π–π interactions hold molecules together and further showed that charge transfer could promote bioactivity and the ability to form biological interactions at the piperidinyl and phenyl moieties.

1. Introduction

Sulfanilamide (4-aminobenzenesulfonyamide) is aptly described as the antecedent of the group of therapeutics known as ‘sulfa drugs’, which ushered in the modern era of antibacterial chemotherapy (Ajani et al., 2012). Although it had been a component of a staple azo dye in the colour industry since the beginning of the 20th century, it did not gain prominence in medicine until the 1930s when Gerhard Domagk and co-workers patented Prontosil, A (Fig. 1), a sulfanilamide prodrug, which not only revolutionized the treatment of bacterial infections, but chemotherapy as a whole, and led to the development of other drugs for non-infectious diseases.

It has been established that the bacteriostatic properties of sulfanilamides (Fig. 1) are predicated based on two major motifs: the aryl amine (–NH2) and sulfonamide (–SO2NH2R) groups (Lesch, 2007). A free or hydrolysable substituted amino (–NHR) moiety that is para to the sulfonamido group has been reported to be crucial for antibacterial activity, whereas modification of the position to the ortho and/or meta position results in non-antibacterial activities (Ajani et al., 2012). The derivatization of the sulfanilamide group with
heterocycles has also produced more potent antibiotics (Ajani et al., 2012; Lesch, 2007). In addition, it has been long reported that no correlations exist between the toxicities and therapeutic efficiencies, as well as toxicities and solubilities, of the three isomers of sulfanilamide, as evidenced by the finding that even though meta-sulfanilamide C was the least toxic of the three, only para-sulfanilamide B possessed bacteriostatic activity (Laug & Morris, 1939). Notably, the inhibitions of the Helicobacter pylori α-class carbonic anhydrase (hpCA) (Nishimori et al., 2006) and tumour-associated transmembrane carbonic anhydrase IX (CA IX) (Vullo et al., 2003) isozymes have been observed with ortho-sulfanilamide D (orthanilamide). Sulfonamides E are derivatives of sulfanilamide and remain an important class of drugs, with antibacterial and non-antibacterial potencies, such as diuretic, antimicrobial, antiepileptic, antileprotic, antimalarial, hypoglycemic, antiretroviral, antithyroid and anti-inflammatory activities (Gül et al., 2016; Henry, 1943; Casini et al., 2002; Mohan et al., 2006; Alex & Storer, 2010).

They also inhibit carbonic anhydrase (Gül et al., 2016; Ghorab et al., 2014; Nocentini et al., 2016) and have been reported to show in vivo and/or in vitro antitumour activities (Boyland, 1946). Many of these sulfonamide-based (sulfa) drugs, reported to be in clinical trials, are devoid of the side effects plaguing most of the current pharmacological agents (Casini et al., 2002; Owa et al., 2002; Lavanya, 2017; Andreucci et al., 2019).

The identification of pharmacologically active moieties in model molecules and lead candidates of physiological significance from a vast array of substances, with the potential of further optimization, is a crucial facet of rational drug design and discovery (Voronin et al., 2020). The process of optimization, it must be noted, typically involves structure–activity relationship studies that facilitate the selection of molecules with optimal receptor affinities (Bloom & Laubach, 1962; Kalgotkar et al., 2010; Sly & Hu, 1995; Lehtonen et al., 2004; Żołnowska et al., 2014; Thiry et al., 2008; Angelī et al., 2020; Güzel-Akdemir et al., 2015; Rutkauskas et al., 2014; Congiu et al., 2014; Temperini et al., 2008a,b; Chiche et al., 2010; Türeci et al., 1998; PDB, http://www.rcsb.org/pdb; Berman et al., 2000).

In continuation of the design of potential ‘sulfa drugs’, we report the synthesis, structural and theoretical studies, and docking application of the o-nitrosulfonamides 1-[(2-nitrophenyl)sulfonyl]pyrrolidine, 1, 1-[(2-nitrophenyl)sulfonyl]piperidine, 2, and 1-[(2-nitrophenyl)sulfonyl]-2,3-dihydro-1H-indole, 3, and the N-cycloamino-o-sulfanilamides 2-(pyrrolidine-1-sulfonyl)aniline, 4, 2-(piperidine-1-sulfonyl)aniline, 5, and 2-(2,3-dihydro-1H-indole-1-sulfonyl)aniline, 6. The crystal structures, density functional theory (DFT) studies, Hirshfeld surface analysis, molecular electrostatic potential and electronic properties of the title sulfonamides and sulfanilamides (1–6) have been discussed. Molecular docking experiments with carbonic anhydrase II (PDB entry 4iwz) and IX (5fl4) active sites were conducted in order to predict their binding interactions with 1–6 (Scheme 1).

2. Experimental

2.1. Instruments and measurements

All reagents were purchased from Millipore Sigma (Germany and South Africa) and were used without purification. The melting points were determined on an Electrothermal digital melting-point apparatus and are uncorrected. Reac-

![Figure 1](https://via.placeholder.com/150)

Figure 1
Sulfanilamides and some prodrugs.
tions were monitored by thin-layer chromatography (TLC) on Merck silica gel 60 F254 precoated plates using a dichloromethane/n-hexane (2 or 1:4:1 v/v) solvent system visualized under a UV lamp (254 nm). Column chromatography was performed with silica gel (70–230 mesh ASTM) and mobile phases were as indicated. Sample crystallization was achieved by the slow evaporation of the indicated solvent systems at ambient temperature. IR spectra were obtained using a Bruker Tensor 27 platinum ATR–FT–IR spectrometer. The ATR–FT–IR spectra were acquired in a single mode with a resolution of 4 cm⁻¹ over 32 scans, in the region 4000–650 cm⁻¹. ¹H and ¹³C NMR spectra were recorded, in CDCl₃, on a Bruker 400 MHz spectrometer. Chemical shift (δ) values were measured in parts per million (ppm) downfield from tetramethylsilane (TMS) and coupling constants (J) are reported in hertz (Hz). Theoretical studies were performed for the compounds and, in each case, their SC-XRD structures were used for optimization and global reactivity descriptor (GRD) calculations.

2.2. Synthesis and crystallization

2.2.1. Synthesis of N-cycloamino-o-nitrobenzenesulfonylamides 1–3. o-Nitrobenzenesulfonyl chloride (1.00 mmol) was added slowly to a stirring dried toluene solution (30 ml) of the cycloamino (2.20 mmol) at ambient temperature and stirred for 12 h, monitored by TLC. The reaction mixture was then diluted with dichloromethane (30 ml) and washed with distilled water (3 × 10 ml). The organic layer was separated, dried over anhydrous sodium sulfate, filtered and concentrated to an oil, which was purified by column chromatography on silica gel (dichloromethane/n-hexane, 2:1 v/v). Crystals were obtained by the slow solvent evaporation of the requisite eluates at ambient temperature, except for 5 which was recrystallized from dichloromethane, slowly evaporated and filtered to give single crystals.

2.2.1.1. N-Pyrrolidinyl-o-nitrobenzenesulfonylamide. 1. o-Nitrobenzenesulfonyl chloride (3.00 g, 13.54 mmol) and pyrrolidine (3.84 g, 3.4 ml, 39.79 mmol). Yellow crystals (3.11 g, 75.5%). Rₚ = 0.79 (CH₂Cl₂/n-hexane, 2:1 v/v); m.p. 81.7–81.9°C. IR (Bruker, ATR, v, cm⁻¹): 3077 (aryl C—H str.), 2947 (sp³C—H str.), 1597 (aryl C=C str.), 1543 (aryl C—NO₂ str.), 1344 (aryl C—NO₂ str.), 1342 (aryl SO₂—N str.), 1163 (sym SO₂—N str.), 1078 (sym C—NO₂ str.), 878 (sym C—NO₂ str.). ¹H NMR (Bruker, 400 MHz, CDCl₃, δH, ppm): 7.96 (1H, J = 4 Hz, ArH), 7.70 (2H, J = 4 Hz, ArH), 7.59 (1H, d, J = 8 Hz, ArH), 3.26–3.24 (4H, m, —CH₂NCH₂—), 1.54–1.54 (2H, m, —CH₂CH₂—). ¹³C NMR (Bruker, 100 MHz, CDCl₃, δC, ppm): 148.5, 133.6, 131.6, 131.5, 130.8, 123.5 (ArH), 47.0 (—CH₂NCH₂—), 25.4 (—CH₂CH₂—), 23.5 (—CH₂CH₂—).

2.2.1.3. N-Indolylno-o-nitrobenzenesulfonylamide. 3. o-Nitrobenzenesulfonyl chloride (3.00 g, 13.54 mmol) and indoline (3.55 g, 3.34 ml, 39.79 mmol). Yellow crystals (3.11 g, 75.5%). Rₚ = 0.79 (CH₂Cl₂/n-hexane, 2:1 v/v); m.p. 81.7–81.9°C. IR (Bruker, ATR, v, cm⁻¹): 3077 (aryl C—H str.), 2947 (sp³C—H str.), 1594 (aryl C=C str.), 1543 (aryl C—NO₂ str.), 1355 (sym SO₂—N str.), 1161 (sym SO₂—N str.), 1051 (C—N str.). ¹H NMR (Bruker, 400 MHz, CDCl₃, δH, ppm): 7.95 (1H, d, J = 8 Hz, ArH), 7.71 (1H, t, J = 8 Hz, ArH), 7.62 (2H, t, J = 8 Hz, ArH), 7.48 (1H, d, J = 8 Hz, ArH), 7.21 (2H, t, J = 8 Hz, ArH), 7.05 (1H, t, J = 8 Hz, ArH), 4.17 (2H, t, J = 8 Hz, –NCH₂—), 3.10 (2H, t, J = 8 Hz, –NCH₂—). ¹³C NMR (Bruker, 100 MHz, CDCl₃, δC, ppm): 148.4, 141.1, 134.1, 131.8, 131.7, 131.6, 130.2, 127.8, 125.5, 124.3, 124.2, 114.5 (ArH), 50.5 (–NCH₂—), 28.0 (–NCH₂—).

2.2.2. N-Cycloamino-o-sulfanilamides 4–6. An evacuated nitrogen-gas-filled round-bottomed flask was charged with N-cycloamino-o-nitrobenzenesulfonylamides 1–3 (15.63 mmol) dissolved in ethanol (30 ml), at ambient temperature, and 10% palladium-on-charcoal catalyst (3.35 mol%) was added, with stirring. Hydrogen gas was then introduced via a balloon and stirring continued at ambient temperature for 12 h. The reaction mixture was filtered and the solvent was evaporated in vacuo. The resulting residue was extracted into dichloromethane (50 ml), dried over anhydrous sodium sulfate, filtered and concentrated under reduced pressure to afford an oil, which was purified on a silica-gel column using dichloromethane/n-hexane (2:1 v/v). Crystals were obtained via slow solvent evaporation of the eluates at ambient temperature.

2.2.2.1. N-Pyrrolidinyl-o-sulfanilamide. 4. N-Pyrrolidinyl-o-nitrobenzenesulfonylamide 1 (4.00 g, 15.63 mmol) with 10% palladium-on-charcoal catalyst (0.56 g, 5.26 mmol). Off-white crystals (2.90 g, 82%). Rₚ = 0.44 (CH₂Cl₂/n-hexane, 2:1 v/v); m.p. 75.2–75.4°C. IR (Bruker, ATR, v, cm⁻¹): 3464, 3363 (N—H str.), 3077 (aryl C—H str.), 2976 (sp³C—H str.), 1594 (aryl C=C str.), 1543 (aryl C—NO₂ str.), 1355 (sym SO₂—N str.), 1161 (sym SO₂—N str.), 1051 (C—N str.). ¹H NMR (Bruker, 400 MHz, CDCl₃, δH, ppm): 7.94 (1H, d, J = 8 Hz, ArH), 7.59 (1H, d, J = 8 Hz, ArH), 7.59 (1H, d, J = 8 Hz, ArH), 3.26–3.24 (4H, m, —CH₂NCH₂—), 1.54–1.54 (2H, m, —CH₂CH₂—). ¹³C NMR (Bruker, 100 MHz, CDCl₃, δC, ppm): 148.4, 141.1, 134.1, 131.8, 131.7, 131.6, 130.2, 127.8, 125.5, 124.3, 124.2, 114.5 (ArH), 50.5 (–NCH₂—), 28.0 (–NCH₂—).

2.2.2.2. N-Piperidinyl-o-sulfanilamide. 5. N-Piperidinyl-o-nitrobenzenesulfonylamide 2 (4.00 g, 18.81 mmol) with 10% palladium-on-charcoal catalyst (0.53 g, 4.98 mmol). Off-white crystals (3.06 g, 86%). Rₚ = 0.57 (CH₂Cl₂/n-hexane, 2:1 v/v); m.p. 76.6–76.8°C. IR (Bruker, ATR, v, cm⁻¹): 3487, 3383 (N—H str.), 3072 (aryl C—H str.), 2974 (sp³C—H str.), 1606 (aryl C=C str.), 1309 (aryl SO₂—N str.), 1186 (sym SO₂—N str.), 1336 (C—N str.). ¹H NMR (Bruker, 400 MHz, CDCl₃, δH, ppm): 7.94 (1H, d, J = 4 Hz, ArH), 7.70 (2H, t, J = 4 Hz, ArH), 7.59 (1H, d, J = 8 Hz, ArH), 3.26–3.24 (4H, m, —CH₂NCH₂—), 1.54–1.54 (2H, m, —CH₂CH₂—). ¹³C NMR (Bruker, 100 MHz, CDCl₃, δC, ppm): 148.4, 141.0, 134.0, 130.2, 119.1, 117.6, 117.1 (ArH), 47.8 (–CH₂NCH₂—), 25.2 (—CH₂CH₂—).
ppm): 7.48 (1H, d, J = 8 Hz, ArH), 7.21 (1H, t, J = 8 Hz, ArH), 6.67 (1H, d, J = 8 Hz, ArH), 6.64 (1H, d, J = 8 Hz, ArH), 4.99 (2H, s, NH), 3.03–3.00 (4H, m, –CH2NCH2–), 1.39–1.37 (2H, m, –CH2CH2CH2–). 13C NMR (Bruker, 100 MHz, CDCl3, δC ppm): 146.4, 142.3, 134.4, 132.1, 129.8, 127.6, 125.1, 123.7, 119.4, 117.7, 117.3, 115.1 (ArH), 50.0 (–NCH2–), 28.1 (–NCH2–). Reaction synthesis of nitrosulfo-namides 3–6 and amino-sulfonamides 4–6 are presented in Scheme S1 in the supporting information. The FT–IR, MS and 1H/13C NMR spectra of compounds 1–6 are also presented in the supporting information.

2.3. Docking studies

2.3.1. Preparation of the ligands for docking. The X-ray crystal structures of synthesized compounds 1–6 (CIF files) were imported directly into the Schrödinger Suite (Schrödinger, 2022) for preparation. The reference drugs N-(5-sulfamoyl-1,3,4-thiadiazol-2-yl)-2-(thiophen-2-yl)acetamide (A) and 5-[1-(naphthalen-1-yl)-1,2,3-triazol-4-yl]thiophene-2-sulfonamide (B) were based on chemical structures downloaded from the PubChem (https://pubchem.ncbi.nlm.nih.gov/) website in SDF format. A and B were used as reference compounds because they are natural ligands in the crystalline state of 5Fl4 and 4iwx. The Ligprep module of the molecular modelling platform of the Schrödinger Suite (Schrödinger, 2022) was then used to prepare the imported structures by assigning bond lengths, bond angles, generating possible ionization states at pH 7 using Epik and finally to optimize using the OPLS4 force field (Nainwal et al., 2018).

2.3.2. Protein preparation. The protein structures of 4iwx and 5Fl4, with resolutions of 1.60 and 1.82 Å, respectively, were downloaded from the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB). Retrieved crystal coordinates were prepared in the ‘Protein Preparation Wizard’ of the Schrödinger Suite (Schrödinger, 2022), with default parameters of assigning bond orders, optimizing and minimization using OPLS4. A receptor grid generation module was applied to the prepared proteins by selecting the corresponding cocrystallized ligand to define the binding site. A default parameter for the radii of van der Waals having a scaling factor of 1 Å with a partial charge cut-off of 0.25 Å was used (Panwar & Singh, 2021; Yang et al., 2022).

2.3.3. Molecular docking. Docking calculations were executed in the extra precision (XP) mode of the Glide module in the molecular modelling platform of the Schrödinger Suite (Schrödinger, 2022). The complexes with the highest negative docking scores have better binding towards the respective proteins 4iwx and 5Fl4. Docking calculations of the synthesized N-cycloamino derivatives against the hCA II (PDB entry 5Fl4) and XII (4iwx) isoforms will provide a selectivity profile that may be interesting for the development of novel anticancer agents with limited side effects. The hCA II (PDB entry 5Fl4) and XII (4iwx) carbonic anhydrase isoforms have recently emerged as excellent targets for the design of novel therapeutic strategies for cancer, due to their involvement in the survival of tumour cells, as well as in the insurmountable resistance of classical anticancer protocols (Milite et al., 2019).

