organic compounds

N-(4-Bromophenyl)pyrazine-2-carbox-amide

Marcelle de Lima Ferreira,[a] Marcus V. N. de Souza,[a] Solange M. S. V. Wardell,[b] James L. Wardell[c]‡ and Edward R. T. Tiekink[d]*

[a]Fundaçao Oswaldo Cruz, Instituto de Tecnologia em Fármacos - Farmanguinhos, R. Sizenando Nabuco 100, Manguinhos, 21041-250 Rio de Janeiro, RJ, Brazil, [b]CHEMSOL, 1 Harcourt Road, Aberdeen AB15 5NY, Scotland, [c]Centro de Desenvolvimento Tecnológico em Saúde (CDTS), Fundação Oswaldo Cruz (FIOCRUZ), Casa Amarela, Campus de Manguinhos, Avenida Brasil 4365, 21040-900 Rio de Janeiro, RJ, Brazil, and [d]Department of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia
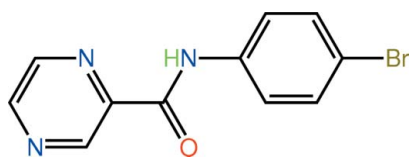Correspondence e-mail: edward.tiekink@gmail.com

The molecule of the title compound, $C_{11}H_8BrN_3O$, is close to planar (r.m.s. deviation of all 16 non-H atoms = 0.103 Å), a conformation stabilized by an intramolecular N—H···N hydrogen bond, which generates an $S(5)$ ring. In the crystal structure, supramolecular chains mediated by C—H···O contacts (along a) are linked into a double layer via N···Br halogen bonds [3.207 (5) Å] and C—Br···π interactions [Br···ring centroid(pyrazine) = 3.446 (3) Å]. The layers stack along the b axis via weak π–π interactions [ring centroid(pyrazine)···ring centroid(benzene) distance = 3.803 (4) Å].

Related literature

For the antimycobacterial activity of pyrazinamide, see: Chaisson et al. (2002); Gordin et al. (2000); de Souza (2006). For structural studies of pyrazinamide derivatives; see: Baddeley et al. (2009); Howie et al. (2010a,b,c,d). For the synthesis, see: Wardell et al. (2008); Vontor et al. (1989). For background to halogen bonding, see: Metrangolo et al. (2008); Pennington et al. (2008). For graph-set nomenclature of hydrogen bonds, see: Bernstein et al. (1995). For details of software used to analyse the shape of the molecule, see: Spek (2009).

‡ Additional correspondence author, e-mail: j.wardell@abdn.ac.uk.

Experimental

Crystal data

$C_{11}H_8BrN_3O$	γ = 110.524 (5)°
M_r = 278.11	V = 512.55 (8) Å³
Triclinic, $P\bar{1}$	Z = 2
a = 5.8396 (4) Å	Mo $K\alpha$ radiation
b = 7.3317 (7) Å	μ = 3.99 mm⁻¹
c = 13.3362 (12) Å	T = 120 K
α = 101.670 (4)°	0.18 × 0.10 × 0.02 mm
β = 96.728 (5)°	

Data collection

Enraf–Nonius KappaCCD diffractometer	8923 measured reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 2007)	2110 independent reflections
T_{min} = 0.764, T_{max} = 1.000	1792 reflections with $I > 2\sigma(I)$
	R_{int} = 0.078

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.054	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2)$ = 0.163	
S = 1.18	
2110 reflections	$\Delta\rho_{max}$ = 0.55 e Å⁻³
148 parameters	$\Delta\rho_{min}$ = −0.52 e Å⁻³
1 restraint	

Table 1
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N1—H1N···N3	0.88 (6)	2.22 (6)	2.708 (7)	115 (5)
C3—H3···O1ⁱ	0.95	2.39	3.177 (8)	140

Symmetry code: (i) $x - 1, y, z$.

Data collection: COLLECT (Nonius, 1998); cell refinement: DENZO (Otwinowski & Minor, 1997) and COLLECT; data reduction: DENZO and COLLECT; program(s) used to solve structure: SHELXS97 (Sheldrick, 2008); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-3 (Farrugia, 1997) and DIAMOND (Brandenburg, 2006); software used to prepare material for publication: publCIF (Westrip, 2010).

