Bulgarian Chemical Communications, Volume 48, Number 1 (pp. 5 – 12) 2016

Structural study of 4-(2-morpholinoethanoylamino)-benzenesulfonamide by X-ray diffraction technique and DFT calculations

M. Durgun[1]*, Ş. P. Yalçın[2], H. Türkmen[1], M. Akkurt[3], E. Eroğlu[4]

[1]*Department of Chemistry, Faculty of Arts and Sciences, Harran University, 63190, Şanlıurfa, Turkey*
[2]*Department of Physics, Faculty of Arts and Sciences, Harran University, 63190 Şanlıurfa,*
[3]*Department of Physics, Faculty of Sciences, Erciyes University, 38039 Kayseri, Turkey*
[4]*Department of Primary School Teaching, Faculty of Education, Akdeniz University, 07058 Antalya, Turkey*

Received January 27, 2014; Revised November 6, 2015

This article presents the synthesis and a combined experimental and computational DFT study of 4-(2-morpholinoethanoylamino)-benzenesulfonamide. The crystal structure of the title compound was determined by single crystal X-ray diffractometry (XRD), which reveals inversion dimers linked by pairs of intermolecular N—H···O hydrogen bonds. The molecular geometry was also optimized by using density functional theory (DFT/B3LYP) methods with the 6-31G and 6-31+G (d) basis sets in ground state and compared with the experimental XRD data. The degree of conformity of the obtained structural parameters between the XRD experiment and DFT calculations was given by two statistical formulas, namely R^2 (squared correlation coefficient) and RMSD (root mean square deviation). Further rise in conformity of the bond lengths was achieved by introducing a bigger, 6-31++G (3df, 3pd) extra basis set on the sulfur atom. The obtained results clearly showed that the size of the used basis set influences the conformity of the structural parameters. DFT optimized structure is in good agreement with the XRD crystal structure of the title compound.

Keywords: X-ray diffraction, Quantum chemical calculations, DFT, Molecular structure, Sulfonamide

INTRODUCTION

Sulfonamides are organic sulfur compounds that contain an $-SO_2NH_2$ group and act as antimicrobial agents by inhibiting bacterial growth and activity. They are called sulfa drug derivatives or variation of sulfanilamides [1]. They are used in the prevention and treatment of bacterial infections, hypertension, and gout. The discovery of sulfonamides is a significant milestone event in human chemotherapeutic history [2]. Since 1935 many thousands of molecules containing sulfanilamide structures have been synthesized and their discovery yielded improved formulations with greater effectiveness and lower toxicity. Sulfonamides are still widely used pharmacological agents for the treatment or prevention of a variety of diseases, such as antimicrobial drugs, antithyroid agents, antitumor agents, antibiotics and inhibitors of carbonic anhydrase as antiglaucoma agents [3-9]. These compounds have also been tested for the inhibition of the major cytosolic isozymes I and II [10]. Due to the wide variety of their biological and biochemical importance, the study of the crystal structure of sulfonamides, along with other physical, chemical and biochemical studies has become an interesting field of research for a long time [11].

Nowadays, quantum chemical methods are widely used for the investigation of large molecules. *Ab initio* and DFT methods provide powerful tools for studying molecular geometry, vibrational and some molecular properties. The results obtained using X-ray diffraction technique and quantum chemical calculations provide lots of information about the structure [12-14].

The title compound, found as an inhibitor of three carbonic anhydrase (CA, EC 4.2.1.1) isozymes, the cytosolic isozymes CA I and II, the catalytic domain of the transmembrane, tumor-associated isozyme CA IX [9] and QSAR study was synthesized and the crystal structure of the title compound was investigated using XRD technique. Using Density Functional Theory (DFT) calculations the bond lengths, bond angles and torsional angles of the title compound were also calculated employing DFT/B3LYP methods using the basis sets 6-31D and 6-31+G(d) and compared them with the X-ray results. It was observed that structural parameters of the title compound obtained using DFT calculations are perfectly consistent with those obtained using XRD technique.

