

John N. Low,<sup>a</sup> James L. Wardell<sup>b</sup>  
 and Christopher Glidewell<sup>c\*</sup>
<sup>a</sup>Department of Chemistry, University of Aberdeen, Meston Walk, Old Aberdeen AB24 3UE, Scotland, <sup>b</sup>Instituto de Química, Departamento de Química Inorgânica, Universidade Federal do Rio de Janeiro, 21945-970 Rio de Janeiro, RJ, Brazil, and <sup>c</sup>School of Chemistry, University of St Andrews, Fife, KY16 9ST, Scotland

Correspondence e-mail: cg@st-andrews.ac.uk

**Key indicators**
 Single-crystal X-ray study  
 T = 120 K  
 Mean  $\sigma(\text{C}-\text{C}) = 0.004 \text{ \AA}$   
 R factor = 0.041  
 wR factor = 0.098  
 Data-to-parameter ratio = 7.8

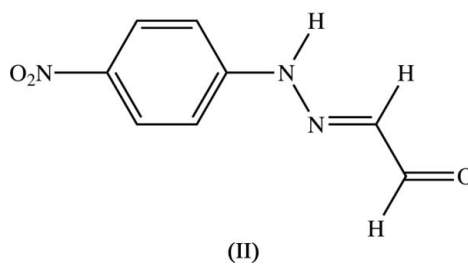
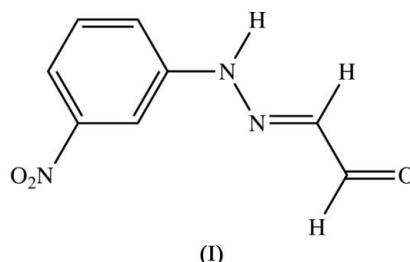
 For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

## A hydrogen-bonded C(6) chain in glyoxal 3-nitrophenylhydrazone

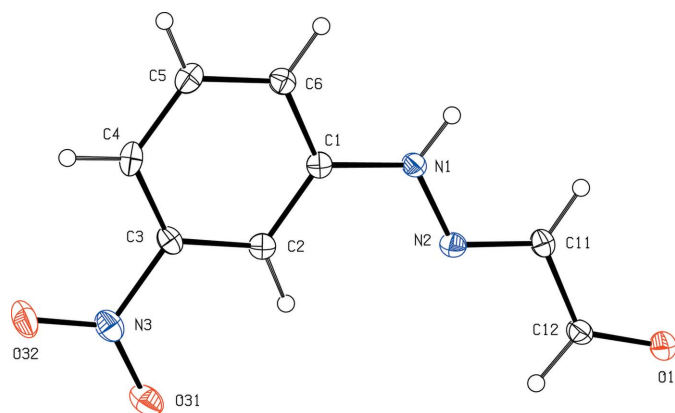
 The molecules of the title compound,  $\text{C}_8\text{H}_7\text{N}_3\text{O}_3$ , which are nearly planar, are linked into simple C(6) chains by an N—H···O hydrogen bond.

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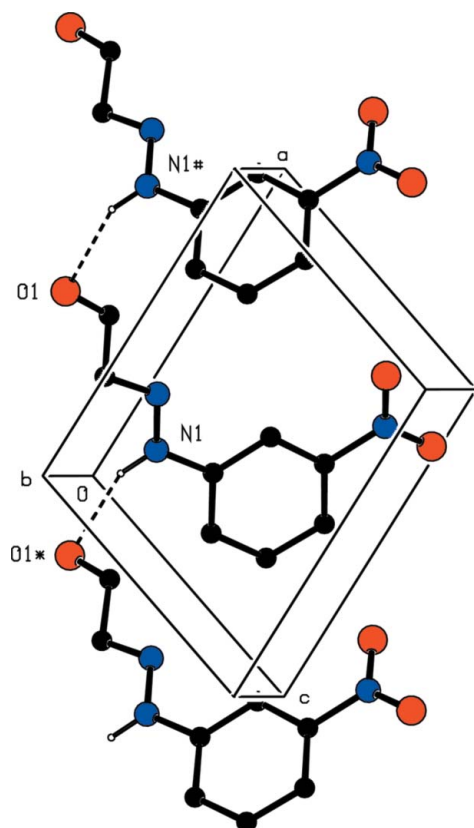
Accepted 31 March 2006

**Comment**
 The title compound, (I), was prepared as part of our continuing study of the supramolecular arrangements of *N*-(nitrophenyl)imide and hydrazone derivatives. We have recently reported the supramolecular structure of the isomeric compound glyoxal 4-nitrophenylhydrazone, (II), in which triple helices enclose two types of channel lying respectively along  $\bar{4}$ , and  $4_1$  or  $4_3$  axes in space group  $I4_1/a$  (Glidewell *et al.*, 2005): the supramolecular structure of (I), by contrast, is very simple.

