

(E)-1-(Naphthalen-1-yl)-3-(1-phenyl-1H-pyrazol-4-yl)prop-2-en-1-one

Abdullah M. Asiri,^{a,b} Abdulrahman O. Al-Youbi,^a Hassan M. Faidallah,^a Khalid A. Alamry^a and Seik Weng Ng^{c,*}

^aChemistry Department, Faculty of Science, King Abdulaziz University, PO Box 80203 Jeddah, Saudi Arabia, ^bCenter of Excellence for Advanced Materials Research, King Abdulaziz University, PO Box 80203 Jeddah, Saudi Arabia, and ^cDepartment of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia
Correspondence e-mail: seikweng@um.edu.my

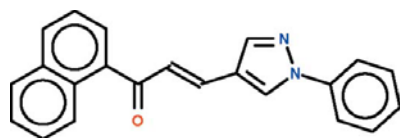
Received 26 August 2011; accepted 27 August 2011

Key indicators: single-crystal X-ray study; *T* = 100 K; mean $\sigma(\text{C}-\text{C})$ = 0.005 Å; *R* factor = 0.060; *wR* factor = 0.140; data-to-parameter ratio = 16.9.

In the title molecule, C₂₂H₁₆N₂O, the phenyl ring is twisted slightly with respect to the plane of the central pyrazole ring [dihedral angle = 14.8 (2)°]; the central ring is connected to the naphthyl ring through a $-\text{CH}=\text{CH}-\text{C}(=\text{O})-$ fragment, whose C=C double bond has an *E* configuration. The pyrazole ring and naphthalene ring system are twisted by 46.3 (1)°. Weak intermolecular C—H···O hydrogen bonds link the molecules, forming supramolecular chains running along the *a* axis. The crystal studied was a non-merohedral twin with a component ratio of 0.544 (2):0.456 (2).

Related literature

For related structures; see: Diáñez & López-Castro (1990); Jones *et al.* (1984). For the synthesis, see: Finar (1961); Finar & Lord (1959); Jones *et al.* (1984).



Experimental

Crystal data

C₂₂H₁₆N₂O

M_r = 324.37

Monoclinic, *P*2₁/*n*
a = 5.8457 (6) Å
b = 10.322 (2) Å
c = 26.626 (2) Å
 β = 92.322 (9)°
V = 1605.3 (4) Å³

Z = 4
Mo *K*α radiation
 μ = 0.08 mm⁻¹
T = 100 K
0.25 × 0.10 × 0.10 mm

Data collection

Agilent SuperNova Dual diffractometer with an Atlas detector
Absorption correction: multi-scan (*CrysAlis PRO*; Agilent, 2010)
T_{min} = 0.980, *T_{max}* = 0.992

3824 measured reflections
3825 independent reflections
2494 reflections with *I* > 2σ(*I*)
R_{int} = 0.105

Refinement

R[*F*² > 2σ(*F*²)] = 0.060
wR(*F*²) = 0.140
S = 0.96
3825 reflections

227 parameters
H-atom parameters constrained
 $\Delta\rho_{\text{max}}$ = 0.31 e Å⁻³
 $\Delta\rho_{\text{min}}$ = -0.34 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> — <i>H</i> ··· <i>A</i>	<i>D</i> — <i>H</i>	<i>H</i> ··· <i>A</i>	<i>D</i> ··· <i>A</i>	<i>D</i> — <i>H</i> ··· <i>A</i>
C9—H9···O1 ⁱ	0.95	2.46	3.397 (4)	167

Symmetry code: (i) *x* − 1, *y*, *z*.

Data collection: *CrysAlis PRO* (Agilent, 2010); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis PRO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *publCIF* (Westrip, 2010).

We thank King Abdulaziz University and the University of Malaya for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: XU5313).

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