organic compounds

Acta Crystallographica Section E **Structure Reports** Online

ISSN 1600-5368

D-Phenylglycinium bromide

Mohanadoss Parthasarathy,^a Kannan Arun Kumar^b and Rengasamy Gopalakrishnan^a*

^aCrystal Research Laboratory, Department of Physics, Anna University, Chennai 600 025, India, and ^bDepartment of Chemistry, Loyola College (Autonomous), Chennai 600 034, India Correspondence e-mail: krgkrishnan@annauniv.edu

Received 30 January 2013; accepted 19 February 2013

Key indicators: single-crystal X-ray study; T = 295 K; mean σ (C–C) = 0.003 Å; R factor = 0.022; wR factor = 0.046; data-to-parameter ratio = 19.0.

In the crystal of the title salt, $C_8H_{10}NO_2^+ \cdot Br^-$, the bromide anions and the phenylglycinium cations are linked through N-H···Br, O-H···Br and C-H···O hydrogen bonds, generating sheets lying parallel to (001).

Related literature

For a similar compound with a different halogen anion, see: Ravichandran et al. (1998). For related structures and background, see: Srinivasan et al. (2001); Bouchouit et al. (2004); Ramaswamy et al. (2001); Bouacida et al. (2006); Thomsen et al. (1994). For biological importance, see: Satyam et al. (1996); Jayasinghe et al. (1994); Chun et al. (2010); Thomas & West (2011).



Experimental

Crystal data

 $C_8H_{10}NO_2^+ \cdot Br^ M_r = 232.08$ Orthorhombic, P212121 a = 5.5240 (5) Åb = 7.4735 (5) Å c = 23.1229 (18) Å

Data collection

Bruker Kappa APEXII CCD diffractometer Absorption correction: multi-scan (SADABS; Bruker, 2004) $T_{\rm min}=0.317,\ T_{\rm max}=0.415$

 $V = 954.60 (13) \text{ Å}^3$ Z = 4Mo $K\alpha$ radiation $\mu = 4.27 \text{ mm}^{-1}$ T = 295 K $0.35 \times 0.30 \times 0.25 \text{ mm}$

5824 measured reflections 2170 independent reflections 2003 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.022$



$R[F^2 > 2\sigma(F^2)] = 0.022$ wR(F^2) = 0.046 S = 1.03	H-atom parameters constrained $\Delta \rho_{\text{max}} = 0.25 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\text{min}} = -0.29 \text{ e } \text{\AA}^{-3}$
2170 reflections	Absolute structure: Flack (1983)
114 parameters	Flack parameter. 0.011 (8)

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	$D-{\rm H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdots Br1^{i}$	0.89	2.54	3.3586 (17)	154
$N1-H1C\cdots Br1^{ii}$	0.89	2.57	3.429 (2)	163
$N1 - H1A \cdots Br1$	0.89	2.45	3.3166 (18)	164
$O1 - H1D \cdot \cdot \cdot Br1^{iii}$	0.82	2.39	3.2027 (17)	171
$C7-H7\cdots O2^{iv}$	0.98	2.59	3.527 (3)	159

Symmetry codes: (i) -x + 1, $y - \frac{1}{2}$, $-z + \frac{3}{2}$; (ii) x - 1, y, z; (iii) x - 1, y - 1, z; (iv) x + 1, v, z

Data collection: APEX2 (Bruker, 2004); cell refinement: APEX2 and SAINT (Bruker, 2004); data reduction: SAINT and XPREP (Bruker, 2004); program(s) used to solve structure: SIR92 (Altomare et al., 1993); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-3 for Windows (Farrugia, 2012) and Mercury (Macrae et al., 2008); software used to prepare material for publication: PLATON (Spek, 2009).

The authors are grateful to Professor K. Sivakumar, Department of Physics, Anna University, Chennai-25, for fruitful scientific discussions. The authors are thankful to the SAIF, IIT Madras, Chennai-36, India, for the X-ray data collection.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: PK2465).