* To whom all correspondence should be sent:
E-mail: mustafadurgun@harran.edu.tr;
mustafadurgun@yahoo.com

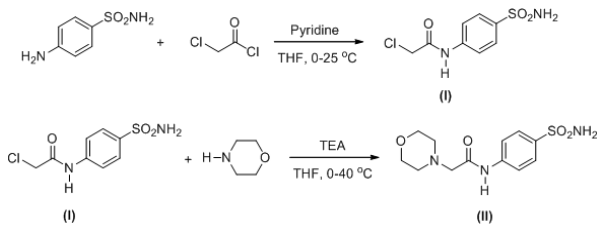
EXPERIMENTAL AND THEORETICAL METHODS

Materials and measurements

All chemicals were obtained from commercial suppliers (Sigma-Aldrich, Merck) and used without further purification. Elemental analysis was carried out on a LECO CHNS model 932 elemental analyzer. ^{1}H and ^{13}C-NMR spectra were recorded on a Bruker-Avance 300 MHz spectrometer for spectroscopic characterization. FT-IR spectra were recorded on a Perkin Elmer Spectrum RXI FT-IR spectrometer in KBr pellets over the wavenumber range of 4000-400 cm^{-1}. Melting points were measured in open capillary tubes with an Electro thermal 9100 melting point apparatus and were uncorrected. Mass spectra were recorded on an Agilent GC/MS spectrometer. TLC (on Merck silica gel 60 F_{254} sheets) was used to follow the course of the reaction and assess product purity. The title compound (II) was synthesized according to the procedure previously described by Turkmen *et al.* [9].

Synthesis of the 4-(2-morpholinoethanoylamino)-benzenesulfonamide

The synthesis of the title molecule (Fig. 1) is outlined in Scheme 1. The starting material, 4-(2-chloroethanoylamino)-benzenesulfonamide, was prepared by the reaction of sulfanilamide with 2-chloroethanoylchloride. The title compound, 4-(2-morpholinoethanoylamino)-benzene sulfonamide, was prepared by the reaction of 4-(2-chloroethanoylamino)-benzenesulfonamide with morpholine. To a stirred solution containing an excess of morpholine (1.04 g, 12.00 mmol) and triethylamine, TEA, (1.84 g, 8.00 mmol) in tetrahydrofuran solvent (30 mL) 4-(2-chloroethanoylamino)-benzenesulfonamide (1.00 g, 4.00 mmol) in tetrahydrofuran (30 mL) was added at 0 ºC in the course of 30 min. After completion of the addition, the reaction mixture was allowed to warm at room temperature and stirred at 40 ºC for 48 h. Excess morpholine and TEA was removed under reduced pressure and the product was also crystallized using ether to remove the excess. After crystallization from ethanol/water (9/1), a pale yellow crystalline product was obtained. Then the compound was dissolved in various organic solvents, namely methanol, chloroform, dichloromethane (4/3/3 v/v) and single crystals suitable for X-ray diffraction studies were grown by the slow evaporation method. The chemical analysis gave the following results: Yield: 70%, mp 208-210 ˚C; Anal. Calculated for $C_{12}H_{17}N_3O_4S$ (299.36 g/mol) (%): C, 48.15; H, 5.72; N, 14.04; S, 10.71. Found (%): C, 48.21; H, 5.80; N, 13.80; S, 10.21; ; FT-IR (KBr pellets, cm^{-1}): 3335, 3305 (NH_2), 3235 (Amid-N-H), 3080 (Ar-C-H), 2990-2810 (Aliph-C-H), 1695 (Amid-C=O), 1325 (asymmetric), 1183 (symmetric) (S=O); ^{1}H-NMR (DMSO-d_6, TMS, 300 MHz, δ ppm): 10.07 (1H, s, -CONH), 7.72-7.78 (4H, m, -Ar-H), 7.26 (2H, s, SO_2NH_2), 3.56 (4H, t, *J* 5 Hz, $C\underline{H_2}OC\underline{H_2}$), 2.52 (2H, s, *J* 7 Hz, $C\underline{H_2}CO$), 2.50 (4H, t, *J* 4 Hz, $C\underline{H_2}NC\underline{H_2}$); ^{13}C-NMR (TMS, 75 MHz, δ ppm): 170.63 (C=O), 143.24 (CNH-), 140,22 (C-SO_2NH_2), 128.24 (2xC-2 Aryl), 120.63 (2xC-3 Aryl), 67.33 ($\underline{C}H_2O\underline{C}H_2$), 63.23 ($\underline{C}H_2CO$), 54.31 ($\underline{C}H_2N\underline{C}H_2$); m/z EI$^+$ 299 [M]$^+$.



Scheme 1. The reaction for the synthesis of the title compound.

Crystallographic study

The needle shaped pale yellow single crystals of the title compound of size 0.12 × 0.15 × 0.24 mm were used for intensity data collection using graphite-monochromatic MoKα radiation in a Rigaku/MSC, 2005 [15] diffractometer at temperature 294 K using CrystalClear software. The structure was solved by direct methods using SIR97 software programme [16]. SHELXL-97 [17] Program was used to refine structure. Molecular graphics were drawn using ORTEP-3 for Windows [18]. WinGX [19] and PLATON [20] softwares were used to prepare the material for publication. The crystallographic data and refinement parameters for the title compound are listed in Table 1, whereas selected bond lengths, bond angles, and torsion angles are shown in Table 2. Full crystallographic data are available as supplementary material.

