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2-Methoxybenzohydroxamic acid: supramolecular aggregation through two-dimensional networks of N—H···O and O—H···O interactions

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Acta Cryst. (2006). E**62**, o4955–o4957 Vembu *et al.* · $C_8H_9NO_3$

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2-Methoxybenzohydroxamic acid: supramolecular aggregation through two-dimensional networks of N—H···O and O—H···O interactions

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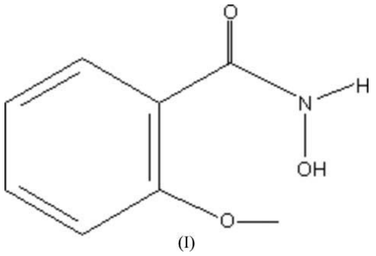
Key indicators
Single-crystal X-ray study
T = 160 K
Mean σ(C–C) = 0.003 Å
R factor = 0.060
wR factor = 0.156
Data-to-parameter ratio = 10.7

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

For the two molecules in the asymmetric unit of the title compound, $C_8H_9NO_3$, the dihedral angles between the mean planes of the benzene ring and the hydroxamic acid group are 4.50 (16) and 10.10 (11)°. The supramolecular aggregation is effected by the formation of two-dimensional networks of N—H···O and O—H···O interactions in addition to C—H···O and π–π interactions.

Comment

Hydroxamic acids are important iron chelators and microbial siderophores. They are associated with diverse biological activities including antibacterial, antifungal and antitumour profiles. Hydroxamate-based compounds are effective urease, ribonucleotide reductase or angiotensin converting enzyme (ACE) inhibitors. Some hydroxamic acids are currently accepted as antineoplastic, anti-inflammatory, analgesic, α-adrenergic agonist and antidepressant drugs (Barbaric *et al.*, 2005). Hydroxamic acids are nitric oxide donors and acetylated hydroxamate derivatives act as effective aspirin analogues by prostaglandin H_2 synthase inhibition (Devocelle *et al.*, 2003). The present investigation is aimed at the study of the molecular and supramolecular architecture of the title compound, (I). This study may serve as a forerunner to the study of the correlation between the molecular and supramolecular features of these compounds and their biological activities.



(I)

There are two independent molecules in the asymmetric unit (Fig. 1). The dihedral angle between the mean planes through atoms O9/C7/N8/O10 and atoms C1–C6 in molecule *A*, and through atoms O21/C19/N20/O22 and atoms C13–C18 in molecule *B*, are 4.50 (16) and 10.10 (11)°, respectively. This near-coplanarity contrasts with the non-coplanar orientation observed for similar groups in 2-amino-5-iodobenzohydroxamic acid [corresponding dihedral angle of 39.1 (1)°; Vembu *et al.*, 2006], 2,4-dichlorobenzohydroxamic acid [49.3 (2)°; Shang *et al.*, 2005] and *o*-methoxy-*N*-phenylbenzohydroxamic acid [63.75 (7)°; Saad *et al.*, 2003].

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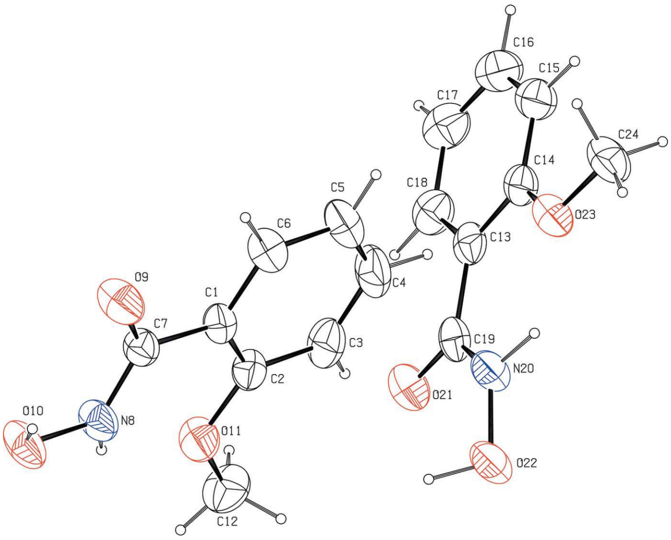

Figure 1
The asymmetric unit of (I), showing 50% probability displacement ellipsoids.