References

Baddeley, T. C., Howie, R. A., da Silva Lima, C. H., Kaiser, C. R., de Souza, M. N., Wardell, J. L. & Wardell, S. M. V. (2009). Z. Kristallogr. **224**, 506–514.
Bernstein, J., Davis, R. E., Shimoni, L. & Chang, N.-L. (1995). Angew. Chem. Int. Ed. Engl. **34**, 1555–1573.
Brandenburg, K. (2006). DIAMOND. Crystal Impact GbR, Bonn, Germany.
Chaisson, R. E., Armstrong, J., Stafford, J., Golub, J. & Bur, S. (2002). J. Am. Med. Assoc. **288**, 165–166.
Farrugia, L. J. (1997). J. Appl. Cryst. **30**, 565.
Gordin, F., Chaisson, R. E., Matts, J. P., Miller, C., Garcia, M. de L., Hafner, R., Valdespino, J. L., Coberly, J., Schechter, M., Klukowicz, A. J., Barry, M. A. & O'Brien, R. J. (2000). J. Am. Med. Assoc. **283**, 1445–1450.
Howie, R. A., da Silva Lima, C. H., Kaiser, C. R., de Souza, M. N., Wardell, J. L. & Wardell, S. M. V. (2010a). Z. Kristallogr. **225**, 19–28.

Howie, R. A., da Silva Lima, C. H., Kaiser, C. R., de Souza, M. N., Wardell, J. L. & Wardell, S. M. V. (2010*b*). *Z. Kristallogr.* **225**, 158–166.

Howie, R. A., da Silva Lima, C. H., Kaiser, C. R., de Souza, M. N., Wardell, J. L. & Wardell, S. M. V. (2010*c*). *Z. Kristallogr.* **225**, 245–252.

Howie, R. A., de Souza, M. V. N., Wardell, S. M. S. V., Wardell, J. L. & Tiekink, E. R. T. (2010*d*). *Acta Cryst.* E**66**, o178–o179.

Metrangolo, P., Resnati, G., Pilati, T. & Biella, S. (2008). *Struct. Bond.* **126**, 105–136.

Nonius (1998). *COLLECT*. Nonius BV, Delft, The Netherlands.

Otwinowski, Z. & Minor, W. (1997). *Methods in Enzymology*, Vol. 276, *Macromolecular Crystallography*, Part A, edited by C. W. Carter Jr & R. M. Sweet, pp. 307–326. New York: Academic Press.

Pennington, W. T., Hanks, T. W. & Arman, H. D. (2008). *Struct. Bond.* **126**, 65–104.

Sheldrick, G. M. (2007). *SADABS*. Bruker AXS Inc., Madison, Wisconsin, USA.

Sheldrick, G. M. (2008). *Acta Cryst.* A**64**, 112–122.

Souza, M. V. N. de (2006). *Recent Pat. Anti-Infec. Drug Discov.* **1**, 33–45.

Spek, A. L. (2009). *Acta Cryst.* D**65**, 148–155.

Vontor, T., Palat, K., Danek, J. & Lycka, A. (1989). *Cesk. Farm.* **38**, 393–397.

Wardell, S. M. S. V., de Souza, M. V. N., Vasconcelos, T. R. A., Ferreira, M. L., Wardell, J. L., Low, J. N. & Glidewell, C. (2008). *Acta Cryst.* B**64**, 84–100.

Westrip, S. P. (2010). *J. Appl. Cryst.* **43**, 920–925.

supplementary materials

N-(4-Bromophenyl)pyrazine-2-carboxamide

M. de Lima Ferreira, M. V. N. de Souza, S. M. S. V. Wardell, J. L. Wardell and E. R. T. Tiekink

Comment

Pyrazinamide has well known anti-mycobacterial activity and is the one of the most important drugs used in tuberculosis treatment (Chaisson *et al.*, 2002; Gordin *et al.*, 2000; de Souza, 2006). In continuation of our studies on pyrazinamide derivatives (Wardell *et al.*, 2008; Baddeley *et al.*, 2009; Howie *et al.*, 2010*a*,*b*,*c*,*d*), we report the structure of *N*-(4-bromophenyl)pyrazine-2-carboxamide, the title compound, (I).

The molecular structure of (I), Fig. 1, is essentially planar with the dihedral angle formed between the pyrazine and benzene rings being 10.2 (3)°; the r.m.s. deviation of all 16 non-H atoms = 0.103 Å (Spek, 2009). The observed conformation is stabilized by an intramolecular N—H···N hydrogen bond, Table 1.