References

- Altomare, A., Cascarano, G., Giacovazzo, C. & Guagliardi, A. (1993). J. Appl. Cryst. 26, 343-350.
- Bouacida, S., Merazig, H. & Benard-Rocherulle, P. (2006). Acta Cryst. E62, 0838-0840.
- Bouchouit, K., Bendheif, L. & Benali-Cherif, N. (2004). Acta Cryst. E60, o272-0274.
- Bruker (2004). SADABS, APEX2, SAINT and XPREP. Bruker AXS Inc., Madison, Wisconsin, USA.
- Chun, L. W., Yang, B. F., Hsiao, H. L., Tung, H. T., Ming, C. T. & Hui, P. W. (2010). J. Biomed. Sci. 17, 71-78.
- Farrugia, L. J. (2012). J. Appl. Cryst. 45, 849-854.
- Flack, H. D. (1983). Acta Cryst. A39, 876-881.
- Jayasinghe, L. R., Datta, A., Ali, S. M., Zymunt, J., Van der Velde, D. G. & Georg, G. I. (1994). J. Med. Chem. 37, 2981-2984.
- Macrae, C. F., Bruno, I. J., Chisholm, J. A., Edgington, P. R., McCabe, P., Pidcock, E., Rodriguez-Monge, L., Taylor, R., van de Streek, J. & Wood, P. A. (2008). J. Appl. Cryst. 41, 466-470.
- Ramaswamy, S., Sridhar, B., Ramakrishnan, V. & Rajaram, R. K. (2001). Acta Cryst. E57, o1149-o1151.
- Ravichandran, S., Dattagupta, J. K. & Chakrabarti, C. (1998). Acta Cryst. C54, 499-501.
- Satyam, A., Hocker, M. D., Kanemaguire, K. A., Morgan, A. S., Villar, H. O. & Lyttle, M. H. (1996). J. Med. Chem. 39, 1736-1747.
- Sheldrick, G. M. (2008). Acta Cryst. A64, 112-122.
- Spek, A. L. (2009). Acta Cryst. D65, 148-155.
- Srinivasan, N., Sridhar, B. & Rajaram, R. K. (2001). Acta Cryst. E57, 0754-0756.
- Thomas, G. & West, G. B. (2011). J. Pharm. Pharmacol. 26, 151-152.
- Thomsen, C., Boel, E. & Suzdak, P. D. (1994). Eur. J. Pharmacol. 267, 77-84.

supporting information

Acta Cryst. (2013). E69, o470 [doi:10.1107/S1600536813004807]

D-Phenylglycinium bromide

Mohanadoss Parthasarathy, Kannan Arun Kumar and Rengasamy Gopalakrishnan

S1. Comment

D-Phenylglycine is an important constituent in the production of semisynthetic penicillins and cephalosporins. Recently the usages of some phenylglycine derivatives in the synthesis of antitumor drugs and other pharmacological applications have been found to be increasing (Satyam et al., 1996; Jayasinghe et al., 1994). Phenylglycine has been reported as a delivery tool for improving l-dopa absorption (Chun et al., 2010) and also found to have anti-inflammatory activity (Thomas et al., 2011). The torsion angle N1-C7-C8-O1, which indicates the relative orientation of the carboxyl group and the amino N atom, is 15.5 (3)° and close to the corresponding value of $18.9^{\circ}(5)$ reported for D-Phenylglycine Hydrochloride (Ravichandran et al., 1998). The orientation of the phenyl ring as described by the torsion angle C5—C6—C7— N1 is 130.05 (3)°. The intermolecular interaction between the molecular ions are primarly decided by hydrogen bonding. The hydrogen bonds N1—H1A···Br1, N1—H1B···Br1ⁱ [Symmetry code: (i) -x+1, y-1/2, -z+3/2], N1—H1C···Br1ⁱⁱ [Symmetry code: (ii) x-1, y-1, z] and C7—H7···O2^{iv} [Symmetry code: (iv) x-1, y-1, z] hydrogen bond interconnects the molecular ions to form an extensive two-dimensional molecular sheet parallel to (001) plane. Parallel stacking of these sheets along [0 0 1] direction constitute the molecular packing of the crystal.

S2. Experimental

The title compound (I), was prepared by mixing a 1:1 ratio of *D*-Phenylglycine and hydrobromic acid in water solvent. The suitable single-crystal of the compound was selected for X-ray analysis from the above solution by slow evaporation method.

S3. Refinement

The hydrogen atoms associated with C atoms were identified from the difference electron density peaks and subsequently treated as riding atoms with distances of d(C-H) = 0.98 Å (for CH) with $U_{iso}(H) = -1.5U_{eq}(C)$ and d(C-H) = 0.93 Å (for aromatic CH) with $U_{iso}(H) = 1.2U_{eq}(C)$. The carboxylic acid hydrogen was constrained to a distance of d(O-H) = 0.82 Å with $U_{iso}(H) = 1.5U_{eq}(C)$ and the positions of NH₃ H atoms were also treated as riding about the parent atom.



Figure 1 Displacement ellipsoid plot of the molecular structure drawn at the 40% probability level.



Figure 2

Part of the crystal structure showing the two dimensional anionic-cationic (0 0 1) sheet formed through N—H···Br, O—H···Br and C—H···O interactions viewed down c axis.

