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N-[2-(4-Bromophenoxy)ethyl]acetamide

Zhen-Hua Shang* and Hui-Li Zhang

College of Chemical and Pharmaceutical Engineering, Hebei University of Science and Technology, Shijiazhuang 050018, People's Republic of China

Correspondence e-mail: zhenhuashang@yahoo.com.cn

Key indicators

Single-crystal X-ray study T = 294 KMean $\sigma(\text{C-C}) = 0.007 \text{ Å}$ R factor = 0.039 wR factor = 0.090Data-to-parameter ratio = 16.0

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

The crystal structure of the title compound, $C_{10}H_{12}BrNO_2$, is stabilized mainly through intermolecular $N-H\cdots O$ hydrogen bonds.

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Comment

2-Phenoxyethanamine is a starting material for the preparation of the antidepressant drug nefazodone (Madding, 1986). The title compound, (I), which can be hydrolyzed to 2-(4-bromophenoxy)ethanamine, was obtained in order to prepare new analogous compounds.

The molecular geometry in (I) is normal (Allen *et al.*, 1987). The crystal structure is stabilized mainly through intermolecular $N-H\cdots O$ hydrogen bonds (Table 1), resulting in C(4) chains (Etter, 1990).

Experimental

A mixture of 4-bromophenol (17.3 g, 0.10 mol) and 2-methyl-4,5-dihydrooxazole (1.2 g, 0.12 mol) was slowly heated to reflux under nitrogen and refluxed for 7 h, monitored by thin-layer chromatography. On completion, the excess 2-methyl-4,5-dihydrooxazole was recovered by distillation, the residue was cooled to room temperature and 10% NaOH solution (50 ml) was added. The product was filtered off and purified by column chromatography. The title compound (20 mg) was dissolved in methanol (15 ml) and after 15 d colourless blocks of (I) were recovered.

Crystal data

 $\begin{array}{lll} \text{C}_{10}\text{H}_{12}\text{BrNO}_2 & V = 543.0 \text{ (3)} \text{ Å}^3 \\ M_r = 258.12 & Z = 2 \\ \text{Monoclinic, } P2_1 & \text{Mo } K\alpha \text{ radiation} \\ a = 4.9957 \text{ (16)} \text{ Å} & \mu = 3.76 \text{ mm}^{-1} \\ b = 9.340 \text{ (3)} \text{ Å} & T = 294 \text{ (2)} \text{ K} \\ c = 11.700 \text{ (4)} \text{ Å} & 0.28 \times 0.24 \times 0.20 \text{ mm} \\ \beta = 95.882 \text{ (6)}^\circ \end{array}$

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Data collection

Bruker SMART CCD area-detector diffractometer Absorption correction: multi-scan (SADABS; Bruker, 1997) $T_{\min} = 0.419$, $T_{\max} = 0.520$ (expected range = 0.380–0.472)

3109 measured reflections 2099 independent reflections 1445 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.026$

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Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.039$ $wR(F^2) = 0.090$ S = 0.982099 reflections 131 parameters 1 restraint H atoms treated by a mixture of independent and constrained refinement

 $\begin{array}{l} \Delta \rho_{\rm max} = 0.24~{\rm e}~\mathring{\rm A}^{-3} \\ \Delta \rho_{\rm min} = -0.39~{\rm e}~\mathring{\rm A}^{-3} \end{array}$

Absolute structure: Flack (1983), with 915 Friedel pairs Flack parameter: 0.006 (16)

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

$D-H\cdots A$	<i>D</i> —Н	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	D $ H$ $\cdot \cdot \cdot A$
N1-H1···O2i	0.83 (4)	2.07 (5)	2.905 (5)	176 (5)

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

The N-bound H atom was located in a difference map and its position was freely refined, with $U_{\rm iso}({\rm H})=1.2U_{\rm eq}({\rm N})$. The C-bound H atoms were positioned geometrically, with C-H = 0.93-0.97 Å, and refined in a riding model, with $U_{\rm iso}({\rm H})=1.2U_{\rm eq}({\rm C})$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

Figure 1 The molecular structure of (I), drawn with 30% probability displacement ellipsoids (arbitrary spheres for the H atoms).

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