X-ray powder diffraction data of the title molecule were recorded with a Rigaku D max 2000 X- ray powder diffractometer at 40kV/30mA using Cu Kα radiation ($\lambda_{k\alpha}$ = 1.5406 Å) . The diffraction pattern was scanned with a step size of 0.02 and an angular range of 5.0–90°.

Table 1. Crystallographic data of the title compound.

Crystal data	
$C_{12}H_{17}N_3O_4S$	V = 672.48 (4) Å^3
M_r = 299.36	Z = 2
Triclinic, $P\bar{1}$	D_x = 1.478 Mg m^{-3}
a = 8.1101 (1) Å	Mo $K\alpha$ radiation
b = 9.6309 (1) Å	Cell parameters from 3426 reflections
c = 9.7079 (1) Å	θ = 2.2–30.6°
α = 73.676 (1)°	μ = 0.26 mm^{-1}
β = 68.060 (9)°	T = 294 (2) K
γ = 79.532 (1)°	Needle, pale yellow
Data collection	
Rigaku R-AXIS RAPID-S diffractomer	θ_{max} = 30.7°
dtprofit.ref scan	h = -11 → 11
Absorption correction: multi-scan (based on symmetry-related measurements)	k = -13 → 13
T_{min} = 0.954, T_{max} = 0.969	l = -13 → 13
20355 measured reflections	
4097 independent reflections	
2589 reflections with $I > 2\sigma(I)$	
R_{int} = 0.090	
Refinement	
Refinement on F^2	Mixture of independent and constrained H-atom refinement
$R[F^2 > 2\sigma(F^2)]$ = 0.069	Calculated weights $w = 1/[\sigma^2(F_o^2) + (0.0441P)^2 + 0.507P]$ where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2)$ = 0.163	$(\Delta/\sigma)_{max} < 0.0001$
S = 1.04	$\Delta\rho_{max}$ = 0.33 e Å^{-1}
4097 reflections	$\Delta\rho_{min}$ = -0.47 e Å^{-1}
191 parameters	Extinction correction: shelxl

Quantum chemical calculations

All calculations were conducted using Density functional theory (DFT) as implemented in the GAUSSIAN 03, Revision B, 05 suite of *Ab initio* quantum chemistry programs [21]. Geometry optimization was started from the X-Ray Diffraction (XRD) experimental atomic position. Initial calculations were performed using the restricted B3LYP exchange and correlation functional and the 6-31G basis set for all atoms. Default SCF and geometry convergence criteria were used and no symmetry constraints were imposed. The harmonic frequency analysis based on analytical second derivatives was used to characterize the optimized geometry as global minimum on the potential energy surface of the title molecule. After initial calculation with the medium size basis set, in order to improve calculated structural parameters, a bigger basis set, namely 6-31+G (d) which takes into account polarized d and diffuse functions on heavy atoms, was used. In the final calculation, due to the involvement of a sulfur atom in the title compound, the extra basis set 6-31++G (3df, 3pd) was employed to improve the structural parameters. These additional extra basis functions have been shown to significantly improve the description of molecules containing second row elements [22].

RESULTS AND DISCUSSION

Structural analysis of the 4-(2-morpholino-ethanoylamino)-benzenesulfonamide

Characterization of the title molecule was achieved using elemental analysis, FT-IR, ^{1}H and ^{13}C NMR, and Mass spectroscopy.

The title compound crystallizes in the triclinic system with the space group $P\bar{1}$ with a = 8.1101 (1) Å, b = 9.6309 (1) Å, c = 9.7079 (1) Å, α = 73.676 (1)°, β = 68.060 (9)°, γ = 79.532 (1)°, V = 672.48 (4) Å^3, Z = 2. In the crystal structure, the morpholine ring (N2/O4/C9–C12) of the title compound (II), (Figs. 1 and 2), adopts a chair conformation, with puckering parameters (Cremer & Pople, 1975) Q_T, θ and ϕ of 0.579(3) Å, 176.7(3)° and 263(5)°. The C4—N3—C7—O3, C4—N3—C7—C8 and N3—C7—C8—N2 torsion angles are 3.2(5), -179.5(3) and 24.7(3), respectively.