D-Phenylglycinium bromide

Crystal data

 $C_8H_{10}NO_2^+ \cdot Br^ M_r = 232.08$ Orthorhombic, $P2_12_12_1$ Hall symbol: P 2ac 2ab a = 5.5240 (5) Å b = 7.4735 (5) Å c = 23.1229 (18) Å V = 954.60 (13) Å³ Z = 4

Data collection

Bruker Kappa APEXII CCD diffractometer Radiation source: fine-focus sealed tube Graphite monochromator ω and φ scan Absorption correction: multi-scan (*SADABS*; Bruker, 2004) $T_{\min} = 0.317, T_{\max} = 0.415$

Refinement

drogen site location: inferred from
eighbouring sites
tom parameters constrained
$\frac{1}{[\sigma^2(F_o^2)]}$
$\sigma_{\rm max} = 0.003$
$h_{max} = 0.25 \text{ e} \text{ Å}^{-3}$
$hin = -0.29 \text{ e} \text{ Å}^{-3}$
inction correction: SHELXL97 (Sheldrick,
2008), Fc [*] =kFc[1+0.001xFc ² λ^{3} /sin(2 θ)] ^{-1/4}
inction coefficient: 0.0530 (13)
solute structure: Flack (1983)
solute structure parameter: 0.011 (8)

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.

F(000) = 464

 $\theta = 2.6 - 28.8^{\circ}$

 $\mu = 4.27 \text{ mm}^{-1}$

Block, colourless

 $0.35 \times 0.30 \times 0.25 \text{ mm}$

5824 measured reflections 2170 independent reflections

 $\theta_{\text{max}} = 27.5^{\circ}, \ \theta_{\text{min}} = 3.3^{\circ}$

2003 reflections with $I > 2\sigma(I)$

T = 295 K

 $R_{\rm int} = 0.022$

 $h = -6 \rightarrow 7$

 $k = -9 \rightarrow 5$

 $l = -28 \rightarrow 30$

 $D_{\rm x} = 1.615 {\rm Mg m^{-3}}$

Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å Cell parameters from 3239 reflections

Refinement. Refinement of F^2 against ALL reflections. The weighted *R*-factor *wR* and goodness of fit *S* are based on F^2 , conventional *R*-factors *R* are based on *F*, with *F* set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating *R*-factors(gt) *etc.* and is not relevant to the choice of reflections for refinement. *R*-factors based on F^2 are statistically about twice as large as those based on *F*, and *R*- factors based on ALL data will be even larger.

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

x	у	Ζ	$U_{ m iso}$ */ $U_{ m eq}$
0.1060 (5)	0.5444 (3)	0.56980 (9)	0.0370 (5)
-0.0251	0.5884	0.5906	0.044*
0.1209 (5)	0.5734 (3)	0.51081 (9)	0.0418 (6)
	x 0.1060 (5) -0.0251 0.1209 (5)	x y 0.1060 (5) 0.5444 (3) -0.0251 0.5884 0.1209 (5) 0.5734 (3)	x y z 0.1060 (5) 0.5444 (3) 0.56980 (9) -0.0251 0.5884 0.5906 0.1209 (5) 0.5734 (3) 0.51081 (9)

H2	-0.0006	0.6372	0.4921	0.050*
C3	0.3119 (5)	0.5092 (3)	0.47991 (9)	0.0424 (6)
H3	0.3196	0.5290	0.4402	0.051*
C4	0.4922 (5)	0.4160 (3)	0.50678 (9)	0.0443 (6)
H4	0.6229	0.3734	0.4855	0.053*
C5	0.4804 (4)	0.3849 (3)	0.56595 (9)	0.0355 (5)
H5	0.6024	0.3204	0.5842	0.043*
C6	0.2866 (4)	0.4500 (2)	0.59770 (7)	0.0264 (4)
C7	0.2695 (4)	0.4057 (2)	0.66152 (7)	0.0282 (5)
H7	0.4217	0.3499	0.6738	0.034*
C8	0.0650 (4)	0.2773 (3)	0.67328 (8)	0.0311 (5)
N1	0.2266 (4)	0.5687 (2)	0.69772 (6)	0.0345 (4)
H1A	0.3369	0.6514	0.6892	0.063 (8)*
H1B	0.2379	0.5399	0.7350	0.063 (8)*
H1C	0.0794	0.6117	0.6905	0.047 (7)*
01	0.1199 (4)	0.1163 (2)	0.65347 (8)	0.0561 (5)
H1D	0.0051	0.0486	0.6586	0.084*
02	-0.1206 (3)	0.3164 (2)	0.69632 (6)	0.0441 (4)
Br1	0.71415 (4)	0.82278 (3)	0.681529 (8)	0.03843 (9)

