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Key indicators

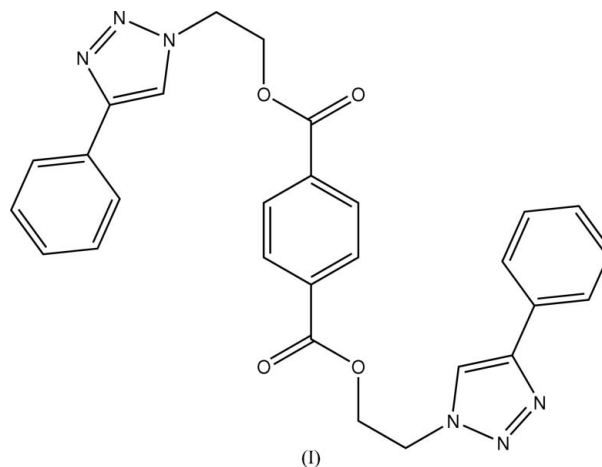
Single-crystal X-ray study
 $T = 293$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.071
 wR factor = 0.137
Data-to-parameter ratio = 14.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Bis[2-(4-phenyl-1*H*-1,2,3-triazol-1-yl)ethyl]
benzene-2,4-dicarboxylate

The title compound, $\text{C}_{28}\text{H}_{24}\text{N}_6\text{O}_4$, crystallizes with one half-molecule in the asymmetric unit, the other half being generated by a center of inversion. In the crystal structure, molecules are linked into ribbons along the a axis by weak $\text{C}-\text{H} \cdots \text{N}$ hydrogen bonds.

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Comment

1,2,3-Triazoles are important target molecules due to their importance as potent pharmacophores. Many 1,2,3-triazoles have been found to be potent antimicrobial (Chen *et al.*, 2000) and anti-inflammatory agents (Banu & Dinakar, 1999). The title triazole, (I), was synthesized *via* [3 + 2]-cycloaddition between azide and acetylene compounds. This reaction generally results in the corresponding 1,4-disubstituted 1,2,3-triazoles in high yields.



The title compound, (I), has a crystallographically imposed center of symmetry. All bond lengths and angles are within normal ranges (Allen *et al.*, 1987). The dihedral angles between the triazole ring and its attached benzene ring is $21.4(2)^\circ$, and that between the triazole ring and the central benzene ring is $56.9(2)^\circ$, while the two benzene rings make an angle of $43.0(2)^\circ$ with each other. In the crystal structure, molecules are linked into a ribbon along the a axis (Fig. 2) by $\text{C8}-\text{H8A} \cdots \text{N1}$ hydrogen bonds (Table 2).

Experimental

To a solution of bis(2-azidoethyl)terephthalate (1 g, 3.3 mmol) in toluene (10 ml), were added successively phenylacetylene (1.6 ml, 16.5 mmol), CuI (0.66 g, 3.3 mmol) and diisopropyl ether (5 ml). The mixture was stirred at 323 K for 20 h. After concentration, the resulting solid was recrystallized from dimethylformamide (DMF),

yielding the title compound, (I). A solution of (I) in DMF was allowed to stand at 323 K for 2 d and colourless needle-shaped crystals suitable for X-ray crystallographic analysis were grown by slow evaporation.

Crystal data

$C_{28}H_{24}N_6O_4$
 $M_r = 508.53$
 Monoclinic, $P2_1/c$
 $a = 5.538$ (3) Å
 $b = 30.783$ (17) Å
 $c = 7.930$ (5) Å
 $\beta = 107.617$ (11)°
 $V = 1288.6$ (12) Å³
 $Z = 2$

$D_x = 1.311$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 535 reflections
 $\theta = 2.6$ – 18.5 °
 $\mu = 0.09$ mm⁻¹
 $T = 293$ (2) K
 Needle, colourless
 $0.43 \times 0.08 \times 0.05$ mm

Data collection

Siemens SMART 1000 CCD area-detector diffractometer
 ω scans
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.962$, $T_{\max} = 0.996$
 7423 measured reflections

2535 independent reflections
 1226 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.066$
 $\theta_{\text{max}} = 26.0$ °
 $h = -5 \rightarrow 6$
 $k = -38 \rightarrow 32$
 $l = -9 \rightarrow 9$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.071$
 $wR(F^2) = 0.137$
 $S = 1.03$
 2535 reflections
 172 parameters

H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0384P)^2]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.12$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.12$ e Å⁻³

Table 1

Selected bond lengths (Å).