An analysis of the crystal packing reveals C—H···O, N···Br, Br···π, and π–π interactions. The C—H···O contacts lead to the formation of a supramolecular chain with a flat topology along the *a* axis. These are sustained in the crystal packing by N···Br halogen bonding [N2···Br1 = 3.207 (5) Å for *i*: 1 + *x*, *y*, 1 + *z*] (Metrangolo *et al.*, 2008; Pennington *et al.*, 2008), as well as Br···π contacts [C5—Br1···*Cg*(N2,N3,C8–C11)[ii] = 3.446 (3) Å, angle at Br1 = 94.59 (18)° for *ii*: 1 - *x*, 1 - *y*, -*z*]. The resulting double layers stack along the *b* axis, Fig. 3, with the closest interactions between them being of the form π–π [ring centroid(N2,N3,C8–C11)···ring centroid(C2–C7)[iii] = 3.803 (4) Å, angle of inclination = 10.2 (3)° for *iii*: 1 - *x*, -*y*, -*z*].

Experimental

N-(4-Bromophenyl)pyrazine-2-carboxamide was prepared following the general procedure for *N*-arylpyrazine-2-carboxamides (Wardell *et al.*, 2008). Yield: 48%; m.p. 473 K, lit. value 471–474 K (Vontor *et al.*, 1989). The colourless plate of (I) used for the structure determination was grown from the slow evaporation of its ethanol solution.

Refinement

The C-bound H atoms were geometrically placed (C—H = 0.95 Å) and refined as riding with $U_{iso}(H) = 1.2U_{eq}(C)$. The N-bound H atom was located from a difference map and refined with the distance restraint N—H = 0.88 (1) Å, and with $U_{iso}(H) = 1.2U_{eq}(N)$.
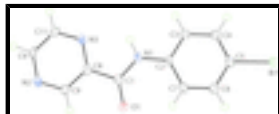
Figures

Fig. 1. The molecular structure of (I) showing displacement ellipsoids at the 50% probability level.
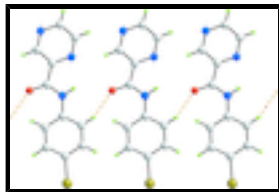
supplementary materials

Fig. 2. Supramolecular chain in (I) aligned along the *a* axis. The C—H···O contacts are as orange dashed lines.

Fig. 3. A view in projection down the *a* axis of the crystal packing in (I) highlighting the stacking of double layers. The C—H···O, N···Br, and Br···π contacts are shown as orange, blue, and purple dashed lines, respectively.

N-(4-Bromophenyl)pyrazine-2-carboxamide

Crystal data

$C_{11}H_8BrN_3O$	$Z = 2$
$M_r = 278.11$	$F(000) = 276$
Triclinic, $P\overline{1}$	$D_x = 1.802$ Mg m^{-3}
Hall symbol: -P 1	Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
$a = 5.8396$ (4) Å	Cell parameters from 22175 reflections
$b = 7.3317$ (7) Å	$\theta = 2.9–27.5°$
$c = 13.3362$ (12) Å	$\mu = 3.99$ mm^{-1}
$\alpha = 101.670$ (4)°	$T = 120$ K
$\beta = 96.728$ (5)°	Plate, colourless
$\gamma = 110.524$ (5)°	$0.18 \times 0.10 \times 0.02$ mm
$V = 512.55$ (8) Å^3	

Data collection

Enraf–Nonius KappaCCD diffractometer	2110 independent reflections
Radiation source: Enraf–Nonius FR591 rotating anode	1792 reflections with $I > 2\sigma(I)$
10 cm confocal mirrors	$R_{int} = 0.078$
Detector resolution: 9.091 pixels mm^{-1}	$\theta_{max} = 26.5°$, $\theta_{min} = 3.1°$
φ and ω scans	$h = -7 \rightarrow 7$
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2007)	$k = -9 \rightarrow 9$
$T_{min} = 0.764$, $T_{max} = 1.000$	$l = -16 \rightarrow 16$
8923 measured reflections	

Refinement

Refinement on F^2	Primary atom site location: structure-invariant direct methods
Least-squares matrix: full	Secondary atom site location: difference Fourier map
$R[F^2 > 2\sigma(F^2)] = 0.054$	Hydrogen site location: inferred from neighbouring sites
$wR(F^2) = 0.163$	H atoms treated by a mixture of independent and constrained refinement