2.4. DFT calculations

Theoretical studies were performed for compounds 1–6 whereupon the SC-XRD structures of the compounds were used for optimization and global reactivity descriptor (GRD) calculations. Computational studies and molecular electrostatic potential (MEP) for 1–6 were carried out using the GAUSSIAN16 (https://www.chemcraftprog.com/). The calculations were performed using the standard hybrid density functional method (B3LYP) with a basis set of the 6-311+G**(p,d) level (Becke, 1993). Optimized molecules were obtained with the Chemcraft visualizazion program.

2.5. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 1. Carbon-bound H atoms were added in idealized geometrical positions in a riding model. Nitrogen-bound H atoms were located in a difference map and refined freely.

3. Results and discussion

3.1. Chemistry

The N-cycloamino-o-sulfanilamides 4–6 were prepared via a two-step reaction, starting from the condensation reaction of 3-nitrobenzenesulfonyl chloride with alicyclic amines in toluene, at ambient temperature, to afford N-cycloamino-o-nitrobenzenesulfonylamide adducts 1–3 (Scheme S1 in the supporting information). The use of toluene as a nonpolar reaction medium was, amongst other reasons, to drive the forward reaction. In the second step, adducts 1–3 were hydrogenated with hydrogen gas, in ethanol at ambient temperature, in the presence of 10% palladium-on-activated charcoal catalyst to give the target N-cycloamino-o-sulfanilamides 4–6 in 72–86% yield. The reactions were monitored by TLC.
All the compounds synthesized were characterized by their melting points and IR, $^1$H/$^{13}$C NMR and MS spectra. In the IR spectra of o-nitrosulfonamide adducts 1-3, the strong absorption bands observed at 1355–1342 and 1171–1161 cm$^{-1}$ were ascribed to the asymmetric and symmetric stretching frequencies, respectively, of the SO$_2$–N moiety, thereby
Table 2
Hydrogen-bond, C—H···π(π) ring and π–π stacking interaction geometry (Å, °) for the crystal structures of p-sulfanilamide (B), o-sulfanilamide (D), o-nitrosulfonamides 1-3 and N-cycloamino-o-sulfanilamides 4-6.

| Compound | Interaction | D—H | H···A | D··A | D—H···A | π–π |
|----------|-------------|------|-------|------|---------|-----|
| 1        | C11—H11A···O1i | 0.99 | 2.56 | 3.398 (7) | 143 |
|          | C11—H11B···O4 | 0.99 | 2.48 | 3.093 (9) | 120 |
|          | C25—H25···O4i | 0.95 | 2.54 | 3.240 (2) | 151 |
|          | C25—H25···O1ii | 0.95 | 2.47 | 3.229 (2) | 137 |
|          | C26—H26···O2 | 0.95 | 2.49 | 2.860 (2) | 103 |
|          | C26—H26···O3v | 0.95 | 2.56 | 3.467 (2) | 160 |
| 2        | C11—H11A···O2 | 0.97 | 2.48 | 2.907 (2) | 107 |
|          | C11—H11A···O2ii | 0.97 | 2.59 | 3.476 (2) | 152 |
|          | C15—H15B···O1 | 0.97 | 2.51 | 2.943 (2) | 107 |
|          | C25—H25···O2ii | 0.93 | 2.57 | 3.334 (2) | 140 |
|          | C26—H26···O1 | 0.93 | 2.53 | 2.877 (2) | 103 |
| 3        | C16—H16···O2 | 0.93 | 2.41 | 2.975 (2) | 119 |
|          | C16—H16···O2vi | 0.93 | 2.55 | 3.195 (2) | 127 |
|          | C23—H23···O1vi | 0.93 | 2.30 | 3.086 (3) | 142 |
|          | C26—H26···N1 | 0.93 | 2.60 | 2.983 (2) | 105 |
|          | Cg1···Cg22 | 3.5967 (11) |
|          | Cg2···Cg11 | 3.6968 (11) |

N-Cycloamino-o-sulfanilamides

| 4        | N1—H12C···O21 | 0.78 (3) | 2.40 (3) | 3.121 (3) | 155 (3) |
|          | N12—H12D···O11 | 0.84 (3) | 2.10 (3) | 2.776 (3) | 138 (3) |
|          | N22—H21C···O1i | 0.82 (3) | 2.30 (3) | 3.106 (2) | 168 (2) |
|          | N22—H21D···O21 | 0.87 (2) | 2.07 (2) | 2.783 (2) | 139 (2) |
|          | C114—H114···O22viii | 0.93 | 2.59 | 3.391 (3) | 144 |
|          | C116—H116···O12 | 0.93 | 2.46 | 2.851 (2) | 105 |
|          | C121—H121···O22' | 0.93 | 2.52 | 2.897 (2) | 105 |
| 5        | N1—H14A···O1x | 0.836 (19) | 2.496 (19) | 3.2999 (16) | 161.8 (16) |
|          | N1—H18B···O2 | 0.852 (16) | 2.156 (16) | 2.8240 (17) | 135.1 (14) |
|          | C16—H16···O1 | 0.95 | 2.48 | 2.8774 (15) | 105 |
|          | C16—H16···O2x | 0.95 | 2.48 | 3.2577 (15) | 139 |
|          | C21—H21A···O1 | 0.99 | 2.55 | 2.9635 (15) | 105 |
|          | C25—H25B···O2 | 0.99 | 2.44 | 2.8675 (16) | 106 |
| 6        | N2—H22C···O2 | 0.86 (3) | 2.19 (3) | 2.857 (2) | 134 (2) |
|          | N2—H22D···O2ii | 0.89 (2) | 2.22 (2) | 3.098 (2) | 168.8 (19) |
|          | C15—H15···O2xii | 0.93 | 2.59 | 3.366 (2) | 141 |
|          | C16—H16···O1 | 0.93 | 2.58 | 3.105 (2) | 117 |
|          | C26—H26···O1 | 0.93 | 2.45 | 2.849 (2) | 106 |
|          | C1—H1B···Cg1xxiv | 0.97 | 2.97 | 3.817 (2) | 147 |
|          | S1—O2···Cg22 | 3.5773 (15) |

Symmetry codes: (i) −x+1, −y+1, −z+1; (ii) +x−y+z−2; (iii) −x+1, y−z+1, z−1; (iv) y+x−z−1; (v) x+y+2; (vi) −x+2, −y+1, −z+1; (vii) −x, y+1, −z+1; (viii) x, y−1, z−1; (ix) −x−1, y−1, z+1; (x) −x−1, y−1, z+1; (xi) −x−1, y−1, z+1; (xii) −x−1, y−1, z+1; Centroids for: 3 Cg1 N1/C1/C2/C2/C12/C11; Cg2 C11/C16; Cg3 C21–C26; for 4 Cg1 C22–C27; for 5 Cg1 C11–C16; Cg2 N1/C2/C1/C12/C11; for 6 Cg1 C25–C26.

alluding to the formation of the sulfonamide bond. The disappearance of the SO2−Cl (1420 and 1220 cm−1) and N−H (3286–3265 cm−1) stretching bands in the IR spectra of o-nitrosulfonamyl chloride and cycloamines, respectively, were good indicators of a successful condensation reaction. This was corroborated by the shift of the sulfonyl (−SO2−) absorption bands from 1420 and 1220 (in o-nitrosulfonamyl chloride) to 1355–1342 and 1171–1161 cm−1 (in 1–3). It is noteworthy that the lower wavenumbers observed in the IR spectra of o-nitrosulfonamides 1–3 for −SO2− were not unusual as the Cl atom bonded to it had been replaced by a less electronegative N atom. In the IR spectra of o-sulfanilamides 4–6, the appearance of two N−H stretching bands in the higher frequency region around 3467 ± 20 and 3383 ± 10 cm−1, and the disappearance of the nitro (NO2) absorption bands (observed at 1550–1536 and 1369–1342 cm−1) in the spectra of 1–3 were attributed to the successful catalytic reduction of the nitro group to the amino group.

The 1H NMR spectra of o-nitrosulfonamides 1–3 were additive of the individual spectra of the starting materials (i.e. o-nitrobenzenesulfonyl chloride and cycloamines), with the disappearance of the nitrogen proton peaks of cycloamines. The aromatic protons of o-sulfanilamides 4–6 resonated upfield in comparison to the same aromatic protons in precursors 1–3. This general shift towards tetramethylsilane (TMS) was credited to the newly formed amino groups whose lone-pair electrons are suspected of having caused the increased mesomeric shielding of the aromatic protons. D2O-exchangeable singlets were also observed in the 1H NMR spectra of 4–6 between 5.13 and 4.99 ppm for the newly-formed amino protons. The success of the catalytic hydrogenation of nitro adducts 1–3 was corroborated by the 13C NMR spectra of 4–6, where the requisite C atoms (C−NO2→ C−NH2) resonated upfield in the range 133.9–130.1 ppm. The spectroscopic data analyses of the synthesized compounds were consistent with the assigned structures of the compounds.
3.2. Crystal structure

The molecules of 1-3 and 4-6 crystallized in the monoclinic space group P2₁/c or P2₁/c (No. 14), except for 5, which crystallized in the orthorhombic space group Pbcn (No. 61). In addition, they all had one molecule in the asymmetric unit, with the exception of 4, with two independent molecules per asymmetric unit cell. The two molecules per unit cell of compound 4 were identical but for the conformation of the pyrrolidine group (cf. Fig. S1 in the supporting information). It is noteworthy that the pyrrolidine ring in 1 is disordered. The molecular structures of 1-3 and 4-6 are shown in Fig. 2, while the crystal data collection parameters of o-nitrosulfonamides 1-3 and N-cycloamoindo-o-sulfanilamides 4-6 are presented in Table 1. They are compared with the crystal structure data of para-sulfanilamide and ortho-sulfanilamide, which crystallize in the orthorhombic Pbcn (No. 61) and monoclinic P2₁/c (No. 14) space groups, respectively (Gelbrich et al., 2008; Shad et al., 2008). Several sulfanamide derivatives have also been reported (El-Gaby et al., 2020). Selected bond lengths and angles, as determined from the SC-XRD experiments, are reported (El-Gaby, 2008). Several sulfonamide derivatives have also been reported (El-Gaby et al., 2020). Selected bond lengths and angles, as determined from the SC-XRD experiments, are collected in Table S1 (see supporting information).

It is instructive to note that the amino (NH₂) group in N-cycloamoindo-o-sulfanilamides 4-6 contributed significantly to their hydrogen-bond interactions (cf. Table 2). In all three structures, there were intramolecular N-H-O=S interactions resulting in ring closures that can be described with S(6) graph-set descriptors (Bernstein et al., 1995; Etter et al., 1990). Furthermore, compounds 5 and 6 exhibited infinite-chain intermolecular N-H-O=S interactions with C(6) descriptors. Interestingly, no infinite chain interaction was observed in 4; instead, four molecules were linked into a ring structure with an R²(24) descriptor. The p-sulfanilamide (Gelbrich et al., 2008) and o-sulfanilamide (Shad et al., 2008) structures also each have a number of infinite-chain interactions and ring structures. Fig. 3 shows selected hydrogen-bond, C-H⋯(π ring) and π-π stacking interactions for sulfonamides 1-3 and sulfanilamides 4-6. All the hydrogen bonds were of moderate (mostly electrostatic) strength (Jeffrey, 1997), with 4 giving the strongest hydrogen bonds (Table 2).

Additionally, the compounds also exhibited both intra- and intermolecular C-H⋯O=S interactions, with the length of the shortest interactions varying in the range 2.30-2.48 Å. The only π-π stacking interaction of note occurred in 3, where two centroid-to-centroid interactions with distances of 3.6967 (11) Å were observed between the centrosymmetric indoline moieties. An N=O⋯O=π ring interaction of 3.657 (2) Å was also evident in 3, whereas intermolecular C-H⋯(π ring) interactions of 2.97 Å and S=O⋯(π ring) interactions of 3.5773 (15) Å were present in the structure of its hydrogenated analogue 6. The packing diagrams of the crystal structures of compounds 1-6 are shown in Fig. S2 in the supporting information.

3.3. Hirshfeld surface analysis

The Hirshfeld surface analyses (Turner et al., 2017) of compounds 1-6 showed intermolecular interactions such as O⋯H⋯O, O⋯H⋯N and C⋯H⋯π. Two sharp O-H spikes

Figure 2
The molecular structures of o-nitrosulfonamides 1-3 and N-cycloamoindo-o-sulfanilamides 4-6 (molecule 2 of 4 shown). Displacement ellipsoids are drawn at the 50% probability level. Minor disorder components have been omitted.

Table 3
Percentage contributions of selected interatomic contacts to the Hirshfeld surface of compounds 1-6.

|                | C⋯H | O⋯H | N⋯H |
|----------------|-----|-----|-----|
| o-Nitrosulfonamides |     |     |     |
| 1              | 15.2| 42.3| 0.6 |
| 2              | 15.3| 41.7| 1.4 |
| 3              | 14.0| 40.3| 0.0 |
| N-Cycloamoindo-o-sulfanilamides |     |     |     |
| 4              | 15.2| 25.9| 3.5 |
| 5              | 16.5| 22.4| 3.4 |
| 6              | 30.4| 19.6| 2.1 |
typical of an O—H···O interaction from 1 contributed the highest O···H interaction of 42.3%. The fingerprint plots showed that C···H contacts were highest for 6 (30.4%), and this is closely related to C—H···π interactions (McKinnon et al., 2007; Kolade et al., 2020). The percentages of the major contributions, e.g. C···H, O···H and N···H interatomic contacts, for each molecule are compiled in Table 3.

The molecular Hirshfeld surfaces, mapped as $d_{norm}$, shape index and curvedness, confirmed interactions between neighbouring molecules of 1–6 and are presented in Fig. S3. The

![Table 4](image)

| Compound | $d_{norm}$ Minimum value | $d_{norm}$ Maximum value | $d_i$ Minimum value | $d_i$ Maximum value | $d_e$ Minimum value | $d_e$ Maximum value |
|----------|--------------------------|--------------------------|---------------------|---------------------|---------------------|---------------------|
| 1        | 0.2565                   | 0.9743                   | 0.9092              | 2.3849              | 0.9083              | 2.4152              |
| 2        | 0.1071                   | 1.0914                   | 1.0665              | 2.4390              | 1.0669              | 2.4804              |
| 3        | 0.3223                   | 1.7007                   | 0.9319              | 2.6809              | 0.9322              | 2.6406              |
| 4        | 0.3784                   | 1.2864                   | 0.8873              | 2.4989              | 0.9319              | 2.4948              |
| 5        | 0.2060                   | 1.3595                   | 0.9944              | 2.6968              | 0.9957              | 2.5141              |
| 6        | 0.3866                   | 1.2989                   | 0.8842              | 2.7791              | 0.8838              | 2.5779              |

Figure 3
Selected hydrogen-bond, C—H···(π ring) and π·π stacking interactions for compounds 1–6. Displacement ellipsoids are drawn at the 50% probability level. Minor disorder components have been omitted.
large circular depressions (deep red) visible on the \( d_{\text{norm}} \) surfaces typically indicate that the molecule has a donor site(s) (e.g. amine and/or sulfone) or interactions with proteins.

Fingerprint plots of \( \alpha \)-nitrosulfonamides 1–3 and \( N \)-cycloamino-\( \alpha \)-sulfanilamides 4–6 in full and resolved into \( C / C_{1} / C_{1} / C_{1} \)H, \( O / C_{1} / C_{1} / C_{1} \)H and \( N / C_{1} / C_{1} / C_{1} \)H are presented in Fig. S4 (supporting information). The intermolecular \( O / C_{1} / C_{1} / C_{1} \)H and \( N / C_{1} / C_{1} / C_{1} \)H interactions appear as two distinct spikes of almost equal length in the 2D (two-dimensional) fingerprint plots in the region \( 1.2 < (d_{e} + d_{i}) < 2.9 \) Å as light-sky-blue patterns in full fingerprint 2D plots and characterized to be \( 2.56 \pm 0.21 \) Å corresponds to \( O \cdot \cdot \cdot H \) contacts which contributes the majority of the surface area. 2D fingerprint plots reveal the contributions of these interactions in the crystal structure quantitatively and are presented in Table 4 (with minimum and maximum values of \( d_{\text{norm}} \), \( d_{l} \) and \( d_{e} \) provided). Complementary regions are also visible in the fingerprint plots (Fig. S4), where one molecule acts as a donor \( (d_{e} > d_{l}) \) and the other acts as an acceptor \( (d_{e} < d_{l}) \). This finding was validated by the calculated molecular electrostatic potential of 1–6 (Fig. S5). The negative potential (acceptor) is indicated as a red surface around the O atoms attached to sulfur (–SO₂) and the N atoms attached to oxygen (–NO₂). The blue/purple surface area indicates that the positive potential (donor) is mapped in the proximity of the H atoms (Fig. S5).

