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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.003 Å R factor = 0.037 wR factor = 0.103 Data-to-parameter ratio = 13.4

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

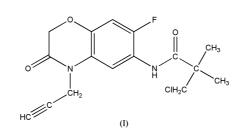
3-Chloro-*N*-[7-fluoro-3-oxo-4-(prop-2-ynyl)-3,4dihydro-2*H*-1,4-benzoxazin-6-yl]-2,2-dimethylpropionamide

The title compound, $C_{16}H_{16}CIFN_2O_3$, known as a protox inhibitor, was synthesized from 7-fluoro-2*H*-benz[1,4]oxazin-3(4*H*)-one. The bond lengths and angles are unexceptional and the heterocyclic ring adopts a screw-boat conformation.

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Comment

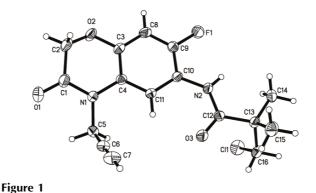
The title compound, (I), is a potent inhibitor of the plant enzyme protoporphyrinogen oxidase (protox; Birchfield *et al.*, 1997). Low dosage provides excellent control for broadleaf weeds and, at high dosage, there is no damage for monocotyledonous plants such as wheat and corn (Chamilleri *et al.*, 1988).



The molecular structure is illustrated in Fig. 1. The conformation of the six-membered heterocyclic ring is close to screw-boat, with atoms C1 and C2 out of the plane of the remaining four atoms by 0.352 (4) and 0.726 (3) Å, respectively. The bond lengths and angles in this ring agree well with those in a related compound (Karolak-Wojciechowska *et al.*, 2001), although the latter adopts a twist-chair conformation.

Experimental

7-Fluoro-2*H*-benz[1,4]oxazin-3(4*H*)-one was prepared according to a previously published method (Terni *et al.*, 1988). It (100 mmol) was then treated with 3-bromoprop-1-yne (100 mmol) to obtain 7-fluoro-



© 2004 International Union of Crystallography Printed in Great Britain – all rights reserved The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level.

4-(prop-2-ynyl)-2*H*-benz[*b*][1,4]oxazin-3(4*H*)-one. After nitration and reduction, the amide was obtained and mixed with pivaloyl chloride (100 mmol). The reaction mixture was poured into ice water, and the precipitated solid was filtered off, washed with water and then dried. The crude product was purified by column chromatography (silica gel, petroleum ether/acetone 2:1) to give (I). ¹H NMR (CDCl₃, p.p.m.): 1.29 (3H, *s*), 1.29 (3H, *s*), 1.82 (1H, *s*), 2.60 (2H, *m*), 3.60 (1H, *m*), 3.63 (2H, *m*), 5.10 (2H, *s*), 6.44 (1H, *m*), 7.36 (1H, *m*), 8.00 (1H, *m*). Compound (I) (20 mg) was dissolved in ethyl acetate (20 ml). Single crystals of (I), suitable for X-ray analysis, were grown by natural evaporation of the solvent.

Crystal data

C₁₆H₁₆ClFN₂O₃ $M_r = 338.76$ Monoclinic, $P2_1/c$ a = 13.292 (4) Å b = 7.529 (2) Å c = 17.213 (5) Å $\beta = 111.607$ (5)° V = 1601.5 (8) Å³ Z = 4

Data collection

Bruker SMART 1000 CCD areadetector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 1997) $T_{min} = 0.930, T_{max} = 0.948$ 6555 measured reflections

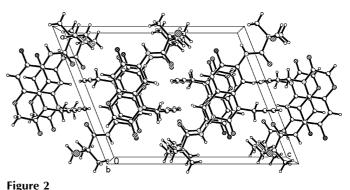
Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.037$ $wR(F^2) = 0.103$ S = 1.032813 reflections 210 parameters H-atom parameters constrained Mo K α radiation Cell parameters from 903 reflections $\theta = 2.6-25.9^{\circ}$ $\mu = 0.27 \text{ mm}^{-1}$ T = 293 (2) KBlock, colorless $0.26 \times 0.24 \times 0.20 \text{ mm}$

 $D_x = 1.405 \text{ Mg m}^{-3}$

2813 independent reflections 2157 reflections with $I > 2\sigma(I)$ $R_{int} = 0.022$ $\theta_{max} = 25.0^{\circ}$ $h = -15 \rightarrow 15$ $k = -8 \rightarrow 8$ $l = -20 \rightarrow 19$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.0478P)^2 \\ &+ 0.4903P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} &= 0.001 \\ \Delta\rho_{\text{max}} &= 0.19 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.23 \text{ e } \text{\AA}^{-3} \end{split}$$



The crystal structure of (I), viewed along the b axis.

H atoms were positioned geometrically, with C–H = 0.93–0.97 Å and N–H = 0.86 Å, and refined in the riding-model approximation, with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}$ (carrier atom).

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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