$S = 1.18$

$w = 1/[\sigma^2(F_o^2) + (0.1P)^2]$
where $P = (F_o^2 + 2F_c^2)/3$

2110 reflections

$(\Delta/\sigma)_{max} = 0.001$

148 parameters

$\Delta\rho_{max} = 0.55$ e Å^{-3}

1 restraint

$\Delta\rho_{min} = -0.52$ e Å^{-3}

Special details

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

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 $F^2 > 2\sigma(F^2)$ 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	y	z	$U_{iso}*/U_{eq}$
Br1	0.20472 (10)	0.24870 (9)	−0.39064 (4)	0.0227 (2)
O1	0.8942 (7)	0.2880 (7)	0.0884 (3)	0.0259 (10)
N1	0.4828 (9)	0.2414 (8)	0.0622 (4)	0.0204 (10)
H1N	0.366 (9)	0.234 (10)	0.099 (5)	0.024*
N2	0.9106 (9)	0.2715 (8)	0.3965 (4)	0.0223 (11)
N3	0.4723 (9)	0.2202 (8)	0.2621 (4)	0.0212 (11)
C1	0.6982 (10)	0.2603 (8)	0.1192 (4)	0.0193 (12)
C2	0.4304 (10)	0.2444 (8)	−0.0435 (4)	0.0170 (11)
C3	0.1796 (10)	0.1859 (9)	−0.0902 (5)	0.0211 (12)
H3	0.0531	0.1461	−0.0512	0.025*
C4	0.1156 (10)	0.1861 (9)	−0.1937 (5)	0.0215 (12)
H4	−0.0549	0.1452	−0.2257	0.026*
C5	0.2979 (11)	0.2453 (8)	−0.2498 (5)	0.0192 (12)
C6	0.5492 (11)	0.3087 (9)	−0.2035 (5)	0.0210 (12)
H6	0.6745	0.3519	−0.2427	0.025*
C7	0.6156 (11)	0.3088 (9)	−0.1011 (5)	0.0205 (12)
H7	0.7868	0.3525	−0.0694	0.025*
C8	0.6915 (11)	0.2522 (9)	0.2304 (4)	0.0203 (12)
C9	0.9064 (11)	0.2777 (9)	0.2980 (5)	0.0198 (12)
H9	1.0565	0.3004	0.2724	0.024*
C10	0.6933 (11)	0.2377 (10)	0.4279 (5)	0.0229 (13)
H10	0.6870	0.2303	0.4979	0.028*
C11	0.4790 (11)	0.2134 (10)	0.3620 (5)	0.0243 (13)
H11	0.3300	0.1909	0.3883	0.029*

Atomic displacement parameters (Å^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
Br1	0.0268 (4)	0.0286 (4)	0.0140 (3)	0.0123 (3)	0.0025 (2)	0.0066 (2)
O1	0.021 (2)	0.040 (3)	0.019 (2)	0.0123 (19)	0.0067 (17)	0.010 (2)
N1	0.018 (2)	0.031 (3)	0.013 (2)	0.011 (2)	0.0028 (18)	0.005 (2)
N2	0.022 (2)	0.030 (3)	0.020 (3)	0.013 (2)	0.003 (2)	0.012 (2)
N3	0.018 (2)	0.024 (3)	0.017 (3)	0.005 (2)	0.0011 (19)	0.004 (2)
C1	0.020 (3)	0.015 (3)	0.019 (3)	0.005 (2)	0.003 (2)	0.002 (2)
C2	0.025 (3)	0.017 (3)	0.008 (3)	0.006 (2)	0.003 (2)	0.005 (2)
C3	0.016 (3)	0.026 (3)	0.020 (3)	0.008 (2)	0.005 (2)	0.004 (2)
C4	0.019 (3)	0.027 (3)	0.019 (3)	0.011 (2)	0.002 (2)	0.004 (2)
C5	0.026 (3)	0.016 (3)	0.018 (3)	0.011 (2)	0.005 (2)	0.007 (2)
C6	0.023 (3)	0.026 (3)	0.017 (3)	0.011 (2)	0.009 (2)	0.008 (2)
C7	0.018 (3)	0.023 (3)	0.021 (3)	0.007 (2)	0.000 (2)	0.010 (2)
C8	0.026 (3)	0.022 (3)	0.015 (3)	0.011 (2)	0.004 (2)	0.004 (2)
C9	0.022 (3)	0.020 (3)	0.019 (3)	0.010 (2)	0.007 (2)	0.004 (2)
C10	0.029 (3)	0.034 (3)	0.013 (3)	0.014 (3)	0.012 (2)	0.013 (2)
C11	0.024 (3)	0.033 (3)	0.021 (3)	0.012 (3)	0.014 (3)	0.012 (3)