### 3.4. Global reactivity descriptors (GRDs)

The full geometry of optimized molecules 1–6 presented bond lengths similar to those obtained from the crystal data. A comparison of selected torsion angles of the crystal structures of 1–6 and the DFT-optimized molecules showed that con-
formation of the molecules did not change significantly in the DFT-optimized state (Fig. S6). Generally, the observed, almost flat, O—S—N—C torsion angle of the DFT-optimized molecules suggest that the lone pairs on sulfur may have contributed to the \( \pi \)-electron delocalization that is observed in the DFT molecules.

The highest occupied molecular orbital (HOMO) and lowest unoccupied molecular orbital (LUMO) electrons are distributed around various moieties within the various molecules (Fig. 4). Generally, electron distribution is mainly scattered in the HOMO over the phenyl, sulfur and indolinyl/pyrrolidinyl rings, with the exception of 3 and 5. The LUMO is mainly spread over the phenyl moieties. This indicates that there is a transfer of charge between the indolinyl/pyrrolidinyl rings and the phenyl moieties within the molecule.

The HOMO–LUMO gap, which describes the stability of molecules and predicts reactivity between species by providing the electrical transport properties, as well as electron carrier and mobility in molecules (Rathi et al., 2020), are provided in Table 5. N-Indolinyl-o-nitrobenzenesulfonamide 3 displayed the smallest energy gap (3.24 eV), indicating that it was the softest molecule with good polarizability and reactivity, whereas \( N \)-piperidinyl-o-sulfanilamide 5 presented the largest energy gap of 4.924 eV, thereby corroborating its high chemical hardness of 2.462 eV (cf. Table 5). The lowest LUMO energy was obtained from 3 (\( E_{\text{LUMO}} = -3.175 \) eV), indicating that it is the best electron acceptor of the molecules analyzed, whereas 6 was the best electron donor in the series, with the highest HOMO energy (\( E_{\text{HOMO}} \)) of \(-6.142 \) eV (Table 5). The observed large energy gap (4.924 eV) in 5 suggests that charge transfer could promote its bioactivity and ability to form biological interactions at the piperidinyl and phenyl moiety (Al-Wahaibi et al., 2019). Therefore, the predicted order of biological interactions are \( 5 > 6 > 4 > 2 > 1 > 3 \).

The ionization potential (\( I \)), electron affinity (\( A \)), chemical potential (\( \mu \)), electronegativity (\( \chi \)), global hardness (\( \eta \)), global softness (\( \xi \)) and global electrophilicity (\( \omega \)) values were calculated using the HOMO and LUMO energy values and are collated in Table 5. The lowest \( I \) value of 6.142 eV originated from sulfanilamide 6, whereas sulfanilamide 3 gave the largest \( A \) value of 3.175 eV. Amongst the compounds studied, 2 gave the highest \( \chi \) value of 5.1795 eV. Interestingly, sulfanilamide 5 displayed the highest \( \eta \) value of 2.462 eV and the lowest chemical softness (\( \xi \)) of 0.406 eV, thus alluding to its having the most reactive nature of all the molecules investi-
The highest global electrophilicity of 29.597 eV was also recorded for sulfonamide 2, indicating that it is a strong electrophile. In general, the chemical reactivities of compounds 1–6 have been shown to vary with the groups attached to the compounds (Abbaz et al., 2018).

### 3.5. Docking studies

Docking studies of synthesized 1–6 with human carbonic anhydrase II and IX inhibitors (hCA II and IX; PDB entries: 4iwz and 5fl4) (Biswas et al., 2013; Leitans et al., 2015), downloaded from the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB) was carried out in Maestro (Version 13.1.137, MMshare Version 5.7.137, Release 2022-1, Platform Windows-x64) (Schrödinger, 2022).

Docking calculations between 4iwz and A (reference drug) displayed a docking score of −2.252 kcal mol⁻¹, which is higher than for all synthesized compounds 1–6 (cf. Table 6). Also, A interacted with amino acid residues GLN_{92} (2.39 Å) and HIE_{64} (2.24 Å) via hydrogen-bonding interactions and with amino acid residue HIS_{64} (4.75 Å) via π–π stacking interactions (cf. Table 7). Some bad interactions/contacts were observed between the amino acid residue GLU_{106} and A (Fig. 5). Compound 2 displayed the best binding affinity among the synthesized compounds, with a docking score of −2.223 kcal mol⁻¹, slightly lower than that of the reference drug. Sulfanilamides 4 and 5 also displayed significantly good binding affinities, with docking scores of −1.645 and −1.636 kcal mol⁻¹, respectively. Sulfanilamide 6 was char-

| Isoenzyme/Entry | Carbonic anhydrase II (PDB entry 4iwz) | Carbonic anhydrase IX (PDB entry 5fl4) |
|-----------------|----------------------------------------|----------------------------------------|
|                 | Hydrogen bond                          | Hydrogen bond                          |
| o-Nitrosulfonamides | π–π or π–cation                         | π–π or π–cation                         |
| 1               | GLN_{92} (2.13)                         | GLN_{92} (2.14)                         |
| 2               | ASN_{62} (2.33), ASN_{67} (2.55)        | GLN_{71} (2.28), THR_{201} (2.13)      |
| 3               | GLN_{92} (2.25), ASN_{62} (2.74)       | GLN_{71} (2.26)                         |
| N-Cycloamino-o-sulfanilamides | π–π or π–cation                         | π–π or π–cation                         |
| 4               | GLN_{92} (2.04), THR_{201} (2.29)      | THR_{201} (2.03)                        |
| 5               | GLN_{92} (1.78), THR_{201} (2.26)      |                                        |
| 6               | GLN_{92} (1.88), TRP_{199} (2.11)      | THR_{201} (1.81) π–π stacking          |
| A               | GLN_{92} (2.39), HIE_{64} (2.24)       | HIS_{64} (4.75) π–π stacking           |
| B               |                                        | ASP_{13} (1.59–2.73), VAL_{130} (2.53) |

Note: A is N-(5-sulfamoyl-1,3,4-thiadiazol-2-yl)-2-(thiophen-2-yl)acetamide and B is 5-[1-(naphthalen-1-yl)-1,2,3-triazol-4-yl]thiophene-2-sulfonamide.

Figure 6
(a) 3D interaction diagram of 5-[1-(naphthalen-1-yl)-1,2,3-triazol-4-yl]thiophene-2-sulfonamide (B) and hCA IX isoenzyme 5fl4, and (b) 2D interaction diagram depicting the binding residues of 5fl4.
acterized by the lowest binding affinity, evidenced by its docking score of $-0.784$ kcal mol$^{-1}$. Compound 6 displayed glide a E-model energy of $-47.945$ kcal mol$^{-1}$ and a ligand efficiency of $-0.041$ kcal mol$^{-1}$. Structurally, sulfanilamide 6 interacted with the protein 4iwz through hydrogen bonding with GLN$_{92}$ (1.88 Å) and TRP$_{5}$ (2.11 Å), and through π–π stacking with THR$_{190}$ (1.81 Å) (Fig. S12).

To determine the mode of interaction of the synthesized compounds with human carbonic anhydrase IX inhibitor (hCA IX), the synthesized compounds were docked into the active site of 5f4, and the results obtained were compared with the docked results of the reference drug B. We observed that the reference drug interacts with amino acid residues ASP$_{13}$ (1.59–2.73 Å) and VAL$_{130}$ (2.53 Å) via hydrogen bonding, and with HID$_{94}$ (5.49 Å) via π–cation interactions (cf. Table 7). Furthermore, B exhibited a docking score of $-1.969$ kcal mol$^{-1}$, a glide E-model energy of $-41.029$ kcal mol$^{-1}$ and a ligand efficiency of $-0.082$ kcal mol$^{-1}$, and is surrounded by several amino acid residues. Some of the residues are TRP$_{6}$, PRO$_{203}$, THR$_{201}$, HID$_{68}$, LEU$_{199}$, HID$_{94}$, GLN$_{92}$, VAL$_{171}$ and ZN$_{264}$, with bad contacts or interactions observed on residue ASP$_{131}$ (Fig. 6). Benzenesulfonamide 2 presented the highest binding affinity, with a docking score of $-1.977$ kcal mol$^{-1}$, higher than the reference drug. All other synthesized compounds, except for N-cycloamino-o-nitro-benzenesulfonamide 1 (docking score = $-0.807$), displayed significantly good docking scores; however, they were lower than the reference drug (cf. Table 6). Compound 3 displayed hydrogen-bond interactions with amino acid residue GLN$_{71}$, with a bond length of 2.26 Å, and a π–cation interaction with amino acid residue HID$_{44}$, with a bond length of 4.05 Å (Fig. S15).

We observed that the docking scores of 2 with 4iwz and 5f4 are close to those obtained for A with 4iwz and B with 5f4. Docking scores of molecules with ring structures 1 and 3–6 (in the range $> -1.67$ kcal mol$^{-1}$) also correlated with the electronegativity and electrophilicity values presented in Table 5. This is informed by the HOMO and LUMO properties (Kumar et al., 2018).

4. Conclusion

ω-Nitrosulfonamides 1–3 and N-cycloamino-o-sulfanilamides 4–6 have been successfully synthesized, characterized and the intermolecular interactions analysed, as well as being tested in silico for carbonic anhydrase II (4iwz) and IX (5f4) inhibitory activities. The results obtained from crystal packing and DFT analysis suggests that the molecules are held together by forces such as hydrogen bonding and π–π interactions. The results of the DFT study of compounds 1–6 were correlated with the molecular docking data and indicate that electronegativity and electrophilicity of the title compounds play an important role in their interaction with carbonic anhydrase II (4iwz) and IX (5f4).

O-Nitrosulfonamide 2 displayed a good docking score against 4iwz (lower than the reference drug) and the best against 5f4 (higher than the reference drug). These results provided a valuable synthesis approach and structural and docking information for compounds 1–6 that may be used for the development of potent antibacterial drugs.

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supporting information

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N-Cycloamino substituent effects on the packing architecture of ortho-sulfanilamide molecular crystals and their in silico carbonic anhydrase II and IX inhibitory activities

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Computing details
For all structures, data collection: APEX2 (Bruker, 2011); cell refinement: APEX2 (Bruker, 2011); data reduction: SAINT (Bruker, 2012); program(s) used to solve structure: SHELXT2018 (Sheldrick, 2015a); program(s) used to refine structure: SHELXL2018 (Sheldrick, 2015b) and ShelXle (Hübschle et al., 2011); molecular graphics: ORTEP-3 for Windows (Farrugia, 2012); software used to prepare material for publication: PLATON (Spek, 2020) and Mercury (Macrae et al., 2020).

1-[(2-Nitrophenyl)sulfonyl]pyrrolidine (ka097)

Crystal data

\[ C_{10}H_{12}N_{2}O_{4}S \]

\[ M_r = 256.28 \]

Monoclinic, \( P_2_1/n \)

\[ a = 8.6173 (5) \text{ Å} \]
\[ b = 14.6662 (9) \text{ Å} \]
\[ c = 9.4885 (6) \text{ Å} \]
\[ \beta = 108.075 (3)^\circ \]

\[ V = 1140.01 (12) \text{ Å}^3 \]

\[ Z = 4 \]

\[ F(000) = 536 \]

\[ D_k = 1.493 \text{ Mg m}^{-3} \]

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

Cell parameters from 9888 reflections

\[ \theta = 2.7–28.3^\circ \]

\[ \mu = 0.29 \text{ mm}^{-1} \]

\[ T = 200 \text{ K} \]

Block, yellow

\[ 0.67 \times 0.67 \times 0.12 \text{ mm} \]

Data collection

Bruker APEXII CCD diffractometer

Radiation source: sealed tube

Graphite monochromator

Detector resolution: 8.3333 pixels mm\(^{-1}\)

\( \phi \) and \( \omega \) scans

Absorption correction: numerical

(SADABS; Bruker, 2008)

\[ T_{\text{min}} = 0.934, T_{\text{max}} = 1.000 \]

Refinement

Refinement on \( F^2 \)

Least-squares matrix: full

\[ R[F^2 > 2\sigma(F^2)] = 0.041 \]

\[ wR(F^2) = 0.111 \]

\[ S = 1.05 \]

24329 measured reflections

2849 independent reflections

2508 reflections with \( I > 2\sigma(I) \)

\[ R_{\text{int}} = 0.018 \]

\[ \theta_{\text{max}} = 28.4^\circ, \theta_{\text{min}} = 2.7^\circ \]

\[ h = -11 \rightarrow 11 \]

\[ k = -17 \rightarrow 19 \]

\[ l = -12 \rightarrow 12 \]

2849 reflections

149 parameters

20 restraints
Primary atom site location: dual
Secondary atom site location: difference Fourier map
Hydrogen site location: inferred from neighbouring sites
H-atom parameters constrained

Special details

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

Refinement. Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with $U_{iso}(H)$ set to 1.2 $U_{eq}(C)$.

The pyrrolidine group is disordered necessitating the use of the restraints SADI, EADP and SAME.

Single-crystal X-ray diffraction (SC-XRD) data were collected at 200 or 296 K on a Bruker APEXII CCD diffractometer with graphite-monochromated Mo $K\alpha$ radiation using the APEX2 data collection software and SAINT (Bruker 2012) for cell refinement and data reduction. The structures were solved by dual-space methods applying SHELXT2018 (Sheldrick, 2015a) and refined by least-squares procedures using SHELXL2018 (Sheldrick, 2015b). Data were corrected for absorption effects using the numerical method implemented in SADABS (Bruker 2012). All non-H atoms were refined anisotropically. The crystal structure diagrams were drawn with ORTEP-3 for Windows (Farrugia 2012).

| Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ($\AA^2$) |
|---|---|---|---|---|
| x | y | z | $U_{iso}/U_{eq}$ | Occ. (<1) |
| S1 0.49089 (5) | 0.66797 (3) | 0.32216 (4) | 0.02954 (13) |
| O1 0.52737 (15) | 0.62543 (9) | 0.46416 (13) | 0.0360 (3) |
| O2 0.41164 (17) | 0.75483 (10) | 0.29726 (18) | 0.0481 (4) |
| O3 0.91161 (16) | 0.56570 (9) | 0.57998 (13) | 0.0374 (3) |
| O4 0.74333 (16) | 0.49165 (8) | 0.40041 (15) | 0.0387 (3) |
| N1 0.3849 (2) | 0.59886 (12) | 0.20100 (17) | 0.0424 (4) |
| N2 0.82322 (16) | 0.55892 (9) | 0.45200 (15) | 0.0261 (3) |
| C21 0.67960 (18) | 0.68563 (10) | 0.28603 (17) | 0.0243 (3) |
| C22 0.82125 (18) | 0.63575 (9) | 0.35184 (16) | 0.0233 (3) |
| C23 0.9678 (2) | 0.6569 (11) | 0.32834 (19) | 0.0300 (3) |
| H23 1.063007 | 0.621352 | 0.376473 | 0.036* |
| C24 0.9742 (2) | 0.72656 (12) | 0.2335 (2) | 0.0347 (4) |
| H24 1.073735 | 0.740356 | 0.214723 | 0.042* |
| C25 0.8355 (2) | 0.77707 (12) | 0.1663 (2) | 0.0348 (4) |
| H25 0.839913 | 0.825347 | 0.100842 | 0.042* |
| C26 0.6899 (2) | 0.75768 (11) | 0.19374 (18) | 0.0304 (3) |
| H26 0.596179 | 0.793966 | 0.149089 | 0.036* |
| C11 0.3771 (10) | 0.4994 (5) | 0.2187 (8) | 0.0525 (5) |
| H11A 0.365697 | 0.483433 | 0.316363 | 0.063* |
| H11B 0.475419 | 0.469108 | 0.207784 | 0.063* |
| C12 0.2269 (6) | 0.4739 (3) | 0.0945 (5) | 0.0525 (5) |
| H12A 0.126167 | 0.490743 | 0.117592 | 0.063* |
| H12B 0.224619 | 0.407828 | 0.072438 | 0.063* |
| C13 0.2474 (6) | 0.5302 (4) | −0.0321 (5) | 0.0525 (5) |
| H13A 0.142720 | 0.536536 | −0.112750 | 0.063* |
### H13B
0.329694 0.502920 −0.072615 0.063* 0.579 (7)

