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Key indicators

Single-crystal X-ray study T = 294 K Mean σ (C–C) = 0.005 Å R factor = 0.035 wR factor = 0.088 Data-to-parameter ratio = 8.3

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

(S)-2-[(S)-2-Acetamido-3-phenylpropanamido]-3-phenylpropanoic acid

In the title compound, $C_{20}H_{22}N_20_4$, the two phenyl rings form a dihedral angle of 89.2 (2)°. The crystal structure is stabilized by weak N-H···O and O-H···O hydrogen bonds. Received 26 November 2006 Accepted 12 December 2006

Comment

N-Acetyl amino acids play an important role in methylation, sulfuration, detoxication and antioxidation. They are very useful in the pharmaceutical and food industries.



The molecular structure of the title compound, (I), is illustrated in Fig. 1. The geometry of the *N*-acetyl-L-phenylalanine system is comparable to that reported for *N*-acetyl-Lphenylalanine (Stout *et al.*, 2000). The dihedral angle between the two phenyl rings is 89.2 (2)°. The crystal structure is stabilized by weak $N-H\cdots O$ and $O-H\cdots O$ intermolecular hydrogen bonds (Fig. 2 and Table 1).

Experimental

A mixture of (S)-2-amino-3-phenylpropanoic acid (0.1 mol), acetic anhydryde (0.2 mol) in water (30 ml) was stirred for 20 min at 298 K. After cooling, filtration and drying, the title compound was obtained. 10 mg of (I) was dissolved in 10 ml ethanol–N,N-dimethylacetamide (1:1 ν/ν) and the solution was allowed to evaporate at room temperature. Colourless single crystals of the title compound were formed after 35 d.

Crystal data

Data collection

Bruker SMART CCD area-detector
diffractometer
φ and ω scans
Absorption correction: multi-scan
(SADABS; Bruker, 1997)
$T_{\min} = 0.970, \ T_{\max} = 0.979$

5164 measured reflections 1978 independent reflections 1573 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.028$ $\theta_{\text{max}} = 26.4^{\circ}$

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Figure 1

The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

Refinement

$w = 1/[\sigma^2(F_o^2) + (0.0407P)^2]$
+ 0.0961P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} = 0.002$
$\Delta \rho_{\rm max} = 0.12 \ {\rm e} \ {\rm \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.14 \text{ e} \text{ Å}^{-3}$

Table 1

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	D-H·	٠·A
$O2-H2A\cdots O3^{i}$	0.82	1.79	2.598 (2)	169	
$N1 - H1 \cdots O4^{ii}$	0.86	1.98	2.819 (3)	166	
$N2-H2\cdots O1^{iii}$	0.86	2.02	2.872 (3)	168	
Symmetry codes: $-x + 1$, $y + \frac{1}{2}$, $-z + 1$.	(i) $-x + 1, y$	$v - \frac{1}{2}, -z + 1;$	(ii) $-x + 1, y - $	$\frac{1}{2}, -z+2;$	(iii

The absolute configuration was known from the synthesis and assumed for the structure. H atoms were initially located in difference maps and then refined in a riding model, with C–H = 0.93–0.98 Å and $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})$ or 1.5 $U_{\rm eq}({\rm methyl}\ {\rm C})$. In the absence of significant anomalous dispersion effects, Friedel pairs were merged prior to refinement.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine



The crystal packing of (I), viewed along the b axis. Dashed lines indicate hydrogen bonds.

structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1997); software used to prepare material for publication: *SHELXTL*.

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