Atomic displacement parameters $(Å^2)$

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0381 (14)	0.0388 (11)	0.0339 (11)	0.0062 (12)	0.0048 (10)	-0.0032 (10)
C2	0.0552 (17)	0.0342 (12)	0.0360 (12)	0.0066 (11)	-0.0030 (11)	0.0072 (10)
C3	0.0638 (18)	0.0364 (12)	0.0270 (10)	-0.0101 (13)	0.0087 (11)	0.0010 (9)
C4	0.0417 (16)	0.0496 (14)	0.0415 (14)	-0.0021 (12)	0.0170 (11)	-0.0082 (11)
C5	0.0277 (13)	0.0429 (12)	0.0360 (12)	0.0004 (11)	0.0035 (9)	-0.0027 (10)
C6	0.0261 (11)	0.0258 (9)	0.0273 (9)	-0.0062 (10)	0.0011 (9)	-0.0013 (7)
C7	0.0261 (13)	0.0316 (10)	0.0269 (9)	-0.0034 (10)	0.0012 (8)	0.0002 (7)
C8	0.0352 (14)	0.0323 (11)	0.0258 (11)	-0.0071 (10)	-0.0018 (9)	0.0014 (8)
N1	0.0377 (13)	0.0396 (9)	0.0262 (9)	-0.0137 (10)	0.0029 (8)	-0.0036 (7)
01	0.0634 (15)	0.0333 (8)	0.0715 (12)	-0.0161 (9)	0.0238 (10)	-0.0057 (8)
O2	0.0328 (9)	0.0448 (9)	0.0547 (9)	-0.0106 (9)	0.0085 (7)	-0.0021 (8)
Brl	0.04061 (14)	0.03701 (12)	0.03766 (12)	-0.01269 (10)	0.00446 (10)	-0.00279 (9)

Geometric parameters (Å, °)

C1—C6	1.382 (3)	C6—C7	1.515 (2)	
C1—C2	1.383 (3)	C7—N1	1.497 (2)	
C1—H1	0.9300	C7—C8	1.507 (3)	
C2—C3	1.361 (3)	C7—H7	0.9800	
С2—Н2	0.9300	C8—O2	1.192 (3)	
C3—C4	1.365 (3)	C8—O1	1.323 (3)	
С3—Н3	0.9300	N1—H1A	0.8900	
C4—C5	1.389 (3)	N1—H1B	0.8900	
C4—H4	0.9300	N1—H1C	0.8900	
C5—C6	1.386 (3)	O1—H1D	0.8200	

С5—Н5	0.9300		
C6—C1—C2	119.8 (2)	C5—C6—C7	119.15 (19)
C6—C1—H1	120.1	N1—C7—C8	107.37 (17)
C2—C1—H1	120.1	N1—C7—C6	112.12 (15)
C3—C2—C1	120.6 (2)	C8—C7—C6	111.19 (16)
С3—С2—Н2	119.7	N1—C7—H7	108.7
C1—C2—H2	119.7	С8—С7—Н7	108.7
C2—C3—C4	120.4 (2)	С6—С7—Н7	108.7
С2—С3—Н3	119.8	O2—C8—O1	125.1 (2)
С4—С3—Н3	119.8	O2—C8—C7	124.73 (19)
C3—C4—C5	120.0 (2)	O1—C8—C7	110.16 (19)
C3—C4—H4	120.0	C7—N1—H1A	109.5
C5—C4—H4	120.0	C7—N1—H1B	109.5
C6—C5—C4	119.9 (2)	H1A—N1—H1B	109.5
С6—С5—Н5	120.0	C7—N1—H1C	109.5
C4—C5—H5	120.0	H1A—N1—H1C	109.5
C1—C6—C5	119.30 (19)	H1B—N1—H1C	109.5
C1—C6—C7	121.4 (2)	C8—O1—H1D	109.5
C6—C1—C2—C3	0.2 (4)	C1C6C7N1	-54.0 (3)
C1—C2—C3—C4	-0.3 (4)	C5—C6—C7—N1	130.1 (2)
C2—C3—C4—C5	0.5 (4)	C1—C6—C7—C8	66.2 (2)
C3—C4—C5—C6	-0.6 (3)	C5—C6—C7—C8	-109.7 (2)
C2-C1-C6-C5	-0.2 (3)	N1—C7—C8—O2	15.6 (3)
C2-C1-C6-C7	-176.2 (2)	C6—C7—C8—O2	-107.4 (2)
C4—C5—C6—C1	0.5 (3)	N1—C7—C8—O1	-165.48 (17)
C4—C5—C6—C7	176.5 (2)	C6—C7—C8—O1	71.5 (2)

Hydrogen-bond geometry (Å, °)

D—H···A	D—H	H···A	$D \cdots A$	D—H···A
N1—H1B····Br1 ⁱ	0.89	2.54	3.3586 (17)	154
N1—H1C···Br1 ⁱⁱ	0.89	2.57	3.429 (2)	163
N1—H1A···Br1	0.89	2.45	3.3166 (18)	164
O1—H1D····Br1 ⁱⁱⁱ	0.82	2.39	3.2027 (17)	171
C7—H7···O2 ^{iv}	0.98	2.59	3.527 (3)	159

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