### C14
0.3052 (11) 0.6216 (4) 0.0416 (7) 0.0525 (5) 0.579 (7)

### H14A
0.384050 0.650475 −0.001515 0.063* 0.579 (7)

### H14B
0.211994 0.663509 0.029701 0.063* 0.579 (7)

### C15
0.3620 (14) 0.5024 (7) 0.2240 (11) 0.0525 (5) 0.421 (7)

### H15A
0.289652 0.492782 0.285820 0.063* 0.421 (7)

### H15B
0.467484 0.471263 0.270293 0.063* 0.421 (7)

### C16
0.2804 (9) 0.4696 (4) 0.0620 (7) 0.0525 (5) 0.421 (7)

### H16A
0.362038 0.441474 0.021428 0.063* 0.421 (7)

### H16B
0.193459 0.424491 0.057238 0.063* 0.421 (7)

### C17
0.2083 (8) 0.5567 (5) −0.0247 (7) 0.0525 (5) 0.421 (7)

### H17A
0.207484 0.551559 −0.128998 0.063* 0.421 (7)

### H17B
0.094759 0.566045 −0.023970 0.063* 0.421 (7)

### C18
0.3140 (15) 0.6354 (6) 0.0501 (10) 0.0525 (5) 0.421 (7)

### H18A
0.399357 0.649069 0.003320 0.063* 0.421 (7)

### H18B
0.248645 0.691003 0.049588 0.063* 0.421 (7)

### Atomic displacement parameters (Å²)

|    | $U^{11}$ | $U^{22}$ | $U^{33}$ | $U^{12}$ | $U^{13}$ | $U^{23}$ |
|----|----------|----------|----------|----------|----------|----------|
| S1 | 0.0263 (2) | 0.0333 (2) | 0.0318 (2) | 0.00668 (14) | 0.01314 (16) | 0.00676 (15) |
| O1 | 0.0363 (6) | 0.0479 (7) | 0.0283 (6) | 0.0048 (5) | 0.0166 (5) | 0.0052 (5) |
| O2 | 0.0392 (7) | 0.0428 (7) | 0.0700 (10) | 0.0185 (6) | 0.0280 (7) | 0.0142 (7) |
| O3 | 0.0405 (7) | 0.0391 (7) | 0.0282 (6) | 0.0012 (5) | 0.0045 (5) | 0.0077 (5) |
| O4 | 0.0373 (7) | 0.0259 (6) | 0.0495 (8) | −0.0061 (5) | 0.0087 (6) | 0.0034 (5) |
| N1 | 0.0400 (8) | 0.0479 (9) | 0.0327 (8) | −0.0083 (7) | 0.0017 (6) | 0.0123 (7) |
| N2 | 0.0242 (6) | 0.0237 (6) | 0.0306 (7) | 0.0030 (5) | 0.0090 (5) | 0.0045 (5) |
| C21 | 0.0261 (7) | 0.0239 (7) | 0.0246 (7) | 0.0026 (5) | 0.0103 (6) | 0.0011 (5) |
| C22 | 0.0276 (7) | 0.0195 (6) | 0.0231 (7) | 0.0016 (5) | 0.0081 (6) | 0.0009 (5) |
| C23 | 0.0270 (8) | 0.0281 (7) | 0.0363 (9) | 0.0030 (6) | 0.0116 (7) | 0.0023 (6) |
| C24 | 0.0350 (8) | 0.0329 (8) | 0.0428 (9) | −0.0009 (7) | 0.0218 (7) | 0.0038 (7) |
| C25 | 0.0446 (10) | 0.0287 (8) | 0.0375 (9) | 0.0036 (7) | 0.0222 (8) | 0.0087 (7) |
| C26 | 0.0351 (8) | 0.0272 (7) | 0.0305 (8) | 0.0080 (6) | 0.0125 (7) | 0.0075 (6) |
| C11 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C12 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C13 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C14 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C15 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C16 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C17 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |
| C18 | 0.0476 (9) | 0.0604 (10) | 0.0421 (7) | −0.0101 (7) | 0.0034 (6) | 0.0040 (7) |

### Geometric parameters (Å, °)

|    |   |   |    |   |
|----|---|---|----|---|
| S1—O1 | 1.4285 (12) | C11—H11A | 0.9900 |
| S1—O2 | 1.4300 (13) | C11—H11B | 0.9900 |
| S1—N1 | 1.5913 (17) | C12—C13 | 1.513 (6) |
| S1—C21 | 1.7818 (15) | C12—H12A | 0.9900 |
O3—N2 1.2209 (18) C12—H12B 0.9900
O4—N2 1.2157 (18) C13—C14 1.522 (6)
N1—C15 1.454 (10) C13—H13A 0.9900
N1—C11 1.472 (8) C13—H13B 0.9900
N1—C18 1.472 (8) C14—H14A 0.9900
N1—C14 1.492 (6) C14—H14B 0.9900
N2—C22 1.4706 (18) C15—C16 1.555 (10)
C21—C26 1.393 (2) C15—H15A 0.9900
C21—C22 1.394 (2) C15—H15B 0.9900
C22—C23 1.380 (2) C16—C17 1.543 (8)
C23—C24 1.387 (2) C16—H16A 0.9900
C23—H23 0.9500 C16—H16B 0.9900
C24—C25 1.382 (2) C17—C18 1.505 (8)
C24—H24 0.9500 C17—H17A 0.9900
C25—C26 1.388 (2) C17—H17B 0.9900
C25—H25 0.9500 C18—H18A 0.9900
C26—H26 0.9500 C18—H18B 0.9900
C11—C12 1.503 (8)

O1—S1—O2 119.93 (9) C13—C12—H12A 111.4
O1—S1—N1 108.19 (8) C11—C12—H12B 111.4
O2—S1—N1 108.08 (9) C13—C12—H12B 111.4
O1—S1—C21 107.34 (7) H12A—C12—H12B 109.3
O2—S1—C21 104.85 (8) C12—C13—C14 102.6 (4)
N1—S1—C21 107.90 (8) C12—C13—H13A 111.2
C15—N1—C18 117.8 (5) C14—C13—H13A 111.2
C11—N1—C14 108.3 (4) C12—C13—H13B 111.2
C15—N1—S1 125.8 (4) C14—C13—H13B 111.2
C11—N1—S1 125.8 (3) H13A—C13—H13B 109.2
C18—N1—S1 116.2 (3) N1—C14—C13 104.5 (4)
C14—N1—S1 124.8 (2) N1—C14—H14A 110.8
O4—N2—O3 124.55 (14) C13—C14—H14A 110.8
O4—N2—C22 118.04 (13) N1—C14—H14B 110.8
O3—N2—C22 117.32 (13) C13—C14—H14B 110.8
C26—C21—C22 117.54 (14) H14A—C14—H14B 108.9
C26—C21—S1 118.12 (12) N1—C15—C16 101.2 (6)
C22—C21—S1 124.21 (11) N1—C15—H15A 111.5
C23—C22—C21 122.31 (14) C16—C15—H15A 111.5
C23—C22—N2 116.04 (13) N1—C15—H15B 111.5
C21—C22—N2 121.64 (13) C16—C15—H15B 111.5
C22—C23—C24 119.09 (15) H15A—C15—H15B 109.4
C22—C23—H23 120.5  C17—C16—C15 104.7 (6)
C24—C23—H23 120.5  C17—C16—H16A 110.8
C25—C24—C23 119.87 (15) C15—C16—H16A 110.8
C25—C24—H24 120.1  C17—C16—H16B 110.8
C23—C24—H24 120.1  C15—C16—H16B 110.8
C24—C25—C26 120.41 (15) H16A—C16—H16B 108.9
C24—C25—H25 119.8  C18—C17—C16 107.4 (6)

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Acta Cryst. (2022). C78, 730-742

sup-4
C26—C25—H25  119.8  C18—C17—H17A  110.2
C25—C26—C21  120.75 (15)  C16—C17—H17A  110.2
C25—C26—H26  119.6  C18—C17—H17B  108.5
C21—C26—H26  119.6  N1—C18—H18A  111.6
N1—C11—H11A  111.3  N1—C18—H18B  111.6
C12—C11—H11A  111.3  C17—C18—H18A  111.6
C12—C11—H11B  111.3  C17—C18—H18B  111.6
H11A—C11—H11B  109.2  C16—C17—H17B  100.8 (5)
C11—C12—C13  101.6 (5)  N1—C18—H18B  111.6
C11—C12—H12A  111.4  H17A—C17—H17B  108.5
N1—C11—C12  102.5 (5)  H17A—C17—H17B  108.5
N1—C11—H11A  111.3  N1—C18—H18A  111.6
C12—C11—H11B  111.3  C17—C18—H18A  111.6
C12—C11—H11B  111.3  C17—C18—H18B  111.6
N1—C11—C12  102.5 (5)  H17A—C17—H17B  108.5
H11A—C11—H11B  109.2  N1—C18—H18B  111.6
C11—C12—C13  101.6 (5)  C17—C18—H18B  111.6
C11—C12—H12A  111.4

C21—S1—N1—C15  102.3 (6)  C18—N1—C15—C16  11.2 (12)
C21—S1—N1—C15  102.3 (6)  C15—N1—C14—C13  1.2 (8)
O1—S1—N1—C15  171.1 (7)  S1—N1—C14—C13  169.7 (3)
O2—S1—N1—C15  171.1 (7)  S1—N1—C14—C13  169.7 (3)
N1—S1—C21—C26  151.82 (14)  S1—N1—C14—C13  169.7 (3)
C26—C21—C22—C23  0.1 (2)  C16—C17—C18—N1  −24.5 (11)
S1—C21—C22—C23  −17.54 (12)  C15—C16—C17—C18  29.7 (11)
C26—C21—C22—C23  151.82 (14)  C15—N1—C18—C17  11.2 (12)
S1—C21—C22—C23  151.82 (14)  C15—N1—C18—C17  11.2 (12)
C25—H25···O4ii  0.95  2.54  3.240 (2)  131
C25—H25···O1iii  0.95  2.54  3.240 (2)  131

Hydrogen-bond geometry (Å, °)

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|-----|------|-------|---------|
| C11···H11A···O1i | 0.99 | 2.56 | 3.398 (7) | 143 |
| C11···H11B···O4 | 0.99 | 2.48 | 3.093 (8) | 120 |
| C25···H25···O4iv | 0.95 | 2.54 | 3.240 (2) | 131 |
| C25···H25···O1v | 0.95 | 2.47 | 3.228 (2) | 137 |
C26—H26···O2 0.95 2.49 2.860 (2) 103
C26—H26···O3iv 0.95 2.56 3.467 (2) 160

Symmetry codes: (i) −x+1, −y+1, −z+1; (ii) −x+3/2, y+1/2, −z+1/2; (iii) x+1/2, −y+3/2, z−1/2; (iv) x−1/2, −y+3/2, z−1/2.

1-[(2-Nitrophenyl)sulfonyl]piperidine (ja198)

Crystal data
C11H14N2O4S  F(000) = 568
Mr = 270.30  Dx = 1.459 Mg m−3
Monoclinic, P21/n  Mo Kα radiation, λ = 0.71073 Å
a = 8.6881 (9) Å  Cell parameters from 9983 reflections
b = 15.0266 (14) Å  θ = 2.6–28.3°
c = 9.8337 (10) Å  μ = 0.27 mm−1
β = 106.526 (4)°  T = 296 K
V = 1230.8 (2) Å3  Block, colourless
Z = 4  0.48 × 0.47 × 0.45 mm

Data collection
Bruker APEXII CCD  25328 measured reflections
diffractometer  3059 independent reflections
Radiation source: sealed tube  2662 reflections with I > 2σ(I)
Graphite monochromator  \( R_{int} = 0.017 \)
Detector resolution: 8.3333 pixels mm−1  \( \theta_{max} = 28.3°, \theta_{min} = 2.6° \)
\( \phi \) and \( \omega \) scans  \( h = -11 \rightarrow 11 \)
Absorption correction: numerical  \( k = -20 \rightarrow 19 \)
(SADABS; Bruker, 2008)  \( l = -13 \rightarrow 13 \)

Refinement
Refinement on \( F^2 \)  Secondary atom site location: difference Fourier map
Least-squares matrix: full  Hydrogen site location: inferred from
\( R[F^2 > 2\sigma(F^2)] = 0.036 \)  neighbouring sites
\( wR(F^2) = 0.106 \)  H-atom parameters constrained
\( S = 1.06 \)  \( w = 1/[\langle \sigma^2(F^2) \rangle + (0.0546P)^2 + 0.3577P] \)
3059 reflections  where \( P = (F^2 + 2F^2_{e})/3 \)
163 parameters  \( \Delta(\sigma)_{max} = 0.001 \)
0 restraints  \( \Delta p_{max} = 0.32 \) e Å\(^{-3}\)
Primary atom site location: dual  \( \Delta p_{min} = -0.31 \) e Å\(^{-3}\)

Special details

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

Refinement. Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with \( U_{iso}(H) \) set to 1.2 \( U_{eq}(C) \).

Single-crystal X-ray diffraction (SC-XRD) data were collected at 200 or 296 K on a Bruker APEXII CCD diffractometer with graphite-monochromated Mo Kα radiation using the APEX2 data collection software and SÁINT (Bruker 2012) for cell refinement and data reduction. The structures were solved by dual-space methods applying SHELXT2018 (Sheldrick, 2015a) and refined by least-squares procedures using SHELXL2018 (Sheldrick, 2015b). Data were corrected for absorption effects using the numerical method implemented in SADABS (Bruker 2012). All non-H atoms were refined anisotropically. The crystal structure diagrams were drawn with ORTEP-3 for Windows (Farrugia 2012).
### Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

|   | x     | y     | z     | U_{iso}*/U_{eq} |
|---|-------|-------|-------|-----------------|
| S1| 0.50241 (4) | 0.66804 (2) | 0.66863 (4) | 0.04006 (12) |
| O1| 0.57946 (15) | 0.75271 (8) | 0.69071 (16) | 0.0609 (3) |
| O2| 0.46987 (14) | 0.62642 (8) | 0.53305 (11) | 0.0521 (3) |
| O3| 0.23990 (17) | 0.49620 (9) | 0.58739 (17) | 0.0705 (4) |
| O4| 0.08960 (18) | 0.57419 (11) | 0.41946 (13) | 0.0734 (4) |
| N1| 0.61016 (14) | 0.60117 (8) | 0.78644 (13) | 0.0416 (3) |
| N2| 0.17049 (15) | 0.56417 (9) | 0.54124 (14) | 0.0463 (3) |
| C11| 0.5872 (2) | 0.50422 (11) | 0.76898 (19) | 0.0517 (4) |
| H11A| 0.564441 | 0.488569 | 0.669528 | 0.062* |
| H11B| 0.496745 | 0.485803 | 0.801683 | 0.062* |
| C12| 0.7374 (2) | 0.45729 (13) | 0.8536 (2) | 0.0627 (5) |
| H212A| 0.720629 | 0.393457 | 0.845762 | 0.075* |
| H212B| 0.825213 | 0.471853 | 0.814835 | 0.075* |
| C13| 0.7814 (2) | 0.48376 (14) | 1.0071 (2) | 0.0606 (5) |
| H13A| 0.881221 | 0.455002 | 1.057712 | 0.073* |
| H13B| 0.698481 | 0.463866 | 1.048463 | 0.073* |
| C14| 0.8004 (2) | 0.58345 (15) | 1.0233 (2) | 0.0662 (5) |
| H14A| 0.819586 | 0.599222 | 1.122396 | 0.079* |
| H14B| 0.892831 | 0.602183 | 0.993857 | 0.079* |
| C15| 0.6533 (2) | 0.63160 (13) | 0.93604 (18) | 0.0582 (4) |
| H15A| 0.564368 | 0.620532 | 0.975063 | 0.070* |
| H15B| 0.673748 | 0.695143 | 0.939930 | 0.070* |
| C21| 0.31422 (16) | 0.68463 (9) | 0.70518 (14) | 0.0357 (3) |
| C22| 0.17424 (16) | 0.63776 (9) | 0.64082 (14) | 0.0372 (3) |
| C23| 0.02972 (18) | 0.65753 (11) | 0.66598 (17) | 0.0468 (3) |
| H23| −0.062624 | 0.626220 | 0.619609 | 0.056* |
| C24| 0.0237 (2) | 0.72436 (12) | 0.76084 (19) | 0.0530 (4) |
| H24| −0.072622 | 0.737406 | 0.780184 | 0.064* |
| C25| 0.1604 (2) | 0.77165 (12) | 0.82675 (18) | 0.0529 (4) |
| H25| 0.156178 | 0.816624 | 0.890548 | 0.063* |
| C26| 0.30433 (19) | 0.75250 (10) | 0.79841 (16) | 0.0449 (3) |
| H26| 0.395471 | 0.785498 | 0.842346 | 0.054* |

