

N-Acetyl-L-phenylalanine

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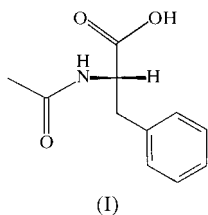
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The structure of the title compound, C₁₁H₁₃NO₃, is characterized by a two-dimensional infinite network of intermolecular N—H...O and O—H...O hydrogen bonds.

Comment

It is important to determine the crystal structures of amino acids and their derivatives because of their importance in defining the preferred conformations of large peptides and proteins. We have determined the structure of the title compound, (I), for a solid-state NMR tensor study. Few N¹⁵



chemical-shielding tensors have been determined (Harbison *et al.*, 1984) and chemical-shielding tensors are important for accurate solution and solid-state NMR experiments (Oas *et al.*, 1987; Hartzell *et al.*, 1987; Lee & Ramamoorthy, 1998; Lee *et al.*, 1998).

Experimental

(I) was obtained from Sigma Chemical Corporation (St Louis, Missouri). Crystals were grown from water and analyzed.

Crystal data

C₁₁H₁₃NO₃, M_r = 207.22
Orthorhombic, P2₁2₁2₁
a = 5.6528 (1) Å
b = 11.1532 (2) Å
c = 16.9897 (1) Å
V = 1071.15 (3) Å³
Z = 4
D_x = 1.285 Mg m⁻³

Mo Kα radiation
Cell parameters from 6900
reflections
θ = 2.40–30.49°
μ = 0.094 mm⁻¹
T = 158 (2) K
Needle, colourless
0.54 × 0.14 × 0.12 mm

Data collection

| | |
|----------------------------------|---------------------------|
| CCD area-detector diffractometer | R _{int} = 0.019 |
| ω scans | θ _{max} = 30.49° |
| 15 627 measured reflections | h = -8 → 7 |
| 1866 independent reflections | k = -15 → 15 |
| 1778 reflections with I > 2σ(I) | l = -24 → 22 |

Refinement

| | |
|---|---|
| Refinement on F ² | w = 1/[σ ² (F _o ²) + (0.0443P) ² |
| R[F ² > 2σ(F ²)] = 0.028 | + 0.1409P] |
| wR(F ²) = 0.077 | where P = (F _o ² + 2F _c ²)/3 |
| S = 1.077 | (Δ/σ) _{max} = 0.001 |
| 1866 reflections | Δρ _{max} = 0.26 e Å ⁻³ |
| 190 parameters | Δρ _{min} = -0.18 e Å ⁻³ |
| All H-atom parameters refined | Extinction correction: SHELXL97 |
| | (Sheldrick, 1997) |
| | Extinction coefficient: 0.010 (3) |

Table 1

Hydrogen-bonding geometry (Å, °).

| D—H...A | D—H | H...A | D...A | D—H...A |
|--------------------------|----------|----------|-------------|------------|
| N1—H1...O3 ⁱ | 0.86 (2) | 2.14 (2) | 2.9835 (11) | 171.3 (14) |
| O2—H2...O1 ⁱⁱ | 0.87 (2) | 1.74 (2) | 2.5502 (10) | 158.4 (18) |

Symmetry codes: (i) 1 + x, y, z; (ii) -x, ½ + y, ½ - z.

H atoms were allowed to refine isotropically. The range of C—H distances is 0.92 (2)–1.01 (2) Å; N—H = 0.86 (2) Å; O—H = 0.87 (2) Å.

Data collection and cell refinement: SMART (Bruker, 1997); data reduction, program used to solve and refine structure, software used to prepare material for publication: SHELXTL (Bruker, 1998).

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