The powder diffraction pattern was auto-indexed with the program Jade 7 (Materials Data Inc., CA). X-ray powder diffraction patterns of title compound are shown in Fig. 4. The best solution fm 33 and fn 56 indicated a triclinic unit cell with a = 9.622 Å, b = 8.106 Å, c = 9.515 Å, α = 72.4°, β = 80.0°, γ = 97.2° and V = 683.8 Å^3.

The experimental details of the title compound are given in Table 1. The selected bond lengths, bond angles, and torsion angles listed in Table 2 are within the normal range and are comparable with those reported for similar structures [23-25].

It can be expected that the carbon - oxygen double bond length (C7=O3 = 1.222 (4) Å) of the amide group is shorter than the other carbon - oxygen single bonds length (C11-O4 = 1.425 (4) Å and O4-C10 = 1.421 (4) Å) of the morpholine group. These distances are also compatible to literature data [26]. The C7=O3 double bond length [1.222 (4)Å] is also within the values observed for a C=O double bond.

The molecular structure of the title compound (II) is stabilized by C—H···O and N—H···N hydrogen bonds forming S(6) and S(5) ring motifs, respectively (Table 3) [27].

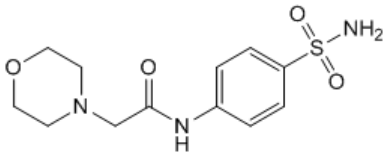


Fig. 1. The chemical structure of 4-(2-morpholinoethanoylamino)-benzenesulfonamide.

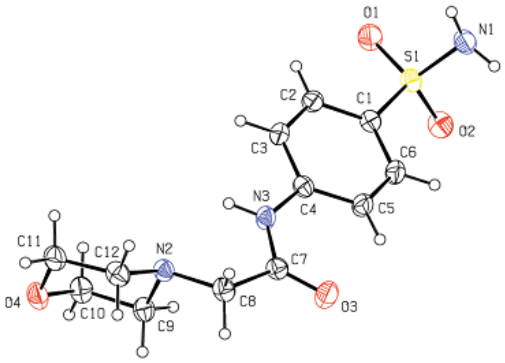


Fig. 2. The ORTEP view of the title molecule with the atom numbering scheme. Displacement ellipsoids for non-H atoms are drawn at the 30% probability level.

In the crystal, both molecules form inversion dimers linked by pairs of intermolecular N—H···O hydrogen bonds (Table 3, Fig. 3), generating $\boldsymbol{R_2^2(8)}$ ring motifs along [010]. The rest of the intermolecular N—H···O hydrogen bonds connects these dimers to another molecule forming two-dimensional layers lying parallel to bc plane. The N1 with the amine hydrogen H2 forms a bifurcated intermolecular short contact with $O3^{ii}$ acceptors [N1–H_2···$O3^{ii}$] (Table 3 and Fig. 3). The molecular structure is further strengthened by C—H···π interactions forming two-dimensional layers and helping in stabilizing the supramolecular structure. The details of the hydrogen bonds are summarized in Table 3. The packing diagram of the title compound is also shown in Fig. 3.

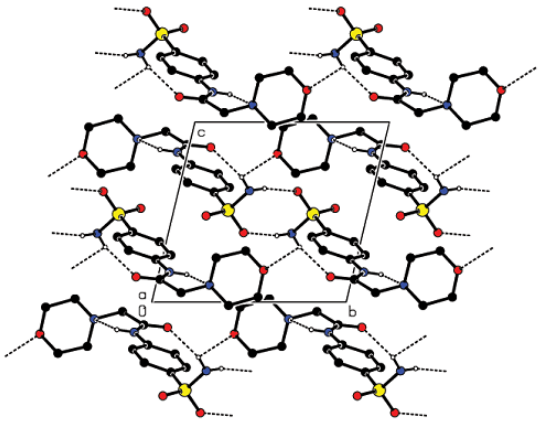


Fig. 3. A partial view of the dimers formed by N—H...O hydrogen bonds of the title compound along the *a* axis. H atoms not involved in hydrogen bondings are omitted for clarity.

Refinement

The H atoms on the NH and NH_2 groups were located from a difference Fourier map and refined with distance restraints of N—H = 0.88(2) Å, with U_{iso}(H) = 1.2U_{eq}(N). The other H atoms were positioned geometrically, with C—H = 0.93 and 0.97 Å, and refined as riding with U_{iso}(H) = 1.2U_{eq}(C).

