

3-(Acetylamino)benzoic acid

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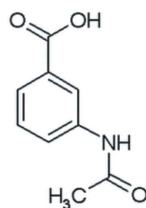
Key indicators: single-crystal X-ray study; $T = 293$ K; mean $\sigma(\text{C}-\text{C}) = 0.003$ Å; R factor = 0.052; wR factor = 0.037; data-to-parameter ratio = 7.8.

The title compound, $\text{C}_9\text{H}_9\text{NO}_3$, was crystallized from methanol. The monoclinic structure features one molecule in the asymmetric unit. The topology of the $\text{O}-\text{H}\cdots\text{O}$ and $\text{N}-\text{H}\cdots\text{O}$ hydrogen-bond network can be characterized by the graph-set assignments $C(9)$ and $R_2^2(14)$.

Related literature

For the crystal structures of the *ortho*- and *para*-isomers of the title compound, see: Feeder & Jones (1992); Kashino *et al.* (1986); Kovalevsky (1999); Mascarenhas *et al.* (1980); Rajnikant & Deshmukh (2004).

For related literature, see: Etter (1990).



Experimental

Crystal data

 $\text{C}_9\text{H}_9\text{NO}_3$ $M_r = 179.17$ Monoclinic, $P2_1/n$ $a = 3.9522$ (15) Å $b = 10.699$ (4) Å $c = 19.831$ (7) Å $\beta = 93.393$ (8)° $V = 837.1$ (5) Å³ $Z = 4$ Mo $K\alpha$ radiation $\mu = 0.11$ mm⁻¹ $T = 293.1$ K $0.60 \times 0.10 \times 0.05$ mm

Data collection

Rigaku Saturn CCD area-detector diffractometer

Absorption correction: multi-scan (Jacobson, 1998)

 $T_{\min} = 0.937$, $T_{\max} = 0.995$

9339 measured reflections

2325 independent reflections

1168 reflections with $F^2 > 2\sigma(F^2)$ $R_{\text{int}} = 0.031$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.052$ $wR(F^2) = 0.037$ $S = 1.50$

1168 reflections

152 parameters

H atoms treated by a mixture of independent and constrained refinement

 $\Delta\rho_{\max} = 0.22$ e Å⁻³ $\Delta\rho_{\min} = -0.17$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{O3}-\text{H7}\cdots\text{O1}^{\text{i}}$	1.02 (3)	1.71 (3)	2.714 (2)	164 (2)
$\text{N1}-\text{H1}\cdots\text{O2}^{\text{ii}}$	1.02 (2)	2.01 (2)	3.022 (2)	173.3 (18)

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

Data collection: *CrystalClear* (Rigaku, 2005); cell refinement: *CrystalClear*; data reduction: *CrystalStructure* (Rigaku, 2005); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *CRYSTALS* (Betteridge *et al.*, 2003); molecular graphics: *CrystalStructure*; software used to prepare material for publication: *CrystalStructure*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB2363).

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