### Atomic displacement parameters (Å²)

|   | U_{11} | U_{22} | U_{33} | U_{12} | U_{13} | U_{23} |
|---|--------|--------|--------|--------|--------|--------|
| S1| 0.03940 (19) | 0.0373 (2) | 0.0487 (2) | −0.00205 (13) | 0.02106 (15) | 0.00020 (13) |
| O1| 0.0540 (7) | 0.0420 (6) | 0.0951 (10) | −0.0107 (5) | 0.0347 (6) | 0.0018 (6) |
| O2| 0.0559 (6) | 0.0647 (7) | 0.0425 (6) | 0.0024 (5) | 0.0248 (5) | −0.0001 (5) |
| O3| 0.0696 (8) | 0.0434 (7) | 0.0929 (10) | 0.0075 (6) | 0.0143 (7) | −0.0118 (7) |
| O4| 0.0767 (9) | 0.0890 (10) | 0.0474 (7) | 0.0056 (8) | 0.0066 (6) | −0.0153 (7) |
| N1| 0.0405 (6) | 0.0379 (6) | 0.0457 (6) | 0.0027 (5) | 0.0110 (5) | −0.0090 (5) |
| N2| 0.0405 (6) | 0.0466 (7) | 0.0525 (7) | −0.0037 (5) | 0.0141 (5) | −0.0078 (6) |
| C11| 0.0540 (9) | 0.0402 (8) | 0.0565 (9) | 0.0011 (7) | 0.0089 (7) | −0.0080 (7) |
| C12| 0.0674 (11) | 0.0466 (9) | 0.0712 (11) | 0.0155 (8) | 0.0150 (9) | −0.0021 (8) |
C13 0.0515 (9) 0.0706 (12) 0.0588 (10) 0.0106 (8) 0.0142 (8) 0.0126 (9)
C14 0.0570 (10) 0.0777 (13) 0.0555 (10) 0.0069 (9) 0.0024 (8) −0.0120 (9)
C15 0.0583 (9) 0.0592 (10) 0.0521 (9) 0.0086 (8) 0.0074 (7) −0.0185 (8)
C21 0.0383 (6) 0.0327 (6) 0.0390 (6) 0.0012 (5) 0.0157 (5) 0.0032 (5)
C22 0.0403 (7) 0.0344 (6) 0.0381 (6) 0.0015 (5) 0.0128 (5) 0.0032 (5)
C23 0.0386 (7) 0.0481 (8) 0.0551 (9) 0.0006 (6) 0.0155 (6) 0.0046 (7)
C24 0.0493 (8) 0.0539 (9) 0.0645 (10) 0.0104 (7) 0.0302 (7) 0.0049 (8)
C25 0.0634 (10) 0.0457 (8) 0.0580 (9) 0.0072 (7) 0.0307 (8) −0.0055 (7)
C26 0.0491 (8) 0.0386 (7) 0.0496 (8) −0.0008 (6) 0.0184 (6) −0.0045 (6)

**Geometric parameters (Å, °)**

| Bond | Distance/Angle (Å/°) | Bond | Distance/Angle (Å/°) |
|------|----------------------|------|----------------------|
| S1—O1 | 1.4252 (12)          | C13—H13B | 0.9700 |
| S1—O2 | 1.4263 (12)          | C14—C15 | 1.506 (3) |
| S1—N1 | 1.6160 (13)          | C14—H14A | 0.9700 |
| S1—C21 | 1.7885 (14)        | C14—H14B | 0.9700 |
| O3—N2 | 1.2070 (19)          | C15—H15A | 0.9700 |
| O4—N2 | 1.2132 (18)          | C15—H15B | 0.9700 |
| N1—C11 | 1.474 (2)           | C21—C26 | 1.390 (2) |
| N1—C15 | 1.4833 (19)         | C21—C22 | 1.3921 (19) |
| N2—C22 | 1.4713 (19)         | C22—C23 | 1.379 (2) |
| C11—C12 | 1.508 (2)           | C23—C24 | 1.382 (2) |
| C11—H11A | 0.9700            | C23—H23 | 0.9300 |
| C11—H11B | 0.9700            | C24—C25 | 1.378 (3) |
| C12—C13 | 1.501 (3)           | C24—H24 | 0.9300 |
| C12—H12A | 0.9700            | C25—C26 | 1.386 (2) |
| C12—H12B | 0.9700            | C25—H25 | 0.9300 |
| C13—C14 | 1.511 (3)           | C26—C21 | 0.9700 |
| C13—H13A | 0.9700            | C26—H26 | 0.9300 |

| Bond | Distance/Angle (Å/°) | Bond | Distance/Angle (Å/°) |
|------|----------------------|------|----------------------|
| O1—S1—O2 | 119.57 (8)          | C15—C14—C13 | 111.53 (16) |
| O1—S1—N1 | 107.14 (7)          | C15—C14—H14A | 109.3 |
| O2—S1—N1 | 108.53 (7)          | C13—C14—H14A | 109.3 |
| O1—S1—C21 | 105.16 (7)         | C15—C14—H14B | 109.3 |
| O2—S1—C21 | 107.43 (7)         | C13—C14—H14B | 109.3 |
| N1—S1—C21 | 108.59 (6)         | H14A—C14—H14B | 108.0 |
| C11—N1—C15 | 114.07 (14)       | N1—C15—C14 | 110.56 (14) |
| C11—N1—S1 | 119.97 (10)        | N1—C15—H15A | 109.5 |
| C15—N1—S1 | 116.79 (10)       | C14—C15—H15A | 109.5 |
| O3—N2—O4 | 124.29 (15)        | N1—C15—H15B | 109.5 |
| O3—N2—C22 | 118.14 (13)       | C14—C15—H15B | 109.5 |
| O4—N2—C22 | 117.42 (14)       | H15A—C15—H15B | 108.1 |
| N1—C11—C12 | 109.30 (14)      | C26—C21—C22 | 117.46 (13) |
| N1—C11—H11A | 109.8            | C26—C21—S1 | 117.79 (11) |
| C12—C11—H11A | 109.8         | C22—C21—S1 | 124.65 (11) |
| N1—C11—H11B | 109.8           | C23—C22—C21 | 122.11 (13) |
| C12—C11—H11B | 109.8         | C23—C22—N2 | 115.62 (13) |
| H11A—C11—H11B | 108.3       | C21—C22—N2 | 122.27 (12) |
C13—C12—C11 111.34 (15) C22—C23—C24 119.28 (15)
C13—C12—H12A 109.4 C22—C23—H23 120.4
C11—C12—H12A 109.4 C24—C23—H23 120.4
C13—C12—H12B 109.4 C25—C24—C23 119.93 (14)
C11—C12—H12B 109.4 C25—C24—H24 120.0
H12A—C12—H12B 108.0 C23—C24—H24 120.0
C12—C13—C14 110.97 (16) C24—C25—C26 120.31 (15)
C12—C13—H13A 109.4 C24—C25—H25 119.8
C14—C13—H13A 109.4 C25—C26—C21 120.88 (15)
C12—C13—H13B 109.4 C25—C26—H26 119.6
H13A—C13—H13B 108.0 C21—C26—H26 119.6

O1—S1—N1—C11 −163.84 (12) O2—S1—C21—C22 21.08 (14)
O2—S1—N1—C11 −33.45 (14) N1—S1—C21—C22 −96.11 (13)
C21—S1—N1—C11 83.04 (13) C26—C21—C22—C23 0.7 (2)
O1—S1—N1—C15 51.20 (14) S1—C21—C22—C23 −175.47 (11)
O2—S1—N1—C15 −178.40 (12) C26—C21—C22—N2 −179.50 (13)
C21—S1—N1—C15 −61.91 (13) S1—C21—C22—N2 4.32 (19)
C15—N1—C11—C12 −56.72 (19) O3—N2—C22—C23 −111.68 (16)
S1—N1—C11—C12 157.43 (13) O4—N2—C22—C23 64.06 (19)
N1—C11—C12—C13 56.4 (2) O3—N2—C22—C21 68.51 (19)
C11—C12—C13—C14 −56.2 (2) O4—N2—C22—C21 −115.74 (16)
C12—C13—C14—C15 54.1 (2) C21—C22—C23—C24 −1.7 (2)
C11—N1—C15—C14 55.3 (2) N2—C22—C23—C24 178.45 (14)
S1—N1—C15—C14 −157.73 (14) C22—C23—C24—C25 1.4 (2)
C13—C14—C15—N1 −52.6 (2) C23—C24—C25—C26 0.0 (3)
O1—S1—C21—C22 −26.70 (14) C24—C25—C26—C21 1.0 (3)
O2—S1—C21—C22 −155.08 (12) C22—C21—C26—C25 0.7 (2)
N1—S1—C21—C22 87.72 (12) S1—C21—C26—C25 177.14 (12)
O1—S1—C21—C22 149.47 (12)

Hydrogen-bond geometry (Å, °)

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|------|------|------|---------|
| C11—H11A···O2 | 0.97 | 2.48 | 2.907 (2) | 107 |
| C11—H11A···O2' | 0.97 | 2.59 | 3.476 (2) | 152 |
| C15—H15B···O1 | 0.97 | 2.51 | 2.943 (2) | 107 |
| C25—H25···O2'' | 0.93 | 2.57 | 3.3337 (19) | 140 |
| C26—H26···O1 | 0.93 | 2.53 | 2.877 (2) | 103 |

Symmetry codes: (i) −x+1, −y+1, −z+1; (ii) x−1/2, −y+3/2, z+1/2.

1-[(2-Nitrophenyl)sulfonyl]-2,3-dihydro-1H-indole (ja250)

Crystal data

C14H12N2O4S

M_r = 304.32
Monoclinic, P2_1/n

a = 7.4701 (5) Å
b = 23.6743 (12) Å
c = 7.8614 (5) Å

Acta Cryst. (2022), C78, 730-742

sup-9
Cell parameters from 9952 reflections

\( \beta = 94.989 (3)^{\circ} \)

\( V = 1385.02 (15) \ \text{Å}^3 \)

\( Z = 4 \)

\( F(000) = 632 \)

\( D_x = 1.459 \ \text{Mg m}^{-3} \)

Mo \( Ka \) radiation, \( \lambda = 0.71073 \ \text{Å} \)

Data collection

Bruker APEXII CCD diffractometer

Radiation source: sealed tube

Graphite monochromator

Detector resolution: 8.3333 pixels mm\(^{-1} \)

\( \theta = 2.7–27.1^{\circ} \)

\( \mu = 0.25 \ \text{mm}^{-1} \)

T = 296 K

Block, yellow

0.62 × 0.51 × 0.43 mm

Data collection

Bruker APEXII CCD diffractometer

Radiation source: sealed tube

Graphite monochromator

Detector resolution: 8.3333 pixels mm\(^{-1} \)

\( R_{int} = 0.024 \)

\( \theta_{\text{max}} = 28.4^{\circ}, \theta_{\text{min}} = 2.7^{\circ} \)

\( h = -9\rightarrow9 \)

\( k = -31\rightarrow28 \)

\( l = -10\rightarrow10 \)

Refinement

Refinement on \( F^2 \)

Least-squares matrix: full

\( R[F^2 > 2\sigma(F^2)] = 0.040 \)

\( wR(F^2) = 0.105 \)

\( S = 1.05 \)

3434 reflections

190 parameters

Hydrogen site location: inferred from neighbouring sites

H-atom parameters constrained

\( w = 1/[\sigma(F_c^2) + (0.0453P)^2 + 0.5135P] \)

\( \Delta/\sigma \)_{\text{max}} = 0.002

\( \Delta \rho_{\text{max}} = 0.26 \ \text{e Å}^{-3} \)

\( \Delta \rho_{\text{min}} = -0.29 \ \text{e Å}^{-3} \)

Special details

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

Refinement. Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with \( U_{	ext{iso}}(H) \) set to 1.2 \( U_{	ext{eq}}(C) \).

Single-crystal X-ray diffraction (SC-XRD) data were collected at 200 or 296 K on a Bruker APEXII CCD diffractometer with graphite-monochromated Mo \( Ka \) radiation using the \textit{APEX2} data collection software and \textit{SAINT} (Bruker 2012) for cell refinement and data reduction. The structures were solved by dual-space methods applying \textit{SHELXTL2018} (Sheldrick, 2015a) and refined by least-squares procedures using \textit{SHELXL2018} (Sheldrick, 2015b). Data were corrected for absorption effects using the numerical method implemented in \textit{SADABS} (Bruker 2012). All non-H atoms were refined anisotropically. The crystal structure diagrams were drawn with \textit{ORTEP-3 for Windows} (Farrugia 2012).

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å\(^2\))

|          | x      | y      | z      | \( \mu^{\circ} \)/\( U_{	ext{eq}} \) |
|----------|--------|--------|--------|---------------------------------|
| S1       | 0.79243 (5) | 0.61702 (2) | 0.46891 (5) | 0.03709 (12) |
| O1       | 0.73327 (18) | 0.65999 (5) | 0.57767 (16) | 0.0546 (3) |
| O2       | 0.91672 (16) | 0.57553 (5) | 0.53509 (15) | 0.0487 (3) |
| O3       | 0.9987 (3) | 0.77311 (7) | 0.5254 (3) | 0.1022 (6) |
| O4       | 1.1144 (3) | 0.69290 (8) | 0.6043 (2) | 0.0839 (5) |
| N1       | 0.61681 (17) | 0.58580 (6) | 0.38325 (18) | 0.0418 (3) |
### Atomic displacement parameters (Å²)

|   | $U^{11}$  | $U^{22}$  | $U^{33}$  | $U^{12}$  | $U^{13}$  | $U^{23}$  |
|---|-----------|-----------|-----------|-----------|-----------|-----------|
| S1 | 0.0407 (2) | 0.0361 (2) | 0.0349 (2) | 0.00043 (15) | 0.00584 (15) | −0.00023 (14) |
| O1 | 0.0670 (8) | 0.0504 (7) | 0.0492 (7) | −0.0017 (6) | 0.0214 (6) | −0.0118 (5) |
| O2 | 0.0468 (7) | 0.0481 (7) | 0.0493 (7) | 0.0008 (5) | −0.0064 (5) | 0.0089 (5) |
| O3 | 0.1429 (18) | 0.0630 (10) | 0.1030 (14) | −0.0190 (11) | 0.0239 (12) | −0.0363 (10) |
| O4 | 0.0995 (13) | 0.0977 (13) | 0.0515 (9) | −0.0136 (10) | −0.0109 (8) | −0.0084 (9) |
| N1 | 0.0335 (7) | 0.0364 (7) | 0.0555 (8) | 0.0049 (5) | 0.0039 (6) | 0.0012 (6) |
| N2 | 0.0699 (11) | 0.0578 (10) | 0.0574 (10) | −0.0260 (9) | 0.0151 (8) | −0.0171 (8) |
| C1 | 0.0417 (9) | 0.0549 (11) | 0.0684 (12) | 0.0155 (8) | 0.0075 (8) | 0.0090 (9) |
| C2 | 0.0349 (9) | 0.0831 (14) | 0.0548 (11) | 0.0060 (9) | 0.0043 (8) | 0.0050 (10) |
| C11 | 0.0387 (8) | 0.0370 (8) | 0.0348 (8) | −0.0030 (6) | 0.0032 (6) | 0.0070 (6) |
| C12 | 0.0381 (8) | 0.0584 (10) | 0.0347 (8) | −0.0066 (7) | 0.0054 (6) | 0.0078 (7) |
| C13 | 0.0530 (11) | 0.0703 (13) | 0.0478 (10) | −0.0229 (10) | 0.0017 (8) | 0.0001 (9) |
| C14 | 0.0835 (15) | 0.0499 (11) | 0.0495 (11) | −0.0217 (10) | 0.0023 (10) | −0.0015 (8) |
| C15 | 0.0749 (13) | 0.0394 (9) | 0.0548 (11) | 0.0063 (9) | −0.0001 (9) | 0.0024 (8) |
| C16 | 0.0457 (9) | 0.0415 (9) | 0.0547 (10) | 0.0042 (7) | −0.0045 (8) | 0.0018 (7) |
| C21 | 0.0382 (8) | 0.0369 (7) | 0.0349 (7) | 0.0017 (6) | 0.0052 (6) | 0.0008 (6) |
| C22 | 0.0528 (10) | 0.0438 (9) | 0.0437 (9) | −0.0075 (7) | 0.0071 (7) | −0.0018 (7) |
C23  0.0842 (15)  0.0601 (12)  0.0616 (13)  −0.0261 (11)  0.0150 (11)  0.0068 (10)
C24  0.0845 (16)  0.0843 (15)  0.0509 (12)  −0.0173 (13)  0.0167 (11)  0.0202 (11)
C25  0.0674 (13)  0.0810 (14)  0.0344 (9)  −0.0051 (11)  0.0056 (8)  0.0028 (9)
C26  0.0474 (9)  0.0527 (10)  0.0376 (8)  −0.0043 (7)  0.0022 (7)  −0.0025 (7)

