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Key indicators

Single-crystal X-ray study
 $T = 173$ K
Mean $\sigma(C-C) = 0.005$ Å
 R factor = 0.048
 wR factor = 0.104
Data-to-parameter ratio = 18.9For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**(2S)-Methyl 1-[(2R)-3-(benzylsulfanyl)-2-(tert-butoxycarbonylamino)propanoyl]pyrrolidine-2-carboxylate**

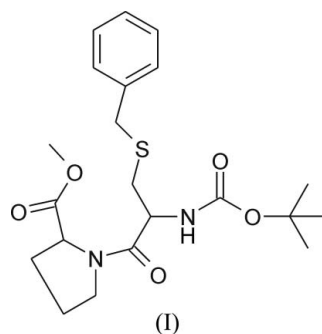
In the title compound, $C_{21}H_{30}N_2O_5S$, all bond lengths and angles are within normal ranges. Several hydrogen bonds stabilize its molecular packing. The secondary structure of the title compound is best described as a β -pleated sheet-type arrangement.

Received 22 March 2007

Accepted 23 March 2007

Comment

The title compound, (I) (Fig. 1), was synthesized as an intermediate for L-cysteine-L-proline methyl ester. All bond lengths and angles are within normal ranges (Kashino *et al.*, 1974; Oku *et al.*, 2003). The observed distance of 3.853 (4) Å between the two C_α atoms (C9 and C14) is typical of the *trans* configuration, whereas the ω angle (C14–N1–C10–C9) of -169.4 (2)° is considerably distorted from the expected 180°. Other peptide backbone torsion angles, φ (C17–N2–C9–C10) and ψ (N2–C9–C10–N1), are -147.0 (2) and 173.2 (2)°, respectively. Hydrogen bonds are commonly found in peptide compounds (Kashino *et al.*, 1974; Oku *et al.*, 2003) and the structure of the title compound is stabilized by C–H...O, C–H...S and NC–H...O hydrogen bonds (Table 1). The secondary structure of the title compound can be best described as a β -pleated sheet-type arrangement.



Experimental

The *N*- and *S*-protected dipeptide *N*-tert-butoxycarbonyl-*S*-benzyl-L-cysteine-L-proline methyl ester, (I), was prepared in a solution phase according to literature procedures. *S*-Benzyl-L-cysteine, (1) (Koerber-Ple & Massiot, 1995), and L-proline methyl ester hydrochloride, (2) (Ryono & Weller, 1987), were prepared first, followed by L-proline methyl ester, (3) (Miles *et al.*, 1985). *N*-tert-Butoxycarbonyl-*S*-benzyl-L-cysteine, (4), was synthesized from (1) by protecting the amine group (Koerber-Ple & Massiot, 1995). Finally, (I) was obtained as white microcrystals by coupling (3) and (4) with *N,N'*-dicyclohexylcarbodiimide (Ondetti & Condon, 1979). Colourless crystals of (I) suitable for X-ray analysis were obtained from CH_2Cl_2 .

Crystal data

$C_{21}H_{30}N_2O_5S$
 $M_r = 422.53$
 Monoclinic, $P2_1$
 $a = 6.013 (1) \text{ \AA}$
 $b = 15.597 (3) \text{ \AA}$
 $c = 12.347 (3) \text{ \AA}$
 $\beta = 103.34 (3)^\circ$

$V = 1126.7 (4) \text{ \AA}^3$
 $Z = 2$
 Mo $K\alpha$ radiation
 $\mu = 0.18 \text{ mm}^{-1}$
 $T = 173 (2) \text{ K}$
 $0.40 \times 0.40 \times 0.06 \text{ mm}$

Data collection

Nonius KappaCCD diffractometer
 Absorption correction: multi-scan
 (SADABS; Sheldrick, 1996)
 $T_{\min} = 0.933$, $T_{\max} = 0.989$

15659 measured reflections
 5015 independent reflections
 3347 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.058$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.048$
 $wR(F^2) = 0.104$
 $S = 1.03$
 5015 reflections
 266 parameters
 2 restraints

H atoms treated by a mixture of independent and constrained refinement
 $\Delta\rho_{\text{max}} = 0.30 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.52 \text{ e \AA}^{-3}$
 Absolute structure: Flack (1983),
 2345 Friedel pairs
 Flack parameter: $-0.06 (9)$

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N2-H22\cdots O1$	0.860 (17)	2.20 (3)	2.617 (3)	109 (2)
$C12-H12B\cdots S1^i$	0.99	2.89	3.689 (3)	138
$C7-H7B\cdots O1^{ii}$	0.99	2.48	3.319 (4)	142
$C8-H8B\cdots O1^{ii}$	0.99	2.53	3.353 (4)	140
$C21-H21B\cdots O2^{iii}$	0.98	2.58	3.405 (4)	142

Symmetry codes: (i) $-x + 2, y - \frac{1}{2}, -z + 2$; (ii) $x + 1, y, z$; (iii) $x - 1, y, z - 1$.

The H atom connected to N was located in a difference map and refined isotropically; $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$. Other H atoms were introduced in their calculated positions [$C-H = 0.95, 0.98, 0.99$ or 1.00 \AA , $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for methyl H atoms] and refined with fixed geometry with respect to their carrier atoms.

Data collection: COLLECT (Nonius, 2002); cell refinement: DIRAX (Duisenberg, 1992); data reduction: EVALCCD (Duisenberg *et al.*, 2003); program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97

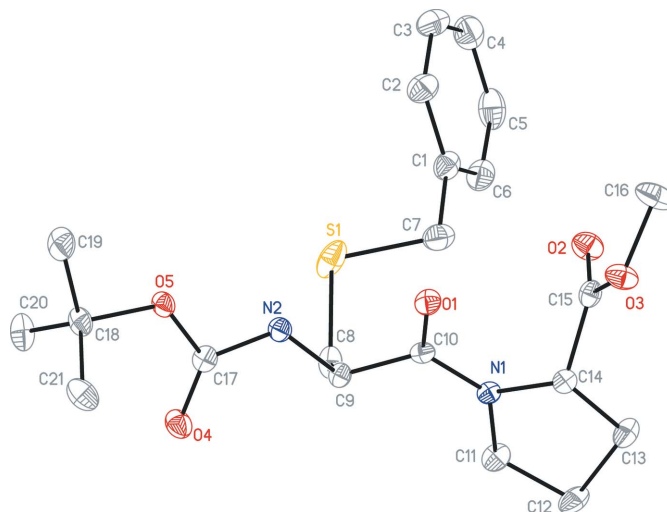


Figure 1

The molecular structure of the title compound with the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms have been omitted for clarity.

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

Financial support from the Magnus Ehrnrooth Foundation is gratefully acknowledged by MR.

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