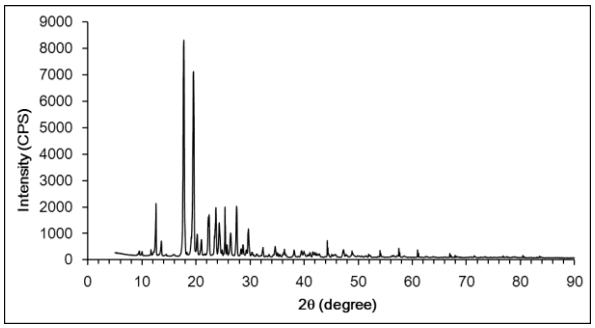


Fig. 4. X-ray powder diffraction pattern of the title compound.

Geometrical structure analysis

The optimized structure parameters of the title compound were calculated by DFT–B3LYP levels with two different basis sets, 6-31G and 6-31+G (d). Additionally, calculation was run by employing an extra basis 6-31++G (3df, 3pd) on the sulfur atom together with the 6-31+G (d) for all other atoms in the molecule. The selected bond lengths, bond angles and torsion angles are compared with the experimental data of the title compound (Table 4). Conformity of the obtained structural parameters between the XRD experiment and the DFT calculations were measured by two statistical formulas, namely R^2 (squared correlation coefficient) and RMSD (root mean square deviation).

A perusal of Table 4 shows that the conformity of the obtained structural parameters between the XRD experiment and the DFT calculation was increased by adding polarized and diffuse functions to the 6-31G basis set. This resulted in the dramatic increment of the conformity of the bond lengths and angles as is evidenced from the increment of the R^2 value from 0.781 to 0.906 and the reduction of the RMSD value from 0.116 to 0.053. Further rise in conformity of the bond lengths was achieved by introducing a bigger, 6-31++G (3df, 3pd) extra basis set on sulfur atom. This resulted in notable changes of the bond lengths of the S1-O1 and S1-O2 from 1.464 to 1.442 Å, the S1-N1 from 1.689 to 1.664 Å and the S1-C1 from 1.797 to 1.781 Å. The maximum bond length difference and bond angle difference between the XRD result and the DFT calculations are 0.061 Å for the bond S-N, 2.21° for

the angle N1-S1-C1 and 13° for the torsion angle N1-S1-C1-C6 in the title compound. As seen from these results, DFT optimized structure is in good agreement with the XRD crystal structure of the title compound.

Table 2. Geometric parameters (bond lengths (Å), bond angles (°), torsion angles (°)).

Bond lengths (Å)			
S1—O1	1.431 (2)	O4—C11	1.425 (4)
S1—O2	1.436 (2)	N2—C8	1.466 (4)
S1—N1	1.603 (3)	N2—C9	1.467 (3)
S1—C1	1.758 (3)	N2—C12	1.475 (3)
O3—C7	1.222 (4)	N3—C4	1.396 (4)
O4—C10	1.421 (4)	N3—C7	1.356 (4)
Bond angles (°)			
O1—S1—O2	118.65 (14)	S1—C1—C2	119.0 (3)
O1—S1—N1	107.01 (16)	N3—C4—C3	116.9 (3)
O1—S1—C1	107.87 (14)	N3—C4—C5	124.1 (3)
O2—S1—N1	106.48 (14)	O3—C7—N3	124.7 (3)
O2—S1—C1	107.10 (15)	N3—C7—C8	114.4 (2)
N1—S1—C1	109.53 (15)	O3—C7—C8	120.9 (3)
C10—O4—C11	109.4 (3)	N2—C8—C7	113.9 (2)
C8—N2—C9	110.9 (2)	N2—C9—C10	109.7 (2)
C8—N2—C12	109.9 (2)	O4—C10—C9	110.4 (3)
C9—N2—C12	108.7 (2)	O4—C11—C12	112.0 (3)
C4—N3—C7	129.7 (2)	N2—C12—C11	110.7 (2)
S1—C1—C6	121.4 (2)		
Torsion Angles (°)			
O1—S1—C1—C2	-10.1 (3)	C4—N3—C7—C8	-179.5 (3)
O2—S1—C1—C2	-138.9 (2)	C7—N3—C4—C3	-177.9 (3)
N1—S1—C1—C2	106.0 (3)	C2—C1—C6—C5	1.6 (4)
O1—S1—C1—C6	170.0 (2)	S1—C1—C2—C3	178.2 (2)
O2—S1—C1—C6	41.2 (3)	S1—C1—C6—C5	-178.5 (2)
N1—S1—C1—C6	-73.9 (3)	C6—C1—C2—C3	-1.9 (4)
C10—O4—C11—C12	-58.3 (4)	C1—C2—C3—C4	0.3 (4)
C11—O4—C10—C9	60.9 (3)	C2—C3—C4—C5	1.6 (4)
C9—N2—C8—C7	79.0 (3)	C2—C3—C4—N3	-177.3 (3)
C12—N2—C8—C7	-160.8 (2)	C3—C4—C5—C6	-1.9 (4)
C12—N2—C9—C10	57.7 (3)	N3—C4—C5—C6	177.0 (3)
C8—N2—C9—C10	178.6 (3)	C4—C5—C6—C1	0.3 (4)
C9—N2—C12—C11	-54.9 (3)	O3—C7—C8—N2	-157.9 (3)
C8—N2—C12—C11	-176.4 (3)	N3—C7—C8—N2	24.7 (3)
C4—N3—C7—O3	3.2 (5)	N2—C9—C10—O4	-61.8 (3)
C7—N3—C4—C5	3.3 (5)	O4—C11—C12—N2	56.0 (4)