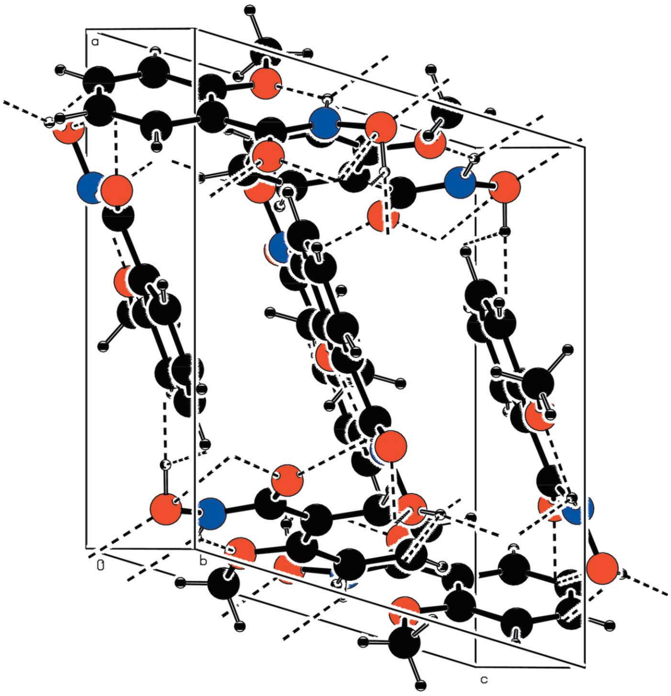

Figure 2
A view of the unit-cell contents of (I), showing the two-dimensional chains and cooperative hydrogen-bonded network of O—H$\cdots$O and N—H$\cdots$O interactions (dashed lines).

The crystal structure of (I) is stabilized by the interplay of O—H$\cdots$O, N—H$\cdots$O, C—H$\cdots$O and π–π interactions (Table 1). The NH groups are involved in bifurcated hydrogen bonds. The N8—H8$\cdots$O11 and N20—H20$\cdots$O23 intramolecular interactions each generate loops with a graph-set motif (Bernstein *et al.*, 1995; Etter, 1990) of $S(6)$. The N8—H8$\cdots$O21^{i} interaction (see Table 1 for symmetry codes) links two independent molecules (*A* and *B*), whereas the N20—H20$\cdots$O22^{iii} interaction links pairs of *B* molecules into dimers. The C24—H24*A*$\cdots$O10^{vi} interaction also links a molecule *B* to a molecule *A*, but there is no corresponding link in the reverse direction. The O10—H10$\cdots$O21^{ii} and O22—H22$\cdots$O9^{iv} interactions combine to give dimers involving the two independent molecules which can be described by a binary motif of $R_2^2(10)$. The combination of all intermolecular N—H$\cdots$O and O—H$\cdots$O interactions forms an extended two-dimensional network which lies parallel to the (100) plane (Fig. 2). The supramolecular aggregation is completed by the presence of a C17–H17$\cdots$O9^{v} interaction (Table 1). The symmetry-related $(2 - x, 2 - y, -z)$ benzene rings of *B* (C13–C18) stack together *via* a π–π interaction in which the centroids of the rings (*Cg*2) are separated by 3.762 (1) Å.

Experimental

Compound (I) was prepared by a reported method (Devocelle *et al.*, 2003). Single crystals suitable for X-ray diffraction were obtained from a methanol solution by slow evaporation.