Geometric parameters (Å, °)

| Bond/Angle | Distance (Å) | Angle (°) |
|------------|-------------|-----------|
| S1—O2      | 1.4190 (12) | C13—C14  | 1.379 (3) |
| S1—O1      | 1.4236 (12) | C13—H13  | 0.9300   |
| S1—N1      | 1.6022 (14) | C14—C15  | 1.376 (3) |
| S1—C21     | 1.7822 (15) | C14—H14  | 0.9300   |
| O3—N2      | 1.216 (2)   | C15—C16  | 1.382 (3) |
| O4—N2      | 1.211 (2)   | C15—H15  | 0.9300   |
| N1—C11     | 1.428 (2)   | C16—H16  | 0.9300   |
| N1—C1      | 1.485 (2)   | C21—C26  | 1.380 (2) |
| N2—C22     | 1.478 (2)   | C21—C22  | 1.381 (2) |
| C1—C2      | 1.517 (3)   | C22—C23  | 1.369 (3) |
| C1—H1A     | 0.9700      | C23—C24  | 1.382 (3) |
| C1—H1B     | 0.9700      | C23—H23  | 0.9300   |
| C2—C12     | 1.497 (3)   | C24—C25  | 1.364 (3) |
| C2—H2A     | 0.9700      | C24—H24  | 0.9300   |
| C2—H2B     | 0.9700      | C25—C26  | 1.387 (2) |
| C11—C16    | 1.377 (2)   | C25—H25  | 0.9300   |
| C11—C12    | 1.386 (2)   | C26—H26  | 0.9300   |
| C12—C13    | 1.377 (3)   | C26—C21  | 1.228 (12) |
| O2—S1—O1   | 120.12 (8)  | C12—C13—C14 | 119.61 (18) |
| O2—S1—N1   | 108.69 (7)  | C12—C13—H13 | 120.2 |
| O1—S1—N1   | 107.25 (8)  | C14—C13—H13 | 120.2 |
| O2—S1—C21  | 108.23 (7)  | C15—C14—C13 | 120.12 (18) |
| O2—S1—C21  | 105.68 (7)  | C15—C14—H14 | 119.9 |
| N1—S1—C21  | 106.04 (7)  | C15—C14—H14 | 119.9 |
| C11—N1—C1  | 109.96 (13) | C14—C15—C16 | 121.33 (19) |
| C11—N1—S1  | 127.90 (11) | C14—C15—H15 | 119.3 |
| C1—N1—S1   | 121.62 (12) | C16—C15—H15 | 119.3 |
| O4—N2—O3   | 125.30 (19) | C11—C16—C15 | 117.77 (17) |
| O4—N2—C22  | 118.03 (17) | C11—C16—H16 | 121.1 |
| O3—N2—C22  | 116.6 (2)   | C15—C16—H16 | 121.1 |
| N1—C1—C2   | 104.61 (14) | C26—C21—C22 | 118.20 (15) |
| N1—C1—H1A  | 110.8       | C26—C21—S1 | 119.31 (12) |
| N1—C1—H1B  | 110.8       | C23—C22—S1 | 122.45 (12) |
| C2—C1—H1A  | 110.8       | C23—C22—C21 | 122.03 (17) |
| C2—C1—H1B  | 110.8       | C23—C22—N2 | 116.49 (16) |
| C1—S1—H1B  | 108.9       | C21—C22—N2 | 121.44 (15) |
| H1A—C1—H1B | 110.8       | C22—C23—C24 | 118.92 (19) |
| C12—C2—C1  | 110.8       | C22—C23—H23 | 120.5 |
| C12—C2—H2A | 110.8       | C24—C23—H23 | 120.5 |
| C12—C2—H2B | 110.8       | C25—C24—C23 | 120.27 (19) |
C1—C2—H2B 110.8 C25—C24—H24 119.9
H2A—C2—H2B 108.8 C23—C24—H24 119.9
C16—C11—C12 121.72 (16) C24—C25—C26 120.26 (18)
C16—C11—N1 129.46 (15) C24—C25—H25 119.9
C12—C11—N1 108.81 (14) C26—C25—H25 119.9
C13—C12—C11 119.44 (17) C21—C26—C25 120.31 (17)
C13—C12—C2 129.88 (17) C21—C26—H26 119.8
C11—C12—C2 110.67 (15) C25—C26—H26 119.8

O2—S1—N1—C11 −26.31 (16) N1—C11—C16—C15 178.24 (16)
O1—S1—N1—C11 −157.59 (13) C14—C15—C16—C11 −0.3 (3)
C21—S1—N1—C11 89.85 (14) O2—S1—C21—C26 90.65 (14)
O2—S1—N1—C1 −139.48 (14) O1—S1—C21—C26 −139.48 (14)
O1—S1—N1—C1 38.16 (16) N1—S1—C21—C26 151.80 (14)
C21—S1—N1—C1 −25.83 (15) O2—S1—C21—C22 −91.72 (15)
C16—C11—C12—C13 1.4 (2) O1—S1—C21—C22 38.16 (16)
N1—C11—C12—C13 −176.87 (17) N1—S1—C21—C22 −125.83 (15)
C16—C11—C12—C13 5.3 (2) O2—S1—C21—C22 −125.83 (15)
O1—S1—C21—C22 176.72 (17) N1—S1—C21—C22 176.87 (17)

Hydrogen-bond geometry (Å, °)

| D—H···A | D—H | H···A | D···A | D—H···A |
|---------|------|-------|-------|---------|
| C16—H16···O2 | 0.93  | 2.41  | 2.975 (2) | 119 |
| C16—H16···O2ii | 0.93  | 2.55  | 3.195 (2) | 127 |
| C23—H23···O1ii | 0.93  | 2.30  | 3.085 (2) | 142 |
| C26—H26···N1 | 0.93  | 2.60  | 2.982 (2) | 106 |

Symmetry codes: (i) −x+2, −y+1, −z+1; (ii) x+1/2, −y+3/2, z−1/2.
2-(Pyrrolidine-1-sulfonyl)aniline (ja192)

Crystal data

C₁₀H₁₄N₂O₂S

\( M_r = 226.29 \)

Monoclinic, \( P_2_1/c \)

\[ a = 16.399 (3) \text{ Å} \]
\[ b = 7.9485 (12) \text{ Å} \]
\[ c = 18.376 (3) \text{ Å} \]
\[ \beta = 113.907 (6)^{\circ} \]

\( V = 2189.7 (6) \text{ Å}^3 \)

\( Z = 8 \)

\( F(000) = 960 \)

\( D_x = 1.373 \text{ Mg m}^{-3} \)

Mo \( K\alpha \) radiation, \( \lambda = 0.71073 \text{ Å} \)

Cell parameters from 9858 reflections

\( \mu = 0.28 \text{ mm}^{-1} \)

\( T = 296 \text{ K} \)

Block, colourless

0.47 × 0.32 × 0.20 mm

Data collection

Bruker APEXII CCD
diffractometer

Radiation source: sealed tube

Graphite monochromator

Detector resolution: 8.3333 pixels mm\(^{-1}\)

\( \phi \) and \( \omega \) scans

Absorption correction: numerical

(SADABS; Bruker, 2008)

\( T_{\text{min}} = 0.927, T_{\text{max}} = 1.000 \)

Refinement

Refinement on \( F^2 \)

Least-squares matrix: full

\( R[F^2 > 2\sigma(F^2)] = 0.035 \)

\( wR(F^2) = 0.107 \)

\( S = 1.04 \)

5477 reflections

287 parameters

0 restraints

Primary atom site location: dual

Secondary atom site location: difference Fourier map

H atoms treated by a mixture of independent and constrained refinement

\( \Delta f^{\text{max}} = 0.33 \text{ e Å}^{-3} \)

\( \Delta f^{\text{min}} = -0.36 \text{ e Å}^{-3} \)

Special details

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

Refinement. Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with \( U_{\text{iso}}(H) \) set to 1.2 \( U_{eq}(C) \).

The nitrogen-bound H atoms were located on a difference map and refined freely. A reflection with large difference between its observed and calculated intensities was omitted. This is due to obstruction by the beam stop.

Single-crystal X-ray diffraction (SC-XRD) data were collected at 200 or 296 K on a Bruker APEXII CCD diffractometer with graphite-monochromated Mo \( K\alpha \) radiation using the APEX2 data collection software and SAINT (Bruker 2012) for cell refinement and data reduction. The structures were solved by dual-space methods applying SHELXT2018 (Sheldrick, 2015a) and refined by least-squares procedures using SHELXL2018 (Sheldrick, 2015b). Data were corrected for absorption effects using the numerical method implemented in SADABS (Bruker 2012). All non-H atoms were refined anisotropically. The crystal structure diagrams were drawn with ORTEP-3 for Windows (Farrugia 2012).
Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

|   | x      | y      | z      | U\(_{eq}\)/U\(_{eq}\) |
|---|--------|--------|--------|-----------------------|
| S1| 0.60593 (2) | 0.11220 (4) | 0.38373 (2) | 0.03995 (10) |
| S2| 0.83675 (3) | 0.54094 (5) | 0.72672 (2) | 0.04473 (11) |
| O11| 0.55812 (7) | 0.21253 (15) | 0.41849 (9) | 0.0639 (3) |
| O12| 0.59914 (8) | 0.15372 (16) | 0.30611 (7) | 0.0604 (3) |
| O21| 0.76909 (9) | 0.41413 (14) | 0.70735 (7) | 0.0567 (3) |
| O22| 0.91886 (9) | 0.51408 (18) | 0.79373 (7) | 0.0691 (4) |
| N11| 0.56877 (8) | -0.07718 (15) | 0.37882 (7) | 0.0403 (3) |
| N12| 0.69275 (18) | 0.1559 (3) | 0.56795 (13) | 0.0824 (7) |
| N21| 0.86112 (9) | 0.55871 (17) | 0.65022 (8) | 0.0461 (3) |
| N22| 0.63790 (10) | 0.6609 (2) | 0.65060 (10) | 0.0564 (4) |
| C11| 0.55387 (14) | -0.1535 (2) | 0.44477 (11) | 0.0597 (5) |
| C11A| 0.508003 | -0.094373 | 0.455235 | 0.072* |
| C11B| 0.608273 | -0.156605 | 0.492981 | 0.072* |
| C12| 0.52380 (17) | -0.3286 (2) | 0.41255 (14) | 0.0740 (6) |
| C12A| 0.533347 | -0.407503 | 0.455504 | 0.089* |
| C12B| 0.461089 | -0.329150 | 0.376874 | 0.089* |
| C13| 0.58061 (14) | -0.3722 (2) | 0.36888 (11) | 0.0592 (4) |
| C13A| 0.549989 | -0.450820 | 0.326115 | 0.071* |
| C13B| 0.636476 | -0.422062 | 0.404671 | 0.071* |
| C14| 0.59696 (11) | -0.2074 (2) | 0.33613 (9) | 0.0490 (4) |
| H14A| 0.659546 | -0.194754 | 0.346526 | 0.059* |
| H14B| 0.561903 | -0.200442 | 0.279189 | 0.059* |
| C21| 0.79052 (12) | 0.5923 (3) | 0.57112 (10) | 0.0560 (4) |
| H21A| 0.756395 | 0.691183 | 0.572202 | 0.067* |
| H21B| 0.750349 | 0.497049 | 0.552570 | 0.067* |
| C22| 0.83964 (15) | 0.6204 (4) | 0.51900 (13) | 0.0842 (7) |
| H22A| 0.830797 | 0.525926 | 0.483167 | 0.101* |
| H22B| 0.818267 | 0.721612 | 0.487506 | 0.101* |
| C23| 0.93579 (15) | 0.6377 (4) | 0.57256 (15) | 0.0835 (7) |
| H23A| 0.960942 | 0.736580 | 0.558485 | 0.100* |
| H23B| 0.96833 | 0.539558 | 0.568498 | 0.100* |
| C24| 0.94016 (12) | 0.6543 (3) | 0.65616 (13) | 0.0707 (5) |
| C24A| 0.994454 | 0.605166 | 0.695106 | 0.085* |
| C24B| 0.936292 | 0.770978 | 0.669874 | 0.085* |
| C11| 0.71909 (9) | 0.11558 (16) | 0.44789 (8) | 0.0362 (3) |
| C11A| 0.74894 (11) | 0.1352 (2) | 0.53050 (9) | 0.0492 (4) |
| C11B| 0.84137 (14) | 0.1302 (3) | 0.57508 (11) | 0.0701 (6) |
| H113| 0.863875 | 0.141455 | 0.630123 | 0.084* |
| C114| 0.89883 (13) | 0.1091 (3) | 0.53914 (14) | 0.0747 (6) |
| H114| 0.959847 | 0.107237 | 0.570304 | 0.090* |
| C115| 0.86913 (11) | 0.0906 (3) | 0.45820 (13) | 0.0648 (5) |
| H115| 0.909391 | 0.076405 | 0.434745 | 0.078* |
| C116| 0.77956 (10) | 0.0933 (2) | 0.41274 (10) | 0.0456 (3) |
| H116| 0.758579 | 0.080195 | 0.357861 | 0.055* |
| C211| 0.79105 (9) | 0.73166 (17) | 0.74078 (8) | 0.0391 (3) |
C212 0.69962 (9) 0.76850 (18) 0.70242 (8) 0.0395 (3)
C213 0.67185 (11) 0.9265 (2) 0.71751 (10) 0.0475 (3)
H213 0.611709 0.954422 0.692911 0.057*
C214 0.73005 (12) 1.0408 (2) 0.76850 (18) 0.70242 (8) 0.0395 (3)
H214 0.709137 1.144299 0.775829 0.067*
C215 0.81985 (13) 1.0037 (2) 0.80430 (12) 0.0638 (5)
H215 0.859590 1.081726 0.837922 0.077*
C216 0.84970 (11) 0.8504 (2) 0.79108 (10) 0.0549 (4)
H216 0.910132 0.825037 0.816091 0.066*
H12C 0.7160 (18) 0.193 (4) 0.6109 (17) 0.095 (9)*
H12D 0.641 (2) 0.190 (4) 0.5399 (19) 0.113 (12)*
H21C 0.5862 (16) 0.690 (3) 0.6389 (13) 0.073 (7)*
H21D 0.6538 (13) 0.556 (3) 0.6567 (12) 0.060 (6)*

Atomic displacement parameters (Å²)

|       | U¹¹   | U¹²   | U¹³   | U²²   | U²³   | U³³   |
|-------|-------|-------|-------|-------|-------|-------|
| S1    | 0.02972 (16) | 0.03424 (17) | 0.0509 (2) | -0.00093 (12) | 0.01122 (14) | 0.00394 (13) |
| S2    | 0.0512 (2) | 0.03890 (19) | 0.03977 (19) | 0.00835 (15) | 0.01394 (16) | 0.00206 (14) |
| O11   | 0.0418 (6) | 0.0440 (6) | 0.1067 (10) | 0.0032 (5) | 0.0311 (6) | -0.0126 (6) |
| O12   | 0.0500 (6) | 0.0649 (7) | 0.0500 (6) | -0.0067 (5) | 0.0034 (5) | 0.0230 (5) |
| O21   | 0.0805 (8) | 0.0364 (5) | 0.0607 (7) | -0.0048 (5) | 0.0364 (6) | 0.0000 (5) |
| O22   | 0.0678 (8) | 0.0739 (8) | 0.0485 (7) | 0.0292 (7) | 0.0060 (6) | 0.0050 (6) |
| N11   | 0.0384 (6) | 0.0377 (6) | 0.0470 (6) | -0.0090 (5) | 0.0196 (5) | -0.0053 (5) |
| N12   | 0.0955 (16) | 0.1087 (16) | 0.0550 (10) | -0.0348 (14) | 0.0430 (11) | -0.0311 (11) |
| N21   | 0.0429 (6) | 0.0480 (7) | 0.0467 (7) | 0.0047 (5) | 0.0174 (5) | -0.0002 (5) |
| N22   | 0.0381 (7) | 0.0600 (9) | 0.0651 (9) | -0.0058 (7) | 0.0148 (7) | -0.0136 (7) |
| C11   | 0.0825 (12) | 0.0509 (9) | 0.0633 (10) | -0.0215 (9) | 0.0475 (10) | -0.0106 (8) |
| C12   | 0.1049 (16) | 0.0496 (10) | 0.0838 (14) | -0.0309 (10) | 0.0550 (13) | -0.0085 (9) |
| C13   | 0.0738 (11) | 0.0421 (8) | 0.0551 (10) | -0.0033 (8) | 0.0192 (9) | -0.0041 (7) |
| C14   | 0.0550 (9) | 0.0456 (8) | 0.0495 (8) | -0.0087 (7) | 0.0242 (7) | -0.0122 (6) |
| C21   | 0.0502 (9) | 0.0693 (11) | 0.0465 (9) | 0.0003 (8) | 0.0175 (7) | 0.0075 (8) |
| C22   | 0.0775 (14) | 0.121 (2) | 0.0628 (12) | 0.0000 (13) | 0.0370 (11) | 0.0190 (12) |
| C23   | 0.0653 (12) | 0.1083 (19) | 0.0937 (16) | 0.0056 (12) | 0.0495 (12) | 0.0194 (14) |
| C24   | 0.0447 (9) | 0.0847 (14) | 0.0824 (13) | -0.0046 (9) | 0.0255 (9) | -0.0003 (11) |
| C111  | 0.0322 (6) | 0.0331 (6) | 0.0394 (7) | -0.0036 (5) | 0.0105 (5) | 0.0005 (5) |
| C112  | 0.0577 (9) | 0.0442 (8) | 0.0423 (8) | -0.0116 (7) | 0.0168 (7) | -0.0070 (6) |
| C113  | 0.0710 (12) | 0.0640 (11) | 0.0459 (9) | -0.0063 (9) | -0.0066 (9) | -0.0071 (8) |
| C114  | 0.0401 (9) | 0.0711 (13) | 0.0851 (15) | 0.0055 (8) | -0.0035 (9) | -0.0100 (11) |
| C115  | 0.0383 (8) | 0.0682 (11) | 0.0867 (14) | 0.0021 (8) | 0.0240 (9) | -0.0051 (10) |
| C116  | 0.0390 (7) | 0.0473 (8) | 0.0508 (8) | -0.0013 (6) | 0.0185 (6) | 0.0010 (6) |
| C211  | 0.0400 (7) | 0.0362 (7) | 0.0388 (7) | 0.0002 (5) | 0.0138 (6) | -0.0023 (5) |
| C212  | 0.0389 (7) | 0.0420 (7) | 0.0405 (7) | -0.0038 (6) | 0.0190 (6) | 0.0014 (6) |
| C213  | 0.0458 (8) | 0.0462 (8) | 0.0578 (9) | 0.0050 (6) | 0.0286 (7) | 0.0064 (7) |
| C214  | 0.0698 (11) | 0.0390 (8) | 0.0714 (11) | -0.0006 (7) | 0.0425 (9) | -0.0054 (7) |
| C215  | 0.0622 (11) | 0.0522 (9) | 0.0772 (12) | -0.0157 (8) | 0.0285 (10) | -0.0267 (9) |
| C216  | 0.0437 (8) | 0.0553 (9) | 0.0582 (10) | -0.0054 (7) | 0.0129 (7) | -0.0162 (8) |
### Geometric parameters (Å, °)