Table 3. Hydrogen-bond parameters (Å, °)

	D—H	H···*A*	D···A	*D*—H···*A*
N1—H1N···O2^{i}	0.88 (3)	2.15 (3)	3.006 (4)	167 (2)
N1—H2N···O3^{ii}	0.87 (3)	2.22 (3)	3.053 (4)	163 (3)
C8—H8B···Cg2^{iv}	0.97	2.73	3.608 (3)	151

Symmetry codes: (i) -x, -1-y, 1-z; (ii) -1+x, y, z; (iii) -1+x, -1+y, z; (iv) 1-x, -y, -z.

Table 4. Comparison of selected structural parameters between the XRD results of the title compound and the DFT optimized geometry *in vacuo*.

Parameter	XRD Results	DFT/B3LYP		
		6-31G	6-31+G(d)	6-31+G(d) 6-31++G (3df.3pd) Extra basis set for S atom
Bond Lengths				
S1-O1	1.431 (2)	1.639	1.464	1.442
S1-O2	1.436 (2)	1.638	1.464	1.442
S1-N1	1.603 (3)	1.824	1.689	1.664
S1-C1	1.758 (3)	1.856	1.797	1.781
O3-C7	1.222 (4)	1.248	1.224	1.224
O4-C10	1.421 (4)	1.458	1.423	1.423
O4-C11	1.425 (4)	1.458	1.423	1.423
N2- C8	1.466 (4)	1.471	1.461	1.461
N2-C9	1.467 (3)	1.483	1.470	1.470
N2-C12	1.475 (3)	1.485	1.472	1.472
N3-C4	1.396 (4)	1.404	1.403	1.403
N3-C7	1.356 (4)	1.373	1.472	1.372
R^2/RMSD		0.799/0.110	0.929/0.045	0.988/0.019
Bond Angles				
N1-S1-CI	109.53	104.67	107.69	107.32
O1-S1-O2	118.65	122.40	123.03	122.85
O1-S1-CI	107.87	108.20	107.42	107.45
C4-N3-C7	129.71	129.02	129.46	129.48
O3-C7-C8	120.90	121.03	121.08	121.06
C7-C8-N2	113.94	113.04	114.12	114.13
C12-N2-C9	108.71	111.49	109.97	109.96
C12-C11-O4	110.40	110.71	111.30	111.29
O4-C10-C9	111.95	110.58	111.37	111.37
R^2/RMSD		0.902/2.328	0.950/1.687	0.949/1.688
Torsion Angles				
N1-S1-C1-C6	-73.90	-89.78	-87.24	-86.90
O1-S1-C1-C6	169.96	157.31	159.98	160.17
C3-C4-N3-C7	-177.88	-179.64	-177.97	-178.18
O3-C7-C8-N2	-157.88	-161.97	-160.01	-159.86
N2-C9-C10-O4	-61.78	-56.24	-56.88	-56.90
C12-C11-O4-C10	-58.31	-58.37	-57.97	-57.96
R^2/RMSD		0.972/8.781	0.982/7.144	0.982/6.985

CONCLUSION

In the present study, the crystal structure of the 4-(2-morpholinoethanoylamino)-benzene sulfonamide was investigated by single crystal XRD technique. Also, the structure was supported by FT-IR and ^{1}H nad ^{13}C spectroscopy. According to the XRD results, the molecular conformation of the title compound is stabilized by the C—H···O and N—H···N hydrogen bonds. In the crystal structure, pairs of molecules are linked as inversion dimers by N—H···O hydrogen bonds. The other intermolecular N—H···O hydrogen bonds connect these dimers to other molecules forming two-dimensional layers lying parallel to bc plane. Furthermore C—H···π interactions between the two-dimensional layers stabilize the supramolecular structure. Using the atomic co-ordinates from XRD results as an input to DFT calculations, a stable conformation of the title compound is theoretically determined. Furthermore, the effect of the used basis set on the conformity of the structure was investigated. The basis set with the polarized and diffuse functions, namely 6-31+G (d) outperformed the 6-31G basis set. The results obtained for the best conformity were achieved by introducing a 6-31++G (3df, 3pd) extra basis set on the sulfur atom while the rest of the molecule was accounted for with the 6-31+G(d). As is seen from these results, DFT optimized structure is in good agreement with the XRD crystal structure of the title compound.