Geometric parameters (Å, °)

Br1—C5	1.901 (6)	C3—H3	0.9500
O1—C1	1.226 (6)	C4—C5	1.369 (8)
N1—C1	1.337 (7)	C4—H4	0.9500
N1—C2	1.413 (7)	C5—C6	1.394 (8)
N1—H1N	0.88 (6)	C6—C7	1.375 (8)
N2—C9	1.321 (8)	C6—H6	0.9500
N2—C10	1.339 (8)	C7—H7	0.9500
N3—C11	1.340 (8)	C8—C9	1.387 (8)
N3—C8	1.352 (8)	C9—H9	0.9500
C1—C8	1.501 (8)	C10—C11	1.376 (8)
C2—C3	1.398 (8)	C10—H10	0.9500
C2—C7	1.402 (8)	C11—H11	0.9500
C3—C4	1.387 (8)		
C1—N1—C2	128.5 (5)	C6—C5—Br1	120.2 (4)
C1—N1—H1N	113 (5)	C7—C6—C5	120.0 (5)
C2—N1—H1N	119 (5)	C7—C6—H6	120.0
C9—N2—C10	116.0 (5)	C5—C6—H6	120.0
C11—N3—C8	115.2 (5)	C6—C7—C2	120.0 (5)
O1—C1—N1	125.4 (6)	C6—C7—H7	120.0
O1—C1—C8	119.5 (5)	C2—C7—H7	120.0
N1—C1—C8	115.1 (5)	N3—C8—C9	121.6 (5)
C3—C2—C7	119.4 (5)	N3—C8—C1	118.2 (5)
C3—C2—N1	117.1 (5)	C9—C8—C1	120.2 (5)
C7—C2—N1	123.5 (5)	N2—C9—C8	122.6 (5)
C4—C3—C2	120.0 (5)	N2—C9—H9	118.7

C4—C3—H3	120.0	C8—C9—H9	118.7
C2—C3—H3	120.0	N2—C10—C11	122.1 (5)
C5—C4—C3	120.1 (5)	N2—C10—H10	119.0
C5—C4—H4	120.0	C11—C10—H10	119.0
C3—C4—H4	120.0	N3—C11—C10	122.6 (5)
C4—C5—C6	120.6 (6)	N3—C11—H11	118.7
C4—C5—Br1	119.1 (4)	C10—C11—H11	118.7
C2—N1—C1—O1	1.4 (10)	N1—C2—C7—C6	−179.5 (6)
C2—N1—C1—C8	179.5 (5)	C11—N3—C8—C9	−0.6 (8)
C1—N1—C2—C3	169.0 (5)	C11—N3—C8—C1	179.6 (5)
C1—N1—C2—C7	−13.3 (9)	O1—C1—C8—N3	−179.6 (5)
C7—C2—C3—C4	2.0 (9)	N1—C1—C8—N3	2.2 (8)
N1—C2—C3—C4	179.8 (5)	O1—C1—C8—C9	0.6 (8)
C2—C3—C4—C5	−0.6 (9)	N1—C1—C8—C9	−177.6 (5)
C3—C4—C5—C6	−1.0 (9)	C10—N2—C9—C8	0.4 (9)
C3—C4—C5—Br1	−178.8 (4)	N3—C8—C9—N2	0.3 (9)
C4—C5—C6—C7	1.2 (9)	C1—C8—C9—N2	−179.9 (5)
Br1—C5—C6—C7	179.0 (4)	C9—N2—C10—C11	−0.8 (9)
C5—C6—C7—C2	0.2 (9)	C8—N3—C11—C10	0.2 (9)
C3—C2—C7—C6	−1.8 (9)	N2—C10—C11—N3	0.5 (10)

Hydrogen-bond geometry (Å, °)

D—H⋯*A*	*D*—H	H⋯*A*	*D*⋯*A*	*D*—H⋯*A*
N1—H1N⋯N3	0.88 (6)	2.22 (6)	2.708 (7)	115 (5)
C3—H3⋯O1[i]	0.95	2.39	3.177 (8)	140

Symmetry codes: (i) *x*−1, *y*, *z*.

Fig. 1

Fig. 2

Fig. 3