Crystal data

$C_8H_9NO_3$
$M_r = 167.16$
Monoclinic, $P2_1/c$
$a = 11.1348$ (4) Å
$b = 16.7669$ (6) Å
$c = 8.8110$ (3) Å
$\beta = 106.761$ (2)°
$V = 1575.09$ (10) Å^3
$Z = 8$
$D_x = 1.410$ Mg m^{-3}
Mo $K\alpha$ radiation
$\mu = 0.11$ mm^{-1}
$T = 160$ (1) K
Prism, orange
0.25 × 0.20 × 0.15 mm

Data collection

Nonius KappaCCD area-detector diffractometer
ω scans
Absorption correction: none
22727 measured reflections
3093 independent reflections
2461 reflections with $I > 2\sigma(I)$
$R_{int} = 0.055$
$\theta_{max} = 26.0$°

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.060$
$wR(F^2) = 0.156$
$S = 1.17$
3092 reflections
290 parameters
All H-atom parameters refined
$w = 1/[\sigma^2(F_o^2) + (0.0749P)^2 + 0.4768P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.52$ e Å^{-3}
$\Delta\rho_{min} = -0.31$ e Å^{-3}
Extinction correction: *SHELXL97*
Extinction coefficient: 0.116 (9)

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

D—H$\cdots A$	D—H	H$\cdots A$	$D\cdots A$	D—H$\cdots A$
N8—H8$\cdots$O11	0.88 (3)	2.00 (3)	2.609 (2)	125 (2)
N8—H8$\cdots$O21^{i}	0.88 (3)	2.41 (3)	3.102 (2)	135 (2)
O10—H10$\cdots$O21^{ii}	0.95 (3)	1.88 (3)	2.798 (2)	162 (3)
N20—H20$\cdots$O22^{iii}	1.05 (3)	2.12 (3)	2.951 (2)	134 (2)
N20—H20$\cdots$O23	1.05 (3)	1.80 (3)	2.588 (2)	129 (2)
O22—H22$\cdots$O9^{iv}	0.98 (4)	1.68 (4)	2.659 (2)	172 (3)
C17—H17$\cdots$O9^{v}	1.00 (3)	2.32 (3)	3.251 (3)	155 (2)
C24—H24*A*$\cdots$O10^{vi}	0.99 (3)	2.27 (3)	3.123 (3)	145 (2)

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

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One low-angle reflection was omitted from the final cycles of refinement because its observed intensity was much lower than the calculated value as a result of being partially obscured by the beam stop. All H atoms were located in difference maps and their positions and isotropic displacement parameters were refined freely. The C—H, N—H and O—H bond lengths are 0.87 (3)–1.05 (3) Å, 0.88 (3) and 1.05 (3) Å, and 0.95 (3) and 0.98 (4) Å, respectively.

Data collection: *COLLECT* (Nonius, 2000); cell refinement: *DENZO*–SMN (Otwinowski & Minor, 1997); data reduction: *DENZO*–SMN and *SCALEPACK* (Otwinowski & Minor, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97*.

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References

Barbaric, M., Ursic, S., Pilepic, V., Zorc, B., Hegold-Brundic, A., Nagl, A., Grdisa, M., Pavelic, K., Snoeck, R., Andrei, G., Balzarini, J., Clerq, E. D. & Mintas, M. (2005). *J. Med. Chem.* **48**, 884–887.

Bernstein, J., Davis, R. E., Shimoni, L. & Chang, N. (1995). *Angew. Chem. Int. Ed. Engl.* **34**, 1555–1573.

Devocelle, M., Mc Loughlin, B. M., Sharkey, C. T., Fitzgerald, D. J. & Nolan, K. B. (2003). *Org. Biomol. Chem.* **1**, 850–853.

Etter, M. C. (1990). *Acc. Chem. Res.* **23**, 120–126.

Nonius (2000). *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. London: Academic Press.

Saad, E. E., Farina, Y. & Yamin, B. M. (2003). *Acta Cryst.* E**59**, o1004–o1005.

Shang, X.-M., Meng, X.-G., Wu, J.-Z. & Li, Q.-S. (2005). *Acta Cryst.* E**61**, o2328–o2329.

Sheldrick, G. M. (1997). *SHELXS97* and *SHELXL97*. University of Göttingen, Germany.

Spek, A. L. (2003). *J. Appl. Cryst.* **36**, 7–13.

Vembu, N., Linden, A., Lee, J., Kelly, J. G., Nolan, K. B. & Devocelle, M. (2006). *Acta Cryst.* E**62**. Submitted.

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