Supplementary data

Crystallographic data for the structure reported in this article are deposited in the Cambridge Crystallographic Data Centre as supplementary publication number CCDC 933007. Copies of the data can be obtained free of charge on application to CCDC 12 Union Road, Cambridge CB21 EZ, UK. (Fax: (+44) 1223 336-033; e-mail: data_request@ccdc.cam. ac.uk).

Acknowledgements: *This research was supported by the Unit of the Scientific Research Projects of Harran University, Turkey for the research grant (HUBAK Project Nos. 1136 and 12060).*

REFERENCES

1. G. Domagk, *Dtsch. Med. Wochenschr.*, **61,** 829 (1935).
2. A.E. Cribb, B.L. Lee, L.A. Trepanier, S.P. Spielberg, *Adverse Drug React. Toxicol. Rev.*, **15,** 9 (1996).
3. M. Remko, C.W.V.D. Lieth, *Bioorgan. Med. Chem.* **12(20),** 5395 (2004).
4. T.H. Maren, *Drug Dev. Res.*, **10,** 255 (1987).
5. M. Rami, A. Innocenti, J.L. Montero, A. Scozzafava, J.Y. Winum, CT. Supuran, *Bioorganic & Medicinal Chemistry Letters*, **21**, 5210 (2011).
6. C.T. Supuran, A. Scozzafava, *Exp. Opin. Ther. Patents*, **10,** 575 (2000).
7. C.T. Supuran, A. Scozzafava, A. Casini, *Med. Res. Rev.*, **23 (2)**, 146 (2003).
8. C. T. Supuran, *Nat. Rev. Drug Discov.*, **7,** 168, (2008).
9. H. Turkmen, M. Durgun, S. Yılmaztekin, M. Emul, A. Innocenti, D. Vullo, A. Scozzafava, C. T. Supuran, *Bioorg. Med. Chem. Lett.*, **15**, 367 (2005).
10. S. Pastorekova, S. Parkkila, J. Pastorek, C.T. Supuran, *J. Enzym. Inhib. Med. Chem.*, **19,** 199, (2004).
11. K. Sarojini, H. Krishnan, Charles C. Kanakam, S. Muthu, *Spectrochimica Acta Part A: Molecular and Biomolecular Spectroscopy*, **96**, 657 (2012).
12. E. Taşal, I. Sıdır, Y. Gülseven, C. Öğretir, T. Önkol, *Spectrochimica Acta Part A*, **72,** 801 (2009).
13. Pirnau, V. Chis, L. Szabo, O. Cozar, M. V. Ovidiu Oniga, R.A. Varga, *Journal of Molecular Structure*, **924–926,** 361 (2009).
14. E. Eroglu, H. Turkmen, S. Güler, S. Palaz, O. Oltulu, *Int. J. Mol. Sci.*, **8,** 145 (2007).
15. Rigaku/MSC, *CrystalClear*. Rigaku/MSC, The Woodlands, Texas, USA, 2005.
16. Altomare, M. C. Burla, M. Camalli, G. L. Cascarano, C. Giacovazzo, A. Guagliardi, A. G. G. Moliterni, G. Polidori, R. Spagna, *J. Appl. Cryst.*, **32,** 115 (1999).
17. G. M. Sheldrick, *Acta Cryst. A***, 64**, 112 (2008).
18. L. J. Farrugia, *J. Appl. Cryst*., **30**, 565 (1997).
19. L. J. Farrugia, *J. Appl. Cryst*., **32,** 837 (1999).
20. L. Spek, *Acta Cryst. D***, 65**, 148 (2009).
21. M.J. Frisch, G.W. Trucks, H.B. Schlegel, G.E. Scuseria, M.A. Robb, J.R. Cheeseman, J.A. Montgomery, Jr. T. Vreven, K.N. Kudin, J.C. Burant, J.M. Millam, S.S. Iyengar, J. Tomasi, V. Barone, B. Mennucci, M. Cossi, G. Scalmani, N. Rega, G.A. Petersson, H. Nakatsuji, M. Hada, M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima, Y. Honda, O. Kitao, H. Nakai, M. Klene, X. Li, J.E. Knox, H.P. Hratchian, J.B. Cross, C. Adamo, J. Jaramillo, R, Gomperts, R. E. Stratmann, O. Yazyev, A.J. Austin, R. Cammi, C. Pomelli, J.W. Ochterski, P.Y. Ayala, K. Morokuma, G.A. Voth, P. Salvador, J.J. Dannenberg, V.G. Zakrzewski, S. Dapprich, A.D. Daniels, M.C. Strain, O, Farkas, D,K, Malick, A,D, Rabuck, K, Raghavachari. J.B. Foresman, J.V. Ortiz, Q. Cui, A.G. Baboul, S. Clifford, J. Cioslowski, B.B. Stefanov, G. Liu, A. Liashenko, P. Piskorz, I. Komaromi, R.L. Martin, D.J. Fox, T. Keith, M.A. Al-Laham, C.Y. Peng, A. Nanayakkara, M. Challacombe, P.M.W. Gill, B. Johnson, W. Chen, M.W. Wong, C. Gonzalez, J.A. Pople, GAUSSIAN 03, Revision B,05, Gaussian, Inc,, Pittsburgh, PA, 2003.
22. T. H, Dunning, K. A. Peterson, A.K. Wilson, *J. Chem. Phys.*, **114,** 9244 (2001).
23. H. Turkmen, S.P. Yalcin, M. Akkurt, and M. Durgun, *Acta Cryst. E*, **68**, 3475 (2012).
24. M. Akkurt, S.P. Yalcin, H. Turkmen, O. Buyukgungor, *Acta Cryst. E*, **66**, 1559 (2010).
25. M. Akkurt, S.P. Yalcin, H. Turkmen and O. Buyukgungor, *Acta Cryst. E*, **66,** 1596 (2010).
26. F. H. Allen, O.Kennard, D. G. Watson, L.Brammer, A. G.Orpen and R. Taylor, *J. Chem. Soc., Perkin Trans.*, **2,** S1 (1987).
27. J. Bernstein, R. E. Davis, L. Shimoni, N.L. Chang, *Angew. Chem. Int. Ed. Engl.*, **34,** 1555 (1995).

