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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.004 Å R factor = 0.057 wR factor = 0.170 Data-to-parameter ratio = 13.2

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

Methyl 2-(methoxyacetylamino)benzoate

The title compound, $C_{11}H_{13}NO_4$, was obtained by reaction of methyl 2-aminobenzoate and 2-methoxyacetyl chloride. The two side chains lie in the same plane as the benzene ring.

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Comment

Methyl 2-(methoxyacetylamino)benzoate, (I), is an important intermediate in the chemical industry (Aavid *et al.*, 1949) and is used extensively in medicine and pesticides (Stephen *et al.*, 2002). For example, it is a precursor of quinazoline derivatives and a potential anticancer medication (Silvana *et al.*, 2004). We report here the synthesis and crystal structure of the title compound, (I). The two side chains lie in the same plane as the benzene ring plane (dihedral angle 1.4°).



Experimental

2-Methoxyacetyl chloride (5.38 g, 0.05 mol) was added dropwise over a period of 30 min to a dichloromethane (60 ml) solution of methyl 2aminobenzoate (5.00 g, 0.033 mol) and pyridine (5.22 g, 0.066 mol) in a cool water bath (273–278 K), then the mixture was stirred for 2 h at room temperature. The resulting solution was washed with 1*M* HCl (50 ml), 1 *M* NaOH (50 ml), saturated NaCl (50 ml) and water (50 ml). The dichloromethane solution was dried over MgSO₄, and the solvent was removed using a rotary evaporator to give (I) as a white solid (yield: 4.80 g, 65%; m.p. 345–346 K). Crystals of (I) suitable for X-ray diffraction were obtained by slow evaporation of a CH₂Cl₂ solution at room temperature. Analysis calculated for C₁₁H₁₃NO₄: C 59.19, H 5.87, N 6.28, O 28.67%; found: C 59.33, H 5.54, N 6.44, O 28.76%.

Crystal data	
C ₁₁ H ₁₃ NO ₄	$V = 555.8 (5) \text{ Å}^3$
$M_r = 223.22$	Z = 2
Triclinic, P1	$D_x = 1.334 \text{ Mg m}^{-3}$
a = 7.149 (4) Å	Mo $K\alpha$ radiation
b = 8.649 (5) Å	$\mu = 0.10 \text{ mm}^{-1}$
c = 9.973 (5) Å	T = 293 (2) K
$\alpha = 67.462 \ (5)^{\circ}$	Prism, colorless
$\beta = 89.982 \ (7)^{\circ}$	$0.24 \times 0.16 \times 0.12 \text{ mm}$
$\gamma = 78.350 \ (7)^{\circ}$	

Data collection

Bruker SMART CCD area-detector	3000 meas
diffractometer	1941 indep
φ and ω scans	1166 reflec
Absorption correction: multi-scan	$R_{\rm int} = 0.02$
(SADABS; Sheldrick, 1996)	$\theta_{\rm max} = 25.0$
$T_{\min} = 0.975, \ T_{\max} = 0.988$	

000 measured reflections 941 independent reflections 166 reflections with $I > 2\sigma(I)$ $R_{int} = 0.029$ $\rho_{max} = 25.0^{\circ}$

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Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.057$	$w = 1/[\sigma^2(F_o^2) + (0.0937P)^2]$
$wR(F^2) = 0.170$	where $P = (F_o^2 + 2F_c^2)/3$
1941 reflections 147 parameters	$\Delta \rho_{\text{max}} = 0.001$ $\Delta \rho_{\text{max}} = 0.21 \text{ e } \text{\AA}^{-3}$ $\Delta \rho_{\text{min}} = -0.23 \text{ e } \text{\AA}^{-3}$

All H atoms were initially located in a difference Fourier map, but were then constrained to an ideal geometry, with C-H = 0.93-0.97 Å and $U_{iso}(H) = 1.2U_{eq}(C)$, and refined as riding on their parent atoms.

Data collection: SMART (Bruker, 2000); cell refinement: SMART; data reduction: SAINT (Bruker, 2000); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997a); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997a); molecular graphics: SHELXTL (Sheldrick, 1997b); software used to prepare material for publication: SHELXTL.

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Figure 1

A view of (I) with the atomic numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

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