O1—C11	1.335 (4)	N3—C9	1.464 (4)
O1—C10	1.446 (3)	C9—C10	1.498 (4)
O2—C11	1.208 (4)		

Table 2

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C8-H8A\cdots N1^i$	0.93	2.49	3.363 (5)	156

Symmetry code: (i) $x + 1, y, z$.

All H atoms were located in difference Fourier maps and constrained to ride on their parent atoms, with C—H distances in the range 0.93–0.97 Å and with $U_{\text{iso}}(\text{H}) = 1.2 U_{\text{eq}}(\text{C})$.

Data collection: SMART (Siemens, 1996); cell refinement: SAINT (Siemens, 1996); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 1997); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL, PARST (Nardelli, 1995) and PLATON (Spek, 2003).

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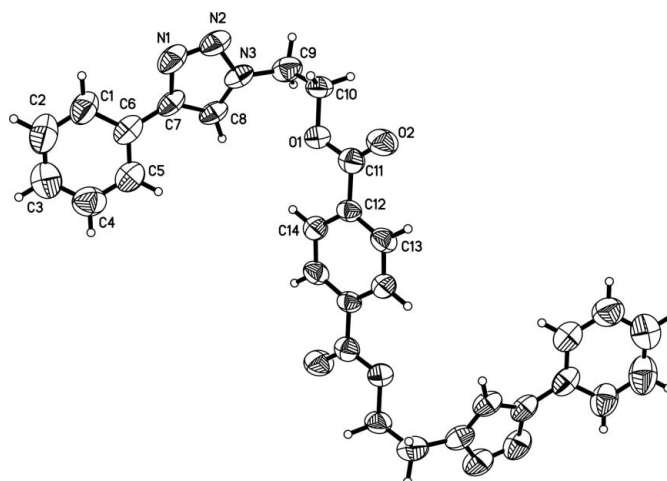


Figure 1

The structure of (I), showing 50% probability displacement ellipsoids and the atom-numbering scheme. Unlabelled atoms are related to labelled atoms by $2 - x, 1 - y, 2 - z$.

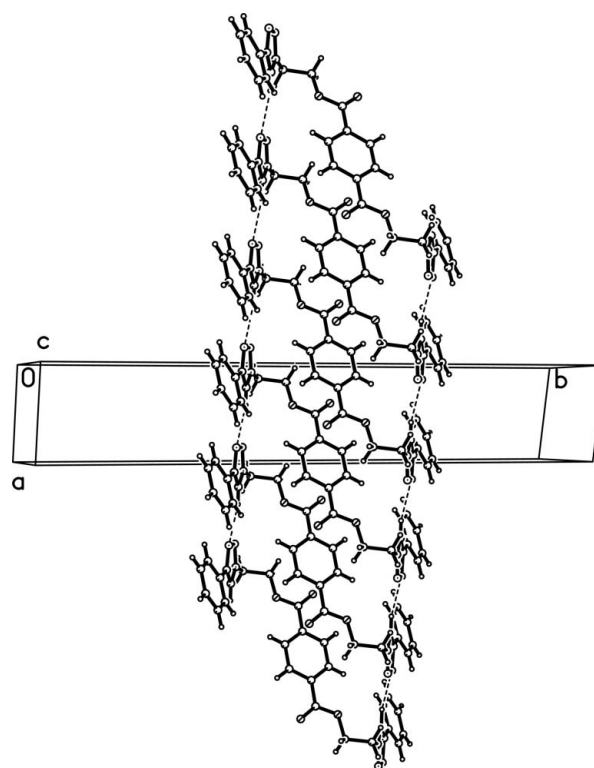


Figure 2

A view down the c axis, showing the ribbon along the a axis. Hydrogen bonds are indicated by dashed lines.

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