СТРУКТУРНО ИЗСЛЕДВАНЕ НА 4-(2-МОРФОЛИНОЕТАНОИЛАМИНО)-БЕНЗЕНСУЛФОНАМИД ЧРЕЗ РЕНТГЕНОВА ДИФРАКЦИЯ И DFT-ИЗЧИСЛЕНИЯ

М. Дургун[1]*, Ш. П. Ялчън[2], Х. Тюркмен[1], М. Аккурт[3], Е. Ероолу[4]

[1]*Департамент по химия, Факултет за изкуства и наука, Университет Харан, Шанлюрфа, Турция*
[2]*Департамент по физика, Факултет за изкуства и наука, Университет Харан, Шанлюрфа и Централна изследователска лаборатория, Университет Харан, Кампус Османбей, Шанлюрфа, Турция*
[3]*Департамент по физика, Факултет по наука, Университет, Кайзери, Турция*
[4]*Департамент по основно образование, Образователен факултет, Университет Акдениз, Анталия, Турция*

Постъпила на 27 януари,2014 г.; коригирана на 6 ноември, 2015 г.

(Резюме)

Тази статия представя съчетание от експериментално и DFT-изчислително изследване на 4-(2-морфолиноетаноиламино)-бензенсулфонамид. Кристалната структура на съединението е определена чрез рентгено-структурен анализ (XRD) на единичен кристал, който разкрива обратими димери свързани с двойки от междумолекулярни N—H...O водородни връзки. Молекулната геометрия е оптимизирана с помощта на метода (DFT/B3LYP) с базисната мрежа 6-31G и 6-31+G (d) в основно състояние и е сравнена с опитните данни от рентгеноструктурния анализ. Степента на съответствие на получените параметри от експеримента и теорията се дава от две статистически формули, т.е. R^2 (коефициент на квадратична корелация) и RMSD (корен от средно-квадратичното отклонение). Следващото съответствие се отнася до дължината на връзките и е постигнато чрез въвеждането на по-голяма базисна мрежа, 6-31++G (3df, 3pd) за серния атом. Получените резултати ясно показват, че размерът на използваната базисна мрежа влияе на съответствието на структурните параметри. DFT-оптимизираната структура е в добро съгласие с рентгенографската структура на изследваното съединение.