 The molecules of compound (I) (Fig. 1) are almost planar, as shown by the leading torsion angles (Table 1); the side chain between atoms N1 and O1 adopts a planar all-*trans* conformation, and the nitro group is nearly coplanar with the aryl ring. There is strong bond fixation in the side chain with very short N2—C11 and C12—O1 bonds, with no evidence for bond polarization in this fragment.

 A single hydrogen bond (Table 2) links the molecules into chains; atom N1 in the molecule at  $(x, y, z)$  acts as hydrogen-bond donor to atom O1 in the molecule at  $(-\frac{1}{2} + x, \frac{1}{2} - y, \frac{1}{2} + z)$ , forming a C(6) chain running parallel to the  $[10\bar{1}]$  direction and generated by the *n*-glide plane at  $y = 0.25$  (Fig. 2). Two such chains pass through each unit cell, but there are no direction-specific interactions between adjacent chains.



**Figure 1**  
A molecule of compound (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.



**Figure 2**  
Part of the crystal structure of compound (I), showing the formation of a C(6) hydrogen-bonded chain along  $[10\bar{1}]$ . For the sake of clarity, H atoms bonded to C atoms have been omitted. Atoms marked with an asterisk (\*) or a hash (#) are at the symmetry positions  $(-\frac{1}{2} + x, \frac{1}{2} - y, \frac{1}{2} + z)$  and  $(\frac{1}{2} + x, \frac{1}{2} - y, -\frac{1}{2} + z)$ , respectively.

## Experimental

Compound (I) was prepared by heating under reflux for 1 h a solution of glyoxal (1 mmol as a 40% aqueous solution) and 3-nitrophenylhydrazine (1 mmol) in methanol (40 ml). The mixture was cooled to ambient temperature and the solvent was removed under reduced pressure. The residue was crystallized from ethanol to yield crystals suitable for single-crystal X-ray diffraction.

## Crystal data

$C_8H_7N_3O_3$   
 $M_r = 193.17$   
Monoclinic,  $Cc$   
 $a = 7.4737$  (4) Å  
 $b = 19.7711$  (13) Å  
 $c = 6.0262$  (4) Å  
 $\beta = 107.080$  (4)°  
 $V = 851.18$  (9) Å<sup>3</sup>

$Z = 4$   
 $D_x = 1.507$  Mg m<sup>-3</sup>  
Mo  $K\alpha$  radiation  
 $\mu = 0.12$  mm<sup>-1</sup>  
 $T = 120$  (2) K  
Lath, yellow  
 $0.16 \times 0.08 \times 0.02$  mm

## Data collection

Bruker–Nonius KappaCCD  
diffractometer  
 $\varphi$  and  $\omega$  scans  
Absorption correction: multi-scan  
(SADABS; Sheldrick, 2003)  
 $T_{\min} = 0.961$ ,  $T_{\max} = 0.998$

7928 measured reflections  
987 independent reflections  
871 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.063$   
 $\theta_{\text{max}} = 27.6^\circ$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.041$   
 $wR(F^2) = 0.098$   
 $S = 1.08$   
987 reflections  
127 parameters  
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0568P)^2 + 0.1446P]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.17$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.26$  e Å<sup>-3</sup>

**Table 1**

Selected geometric parameters (Å, °).

C1–N1	1.395 (3)	C11–C12	1.445 (4)
N1–N2	1.331 (3)	C12–O1	1.224 (3)
N2–C11	1.294 (3)		
C2–C1–N1–N2	−3.6 (4)	N2–C11–C12–O1	−177.1 (3)
C1–N1–N2–C11	−175.8 (2)	C2–C3–N3–O31	6.7 (4)
N1–N2–C11–C12	−179.1 (2)		

**Table 2**

Hydrogen-bond geometry (Å, °).

$D-H \cdots A$	$D-H$	$H \cdots A$	$D \cdots A$	$D-H \cdots A$
N1–H1 <sup>i</sup> ⋯O1 <sup>i</sup>	0.88	2.15	2.940 (3)	149

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

All H atoms were located in difference maps and then treated as riding atoms, with C–H = 0.95 Å and N–H = 0.88 Å, and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$ . In the absence of significant anomalous dispersion the Flack (1983) parameter was indeterminate and it was not possible to determine the correct orientation of the structure with respect to the polar axis directions. Accordingly, the Friedel-equivalent reflections were merged prior to the final refinement.

Data collection: *COLLECT* (Hooft, 1999); cell refinement: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *OSCAIL* (McArdle, 2003) and *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *OSCAIL* and *SHELXL97* (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2003); software used to prepare material for publication: *SHELXL97* and *PRPKAPPA* (Ferguson, 1999).

X-ray data were collected at the EPSRC X-ray Crystallographic Service, University of Southampton, England. The

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