| Bond/Angle | Length/Distance | Bond/Angle | Length/Distance |
|------------|----------------|------------|----------------|
| S1—O12     | 1.4236 (13)    | C21—H21A   | 0.9700         |
| S1—O11     | 1.4369 (12)    | C21—H21B   | 0.9700         |
| S1—N11     | 1.6127 (12)    | C22—C23    | 1.489 (3)      |
| S1—C11     | 1.7496 (14)    | C22—H22A   | 0.9700         |
| S2—O22     | 1.4252 (12)    | C22—H22B   | 0.9700         |
| S2—O21     | 1.4330 (13)    | C23—C24    | 1.514 (3)      |
| S2—N21     | 1.6161 (14)    | C23—H23A   | 0.9700         |
| S2—C21     | 1.7558 (14)    | C23—H23B   | 0.9700         |
| N11—C11    | 1.462 (2)      | C24—H24A   | 0.9700         |
| N11—C14    | 1.4813 (19)    | C24—H24B   | 0.9700         |
| N12—C112   | 1.365 (3)      | C111—C112  | 1.397 (2)      |
| N12—H12C   | 0.78 (3)       | C111—C112  | 1.402 (2)      |
| N12—H12D   | 0.84 (3)       | C112—C113  | 1.401 (3)      |
| N21—C24    | 1.468 (2)      | C113—C114  | 1.363 (3)      |
| N21—C21    | 1.470 (2)      | C113—H113  | 0.9300         |
| N22—C212   | 1.372 (2)      | C114—C115  | 1.373 (3)      |
| N22—H21C   | 0.82 (2)       | C114—H114  | 0.9300         |
| N22—H21D   | 0.87 (2)       | C115—C116  | 1.364 (2)      |
| C11—C12    | 1.514 (2)      | C115—H115  | 0.9300         |
| C11—H11A   | 0.9700         | C116—H116  | 0.9300         |
| C11—H11B   | 0.9700         | C211—C216  | 1.396 (2)      |
| C12—C13    | 1.496 (3)      | C211—C212  | 1.405 (2)      |
| C12—H12A   | 0.9700         | C212—C213  | 1.402 (2)      |
| C12—H12B   | 0.9700         | C213—C214  | 1.364 (2)      |
| C13—C14    | 1.510 (2)      | C213—H213  | 0.9300         |
| C13—H13A   | 0.9700         | C214—C215  | 1.381 (3)      |
| C13—H13B   | 0.9700         | C214—H214  | 0.9300         |
| C14—H14A   | 0.9700         | C215—C216  | 1.371 (2)      |
| C14—H14B   | 0.9700         | C215—H215  | 0.9300         |
| C21—C22    | 1.497 (3)      | C216—H216  | 0.9300         |


| Bond/Distance | Length/Distance |
|---------------|----------------|
| O12—S1—O11   | 118.78 (8)     |
| O12—S1—N11   | 106.62 (7)     |
| O11—S1—N11   | 106.32 (7)     |
| O12—S1—C11   | 107.62 (7)     |
| O11—S1—C111  | 108.23 (7)     |
| N11—S1—C111  | 109.00 (6)     |
| O22—S2—O21   | 118.33 (8)     |
| O22—S2—N21   | 106.53 (8)     |
| O21—S2—N21   | 106.55 (7)     |
| O22—S2—C211  | 108.20 (7)     |
| O21—S2—C211  | 108.07 (7)     |
| N21—S2—C211  | 108.86 (7)     |
| N21—N11—C14  | 110.00 (13)    |
| C11—N11—S1   | 121.83 (10)    |
| C14—N11—S1   | 119.32 (10)    |
C112—N12—H12C 114 (2)  N21—C24—H24B 111.4
C112—N12—H12D 117 (2)  C23—C24—H24B 111.4
H12C—N12—H12D 117 (3)  H24A—C24—H24B 109.3
C24—N21—C21 107.31 (14)  C116—C111—C112 120.86 (14)
C24—N21—S2 120.18 (12)  C116—C111—S1 116.38 (11)
C21—N21—S2 120.19 (11)  C112—C111—S1 122.75 (11)
C212—N22—H21C 113.7 (16)  N12—C112—C113 119.99 (18)
C212—N22—H21D 114.3 (13)  N12—C112—C111 123.25 (17)
H21C—N22—H21D 117 (3)  H24A—C24—H24B 109.3
N11—C11—C12 101.23 (14)  C114—C113—C112 121.12 (17)
N11—C11—H11A 111.5  C114—C113—H113 119.4
C12—C11—H11A 111.5  C112—C113—H113 119.4
N11—C11—H11B 111.5  C113—C114—C115 121.80 (17)
C12—C11—H11B 111.5  C113—C114—H114 119.1
H11A—C11—H11B 109.3  C115—C114—H114 119.1
C13—C12—C11 104.33 (14)  C116—C115—C114 118.88 (18)
C13—C12—H12A 110.9  C116—C115—H115 120.6
C11—C12—H12A 110.9  C114—C115—H115 120.6
C13—C12—H12B 110.9  C115—C116—C111 120.58 (16)
C11—C12—H12B 110.9  C115—C116—H116 119.7
H12A—C12—H12B 108.9  C111—C116—H116 119.7
C12—C13—C14 105.24 (14)  C216—C211—C212 119.99 (14)
C12—C13—H13A 110.7  C216—C211—S2 117.42 (11)
C14—C13—H13A 110.7  C212—C211—S2 122.57 (11)
C12—C13—H13B 110.7  N22—C212—C213 119.25 (14)
C14—C13—H13B 110.7  N22—C212—C211 123.75 (14)
H13A—C13—H13B 108.8  C213—C212—C211 116.98 (13)
N11—C14—C13 104.53 (13)  C214—C213—C212 122.24 (15)
N11—C14—H14A 110.8  C214—C213—H213 118.9
C13—C14—H14A 110.8  C212—C213—H213 118.9
N11—C14—H14B 110.8  C213—C214—C215 120.37 (15)
C13—C14—H14B 110.8  C213—C214—H214 119.8
H14A—C14—H14B 108.9  C215—C214—H214 119.8
N21—C21—C22 104.32 (15)  C216—C215—C214 119.19 (16)
N21—C21—H21A 110.9  C216—C215—H215 120.4
C22—C21—H21A 110.9  C214—C215—H215 120.4
N21—C21—H21B 110.9  C215—C216—C211 121.23 (16)
C22—C21—H21B 110.9  C215—C216—H216 119.4
H21A—C21—H21B 108.9  C211—C216—H216 119.4
O12—S1—N11—C11 −171.19 (13)  O11—S1—C111—C112 29.11 (14)
O11—S1—N11—C11 −43.54 (15)  N11—S1—C111—C112 −86.12 (13)
C111—S1—N11—C11 72.91 (14)  C116—C111—C112—N12 −179.45 (18)
O12—S1—N11—C14 44.67 (13)  S1—C111—C112—N12 0.4 (2)
O11—S1—N11—C14 172.32 (12)  C116—C111—C112—C113 178.01 (13)
C111—S1—N11—C14 −71.23 (13)  S1—C111—C112—C113 −71.23 (13)
O22—S2—N21—C24 −40.89 (16)  N12—C112—C113—C114 179.8 (2)
O21—S2—N21—C24 −168.09 (14)  C111—C112—C113—C114 0.7 (3)
Hydrogen-bond geometry (Å, °)

| D—H···A     | D—H | H···A | D···A | D—H···A |
|-------------|------|-------|-------|---------|
| N12—H12C···O21 | 0.78 (3) | 2.39 (3) | 3.121 (2) | 155 (3) |
| N12—H12D···O11  | 0.84 (3) | 2.10 (3) | 2.776 (3) | 138 (3) |
| N22—H21C···O11i | 0.82 (2) | 2.30 (2) | 3.106 (2) | 168 (2) |
| N22—H21D···O21  | 0.87 (2) | 2.07 (2) | 2.783 (2) | 138.8 (17) |
| C114—H114···O22a | 0.93 | 2.59 | 3.391 (2) | 144 |
| C116—H116···O12  | 0.93 | 2.46 | 2.8505 (19) | 105 |
| C216—H216···O22  | 0.93 | 2.52 | 2.897 (2) | 105 |

Symmetry codes: (i) −x+1, −y+1, −z+1; (ii) −x+2, y−1/2, −z+3/2.

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### 2-(Piperidine-1-sulfonyl)aniline (ka115)

#### Crystal data

C₁₁H₁₆N₂O₂S

Mᵣ = 240.32

Orthorhombic, Pbca

| Parameter       | Value                  |
|-----------------|------------------------|
| a               | 11.1747 (4) Å          |
| b               | 10.4850 (4) Å          |
| c               | 20.1368 (8) Å          |
| V               | 2359.36 (15) Å³        |
| Z               | 8                      |
| F(000)          | 1024                   |

\(D_\lambda = 1.353 \text{ Mg m}^{-3}\)

Mo Kα radiation, \(\lambda = 0.71073 \text{ Å}\)

Cell parameters from 9577 reflections

\(\theta = 2.9−28.3^\circ\)

\(\mu = 0.26 \text{ mm}^{-1}\)

\(T = 200 \text{ K}\)

Block, colourless

0.49 × 0.26 × 0.25 mm
**Data collection**

- **Bruker APEXII CCD**
- **Radiation source**: sealed tube
- **Graphite monochromator**: 8.3333 pixels mm\(^{-1}\)
- **Detector resolution**: 8.3333 pixels mm\(^{-1}\)
- **φ and ω scans**
- **Absorption correction**: numerical (SADABS; Bruker, 2008)
- **T\(_{\text{min}}\) = 0.944, T\(_{\text{max}}\) = 1.000

**Refinement**

- **Refinement on F\(^2\)**
- **Least-squares matrix**: full
- **R\([F^2 > 2\sigma(F^2)]\) = 0.029**
- **wR(F^2) = 0.087**
- **S = 1.05**
- **2935 reflections**
- **153 parameters**
- **0 restraints**
- **Primary atom site location**: dual
- **Secondary atom site location**: difference Fourier map
- **Hydrogen site location**: mixed
- **H atoms treated by a mixture of independent and constrained refinement**

**Special details**

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

**Refinement.** Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with U\(_{\text{iso}}\)(H) set to 1.2 U\(_{\text{eq}}\)(C). The nitrogen-bound H atoms were located on a difference map and refined freely.

**Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å\(^2\))**

|     | x     | y     | z     | U\(_{\text{iso}}\)/U\(_{\text{eq}}\) |
|-----|-------|-------|-------|-----------------------------------|
| S1  | 0.66247 (2) | 0.46255 (3) | 0.35628 (2) | 0.02489 (10) |
| O1  | 0.78413 (7)  | 0.45299 (8)  | 0.37905 (5)  | 0.0331 (2)    |
| O2  | 0.60807 (8)  | 0.58657 (8)  | 0.35302 (5)  | 0.0344 (2)    |
| N1  | 0.48648 (11) | 0.51544 (13) | 0.23579 (7)  | 0.0417 (3)    |
| N2  | 0.58073 (8)  | 0.37768 (9)  | 0.40733 (5)  | 0.0257 (2)    |
| C11 | 0.65595 (9)  | 0.38973 (11) | 0.27755 (6)  | 0.0245 (2)    |
| C12 | 0.56770 (10) | 0.41892 (11) | 0.22957 (6)  | 0.0281 (2)    |
| C13 | 0.56702 (11) | 0.34467 (13) | 0.17139 (6)  | 0.0340 (3)    |
| H13 | 0.509126     | 0.361787     | 0.138016     | 0.041*        |
| C14 | 0.64803 (12) | 0.24808 (13) | 0.16172 (6)  | 0.0357 (3)    |
| H14 | 0.644395     | 0.199006     | 0.122112     | 0.043*        |
### Atomic displacement parameters (Å²)

|   | $U^{11}$  | $U^{22}$  | $U^{33}$  | $U^{12}$  | $U^{13}$  | $U^{23}$  |
|---|-----------|-----------|-----------|-----------|-----------|-----------|
|S1 | 0.02117 (15) | 0.02347 (15) | 0.03003 (16) | $-0.00296$ (9) | $-0.00057$ (10) | $-0.00017$ (10) |
|O1 | 0.0226 (4) | 0.0393 (5) | 0.0373 (5) | $-0.0060$ (3) | $-0.0045$ (3) | $-0.0021$ (4) |
|O2 | 0.0350 (5) | 0.0231 (4) | 0.0451 (5) | $-0.0009$ (3) | 0.0032 (4) | 0.0006 (4) |
|N1 | 0.0315 (6) | 0.0460 (7) | 0.0476 (7) | 0.0119 (5) | $-0.0111$ (5) | 0.0009 (6) |
|N2 | 0.0240 (4) | 0.0249 (5) | 0.0280 (5) | $-0.0019$ (4) | 0.0011 (4) | 0.0007 (4) |
|C11| 0.0214 (5) | 0.0253 (5) | 0.0267 (5) | $-0.0027$ (4) | 0.0000 (4) | 0.0037 (4) |
|C12| 0.0223 (5) | 0.0299 (6) | 0.0319 (6) | $-0.0030$ (4) | $-0.0010$ (4) | 0.0078 (5) |
|C13| 0.0318 (6) | 0.0419 (7) | 0.0284 (6) | $-0.0068$ (5) | $-0.0052$ (5) | 0.0056 (5) |
|C14| 0.0425 (7) | 0.0369 (7) | 0.0277 (6) | $-0.0089$ (5) | 0.0021 (5) | $-0.0001$ (5) |
|C15| 0.0360 (6) | 0.0300 (6) | 0.0349 (6) | 0.0010 (5) | 0.0073 (5) | 0.0021 (5) |
|C16| 0.0251 (5) | 0.0287 (6) | 0.0303 (5) | 0.0002 (4) | 0.0008 (4) | 0.0056 (4) |
|C21| 0.0366 (6) | 0.0278 (6) | 0.0315 (6) | 0.0029 (5) | 0.0030 (5) | 0.0057 (5) |
|C22| 0.0485 (8) | 0.0458 (8) | 0.0344 (7) | 0.0000 (6) | 0.0024 (6) | 0.0149 (6) |
|C23| 0.0457 (8) | 0.0512 (8) | 0.0409 (7) | $-0.0114$ (7) | 0.0090 (6) | 0.0132 (6) |
|C24| 0.0321 (6) | 0.0338 (9) | 0.0486 (8) | $-0.0040$ (6) | 0.0118 (6) | 0.0041 (7) |
|C25| 0.0234 (5) | 0.0384 (7) | 0.0455 (7) | $-0.0019$ (5) | 0.0014 (5) | 0.0089 (6) |

### Geometric parameters (Å, °)

- **S1—O2**: 1.4369 (9)
- **C15—H15**: 0.9500
- **S1—O1**: 1.4382 (8)
- **C16—H16**: 0.9500
- **S1—N2**: 1.6381 (10)
- **C21—C22**: 1.5178 (17)
- **S1—C11**: 1.7611 (12)
- **C21—H21A**: 0.9900

*Acta Cryst. (2022), C78, 730-742*
| Bond          | Distance (Å) | Bond          | Distance (Å) |
|---------------|--------------|---------------|--------------|
| N1—C12        | 1.3652 (17)  | C21—H21B     | 0.9900       |
| N1—H1A        | 0.836 (19)   | C22—C23      | 1.518 (2)    |
| N1—H1B        | 0.852 (17)   | C22—H22A     | 0.9900       |
| N2—C21        | 1.4780 (15)  | C22—H22B     | 0.9900       |
| N2—C25        | 1.4804 (15)  | C23—C24      | 1.518 (2)    |
| C11—C16       | 1.4014 (16)  | C23—H23A     | 0.9900       |
| C11—C12       | 1.4141 (15)  | C23—H23B     | 0.9900       |
| C12—C13       | 1.4066 (18)  | C24—C25      | 1.5200 (18)  |
| C13—C14       | 1.3723 (19)  | C24—H24A     | 0.9900       |
| C13—H13       | 0.9500       | C24—H24B     | 0.9900       |
| C14—C15       | 1.3901 (18)  | C25—H25A     | 0.9900       |
| C14—H14       | 0.9500       | C25—H25B     | 0.9900       |
| C15—C16       | 1.3759 (17)  |               |              |
| O2—S1—O1      | 118.52 (5)   | N2—C21—C22   | 109.85 (11)  |
| O2—S1—N2      | 106.51 (5)   | N2—C21—H21A  | 109.7        |
| O1—S1—N2      | 106.81 (5)   | C22—C21—H21A | 109.7        |
| O2—S1—C11     | 109.50 (5)   | N2—C21—H21B  | 109.7        |
| O1—S1—C11     | 107.21 (5)   | C22—C21—H21B | 109.7        |
| C12—N1—H1A    | 117.2 (12)   | H21A—C21—H21B| 108.2        |
| C12—N1—H1B    | 119.7 (10)   | C21—C22—C23  | 111.39 (11)  |
| H1A—N1—H1B    | 122.5 (16)   | C21—C22—C23  | 109.4        |
| C21—N2—C25    | 112.41 (10)  | C23—C22—C23  | 109.4        |
| C21—N2—S1     | 115.21 (8)   | C23—C22—H22B | 109.4        |
| C25—N2—S1     | 115.59 (8)   | H22A—C22—H22B| 108.0        |
| C16—C11—C12   | 120.52 (11)  | C24—C23—C22  | 109.84 (12)  |
| C16—C11—S1    | 115.92 (8)   | C24—C23—H23A | 109.7        |
| C12—C11—S1    | 123.37 (9)   | C22—C23—H23A | 109.7        |
| N1—C12—C13    | 118.89 (11)  | C24—C23—H23B | 109.7        |
| N1—C12—C11    | 124.15 (12)  | C22—C23—H23B | 109.7        |
| C13—C12—C11   | 116.94 (11)  | H23A—C23—H23B| 108.2        |
| C14—C13—C12   | 121.54 (11)  | C23—C24—C25  | 111.08 (12)  |
| C14—C13—H13   | 119.2        | C23—C24—H24A | 109.4        |
| C12—C13—H13   | 119.2        | C25—C24—H24A | 109.4        |
| C13—C14—C15   | 121.24 (12)  | C23—C24—H24B | 109.4        |
| C13—C14—H14   | 119.4        | C25—C24—H24B | 109.4        |
| C15—C14—H14   | 119.4        | H24A—C24—H24B| 108.0        |
| C16—C15—C14   | 118.73 (12)  | N2—C25—C24   | 109.28 (11)  |
| C16—C15—H15   | 120.6        | N2—C25—H25A  | 109.8        |
| C14—C15—H15   | 120.6        | C24—C25—H25A | 109.8        |
| C15—C16—C11   | 121.03 (11)  | N2—C25—H25B  | 109.8        |
| C15—C16—H16   | 119.5        | C24—C25—H25B | 109.8        |
| C11—C16—H16   | 119.5        | H25A—C25—H25B| 108.3        |
| O2—S1—N2—C21  | 177.25 (8)   | N1—C12—C13—C14| 178.65 (12)  |
| O1—S1—N2—C21  | 55.17 (9)    | C11—C12—C13—C14| 0.20 (17)    |
| C11—S1—N2—C21 | 59.79 (9)    | C12—C13—C14—C15|−0.85 (19)    |

*Acta Cryst. (2022), C78, 730-742*
| Bond                  | Distance (Å) | Angle (°) |
|-----------------------|--------------|-----------|
| O2—S1—N2—C25         | 43.41 (10)   |           |
| O1—S1—N2—C25         | 170.99 (9)   |           |
| C11—S1—N2—C25        | −74.05 (10)  |           |
| O2—S1—C11—C16        | 158.65 (8)   |           |
| O1—S1—C11—C16        | 28.86 (10)   |           |
| N2—S1—C11—C16        | −85.83 (9)   |           |
| O2—S1—C11—C12        | −26.31 (11)  |           |
| O1—S1—C11—C12        | −156.11 (9)  |           |
| N2—S1—C11—C12        | 89.20 (10)   |           |
| C16—C11—C12—N1       | −177.75 (12) |           |
| C16—C11—C12—N1       | 7.43 (17)    |           |
| C16—C11—C12—C13      | 0.61 (16)    |           |
| S1—C11—C12—C13       | −174.21 (8)  |           |

Hydrogen-bond geometry (Å, °)

|        | D—H···A  |        | D—H···A  | D···A  |       | D—H···A  |
|--------|---------|--------|---------|--------|--------|---------|
| N1—H1A···O1i | 0.836 (19) | 2.496 (19) | 3.3000 (16) | 161.8 (16) |
| N1—H1B···O2  | 0.852 (17) | 2.156 (17) | 2.8240 (17) | 135.1 (14) |
| C16—H16B···O1 | 0.95     | 2.48    | 2.8774 (15) | 105    |
| C16—H16B···O2ii | 0.95   | 2.48    | 3.2576 (14) | 139    |
| C21—H21A···O1 | 0.99    | 2.55    | 2.9635 (15) | 105    |
| C25—H25B···O2ii | 0.99 | 2.44 | 2.8675 (15) | 106    |

Symmetry codes: (i) x−1/2, y, −z+1/2; (ii) −x+3/2, y−1/2, z.

2-(2,3-Dihydro-1H-indole-1-sulfonyl)aniline (ja189)

Crystal data

C14H14N2O2S

F(000) = 576
d = 1.397 Mg m−3
Monoclinic, P2₁/n

Cell parameters from 9932 reflections

θ = 2.4–28.4°
µ = 0.25 mm⁻¹

T = 296 K

Block, colourless

0.54 × 0.34 × 0.34 mm

Data collection

Bruker APEXII CCD
diffractometer

28600 measured reflections
3275 independent reflections

Radiation source: sealed tube

2726 reflections with I > 2σ(I)

Graphite monochromator

Rint = 0.031

Detector resolution: 8.3333 pixels mm⁻¹

θmax = 28.7°, θmin = 2.4°

h = −13→13

k = −13→12

l = −16→17

Tmin = 0.925, Tmax = 1.000

Acta Cryst. (2022). C78, 730-742
Refinement

Refinement on \( F^2 \)
Least-squares matrix: full
\( R[F^2 > 2\sigma(F^2)] = 0.039 \)
\( wR(F^2) = 0.113 \)
\( S = 1.05 \)
3275 reflections
180 parameters
0 restraints
Primary atom site location: dual
Secondary atom site location: difference Fourier map
Hydrogen site location: mixed
H atoms treated by a mixture of independent and constrained refinement
\( w = 1/[\sigma^2(F_o^2) + (0.053P)^2 + 0.4178P] \)
where \( P = (F_o^2 + 2F_c^2)/3 \)
\( \Delta/\sigma \) max < 0.001
\( \Delta \rho_{\text{max}} = 0.27 \text{ e Å}^{-3} \)
\( \Delta \rho_{\text{min}} = -0.42 \text{ e Å}^{-3} \)

Special details

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

Refinement. Carbon-bound H atoms were placed in calculated positions and were included in the refinement in the riding model approximation, with \( U_{	ext{iso}}(H) \) set to 1.2 \( U_{eq}(C) \).
The nitrogen-bound H atoms were located on a difference map and refined freely.

Single-crystal X-ray diffraction (SC-XRD) data were collected at 200 or 296 K on a Bruker APEXII CCD diffractometer with graphite-monochromated Mo \( K\alpha \) radiation using the APEX2 data collection software and SAINT (Bruker 2012) for cell refinement and data reduction. The structures were solved by dual-space methods applying SHELXT2018 (Sheldrick, 2015a) and refined by least-squares procedures using SHELXL2018 (Sheldrick, 2015b). Data were corrected for absorption effects using the numerical method implemented in SADABS (Bruker 2012). All non-H atoms were refined anisotropically. The crystal structure diagrams were drawn with ORTEP-3 for Windows (Farrugia 2012).

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

|    | x      | y      | z      | \( U_{\text{iso}}^*/U_{eq} \) |
|----|--------|--------|--------|---------------------|
| S  | 0.38977 (4) | 0.26951 (4) | 0.46693 (3) | 0.04455 (13) |
| O1 | 0.46972 (13) | 0.21097 (14) | 0.55683 (9) | 0.0646 (4) |
| O2 | 0.45941 (11) | 0.31734 (14) | 0.38820 (9) | 0.0593 (3) |
| N1 | 0.31329 (14) | 0.39561 (13) | 0.50488 (10) | 0.0476 (3) |
| N2 | 0.1992 (2) | 0.27928 (18) | 0.25271 (12) | 0.0630 (4) |
| C1 | 0.20394 (18) | 0.60239 (17) | 0.50168 (14) | 0.0536 (4) |
| H1A| 0.262936 | 0.675102 | 0.528584 | 0.064* |
| H1B| 0.119055 | 0.635928 | 0.460230 | 0.064* |
| C2 | 0.27807 (18) | 0.51224 (17) | 0.43895 (13) | 0.0532 (4) |
| H2A| 0.218044 | 0.489119 | 0.374487 | 0.064* |
| H2B| 0.361389 | 0.553051 | 0.423985 | 0.064* |
| C11| 0.23714 (14) | 0.39828 (15) | 0.58651 (11) | 0.0418 (3) |
| C12| 0.17276 (15) | 0.51848 (15) | 0.58744 (12) | 0.0457 (3) |
| C13| 0.09543 (18) | 0.5451 (2) | 0.66236 (15) | 0.0621 (5) |
| H13| 0.052108 | 0.625529 | 0.663818 | 0.074* |
| C14| 0.08286 (19) | 0.4512 (2) | 0.73524 (14) | 0.0681 (5) |
| H14| 0.030634 | 0.468525 | 0.785769 | 0.082* |
| C15| 0.1472 (2) | 0.3326 (2) | 0.73330 (13) | 0.0626 (5) |
| H15| 0.137895 | 0.270445 | 0.782820 | 0.075* |
| C16| 0.22563 (19) | 0.30382 (18) | 0.65894 (13) | 0.0542 (4) |
| H16| 0.269140 | 0.223417 | 0.657880 | 0.065* |
### Atomic displacement parameters (Å²)

|       | U₁¹ | U₂² | U₃³ | U₁₂ | U₁₃ | U₂₃ |
|-------|-----|-----|-----|-----|-----|-----|
| S1    | 0.03429 (19) | 0.0609 (3) | 0.0368 (2) | 0.00384 (14) | 0.00238 (14) | −0.00607 (15) |
| O1    | 0.0543 (7) | 0.0854 (9) | 0.0466 (6) | 0.0190 (6) | −0.0106 (5) | −0.0049 (6) |
| O2    | 0.0413 (6) | 0.0893 (9) | 0.0505 (6) | −0.0069 (6) | 0.0168 (5) | −0.0118 (6) |
| N1    | 0.0533 (7) | 0.0477 (7) | 0.0460 (7) | −0.0005 (5) | 0.0201 (6) | 0.0009 (5) |
| N2    | 0.0658 (10) | 0.0767 (11) | 0.0394 (7) | −0.0037 (8) | −0.0085 (7) | 0.0020 (7) |
| C1    | 0.0514 (9) | 0.0459 (8) | 0.0602 (10) | −0.0043 (7) | 0.0018 (7) | −0.0025 (7) |
| C2    | 0.0580 (9) | 0.0544 (9) | 0.0467 (8) | −0.0048 (7) | 0.0082 (7) | 0.0049 (7) |
| C11   | 0.0386 (7) | 0.0491 (8) | 0.0382 (7) | −0.0074 (6) | 0.0089 (5) | −0.0069 (6) |
| C12   | 0.0367 (7) | 0.0504 (8) | 0.0478 (8) | −0.0058 (6) | 0.0021 (6) | −0.0117 (6) |
| C13   | 0.0494 (9) | 0.0730 (12) | 0.0643 (11) | 0.0018 (8) | 0.0120 (8) | −0.0241 (9) |
| C14   | 0.0543 (10) | 0.1020 (16) | 0.0522 (10) | −0.0112 (10) | 0.0210 (8) | −0.0224 (10) |
| C15   | 0.0631 (10) | 0.0831 (13) | 0.0444 (8) | −0.0183 (10) | 0.0172 (8) | −0.0028 (9) |
| C16   | 0.0612 (10) | 0.0570 (9) | 0.0472 (8) | −0.0061 (8) | 0.0174 (7) | 0.0004 (7) |
| C21   | 0.0431 (7) | 0.0464 (8) | 0.0408 (7) | 0.0043 (6) | 0.0059 (6) | −0.0059 (6) |
| C22   | 0.0404 (7) | 0.0561 (9) | 0.0410 (7) | 0.0047 (6) | 0.0063 (6) | −0.0137 (7) |
| C23   | 0.0492 (9) | 0.0793 (13) | 0.0604 (10) | −0.0090 (8) | 0.0090 (8) | −0.0296 (9) |
| C24   | 0.0846 (15) | 0.0786 (14) | 0.0913 (16) | −0.0327 (12) | 0.0343 (13) | −0.0391 (13) |
| C25   | 0.126 (2) | 0.0500 (11) | 0.0938 (17) | −0.0192 (12) | 0.0453 (16) | −0.0082 (11) |
| C26   | 0.0888 (14) | 0.0504 (10) | 0.0582 (10) | 0.0058 (9) | 0.0139 (9) | 0.0003 (8) |

### Geometric parameters (Å, °)

|       |        |       |       |       |       |       |
|-------|--------|-------|-------|-------|-------|-------|
| S1—O1 | 1.4277 (12) | C13—C14 | 1.383 (3) |
| S1—O2 | 1.4317 (12) | C13—H13 | 0.9300 |
| S1—N1 | 1.6205 (14) | C14—C15 | 1.373 (3) |
| S1—C21| 1.7486 (16) | C14—H14 | 0.9300 |
| N1—C11| 1.4203 (18) | C15—C16 | 1.387 (2) |
| N1—C2 | 1.482 (2) | C15—H15 | 0.9300 |
| N2—C22| 1.358 (2) | C16—H16 | 0.9300 |
| N2—H2C| 0.86 (3) | C21—C26 | 1.389 (2) |
| N2—H2D| 0.89 (2) | C21—C22 | 1.414 (2) |
| C1—C12| 1.498 (2) | C22—C23 | 1.396 (2) |
| Bond/Angle                  | Distance/Value     |
|----------------------------|--------------------|
| C1—C2                      | 1.514 (2)          |
| C1—H1A                     | 0.9700             |
| C1—H1B                     | 0.9700             |
| C2—H2A                     | 0.9700             |
| C2—H2B                     | 0.9700             |
| C11—C16                    | 1.381 (2)          |
| C11—C12                    | 1.386 (2)          |
| C12—C13                    | 1.380 (2)          |
| O1—S1—O2                   | 119.06 (8)         |
| O1—S1—N1                   | 107.04 (7)         |
| O2—S1—N1                   | 105.10 (8)         |
| O1—S1—C21                  | 107.35 (8)         |
| O2—S1—C21                  | 109.61 (7)         |
| N1—S1—C21                  | 108.24 (7)         |
| C11—N1—C2                  | 109.39 (13)        |
| C11—N1—S1                  | 126.02 (11)        |
| C2—N1—S1                   | 122.27 (11)        |
| C22—N2—H2C                 | 115.9 (18)         |
| C22—N2—H2D                 | 116.2 (15)         |
| H2C—N2—H2D                 | 120 (2)            |
| C12—C1—C2                  | 104.35 (13)        |
| C12—C1—H1A                 | 110.9              |
| C2—C1—H1A                  | 110.9              |
| C12—C1—H1B                 | 110.9              |
| C2—C1—H1B                  | 110.9              |
| H1A—C1—H1B                 | 108.9              |
| N1—C2—C1                   | 104.80 (13)        |
| N1—C2—H2A                  | 110.8              |
| C1—C2—H2A                  | 110.8              |
| N1—C2—H2B                  | 110.8              |
| C1—C2—H2B                  | 110.8              |
| H2A—C2—H2B                 | 108.9              |
| C16—C11—C12                | 121.52 (14)        |
| C16—C11—N1                 | 129.33 (15)        |
| C12—C11—C12                | 109.13 (13)        |
| C13—C12—C11                | 119.57 (16)        |
| C13—C12—C1                 | 130.07 (16)        |
| C11—C12—C1                 | 110.35 (14)        |
| O1—S1—N1—C11               | −48.70 (15)        |
| O2—S1—N1—C11               | −176.21 (12)       |
| C21—S1—N1—C11              | 66.72 (14)         |
| O1—S1—N1—C2                | 150.47 (13)        |
| O2—S1—N1—C2                | 22.96 (14)         |
| C21—S1—N1—C2               | −94.10 (13)        |
| C11—N1—C2—C1               | 14.13 (17)         |
| S1—N1—C2—C1                | 177.78 (11)        |

**sup-26**

_Acta Cryst._ (2022), C78, 730-742
Hydrogen-bond geometry (Å, °)

| D—H···A   | D—H | H···A  | D···A | D—H···A |
|-----------|-----|--------|-------|---------|
| N2—H2C···O2 | 0.86 (3) | 2.19 (3) | 2.857 (2) | 134 (2) |
| N2—H2D···O1<sup>i</sup> | 0.89 (2) | 2.22 (3) | 3.098 (2) | 169 (2) |
| C15—H15···O2<sup>a</sup> | 0.93 | 2.59 | 3.366 (2) | 141 |
| C16—H16···O1 | 0.93 | 2.58 | 3.105 (2) | 117 |
| C26—H26···O1 | 0.93 | 2.45 | 2.849 (3) | 106 |

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